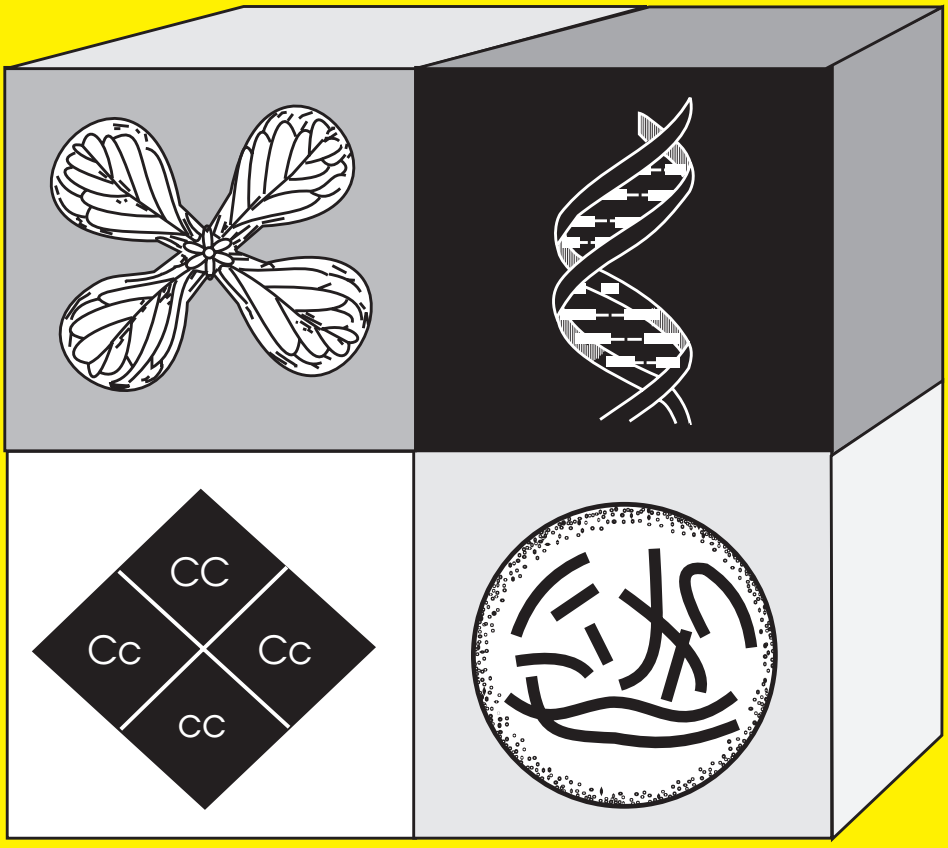
CRUCIFERAE: COMPENDIUM OF TRAIT GENETICS



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CRUCIFERAE: COMPENDIUM OF TRAIT GENETICS

by

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FOREWORD

The **Cruciferae: Genetics Review** brings together genetic information on crucifers with the exception of the genus *Arabidopsis*. The **Cruciferae: Compendium of Trait Genetics** builds on S.H. Yarnell's contribution on vegetable brassicas in 1956 and the Resource Book of the Crucifer Genetics Cooperative (Williams, 1985). We have endeavoured to include all papers where the inheritance of a trait was described. Some papers may have been inadvertently omitted; for this, we apologize.

When identical gene symbols have been used for different traits, the symbols have been listed in chronological order. The isozyme nomenclature follows the classification of Murphy *et al.* (1990).

An electronic version of the **Cruciferae: Compendium of Trait Genetics** is available at the Internet address: http://res.agr.ca/ecorc/ program2/botany/crucifers/genetics/genetrev.pdf. Updates of the Internet version will be released periodically. Authors wishing to contribute information to the updates are kindly asked to forward reprints to Dr. G. Séguin-Swartz, Saskatoon Research Centre, AAFC, Saskatoon, Canada.

The **Cruciferae: Compendium of Trait Genetics** is dedicated to Dr. P.H. Williams whose love and enthusiasm for crucifer genetics inspired the undertaking of this work. Finally, we are indebted to Ms. G.M. Charabin, Saskatoon Research Centre, AAFC, Saskatoon, for expert assistance in searching literature and verifying citations, to Dr. G. Baillargeon and his team, ECORC, AAFC, Ottawa, for preparing the Internet version, and to Dr. D.R. Sampson for critical comments on the manuscript.

G. Séguin-Swartz
S.I. Warwick
R. Scarth

November 1997

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Brassica atlantica (Coss.) O.E. Schulz
Brassica bourgeaui (Webb) Kuntze
*Brassica campestris** L. [see *Brassica rapa*]
subsp. *chinensis* (L.) Makino (pak choi)
subsp. *dichotoma* (Roxb.) Olsson (brown sarson)
subsp. *narinosa* (L.H. Bailey) Olsson (broad beet mustard)
subsp. *nipposinica* (L.H. Bailey)
subsp. *parachinensis* (choy sum)
subsp. *pekinensis* (Lour.) Olsson (Chinese cabbage)
subsp. *rapifera* (Metzger) Sinsk. (turnip)
subsp. *sylvestris* (L.) Janchen (bird's rape)
subsp. *trilocularis* (Roxb.) Olsson (yellow sarson)
var. *napobrassica* L.
Brassica carinata A. Braun (Ethiopian mustard)
Brassica chinensis L. [see *Brassica rapa*]
Brassica cretica Lam.
Brassica incana Ten.
Brassica insularis Moris
Brassica japonica (Thunb.) Siebold ex Miq. [see *Brassica rapa*]
Brassica juncea (L.) Czern. (oriental and brown mustard, rai)
Brassica juncea (L.) Czern. subsp. *gracilis* Tsen & Lee (Meitan da-yu-tsai)
Brassica napus L.
subsp. *oleifera* (DC.) Metzger (oilseed rape, forage rape)
subsp. *rapifera* Metzger (rutabaga, swede)
Brassica narinosa L.H. Bailey [see *Brassica rapa*]
Brassica nigra (L.) Koch (black mustard)
Brassica nipposinica L.H. Bailey [see *Brassica rapa*]
Brassica oleracea L. (cole-crops)
var. *acephala* DC. (kales)
var. *albiflora* Sun [= *B. alboglabra*] (Chinese kale)
var. *alboglabra* [= *B. alboglabra*] (Chinese kale)
var. *botrytis* L. (cauliflower, heading broccoli)
var. *capitata* L. (cabbage)
var. *chinensis* Prain (burma sarson)
var. *fimbriata* Mill. (kitchen kale)
var. *fruticosa* Metz. (thousand-head kale)
var. *gemmifera* DC. (brussels sprouts)
var. *gongylodes* L. (kohlrabi)
var. *italica* Plenck. (broccoli, calabrese)
var. *sabauda* L. (savoy cabbage)
var. *sabellica* (collards)
var. *tronchuda* L.H. Bailey (tronchuda cabbage)
Brassica parachinensis L.H. Bailey [see *Brassica rapa*]
Brassica pekinensis (Lour.) Rupr. [see *Brassica rapa*]

*Brassica rapa** L.
subsp. *chinensis* (L.) (pak choi, Chinese mustard, celery mustard)
subsp. *dichotoma* (Roxb.) (brown sarson)
subsp. *japonica* (Thunb.)
subsp. *narinosa* L.H. Bailey (broad beet mustard)
subsp. *nipposinica* L.H. Bailey
subsp. *oleifera* Metzger (turnip rape, toria)
subsp. *parachinensis* (L.H. Bailey) (choy sum)
subsp. *pekinensis* (Lour.) (Chinese cabbage, Pe-tsai, celery cabbage)
subsp. *rapifera* Metzger (turnip)
subsp. *sylvestris* (L.) Janchen (bird's rape)
subsp. *trilocularis* (yellow sarson)
subsp. *utilis* (spring broccoli)
Brassicoraphanus Sageret
Capsella bursa-pastoris (L.) Medic. (shepherd's purse)
Capsella grandiflora (Fauché and Chaub.) Boiss.
Capsella rubella Reuter
Cardamine pratensis L.
Crambe abyssinica Hochst. ex O.E. Schulz (crambe)
Crambe hispanica L.
Diplotaxis muralis (L.) DC. (sand rocket)
Eruca sativa Mill. [see *Eruca vesicaria*]
Eruca vesicaria (L.) Cav. subsp. *sativa* (Mill.) Thell. (taramira, roquette, rocket)
Iberis amara L.
Leavenworthia crassa Rollins
Lesquerella densipila Rollins
Lesquerella lescurii (A. Gray) S. Watson
Raphanus raphanistrum L. (wild radish)
Raphanus sativus L. (radish)
var. *caudatus* Alef. (rat tail radish)
var. *radicula* (DC.)
Sinapis alba L. (white mustard)
Sinapis arvensis L. (wild mustard)
Thlaspi arvense L. (stinkweed)

**Brassica rapa* and *B. campestris* are considered the same species under the name *B. rapa*. Only two of the many cultivated subspecies under *B. campestris* have been legitimately named under *B. rapa* (subsp. *oleifera* and subsp. *rapifera*), the others were proposed for transfer to subspecific rank in the paper by Oost (1986). In this review, they will be treated as part of *B. rapa*.

LIST OF GENES

Brassica carinata

E_B	Seed fatty acids (erucic acid)
E_C	Seed fatty acids (erucic acid)

Brassica juncea

A	Seed coat colour (brown)
ac_1	Disease susceptibility (white rust)
Ac_2	Disease susceptibility (white rust)
B	Seed coat colour (light brown)
Cr	Petal colour (cream-yellow)
E	Seed fatty acids (erucic acid)
E_0	Seed fatty acids (erucic acid allele)
E_1	Seed fatty acids (erucic acid allele)
E_2	Seed fatty acids (erucic acid allele)
E_A	Seed fatty acids (erucic acid)
E_B	Seed fatty acids (erucic acid)
gl	Leaf colour (chlorophyll deficient mutant)
gl^l	Leaf colour (chlorophyll deficient mutant)
p_1	Petal number (apetalous)
p_2	Petal number (apetalous)
Pl	Leaf colour (purple pigmentation)
R_1	Seed coat colour (brown)
R_2	Seed coat colour (brown)
Rf	Male fertility restoration
Wl	Leaf waxiness (glossy)
Y	Petal colour (yellow)
Y_1	Petal colour (cream)
Y_1	Petal colour (yellow)
Y_2	Petal colour (cream)
Y_2	Petal colour (light yellow)
Y_2	Petal colour (yellow)
Y_3	Petal colour (yellow)

Brassica napus

A	Petal colour (lemon-yellow)
A	Seed fatty acids (erucic acid)
A	Vernalization
Ac7-1	Disease resistance (white rust race 7)
Ac7-2	Disease resistance (white rust race 7)
Ac7-3	Disease resistance (white rust race 7)

Brassica napus (con'd)

*Al1**	Seed coat colour (dotted, aleurone 1*)
apet-1	Petal number (apetalous)
apet-2	Petal number (apetalous)
apet-3	Petal number (apetalous)
B	Petal colour (pale yellow)
B	Petal colour (cream)
B	Vernalization
Bl_1	Seed coat colour (black)
Bl_2	Seed coat colour (black)
Bl_3	Seed coat colour (black)
Bl1	Seed coat colour (black palisade)
*Bl1**	Seed coat colour allele (black palisade, variegated form of gene *Bl1*)
Bl_1	Disease resistance (blackleg)
Bl_2	Disease resistance (blackleg)
Bl_3	Disease resistance (blackleg)
bm	Disease resistance (black rot)
Br	Disease resistance (black rot)
C	Petal colour (light orange)
E	Seed fatty acids (erucic acid)
Ea	Seed fatty acids (erucic acid allele)
Eb	Seed fatty acids (erucic acid allele)
Ec	Seed fatty acids (erucic acid allele)
Ed	Seed fatty acids (erucic acid allele)
E^d	Seed fatty acids (eicosenoic acid allele, erucic acid allele)
e	Seed fatty acids (eicosenoic acid allele, erucic acid allele)
E_A	Seed fatty acids (erucic acid)
E_C	Seed fatty acids (erucic acid)
E1	Seed fatty acids (erucic acid, eicosenoic acid)
E2	Seed fatty acids (erucic acid, eicosenoic acid)
E_1	Leaf shape (entire)
E_2	Leaf shape (entire)
El3	Seed glucosinolates (C4 to C5 amino acid precursor elongation)
G	Leaf waxiness (glossy)
Gl_D	Leaf waxiness (glossy leaves and small amounts of wax on stems)
gl_R	Leaf waxiness (glossy)
Gsl-elong-A	Seed glucosinolates (butyl and pentyl glucosinolates)
Gsl-elong-C	Seed glucosinolates (butyl and pentyl glucosinolates)
Gsl-oh-C	Seed glucosinolates (butenyl and pentenyl glucosinolate hydroxylation)
Gsl-oh-A	Seed glucosinolates (butenyl and pentenyl glucosinolate hydroxylation)
Gsl-pro	Seed glucosinolates (propyl glucosinolates)
GPI	Isozymes (glucose-6-phosphate isomerase)
L_1	Silique length
L_2	Silique length
LmFr1	Disease resistance (blackleg)
LmR1	Disease resistance (blackleg)
Lm1	Disease resistance (blackleg)
Lm2	Disease resistance (blackleg)

Brassica napus (con'd)

M_1	Root colour (white flesh)
M_2	Root colour (white flesh)
Ms	Male sterility
Ms_1	Male sterility
ms_1	Male sterility
ms_2	Male sterility
Ms_A	Male fertility restoration
Ms_C	Male fertility restoration
Ms_j	Male sterility
N_1	Root colour (purple neck)
N_2	Root colour (purple neck)
npet-1	Petal number (apetalous)
npet-2	Petal number (apetalous)
npet-3	Petal number (apetalous)
npet-4	Petal number (apetalous)
npet-5	Petal number (apetalous)
npet-6	Petal number (apetalous)
P_1	Root colour (light purple pigmentation of the underground portion)
P_2	Root colour (dark purple pigmentation)
p	Petal number (apetalous)
p_1	Petal number (apetalous)
p_2	Petal number (apetalous)
p_3	Petal number (apetalous)
p_4	Petal number (apetalous)
Rf	Male fertility restoration
Rfp1	Male fertility restoration
Rfp2	Male fertility restoration
Rlm1	Disease resistance (blackleg)
Rlm2	Disease resistance (blackleg)
S	Self-incompatibility
stap-1	Petal number (apetalous)
stap-2	Petal number (apetalous)
Ts	Temperature sensitive
V1	Vernalization
V2	Vernalization
V3	Vernalization
V4	Vernalization
W_C	Petal colour (white)
Wl	Leaf waxiness (waxless)
Nwl	Leaf waxiness allele (waxy)

Brassica nigra

a_1	Leaf colour (purple pigmentation absence)
a_2	Hypocotyl colour (purple pigmentation absence)
Ac2	Disease resistance (white rust race 2)
Aco-1	Isozymes (aconitase hydratase)
Aco-2	Isozymes (aconitase hydratase)
Aco-3	Isozymes (aconitase hydratase)
Aco-4	Isozymes (aconitase hydratase)
Aps-1L	Isozymes (acid phosphatase)
cp	Pollen colour (cream)
E_B	Seed fatty acids (erucic acid)
fp	Petal shape (folded)
fr	Flower retention
glb	Plant trichomes (pubescence/glabrous)
Lap-1	Isozymes (leucine aminopeptidase)
Lap-2	Isozymes (leucine aminopeptidase)
lu	Cotyledon colour (lutescence)
6Pgd-1	Isozymes (phosphogluconate dehydrogenase, plastidic)
6Pgd-1'	Isozymes (phosphogluconate dehydrogenase, plastidic)
6Pgd-2	Isozymes (phosphogluconate dehydrogenase, cytosolic)
6Pgd-2'	Isozymes (phosphogluconate dehydrogenase, cytosolic)
Pgi-1	Isozymes (glucose-6-phosphate isomerase, plastidic)
Pgi-2	Isozymes (glucose-6-phosphate isomerase, cytosolic)
Pgm-1	Isozymes (phosphoglucomutase)
Pgm-2	Isozymes (phosphoglucomutase)
Rf_1	Male fertility restoration
Rf_2	Male fertility restoration
Tpi-1	Isozymes (triose-phosphate isomerase, plastidic)
Tpi-1'	Isozymes (triose-phosphate isomerase, plastidic)
Tpi-2	Isozymes (triose-phosphate isomerase, cytosolic)
Tpi-2'	Isozymes (triose-phosphate isomerase, cytosolic)
vl	Leaf colour (virescence)
yg1	Plant colour (yellow-green)
ygc1	Cotytelon colour (green at emergence; yellow-green 6 days after)
ygc2	Cotytelon colour (yellow-green at emergence; green 4 days after)
Xv	Leaf colour (xanthovirescence)

Brassica oleracea

A	Leaf colour (with gene *D*, red leaves)
A	Leaf shape ("asparagodes" phenotype) [superseded by symbol *As*]
A	Leaf colour (with gene *C*, red midrib)
A	Stem colour (purple), petiole colour (purple), ovary colour (purple)
A	Stem colour (purple), petiole colour (purple), ovary colour (slightly purple-tinged)
A^{ck}	Stem colour (purple), petiole colour (purple), ovary colour (deep purple)
A^{pb}	Stem colour (purple), petiole colour (purple), ovary colour (purple)

Brassica oleracea (con'd)

A^{rc}	Stem colour (purple), petiole colour (purple), leaf colour (purple), ovary colour (deep purple) [= gene *D* of Kristofferson]
a	Plant colour (traces of anthocyanins)
A	Hypocotyl colour (pigmented)
A^{o}	Ovary colour (pigmented)
a	Disease resistance (black rot)
a	Leaf waxiness (glossy/waxless)
Aco-1	Isozymes (aconitase)
Aco-2	Isozymes (aconitase)
Aco-3	Isozymes (aconitase)
Aco-4	Isozymes (aconitase)
Adh-1	Isozymes (alcohol dehydrogenase)
Adh-2	Isozymes (alcohol dehydrogenase)
Ap	Pollen (abortive)
Aps-1	Isozymes (acid phosphatase)
Aps-1L	Isozymes (acid phosphatase)
Aps-3L	Isozymes (acid phosphatase)
As	Leaf shape ("asparagodes" phenotype) [supersedes symbol *A*]
As	Anther tip colour (anther purple spot)
B	Leaf colour (light red midrib; with gene *A*, dark violet midrib)
B	Enlarged stem [superseded by symbol *Br*]
B	Disease resistance (black rot)
b	Leaf waxiness (dull waxless)
B_1	Enlarged stem (bulb formation)
B_2	Enlarged stem (bulb formation)
B_3	Enlarged stem (bulb formation)
bl	Meristem mutant (blind)
Br	Enlarged stem [supersedes symbol *B*]
C	Leaf colour (with gene *A*, dark violet midrib)
C	Leaf colour (with gene *A*, red midrib)
c	Plant colour (anthocyanin synthesis inhibitor) [superseded by symbol *c-1*]
c-1	Plant colour (anthocyanin synthesis inhibitor) [supersedes symbol *c*]
c-2	Plant colour (anthocyanin synthesis inhibitor)
cf	Flowers clustered
cp-1	Petal shape (crinkly)
cr	Petal colour (cream)
D	Leaf colour (with gene *A*, red leaves)
D	Leaf colour (purple, blue)
▵	Leaf colour (blue)
E	Leaf colour (dark violet areas)
E	Leaf shape (entire) [superseded by symbol *En*]
Ea	Earliness
E_C	Seed fatty acids (erucic acid)
En	Leaf shape (entire) [supersedes symbol *E*]
f	Disease resistance (black rot)
fc1	Cotyledon shape (fused)

Brassica oleracea (con'd)

fc2	Cotyledon shape (fused)
Fn	Leaf shape (fern-leaf)
G	Leaf colour (purple pigmentation)
gl	Leaf waxiness (glossy)
gl-1	Leaf waxiness (glossy) [= gene *gl*]
gl-3	Leaf waxiness (glossy)
gl-e3	Leaf waxiness (glossy)
gl-el	Leaf waxiness (glossy)
gl-y	Leaf waxiness (glossy)
Go	Leaf waxiness (glossy)
Got-3	Isozymes (aspartate aminotransferase)
H	Leaf colour (pigmentation)
Hr-1	Leaf trichomes (pubescence, first leaf margins)
Hr-2	Leaf trichomes (pubescence, first leaf margins and petioles)
Hr-y	Leaf trichomes (pubescence)
K	Heading
k_1	Heading
k_2	Heading
k_3	Heading
L	Head (presence of leaves in heads)
Lap-1	Isozymes (leucine aminopeptidase)
Lap-2	Isozymes (leucine aminopeptidase)
Lc	Cotyledon size (large)
le	Leaf excrescence
M	Leaf colour (magenta)
Mdh-1	Isozymes (malate dehydrogenase)
ms	Male sterility
ms_B	Male sterility
ms_c	Male sterility
ms_1	Male sterility
ms_2	Male sterility
ms_4	Male sterility
ms_5	Male sterility
ms_6	Male sterility
ms-1	Male sterility
ms-2	Male sterility
ms-4	Male sterility
n	Leaf necrosis
N_1	Head (heading habit)
N_2	Head (heading habit)
NOR-1	Ribosomal RNA
NOR-2	Ribosomal RNA
NOR-3	Ribosomal RNA
Ns_1	Plant branching habit (suppression of lateral branching)
Ns_2	Plant branching habit (suppression of lateral branching)
O	Flower bud shape (open bud)
Or	Curd colour (orange)

Brassica oleracea (con'd)

P	Leaf petiolate [superseded by symbol *Pet*]
P	Leaf colour (red)
p	Petaloid sterility
pb	Flower bud shape (puffy bud)
pb_1	Disease resistance (clubroot)
pb_2	Disease resistance (clubroot)
pBOS5-1	Self-incompatibility
pBOS5-2	Self-incompatibility
pBOS5-3	Self-incompatibility
pBSIL9-1	Isozymes (isocitrate lyase)
pBSIL9-3	Isozymes (isocitrate lyase)
pBSMS-1	Isozymes (malate synthase)
pBSMS-2	Isozymes (malate synthase)
pCl-1	Seed proteins (cruciferin)
pCl-2	Seed proteins (cruciferin)
Pet	Leaf petiolate [supersedes symbol *P*]
pg	Leaf colour (pale green)
pg-1	Leaf colour (pale green foliage)
pg-2	Leaf colour (pale green foliage)
6Pgd-1	Isozymes (phosphogluconate dehydrogenase, plastidic)
6Pgd-1'	Isozymes (phosphogluconate dehydrogenase, plastidic)
6Pgd-2	Isozymes (phosphogluconate dehydrogenase, cytosolic)
6Pgd-2'	Isozymes (phosphogluconate dehydrogenase, cytosolic)
Pgi-1	Isozymes (glucose-6-phosphate isomerase, plastidic)
Pgi-2	Isozymes (glucose-6-phosphate isomerase, cytosolic)
Pgm-1	Isozymes (phosphoglucomutase)
Pgm-2	Isozymes (phosphoglucomutase)
Pgm-3	Isozymes (phosphoglucomutase)
pN2-1	Seed proteins (napin)
pN2-2	Seed proteins (napin)
pN2-3	Seed proteins (napin)
pN2-4	Seed proteins (napin)
pN2-5	Seed proteins (napin)
pN2-6	Seed proteins (napin)
po	Cotyledon number (polycotyledony)
PPA3	Disease resistance (downy mildew)
ps	Sepal persistence
R1	Disease resistance (downy mildew)
R2	Disease resistance (downy mildew)
R_1	Leaf colour (purple pigmentation)
R_2	Leaf colour (purple pigmentation)
S	Self-incompatibility
Sa	Self-incompatibility allele
Sb	Self-incompatibility allele
Sc	Self-incompatibility allele
Sd	Self-incompatibility allele
S1	Self-incompatibility allele

Brassica oleracea (con'd)

S2	Self-incompatibility allele
S3	Self-incompatibility allele
S	Leaf colour (purple pigmentation)
S	Leaf shape (wrinkled) [superseded by symbol *Sm*]
Sm	Leaf shape (wrinkled) [supersedes symbol *S*]
S_p	Self-incompatibility
S_{p1}	Self-incompatibility allele
S_{p2}	Self-incompatibility allele
S_{p3}	Self-incompatibility allele
S_q	Self-incompatibility
S_{q1}	Self-incompatibility allele
S_{q2}	Self-incompatibility allele
S_{q3}	Self-incompatibility allele
St	Flower bud (starring, rosetting)
T	Plant height (tall)
T	Self-incompatibility
T1	Self-incompatibility allele
T2	Self-incompatibility allele
t	Growth habit (annual)
Tpi-1	Isozymes (triose-phosphate isomerase, plastidic)
Tpi-1'	Isozymes (triose-phosphate isomerase, plastidic)
Tpi-2	Isozymes (triose-phosphate isomerase, cytosolic)
Tpi-2'	Isozymes (triose-phosphate isomerase, cytosolic)
W	Leaf size (broad)
W	Leaf shape (wrinkled) [superseded by symbol *Wr*]
W	Petal colour (white) [superseded by symbol *Wh*]
Wh	Petal colour (white)
Wh	Petal colour (white) [supersedes symbol *W*]
Wr	Leaf shape (wrinkled) [supersedes symbol *W*]

Brassica rapa

A	Disease resistance (clubroot)
A	Seed fatty acids (erucic acid)
a-1	Hypocotyl colour (purple pigmentation/absence)
a-2	Hypocotyl colour (purple pigmentation/absence)
a-3	Hypocotyl colour (purple pigmentation/absence)
a-4	Hypocotyl colour (purple pigmentation/absence)
aa	Anther tip colour (anthocyaninless)
ab	Sepal tip colour (anthocyaninless)
Aco-1	Isozymes (aconitase hydratase)
Aco-2	Isozymes (aconitase hydratase)
Aco-3	Isozymes (aconitase hydratase)
Aco-4	Isozymes (aconitase hydratase)
Adh-2	Isozymes (alcohol dehydrogenase)
ahd	Leaf hydathode colour (anthocyaninless)

Brassica rapa (con'd)

Aps-1L	Isozymes (acid phosphatase)
as	Asynaptic mutant
as	Pistil, style tip colour (anthocyaninless)
as_2	Asynaptic mutant
as_3	Asynaptic mutant
B	Disease resistance (clubroot)
b	Leaf waxiness (waxless)
b-2	Leaf waxiness (waxless)
b-3	Leaf waxiness (waxless)
Br1	Seed coat colour
Br3	Seed coat colour
Br_1	Seed coat colour (dark reddish brown)
br^1_1	Seed coat colour allele (yellow)
$br^2 1$	Seed coat colour allele (yellow)
Br_2	Seed coat colour (reddish brown)
Br_3	Seed coat colour (yellowish brown)
Br_4	Seed coat colour
Br_5	Seed coat colour
Br_6	Seed coat colour
br^1_6	Seed coat colour allele (yellow)
br^2_6	Seed hilum colour allele (light)
Br_7	Seed coat colour
Br_8	Seed hilum colour
C	Disease resistance (clubroot)
C	Cotyledon colour (chlorotic/green/albino)
C	Leaf shape
C	Root colour (purple)
cr	Petal colour (cream)
cup	Petal shape (cupped)
Dia-2A	Isozymes (dihydrolipoamide dehydrogenase)
dw	Plant height (dwarf)
dy	Petal colour (dark yellow)
E	Root colour (purple)
E_A	Seed fatty acids (erucic acid)
El3	Seed glucosinolates (C4 to C5 amino acid precursor elongation)
en	Leaf shape (entire)
Est-2A	Isozymes (esterase)
F	Root shape
Fbp-3A	Isozymes (fructose-bisphosphatase)
G	Self-incompatibility (gametophytic)
gal	Isozymes (ß-galactosidase)
Got-1A	Isozymes (aspartate aminotransferase)
Got-3	Isozymes (aspartate aminotransferase)
Gpi-2	Isozymes (glucose-6-phosphate isomerase)
Gpi-2A	Isozymes (glucose-6-phosphate isomerase)
H	Leaf trichomes (pubescence/glabrous)

Brassica rapa (con'd)

HY	Seed glucosinolates (hydroxylation)
Icd-1A	Isozymes (isocitrate dehydrogenase)
jp	Petal shape (jagged)
L_1	Root size (length)
L_2	Root size (length)
Lap-1	Isozymes (leucine aminopeptidase)
Lap-2	Isozymes (leucine aminopeptidase)
Lap-2A	Isozymes (leucine aminopeptidase)
Lob	Leaf lobe number
ly	Petal colour (light yellow)
M	Root colour (white flesh)
M1	Seed mucilage
M2	Seed mucilage
m	Self-incompatibility supressor
Mdh-2A	Isozymes (malate dehydrogenase)
mod	Self-incompatibility (repressor of *S*-alleles in pistil)
ms	Male sterility
MT	Seed glucosinolates (maturation)
nsep	Sepal width (narrow)
o	Petal colour (pale orange)
P	Root colour (red skin)
P	Seed coat colour (brown)
Pb1	Disease resistance (clubroot race 6)
Pb2	Disease resistance (clubroot race 6)
Pb3	Disease resistance (clubroot race 6)
6Pgd-1	Isozymes (phosphogluconate dehydrogenase, plastidic)
6Pgd-1'	Isozymes (phosphogluconate dehydrogenase, plastidic)
6Pgd-2	Isozymes (phosphogluconate dehydrogenase, cytosolic)
6Pgd-2'	Isozymes (phosphogluconate dehydrogenase, cytosolic)
6Pgd-2Ac	Isozymes (phosphogluconate dehydrogenase)
Pgi-1	Isozymes (glucose-6-phosphate isomerase, plastidic)
Pgi-2	Isozymes (glucose-6-phosphate isomerase, cytosolic)
Pgm-1	Isozymes (phosphoglucomutase)
Pgm-1A	Isozymes (phosphoglucomutase)
Pgm-2	Isozymes (phosphoglucomutase)
Pgm-3A	Isozymes (phosphoglucomutase)
pkl	Leaf shape (puckered)
pl	Petal number (apetalous)
Pp	Petal number (polypetalous)
Pub	Leaf trichomes (pubescence/glabrous)
R	Seed coat colour (red)
R	Root colour (red)
r	Chlorophyll synthesis repressor mutant
Rf_1'	Male fertility restoration
Rf_2'	Male fertility restoration
ro	Plant height (rosette)
Ropm	Petal shape (rolled)

Brassica rapa (con'd)

rpm	Petal margin colour (red)
S	Self-incompatibility
S_1	Self-incompatibility allele
S_2	Self-incompatibility allele
S_3	Self-incompatibility allele
S_4	Self-incompatibility allele
s_c	Self-compatibility allele
Sdh-1A	Isozymes (shikimate dehydrogenase)
Sdh-2A	Isozymes (shikimate dehydrogenase)
sp	Petal colour (bicoloured)
Tpi-1	Isozymes (triose-phosphate isomerase, plastidic)
Tpi-1'	Isozymes (triose-phosphate isomerase, plastidic)
Tpi-2	Isozymes (triose-phosphate isomerase, cytosolic)
Tpi-2'	Isozymes (triose-phosphate isomerase, cytosolic)
tu	Petal shape (tucked)
V	Root colour (green skin)
V	Silique valve number
Y_1	Petal colour (yellow)
Y_2	Petal colour (yellow)
y	Petal colour (white)
y	Embryo colour (yellow)
yg-1	Cotyledon and true-leaf colour (yellow-green)
yg-2	Cotyledon and true-leaf colour (yellow-green)
yg-3	Cotyledon and true-leaf colour (yellow-green)
yg-4	Cotyledon and true-leaf colour (yellow-green)
yg-5	Cotyledon and true-leaf colour (yellow-green)
yg-6	Cotyledon and true-leaf colour (yellow-green)
yg-7	Cotyledon and true-leaf colour (yellow-green)

Capsella bursa-pastoris

Gdh-1	Isozymes (glutamate dehydrogenase)
Gdh-2	Isozymes (glutamate dehydrogenase)

Capsella grandiflora

Gdh-1	Isozymes (glutamate dehydrogenase)
Gdh-2	Isozymes (glutamate dehydrogenase)
S	Self-incompatibility
S1	Self-incompatibility allele
S2	Self-incompatibility allele
S3	Self-incompatibility allele

Capsella rubella

Gdh-1	Isozymes (glutamate dehydrogenase)
Gdh-2	Isozymes (glutamate dehydrogenase)

Cardamine pratensis

B	Self-incompatibility
G	Self-incompatibility
S	Self-incompatibility
S_1	Self-incompatibility allele
S_3	Self-incompatibility allele
Z	Self-incompatibility
Z_1	Self-incompatibility allele
Z_2	Self-incompatibility allele
Z_3	Self-incompatibility allele
Z_4	Self-incompatibility allele

Crambe abyssinica

P	Leaf trichomes (pubescence/glabrous)
p	Leaf trichomes (pubescence/glabrous)

Crambe hispanica

P	Leaf trichomes (pubescence/glabrous)
p	Leaf trichomes (pubescence/glabrous)

Iberis amara

S	Self-incompatibility

Leavenworthia crassa

S	Self-incompatibility

Lesquerella densipila

S	Self-incompatibility

Lesquerella lescurii

S	Self-incompatibility

Raphanus raphanistrum

G	Self-incompatibility
S	Self-incompatibility

Raphanus sativus

A	Root colour (violet)
A	Root colour (presence of colour)
B	Root colour (with gene *R*, purple roots)
B	Root colour (violet)
B	Root colour (expression)
Ac1	Disease resistance (white rust race 1) [supersedes symbol *R*]
Aco	Isozymes (aconitase hydratase)
Acp	Isozymes (acid phosphatase)
Apl	Plant colour (purple pigmentation)
Ar	Root colour (purple)
C	Root colour (white)
C	Root colour
C	Hypocotyl colour (violet)
C	Root colour (purple)
c	Regenerative ability (tissue culture/callogenesis)
cp	Pollen colour (cream)
Est	Isozymes (esterase)
G	Root colour (pale green neck) and hypocotyl colour (pale green)
G	Self-incompatibility
G_1	Self-incompatibility allele
G_2	Self-incompatibility allele
gf_1	Leaf colour (yellow-green mutant/green fleck)
gf_2	Leaf colour (yellow-green mutant/green fleck)
H	Root colour (white)
I	Self-incompatibility
Idh	Isozymes (isocitrate dehydrogenase)
L	Root shape (long)
Lap	Isozymes (leucine aminopeptidase)
ms	Male sterility
ms1	Male sterility
P	Root colour (purple)
Pgd	Isozymes (phosphogluconate dehydrogenase)
Pgi	Isozymes (phosphoglucoisomerase)
Pgm-1	Isozymes (phosphoglucomutase)
Pgm-2	Isozymes (phosphoglucomutase)
Pgm-3	Isozymes (phosphoglucomutase)
Pi	Plant colour (pink)
Prx	Isozymes (peroxidase)
Pu	Silique colour (purple)
R	Root colour (purple)
R	Root colour (red)
R	Root colour allele

Raphanus sativus (con'd)

R^p	Root colour allele
R^s	Root colour allele
r	Root colour allele
R	Disease resistance (white rust race 1) [superseded by symbol *Ac1*]
R^p	Root colour (purple)
R^s	Root colour (red striping)
R_1	Seedling colour (red cortex)
R_2	Seedling colour (red cortex)
R_2	Root colour
R_3	Root colour
rl	Regenerative ability (tissue culture/rhizogenesis)
rs	Regenerative ability (tissue culture/rhizogenesis)
S	Self-incompatibility
S_1	Self-incompatibility allele
S_2	Self-incompatibility allele
S_3	Self-incompatibility allele
S_4	Self-incompatibility allele
S_5	Self-incompatibility allele
S_6	Self-incompatibility allele
Tpi	Isozymes (triose-phosphase isomerase)
vg	Root colour (white neck)
x_a	Seedling colour (yellow)
Y	Root colour (yellow)
Y^b	Root colour (black)
yg	Leaf colour (yellow green mutant)

Sinapis alba

py	Petal colour (pale yellow)

Sinapis arvensis

E	Seed fatty acids (erucic acid)
Fbp-2	Isozymes (fructose-bisphosphatase)
Gpi-2	Isozymes (glucose-6-phosphate isomerase)
I	Seed dormancy
Idh-2	Isozymes (isocitrate dehydrogenase)
Pgm-2	Isozymes (phosphoglucomutase)
Pgm-2'	Isozymes (phosphoglucomutase)
S	Self-incompatibility
Tpi-1	Isozymes (triose-phosphate isomerase)
Tpi-1'	Isozymes (triose-phosphate isomerase)

TRAIT GENETICS

MORPHOLOGICAL TRAITS

Anther/Filament length/*Raphanus raphanistrum*

Conner and Via (1993)
Genetic half-sibling analyses were conducted on plants grown from seed from a population from Binghamton, New York, U.S.A. Narrow-sense heritability estimates for ten phenotypic traits were 0.25 for seedling emergence time, 0.28 for leaf length, 0.40 for leaf width, 0.52 to 0.58 for short and long filament lengths, 0.63 for petal length and flowering time, 0.68 for flower tube length, 0.92 for pistil length, and 1.16 for petal width. The three traits with the lowest narrow-sense heritabilities (0.25 to 0.40) were the most phenotypically variable, whereas floral traits were less affected by the environment. Genetic correlations for flower traits were moderately positive (r = 0.13 to 0.53), with the exception of a high correlation between flower tube and filament lengths (r = 0.8 to 0.9). Leaf length and leaf width were highly correlated (r = 0.84). Additive genetic correlations between the morphological and life-history traits were generally similar to the phenotypic correlations (*i.e.* small and mostly negative). Additive genetic correlations among the traits were very similar to the phenotypic correlations.

Anther/Tip colour/*Brassica oleracea*

Sampson (1967a)
Gene *c* completely blocks anthocyanin synthesis in curly kale [= var. *acephala*]. A similar gene, designated *c-2*, was found in brussels sprouts [= var. *gemmifera*]. The allelic relationships between various alleles of gene *A* for anthocyanin production were described. Allele A^{rc} (= gene *D* of Kristofferson) from purple cabbage [= var. *capitata*] gave purple stems, petioles, leaf blades and midribs, and deep purple ovaries; allele A^{ck} from curly kale [= var. *acephala*] gave purple stems, petioles, and deep purple ovaries; allele A^{pb} from purple broccoli [= var. *italica*] gave medium purple ovaries and somewhat more purple plant parts than the fourth allele, *a*, from green sprouting broccoli [= var. *italica*], that gave only traces of anthocyanin. A fifth allele *A* from curly kale which gave purple stems and petioles but only slightly tinged ovaries, was postulated. Linkage was observed between genes *A* and *As* (large purple anther spot; from marrowstem kale [= var. *acephala*]); percent recombination between the genes *A* and *As* was 44.47 ± 2.31.

Wills and Smith (1972)
Linkage studies in various *B. oleracea* genotypes indicated linkage between the glossy foliage genes *gl-y* and *gl-e3* and genes of linkage group 1 [*Ap* (abortive pollen), *S* (self-incompatibility), *ps* (persistent sepal), *As* (anther spot), *A* (pigmented hypocotyl), and *cp-1* (crinkly petal)] and linkage between gene *Hr-y* (hairy leaf) and genes of linkage group 3 [*Wh* (white petal) and *gl-1* (glossy foliage)]. Linkage was also detected between the genes *Fn* (fern-leaf) and *c-2* (anthocyanin suppressor) and between the genes *cp-1* (crinkly petal) and A^{o} (pigmented ovary).

Wills and Smith (1973)
Linkage was reported in *B. oleracea* between the genes *cp-1* (crinkly petal), *As* (anther spot), and *gl-el* (glossy foliage). The genes *fc1* and *fc2* (fused cotyledon) were found to be different.

Anther/Tip colour/*Brassica rapa*

Cours (1977)
The inheritance of non-pigmented anther tip (probably due to the absence of anthocyanin) was studied in USDA introduction PI 175079. The trait was conditioned by a single recessive gene, designated *aa*. Gene *aa* was linked to gene *as* (anthocyaninless style tip).

Corolla width/*Raphanus sativus*

Young *et al.* (1994)
Heritability and genetic correlations of three floral traits (corolla width, pollen production per flower, and pollen size) were examined in a wild population originating from Davis, California, U.S.A., in the greenhouse and under field conditions. The first generation (parents in the field, crosses between 36 pairs of mated plants, resulting offspring grown in the greenhouse) and the second generation (parents grown in the greenhouse, offspring grown in the greenhouse and at two field sites) were examined. Corolla width and pollen production showed significant heritabilities in both generations and under all growth environments, with mean values of 54% and 56%, respectively, while pollen size variation appeared to be under little genetic control. Heritability estimates did not vary significantly among generations or among the growth environments. Genotype-environment interactions were not apparent for any trait. Only corolla width and pollen production were significantly genetically correlated, *i.e.* families with large corollas also had large pollen production per flower.

Cotyledon/Colour/Chlorotic/green/albino/*Brassica rapa*

Stringam (1969)
The inheritance of the trait chlorotic cotyledon was examined in M3 progenies from ethylene imine-treated seed of yellow sarson [= subsp. *trilocularis*]. The trait was controlled by a single partially dominant gene, designated *C*. The postulated genotypes were *CC* (green), *Cc* (chlorotic), and *cc* (albino). F_1 progenies of crosses between chlorotic cotyledon plants or albino cotyledon plants and a wild-type line fitted the expected segregation ratios.

Cotyledon/Colour/Lutescence/*Brassica nigra*

Delwiche and Williams (1981)
Lutescence, *i.e.* an irregular pattern of yellowing on cotyledons visible eight to ten days after germination, was observed in USDA Plant Introduction PI 197401. The trait was found in testcross and F_2 segregation studies to be controlled by a single recessive gene, designated *lu*.

Cotyledon/Colour/Yellow-green/*Brassica nigra*

Delwiche and Williams (1981)
The expression of yellow-green cotyledons in USDA Plant Introductions PI 197401 and PI 179846 was found in testcross and F_2 segregation studies to be separately controlled by two recessive genes, *ygc1* and *ygc2*. Gene *ygc1* controlled the expression of yellow-green colour in the cotyledon about six days after germination, whereas gene *ygc2* controlled the reverse condition, *i.e.* where the cotyledons were yellow-green upon emergence and became normal green about four days after germination.

Cotyledon/Colour/Yellow-green/*Brassica rapa*

Stringam (1973)
The inheritance of chlorophyll-deficient cotyledons and true leaves was studied in seven mutant lines derived from ethylene imine-treated seed of yellow sarson [= subsp. *trilocularis*]. All mutant phenotypes were controlled by single recessive genes, designated *yg-1*, *yg-2*, *yg-3*, *yg-4*, *yg-5*, *yg-6*, and *yg-7*. None of of the genes was linked.

Cotyledon/Number (polycotyledony)/*Brassica oleracea*

Wills and Smith (1974)
Linkage was reported in *B. oleracea* between genes *po* (polycotyledony) and *le* (leaf excrescence) (14.56 ± 0.05% recombination), between genes *gl-3* (glossy) and *pg* (pale green) (37.38 ± 0.31% recombination) and, as reported by Sampson (1967b), between genes *pg-2* (pale green foliage) and *Hr-1* (hairy leaf) (18.86 ± 4.73% recombination).

Cotyledon/Shape (fused)/*Brassica oleracea*

Wills and Smith (1973)
See Morphological traits/Anther/Tip colour/*Brassica oleracea*.

Cotyledon/Size/*Brassica oleracea*

Dickson (1968)
The trait “large cotyledon” in broccoli [= var. *italica*] was controlled by a single dominant gene, designated *Lc*.

Cotyledon/Size/*Brassica rapa*

Prasad (1993)
A comparison of F_1 intervarietal turnip [= subsp. *rapifera*] hybrids showed heterosis for the traits seed germination, mean hypocotyl length, mean cotyledon area, and relative width of cotyledon. Turnip root colour was inherited monogenically while hypocotyl length was under the control of a polygenic system. Plant height and days to flower were negatively correlated.

Cotyledon/Size/*Raphanus sativus*

Kubka *et al.* (1974)
Heritability estimates were made for 11 agronomic traits in radish cv. Saxa. The estimates were: seed yield (33.4%), weight of roots (41.5%), silique number (44.3%), weight of siliques (53.9%), shoot number and plant weight (65.6%), cotyledon width (79.9%), cotyledon length (80.6%), number of seeds per silique (86.0%), plant height (87.6%), and weight of seeds (92.2%). The correlation coefficient between seed weight of the mother plants was positive (with the exception of the number of seeds per silique which was negatively correlated) and significant for all above traits, with the exception of the number of siliques and seed yield.

Curd/Colour/*Brassica oleracea*

Crisp *et al.* (1975)
A cauliflower [= var. *botrytis*] mutant with orange curd was found in white-curded cv. Extra Early Snowball. Studies indicated monogenic dominant expression. *OrOr* genotypes had a stunted orange curd while the *Oror* genotypes had a normal orange curd; *oror* genotypes had a normal white curd.

Curd/Riceyness/*Brassica oleracea*

Watts (1966)
Segregating ratios of crosses in early summer cauliflower [= var. *botrytis*] between plants of cv. van den Berg's No. 35 with no riceyness (riceyness grade 1) x plants of cv. Cambridge 6 with a high degree of riceyness indicated that trait was under polygenic control with slight dominance of the poorer curd quality (riceyness grade 4).

Curd/Size/*Brassica oleracea*

Swarup and Pal (1966)
The inheritance of curd maturity, net weight, and size in cauliflower [= var. *botrytis*] was studied in eight inbreds (Takii Extra Early Market, Success, Delft Market, Snowball, Snowball-16, E.C. 12012, E.C. 12013, E.C. 12016), 14 F_1 hybrids, F_2 and backcross progenies. For curd maturity and size, dominance was more important than additiveness. Significant additive and dominance gene effects were observed in several crosses for curd weight. Heterosis in the F_1s was observed for early curd maturity, higher curd weight, and larger curds. Transgressive segregants for these traits were observed in several crosses in the F_2 progenies.

Curd/Texture/*Brassica oleracea*

Nieuwhof and Garretsen (1961)
The inheritance of curd texture in cauliflower [= var. *botrytis*] was investigated in crosses between plants with solid x plants with loose curds. Curd solidity was under polygenic control.

Embryo colour (yellow)/*Brassica rapa*

Stringam and McGregor (1980)
The inheritance of a yellow-embryo mutant of cv. Arlo [= subsp. *oleifera*] was controlled by a single recessive gene, designated *y*, under embryonic control.

Flower/Clustered/*Brassica oleracea*

Chiang (1983)
The inheritance of the trait “clustered flowers” was studied in reciprocal crosses between a cabbage [= var. *capitata*] line with clustered flowers (2-9 fertile flowers with fused pedicels) x wild-type cabbage cv. April Green. The segregation of the F_2 and backcross (BC) generations was consistent with control by a single recessive gene, designated *cf*.

Flower/Number/*Brassica rapa*

Ågren and Schemske (1992)
Estimated heritabilities of trichome number and days to first flower on rapid-cycling population CrCG#1 from Wisconsin, U.S.A., were not significantly different from 1.0. The trichome number on the edge of the first leaf was significantly correlated with the trichome number on the petiole of the first leaf (r = 0.80) and with the number of days to first flower (r = 0.31); leaf edge trichome number was not correlated with total number of flowers (r = 0.17).

Ågren and Schemske (1994)
Studies were conducted on plants from a naturalized population from California, U.S.A. [= subsp. *sylvestris*]. Greenhouse-grown paternal and maternal sibships were used to estimate the correlation between trichome number, days to first flower, and flower production. Genetic correlations between total number of flowers and trichome number (r = -0.03 to 0.13) were weak. Genetic correlation between total number of flowers and days to first flower were large and negative (r = -0.72 to 0.79) and significant for all methods.

Flower/Retention/*Brassica nigra*

Delwiche and Williams (1981)
Floral retention (stamens, sepals, and petals wither and fade but do not abscise) observed in USDA Plant Introduction PI 173860, was found in F_2 segregation studies to be controlled by a single recessive gene, designated *fr*.

Flower bud/Shape/Open bud/*Brassica oleracea*

Dickson (1968)
The inheritance of the trait “open bud” (sepals do not completely meet at the tip of the bud so that the stigma is exposed) was studied in crosses between broccoli [= var. *italica*] accession USDA PI 189028 (open bud) x broccoli accessions USDA PI 231997 and PI 271445 and cauliflower [= var. *botrytis*]

accessions USDA PI 241621 and PI 217934 (closed bud). The trait “open bud” was found to be sensitive to the environment, being dominant to “closed bud” under hot summer and recessive to “closed bud” under winter greenhouse conditions. The gene was designated *O.*

Flower bud/Shape/Puffy bud/*Brassica oleracea*

Dickson (1968)
The inheritance of the trait “puffy bud” (large and loose sepals resulting in a puffy bud) was studied in crosses between broccoli [= var. *italica*] accessions. The trait puffy bud was inherited as a single recessive gene, designated *pb*.

Flower bud/Starring (rosetting)/*Brassica oleracea*

Dickson (1968)
The trait “starring or rosetting” (flower buds in the centre of the inflorescence turn yellow and often fail to mature) in broccoli [= var. *italica*] was controlled by a single dominant gene, designated *St.* The expression of gene *St* was more pronounced in hot weather.

Head/Core length/*Brassica oleracea*

Dickson and Carruth (1967)
The inheritance of core length in cabbage [= var. *capitata*] was conditioned by two incompletely dominant genes for short core length. Short core length was correlated (r = 0.55) with round head. Heritability estimates were 0.70 for core length and 0.51 for head shape.

Chiang (1969)
The inheritance in cabbage [= var. *capitata*] of inner core length, days to maturity, polar and equatorial diameters of heads, number of wrapper leaves, and yield, was studied in a diallel cross with the cultivars Early Greenball, Baby Head, and Early Marvel and the inbred lines 192265B and W60. The inheritance of inner core length and days to maturity was mainly additive. Additive and dominance were equally important in the inheritance of polar and equatorial diameters of heads. Dominance effects were important for yield. Heritability estimates were high for polar diameter (68.94%) and days to maturity (82.68%), moderate for number of wrapper leaves and length of inner core (34.56%), and low for equatorial diameter and yield (3.81%).

Head/Heading habit/*Brassica oleracea*

Pease (1926)
In a cross between cabbage [= var. *capitata*] x kale [= var. *acephala*] and kohlrabi [= var. *gongylodes*], the non-heading habit of kale and kohlrabi was dominant over the heading habit of cabbage. The trait was controlled by two genes, designated N_1 and N_2.

Allgayer (1928)
In a cross between cabbage [= var. *capitata*] x kitchen kale [= var. *fimbriata*], one dominant gene, designated *K*, and three minor recessive genes, designated k_1, k_2, and k_3, were postulated for the control of heading.

Head/Heading habit/*Brassica rapa*

Stout (1922)
The heading habit was recessive in crosses between Pe-tsai [= subsp. *pekinensis*] (heading) x pak-choi [= subsp. *chinensis*] (non-heading).

Head/Number of non-wrapper leaves/*Brassica oleracea*

Pearson (1934)
The inheritance of the number of non-wrapper leaves attached to the main stem in cabbage [= var. *capitata*] was determined. Lower leaf number was dominant to higher leaf number and a number of modifying factors were implicated.

Head/Number of wrapper leaves/*Brassica oleracea*

Chiang (1969)
See Morphological traits/Head/Core length/*Brassica oleracea*.

Head/Presence of leaves in heads (leafy)/*Brassica oleracea*

Dickson (1968)
The inheritance of the trait “leafy” (presence of leaves in heads) was studied in crosses between leafy broccoli [= var. *italica*] accessions USDA PI 189028, PI 249556, PI 250128 (leafy) and cauliflower [= var. *botrytis*] accession PI 231210 (cv. Romano) x non-leafy cauliflower cv. Coastal and accession PI 241621. Leafy was inherited as a single dominant gene, designated *L*. The expression of gene *L* was enhanced by high temperature.

Head/Shape/*Brassica oleracea*

von Tschermak (1916)
The trait “pointed head” in cabbage [= var. *capitata*] was reported to be dominant to the trait “round head”.

Dickson and Carruth (1967)
See Morphological traits/Head/Core length/*Brassica oleracea*.

Head/Size/*Brassica oleracea*

Chiang (1969)
See Morphological traits/Head/Core length/*Brassica oleracea*.

Head/Size/*Brassica rapa*

Tan *et al.* (1982)
The heritability of quantitative traits was determined in two crosses of Chinese cabbage [= subsp. *pekinensis*]. Narrow-sense heritability estimates for plant diameter, head firmness, and plant height were about 50%; narrow-sense heritability estimates for leaf differentiation rate, head diameter, leaf number per plant, gross weight, and net weight were about 30%.

Hypocotyl/Colour/Green/*Brassica oleracea*

Sampson (1966a)
Linkage was observed between male sterility gene *ms-1* of green sprouting broccoli [= var. *italica*] and gene *c* (anthocyanin-free plant with bright green hypocotyl) of curly kale [= var. *acephala*] and variegated ornamental kale.

Hypocotyl/Colour/Green/*Brassica rapa*

Hawk (1982a)
Crosses were made between a green hypocotyl, yellow-seeded selection of an early-flowering line of *B. campestris* x a purple hypocotyl, brown-seeded selection of an early-flowering line of *B. campestris* and cv. Torch [= subsp. *oleifera*]. Segregation ratios were consistent with a single recessive gene which controlled both green hypocotyl colour and yellow seed coat colour. The gene for green hypocotyl colour was epistatic to the dominant alleles at the Br_1 and Br_3 (Stringam, 1980) seed coat colour loci.

Hawk (1982b)
Tight linkage was identified between two seedling mutants isolated from early flowering plants of *B. campestris* USDA Plant Introductions PI 175054 and PI 175079. A green hypocotyl mutant allelic to previously reported gene *a-2* (Stringam, 1971) was found to be linked to a mutant with wrinkled leaves and jagged petal margins (gene *jp*). Genes *a-2* and *jp* were assigned to linkage group I.

Hypocotyl/Colour/Pale green/*Raphanus sativus*

Tatebe (1937a)
Pale green neck or hypocotyl in radish was conditioned by dominant gene *G*.

Hypocotyl/Colour/Purple pigmentation/*Brassica oleracea*

Wills and Smith (1972)
See Morphological traits/Anther/Tip colour/*Brassica oleracea*.

Hypocotyl/Colour/Purple pigmentation (absence)/*Brassica nigra*

Delwiche and Williams (1981)
The absence of purple pigmentation (anthocyanins) in the first true leaves and hypocotyls was observed in USDA Plant Introductions PI 179846 and PI 173855, respectively. These two traits were found in F_2 segregation studies to be controlled by two unlinked recessive genes, designated a_1 and a_2, respectively.

Hypocotyl/Colour/Purple pigmentation (absence)/*Brassica rapa*

Stringam (1971)
Segregation progenies of crosses between four green hypocotyl mutants of yellow sarson [= subsp. *trilocularis*] and a wild-type genotype were consistent with each mutation being controlled by a single recessive gene. The genes were designated *a-1*, *a-2*, *a-3*, and *a-4*. Evidence was presented for the linkage of genes *a-1*, *a-2*, and *a-3*.

Hypocotyl/Colour/Violet/*Raphanus sativus*

Dayal and Prasad (1983)
In the crosses cv. Rainy Season Red (violet hypocotyls) x cv. Jaupur Giant (white hypocotyls) and cv. Kalamikati Red (violet hypocotyls) x cv. Jaupur Giant (white hypocotyls), F_1 seedlings were found to have light violet hypocotyls. F_2 segregation data from both crosses fitted a ratio of 1 violet: 2 light violet: 1 white, indicating that hypocotyl colour was controlled by a single gene, with two alleles, with the violet allele, *C*, being incompletely dominant to the white allele, *c*.

Hypocotyl/Length/*Brassica rapa*

Prasad (1993)
See Morphological traits/Cotyledon/Size/*Brassica rapa*.

Hypocotyl/Length/*Raphanus sativus*

Dayal and Prasad (1983)
In the crosses cv. Japanese White (long hypocotyls) x cv. Jaupur Giant (short hypocotyls) and cv. Kalamikati Red (long hypocotyls) x cv. Jaupur Giant (short hypocotyls), F_1 segregation data indicated that long hypocotyls were dominant over short hypocotyls. However, in the F_2 generations, hypocotyl length varied widely with values both shorter and longer than in the parents and F_1 hybrids.

Segregation data indicated that the trait was probably polygenically controlled; the apparent dominance of long hypocotyls was attributed to interallelic and nonallelic interactions.

Leaf/Area/*Brassica napus*

Paul (1992a)
The inheritance of growth attributes (relative growth rate, net assimilation rate, leaf area ratio, relative leaf growth rate, and specific leaf area), leaf length and width, and anatomical leaf traits was studied in forage oilseed rape [= subsp. *oleifera*] in a 5 x 5 diallel cross. Additive effects were observed for leaf length and number. Dominance effects were observed for net assimilation rate. Both additive and dominance effects were significant for the remaining traits, additive affects being more important than the dominance effects. Broad-sense heritability was very high for all traits. Narrow-sense heritability was high for all traits except for net assimilation rate, relative leaf growth rate, total leaf area, and mean cross-sectional area of spongy parenchyma. A positive correlation for dry matter yield was observed between leaf area ratio and specific leaf area.

Leaf/Area/*Raphanus sativus*

Ling *et al.* (1986)
Heterosis and combining ability were studied in radish. Analysis of a 3 x 4 diallel cross showed positive correlations between parents and progenies for leaf area and root length. Nine of the 12 hybrids performed better than the high parent for root weight per plant and all hybrids had a greater leaf area. Only four hybrids showed positive heterosis for root length; of these, one was better than the high parent. Eleven hybrids were better than the high parent for root diameter. Among F_1s, leaf area was positively correlated with root weight per plant. Leaf area, root length, and root weight per plant had high general combining ability (in the region of or above 90%); broad- and narrow-sense heritabilities for these three traits were greater than 60%.

Leaf/Colour/Chlorophyll deficient mutant/*Brassica juncea*

Singh *et al.* (1964)
In this mutant, leaves were white at the early stage, but became light green at the time of flowering. The trait was recessive and controlled by two duplicate genes, designated *gl* and *gl'*.

Leaf/Colour/Dark green/*Brassica oleracea*

Kianian and Quiros (1992a)
Segregation ratios in F_2 populations (46:14 and 41:19 dark green to light green plants) derived from a cross between commercial Chinese kale [= var. *alboglabra*] accessions with dark green foliage (B479) and light green foliage (B478) fitted a dominant monogenic model.

Leaf/Colour/Pale green foliage/*Brassica oleracea*

Sampson (1966b)
The gene *pg-1* for pale green foliage (pale true leaves and dwarfness) in broccoli [= var. *italica*] was completely recessive and linked to gene *cr* (cream petal) with 11.0 ± 0.8% recombination. The gene *pg-2* for pale green foliage (yellowish cotyledons, true leaves paler than in *pg-1* plants, reduced vigor, and delayed flowering) was completely recessive.

Wills and Smith (1974)
See Morphological traits/Cotyledon/Number (polycotyledony)/*Brassica oleracea*.

Leaf/Colour/Pink margins/*Brassica juncea*

Dixit (1972)
The inheritance of pink leaf margins was investigated in a cross between an Indian mustard mutant with pink leaf margins x an albino type with white leaves. F_1 plants had leaves with pink margins. The F_2 and BC segregation ratios were consistent with a single dominant gene for pink leaf margins.

Leaf/Colour/Purple pigmentation/*Brassica juncea*

Singh *et al.* (1964)
Genetic studies were conducted on plants of a mutant in which leaves were initially green and became purple in about 20 days, with the colouration developing from the leaf margins towards the mid-rib. Purple leaf colour was dominant and controlled by a single gene, designated *Pl*. Purple colour was found to be epistatic to gene *gl* and/or *gl'* for a chlorophyll deficient mutant.

Yadav *et al.* (1976)
In crosses of wild-type cvs. Prakash, Varuna, and RH-30 x line RC-781 with purple leaves, the F_1 plants had purple foliage. F_2 segregation ratios were 9 plants with purple leaves: 7 plants with green leaves, indicating complementary action of two genes.

Chen and Tong (1985)
Crosses were made between mustard morphotypes. Leaf colour, leaf shape, and basal branching were conditioned by one pair of genes, while petal colour was controlled by two pairs of interacting genes. Red leaf colour, yellow petal colour, basal branching, enlarged root, incised leaf, large foliage, and large terminal lobed leaf were dominant traits.

Leaf/Colour/Purple pigmentation/*Brassica oleracea*

Wiegmann (1828)
The author is reported to have discovered that purple colour in cabbage [= var. *capitata*] was incompletely dominant over green.

Kristofferson (1924)
Crosses were made between red and green cabbage [= var. *capitata*]. Colour was determined by the interaction of several genes: gene *A* alone had no effect (green leaves), but in combination with gene *D* produced red leaves. Gene *B* alone produced leaves with a light red midrib and in combination with gene *A* produced leaves with a dark violet midrib. Gene *C* alone was colourless, but in combination with gene *A* produced leaves with a dark violet midrib. The presence of gene *E* extended the dark violet areas. Genes *B* and *C* produced the same phenotype as gene *B* alone. It was postulated that green cabbage was *Dabce* and red cabbage, *daBCE*.

Sutton (1924)
The F_2 segregation ratios of a cross in cabbage [= var. *capitata*] between Red Pickling Cabbage (tendency to bolt) x a green heading cabbage suggested that the traits “tendency to bolt” and “green leaf colour” were conditioned by unlinked, single recessive genes.

Pease (1926)
Incomplete dominance of red over green colour in cabbage [= var. *capitata*] was reported.

Kristofferson (1927)
Crosses were made between broccoli [= var. *italica*] and dwarf kale [= var. *acephala*]. The parents had green leaves with a whitish midrib in broccoli and a green midrib in kale. The colour of the midrib of the F_1 plants was dark red violet. The F_2 segregation ratios approximated a 9:7 distribution of plants with a dark red violet midrib or with light red to green midribs. A two gene control with complementary gene action was suggested for the colour of the midrib. Genes were designated *A* and *C*.

Moldenhawer (1927)
The inheritance of purple colour in kohlrabi [= var. *gongylodes*] x green brussels sprouts [= var. *gemmifera*] was controlled by two complementary factors (F_2 ratio: 9:7).

Pease (1927)
The inheritance of blue colour in kohlrabi [= var. *gongylodes*] cv. Vienna x green savoy cabbage [= var. *sabauda*] was controlled by two complementary factors, designated *D* and ∆.

Allgayer (1928)
A single dominant gene, designated *P*, controlled the inheritance of red leaf blade in crosses between purple cabbage [= var. *capitata*] x green curly kale [= var. *acephala*]. The heterozygous condition resulted in green leaves with red veins.

Magruder and Myers (1933)
The inheritance of plant colour in cabbage [= var. *capitata*] was reported to be under the control of two genes, designated *M* and *S*. Postulated genotypes were *S_M_* (purple), *S_m_* (sun, purple pigmentation only on portions of plants exposed to the sun), *s_M_* (magenta), and *s_m_* (green, light green on the whole plant).

Kwan (1934)
Inheritance studies of anthocyanins in a cabbage [= var. *capitata*] cross between a deep purple strain of cabbage x a sun-red strain indicated two duplicate genes (F_2 ratio: 15 deep purple plants: 1 sun-red plant), designated R_1 and R_2. The F_2 segregation ratio for a cross between a purple strain x a green strain was consistent with two genes with recessive epistasis (9 purple: 3 sun red: 4 green plants); the genes were designated *G* for pigment production and *H* for purple (genotype of sun-red plants: *G_hh*).

Wrinkled foliage was controlled by two complementary genes, designated *W* and *S*. Plant height and head weight were controlled by several genes.

Tan *et al.* (1964)
The inheritance of purple leaf colour in cabbage was studied in crosses between green x purple plants. Results suggested monogenic dominant inheritance in some progenies and more complex inheritance in others.

Sampson (1967a)
See Morphological traits/Anther/Tip colour/*Brassica oleracea*.

Kianian and Quiros (1992a)
Segregation ratios in a F_2 population (35:17 plants) obtained from an interspecific cross between purple-tinged kohlrabi [= *Brassica oleracea* var. *gongylodes*] x *Brassica incana* (green) best fitted a dihybrid ratio with complementary gene action.

Segregation ratios in a F_2 population (39:21 plants) obtained from a cross between a purple-tinged genotype of collards [= *Brassica oleracea* var. *sabauda*] x green cauliflower [= *Brassica oleracea* var. *botrytis*] best fitted a monohybrid ratio.

Leaf/Colour/Purple pigmentation/*Brassica rapa*

Shibutani and Okamura (1957)
The F_1 generation of crosses between turnips [= subsp. *rapifera*] with purple vs. green leaves showed complete dominance of purple pigmentation over red pigmentation. No F_2 segregation ratios were provided.

Leaf/Colour/Purple pigmentation (absence)/*Brassica nigra*

Delwiche and Williams (1981)
The absence of purple pigmentation (anthocyanins) in the first true leaves and hypocotyls was observed in USDA Plant Introductions PI 179846 and PI 173855, respectively. These two traits were found in F_2 segregation studies to be controlled by two unlinked recessive genes, designated *a1* and *a2*, respectively.

Leaf/Colour/Variegated/*Brassica oleracea*

Martin (1959)
The inheritance of variegation in ornemental kale [= var. *acephala*] was studied in a cross between a true-breeding variegated mutant and broccoli [= var. *italica*] cv. Yates Green Sprout. Variegation was dominant and conditioned by a single gene. In homozygous individuals, the expression of the variegation was constant, but less pronounced at high temperature (21° C); in heterozygous individuals, the trait was expressed at cool temperature (7° C), but not at high temperature (21° C).

Leaf/Colour/Variegated/*Brassica rapa*

Orakwue and Crowder (1983)
Variegated mutants were identified in self-progenies of normal *B. campestris* or in natural populations in the *B. campestris* genetics program at the Department of Plant Breeding, Cornell University, Ithaca, U.S.A. The variegation (white and pinkish-purple on the foliage, stems, and siliques) was most evident at the peak of foliage development. The trait was recessive and linked to cream petal colour. Penetrance of the trait was complete, but its expressivity was variable.

Leaf/Colour/Virescence/*Brassica nigra*

Delwiche and Williams (1981)
Virescent leaf (emerging true leaves are initially yellow-green and turn normal green as they expand) was observed in USDA Plant Introduction PI 1733860. The trait was found in F_2 segregation studies to be controlled by a single recessive gene, designated *vl*.

Leaf/Colour/Xanthovirescence/*Brassica nigra*

Delwiche and Williams (1981)
Xanthovirescence (cotyledons and true leaves are yellow upon emergence and turn green as they mature) was observed in USDA Plant Introduction PI 179846. The trait was found in testcross and F_2 segregation studies to be controlled by a single dominant gene, *Xv*, which was lethal in the homozygous condition (*XvXv*).

Leaf/Colour/Yellow-green mutant/*Raphanus sativus*

Humaydan and Williams (1976)
Inheritance studies of a yellow-green leaf mutant in the F_1 and F_2 generations indicated that the trait was controlled by a single gene, designated *yg*, with recessiveness for yellow-green leaf. A chlorophyll-deficient mutant with yellow-green cotyledons and yellow-green true leaves with normal green flecks was identified in cv. Early Scarlet Globe. The inheritance of the green fleck trait was controlled by recessive alleles, designated gf_1 and gf_2, at two duplicate genes. F_1 progenies of a cross made between a yellow-green parent (*yg*) and a green-fleck parent (*gf1gf2*) indicated that different genes were involved.

Leaf/Excrescence/*Brassica oleracea*

Wills and Smith (1974)
See Morphological traits/Cotyledon/Number (polycotyledony)/*Brassica oleracea*.

Wills and Smith (1975)
Linkage was reported in *B. oleracea* between genes *Fn* (fern-leaf) and *le* (leaf excrescence).

Sampson (1978a)
A spontaneous mutant from green sprouting broccoli [= var. *italica*], probably cv. Calabrese, showed small outgrowths on the upper surface of leaves and strong apical dominance. The phenotype was conditioned by a single recessive gene, designated *le*. Gene *le* was loosely linked to gene *Hr-1* (hairy first leaf) with 46.8 ± 1.2% recombination.

Leaf/Hydathode colour/*Brassica rapa*

Cours (1977)
The inheritance of non-pigmented hydathodes (probably due to the absence of anthocyanin) was studied in USDA introduction PI 175059. The trait was conditioned by a single recessive gene, designated *adh*.

Leaf/Lobe number/*Brassica rapa*

Song *et al.* (1995)
The segregation of 220 RFLP loci and the variation for a number of traits were studied in 95 F_2 plants derived from a cross between Chinese cabbage [= subsp. *pekinensis*] cv. Michihili x spring broccoli (*B. rapa* subsp. *utilis*). Zero to five quantitative trait loci were detected for each of 28 traits. Unequal gene effects on the expression of many traits were observed. Petiole length was positively correlated with petiole thickness (r = 0.76) and number of leaf lobes (r = 0.89), and negatively correlated with lamina width (r = -0.66) and petiole width (r = -0.49). Days to flower was positively correlated with days to bud (r = 0.62) and days from bud to flower. Pubescence was controlled by a dominant allele at one locus, designated *Pub*; the degree of pubescence was controlled by polygenes. The number of leaf lobes was controlled by a dominant allele at one locus, designated *Lob*. Locus *Lob* seemed to have a large effect on petiole and lamina length.

Leaf/Necrosis/*Brassica oleracea*

Pound and Walker (1953)
Leaf necrosis (spotting) in cabbage [= var. *capitata*] was found to be recessive and conditioned by a number of genes. Petiole necrosis was also recessive, but appeared to be controlled by a different set of genes.

Nieuwhof and Wiering (1962)
Cabbage [= var. *capitata*] leaf necrosis is characterized by black, sunken, circular to oval necrotic spots on the upper and lower surfaces of leaves appearing during storage. The inheritance of leaf necrosis in cabbage cv. Langedijker Storage Red was conditioned by an incompletely recessive gene, designated *n*. The action of minor genes was postulated. Genotypes were *NN* (healthy heads), *Nn* (weak symptoms in the second half of the storage period), and *nn* (necrotic heads early in the storage period).

Leaf/Number/*Brassica napus*

Lefort-Buson and Dattée (1982a)
140 F_1 hybrids of winter oilseed rape [= subsp. *oleifera*] (reciprocal and direct combinations) were evaluated for yield, yield components (number of siliques, number of siliques per branch, number of seeds per silique, 1,000 seed weight), and morphological traits (plant height and leaf number at rosette stage, plant height and branch number at maturity). Heterosis for seed yield averaged 11% in one year, 23.5% in the second year, on the basis of the mid-parent value. Heterosis for yield components number of siliques and seeds per silique was significant in one year. There was heterosis for plant height throughout development. The highest heterosis was for dry matter at rosette stage (18% over mean parent) and at the beginning of flowering. Significant reciprocal effects were shown for flowering date, height and leaf canopy at beginning of flowering, and density at maturity. The following traits were highly correlated: total yield and yield of secondary branches, secondary branch yield and mean number of siliques per secondary branch. 1,000 seed weight was negatively correlated to the number of seeds per silique.

Lefort-Buson and Dattée (1982b)
Twenty-five winter rape [= subsp. *oleifera*] inbred lines were crossed in an incomplete diallel design and assessed for general (GCA) and specific combining ability (SCA), general (MRE) and specific reciprocal effects (SRE) of several traits. Additive gene action was identified for leaf number at rosette stage, lodging susceptibility, leaf canopy and density at maturity. MRE were significant for plant height at the beginning of flowering, earliness, leaf canopy, and density at maturity. Total yield fitted an additive symmetrical model. Heritability of plot yield was intermediate (0.32). Yield and yield components on the main branch of individual plants showed average to high heritability (0.32 to 0.60). For individual plants, the variability of main branch yield was due to GCA effects. Correlation between GCA of plot leaf canopy and of plot seed yield was high (0.79). The genetic correlations between GCA of plant silique number and of plant seed yield and GCA of plant seed number per silique and of plant seed yield were significant.

Ringdahl *et al.* (1986)
The inheritance of earliness (days to bud, days to first flower, and days to maturity), plant height, and leaf number was studied in crosses between dwarf early line D-001, derived from intergeneric crosses with sand rocket [= *Diplotaxis muralis*], and oilseed rape [= *Brassica napus* subsp. *oleifera*] cvs. Regent and Pivot. Plants of P_1, P_2, F_1, F_2, BC_1, and BC_2 generations for both crosses were grown in a completely randomized design at two locations in Manitoba, Canada, in 1984. Additive gene action predominated for all traits for both crosses and both locations. In addition, dominance gene action was found to influence days to first flower, days to maturity, and leaf number for the D-001 x Regent cross and all traits for the D-001 x Pivot cross. Nonallelic interactions were nonsignificant in all cases. Genotype x environment interactions were significant only for plant height. Broad-sense heritabilities for phenological traits ranged from 55 to 90%, while narrow-sense heritabilities ranged from 0 to 81%. For plant height, broad- and narrow-sense heritability estimates were equal and ranged from 51 to 84%. Heritability for leaf number ranged from 73 to 82% for broad-sense and from 49 to 77% for narrow-sense estimates.

Paul (1992a)
See Morphological traits/Leaf/Area/*Brassica napus*.

Leaf/Number/*Brassica oleracea*

Pal and Swarup (1966)
The inheritance of number of leaves, leaf size index, plot yield, and number of marketable curds was studied in 14 crosses of cauliflower [= var. *botrytis*] lines described by Swarup and Pal (1966). Dominance and epistasis, particularly dominance x dominance, played a major role in the inheritance of the traits. Heterosis over the better parent was observed for leaf number, leaf size index and plot yield. There was no significant heterosis for number of marketable curds.

Johnston (1968)
Diallel crosses were made between two inbred lines each of marrowstem kale [= var. *acephala*], thousand-headed kale [= var. *fruticosa*], and Scotch curled kale, and one line each of Chou Fourrager Jaune, Brussels sprouts [= var. *gemmifera*], and cabbage [= var. *capitata*] cv. January King. Analysis of the F_1s indicated highly significant general combining ability for all yield components (total yield, leaf yield, leaf weight, number of leaves, and stem yield). Specific combining ability was also significant for all traits but at a lower level. Heterosis was observed for leaf yield.

Keyes and Honma (1986)
Examination of F_2 distribution from crosses between broccoli [= var. *italica*] plants with high (22) and low (16) leaf numbers suggested dominance for low leaf number, with two major genes and modifiers. The F_2 data fitted a 13:3 recessive supressor gene model.

Leaf/Number/*Brassica rapa*

Tan *et al.* (1982)
See Morphological traits/Head/Diameter/*Brassica rapa*.

Leaf/Number/*Raphanus sativus*

Prasad and Prasad (1978)
Heritability values of agronomic traits were based on a trial of 14 radish cultivars. Moderate to high heritability values were observed for leaf width and number of leaves per plant (50 to 56%), percent germination, leaf length and root weight loss during storage (81 to 85%), top fresh weight, and root length, diameter, weight, yield, and storage weight (>90%), and leaf dry matter (99.5%).

Pandey *et al.* (1981)
The inheritance of root yield per plot and root yield components (root length, root width, root weight, plant height, number of leaves, and root top ratio) was determined from the results of a 6 x 6 diallel cross with six radish lines (Pusa Chetki, Kalyanpur T-I, H.R.I., Jaunpuri, Kashmiri Local Round, and Japanese White). Overdominance was observed for all traits. The dominant components H_1 and H_2 were greater than the additive component (D) for all traits.

Leaf/Petiolate/*Brassica oleracea*

Pease (1926)
In crosses between cabbage [= var. *capitata*] x kohlrabi [= var. *gongylodes*], the petiolate leaf of the kohlrabi was dominant over the sessile leaf of the cabbage. The trait was controlled by a single gene, designated *P* [= *Pet* in Yarnell, 1956].

Leaf/Shape/*Brassica juncea*

Singh (1961a)
The inheritance of a cupped leaf trait (leaf margins rolled towards the midrib on the upper surface) in rai [= *B. juncea*] was investigated in a cross between a cupped leaf mutant x a normal rai cultivar, Laha 101. The leaves of F_1 plants had a leaf shape intermediate between flat and cupped. F_2 and F_3 plants were classified as having either normal leaves or cupped leaves. On the basis of the F_2 and F_3 segregation ratios, the trait was found to be controlled by three genes.

Pokhriyal *et al.* (1964)
Normal leaf type was dominant over a deeply laciniate leaf type observed in a rai mutant. The trait was controlled by a single gene.

A “cuppish leaf” mutant (leathery, round leaf with a central depression) was controlled by two recessive genes.

Singh *et al.* (1964)
A mutant with leaves with marked wavy margins and a number of folds was recovered in rai. The trait was controlled by a single dominant gene.

Singh *et al.* (1968)
The segregation ratios of F_1, F_2, and BC generations of crosses between Indian mustard line 257(curly leaves) x lines 259 and 260 (wild-type leaves) were consistent with a monogenic model of inheritance, with the trait curly leaf being dominant to wild-type leaf.

The segregation ratios of F_1, F_2, and BC generations of crosses between Indian mustard line 257(laciniate leaves) x line 261 (entire leaves) were consistent with a monogenic model of inheritance, with the entire leaf edges being dominant over laciniate leaf edges.

Chen and Tong (1985)
See Morphological traits/Leaf/Colour/Purple pigmentation/*Brassica juncea*.

Leaf/Shape/*Brassica napus*

Hallqvist (1916)
The F_2 segregation ratios of a cross between rutabaga [= subsp. *rapifera*] genotypes ‘Blanc hâtif à feuille entière’ (entire leaf) x Bangholm (cut leaf) were consistent with a digenic model of inheritance, with the trait entire leaf being dominant to cut leaf.

Schulz (1961)
A curly leaf mutation in winter oilseed rape [= subsp. *oleifera*] was conditioned by a single dominant gene.

Salam and Downey (1978)
F_2 and BCF_1 segregation ratios for leaf margin and pubescence in an interspecific cross between oilseed rape [= *Brassica napus* subsp. *oleifera*] cv. Bronowski (non-dissected basal stem leaves, serrated upper stem leaf margins, glabrous young stem and leaf surface) and turnip rape [= *Brassica rapa* subsp. *oleifera*] cv. Polish [(dissected basal stem leaves, entire upper stem leaf margins, pubescent young stem and leaf surface) were consistent with monogenic inheritance for dissected vs. non-dissected basal stem leaves, pubescent vs. glabrous leaves, and serrated vs. entire upper stem leaves. The genes were unlinked.

Klein Geltink (1983)
In the crosses between oilseed rape [= subsp. *oleifera*] cv. Lonto (entire leaves) x cvs. Liragold and Orma (cut leaves), F_1 plants had a leaf shape somewhat close to that of the entire leaf parent. F_2 progenies of both crosses segregated in a 3:1 ratio of plants with entire leaves to plants with cut leaves, indicating a single dominant gene. Because of the phenotype of the F_1 progeny, it was concluded that the gene for entire leaves was incompletely dominant. The genotypes for the cultivars were postulated as being $E_1E_1e_2e_2$ or $e_1e_1E_2E_2$ for cv. Lonto, and $e_1e_1e_2e_2$ for cvs. Liragold and Orma.

Leaf/Shape/*Brassica oleracea*

Pease (1926)
In crosses between cabbage [= var. *capitata*] x kohlrabi [= var. *gongylodes*], the entire leaf of the cabbage was dominant over the lyrate leaf of the kohlrabi. The trait was controlled by a single gene, designated *E*, superseded by symbol *En* (Yarnell, 1956). The presence of leaf protuberances ("asparagodes" phenotype) in cabbage was determined to be under the control of a dominant or partially dominant gene, designated *A*. Symbol *A* was superseded by symbol *As* (Yarnell, 1956).

Kwan (1934)
Inheritance studies of anthocyanins in a cabbage [= var. *capitata*] cross between a deep purple strain of cabbage x a sun-red strain indicated two duplicate genes (F_2 segregation: 15 deep purple plants: 1 sun-red plant), designated R_1 and R_2. The F_2 segregation ratio for a cross between a purple strain x a green strain was consistent with two genes with recessive epistasis (9 purple: 3 sun red: 4 green plants); the genes were designated *G* for pigment production and *H* for purple (genotype of sun-red plants: *G_hh*). Wrinkled foliage was controlled by two complementary genes, designated *W* and *S*. Plant height and head weight were controlled by several genes.

Wills and Smith (1972)
See Morphological traits/Anther/Tip colour/*Brassica oleracea*.

Wills and Smith (1975)
Linkage was reported in *B. oleracea* between genes *Fn* (fern-leaf) and *le* (leaf excrescence).

Leaf/Shape/*Brassica rapa*

Ragionieri (1920)
In reciprocal crosses between Pe-tsai [= subsp. *pekinensis*] x white turnip [= subsp. *rapifera*], a single recessive gene controlled the expression of entire leaves.

Brune (1949a)
The trait “entire leaf” was dominant over “cut leaf” and conditioned by two or three genes.

Singh (1955)
A plant with leaves whose shape differed significantly from that of normal leaves (lyrate) was isolated in a cultivar of yellow sarson [= subsp. *trilocularis*]. The leaves had a small terminal lobe with an acute apex; lobes in the distal part of the leaf formed an angle with the midrib instead of being perpendicular to it; and the sinuses between the proximal lobes did not reach the midrib. Crosses between plants with lyrate leaves x plants with mutant leaves were made. The leaf shape of the F_1 plants was intermediate to that of the parents.

Shibutani and Okamura (1957)
The F_1 generation of crosses between turnips [= subsp. *rapifera*] with deeply dissected leaves vs. entire or shallowly dissected leaves had intermediate leaf shapes. No F_2 segregation ratios were provided.

Brar *et al.* (1969)
The inheritance of root skin colour, root shape, and leaf shape was investigated in turnips [= subsp. *rapifera*]. Root colour in the crosses cv. Purple White Top Globe (purple rooted) x Desi Red (red rooted) and cv. Purple White Top Globe (purple rooted) x cv. Desi White (white rooted) was conditioned by two genes, designated *R* (red colour) and *P* (purple colour). Root shape in the cross cv. Purple White Top Globe (round) x cv. Desi White (flat) was conditioned by a single incompletely dominant gene, designated *F*. Leaf shape in the cross cv. Purple White Top Globe (compound leaf) x cv. Desi White (simple leaf) was conditioned by a single dominant gene, designated *C*, for compound leaf. Genes for root colour and leaf shape were linked (recombination frequency: 46.3%).

Cours (1977)
The inheritance of puckered leaves (leaf surface with numerous interveinal concave depressions) was studied in progeny of a cross between USDA introduction PI 175054 x open-pollinated plants of genetic stock 3277-1 (G.R. Stringam, University of Alberta, Canada). The trait was conditioned by a single recessive gene, designated *pkl*.

Stringam (1977)
A mutant with entire leaves was recovered among seed of yellow sarson [= subsp. *trilocularis*] treated with ethylene imine. The trait was controlled by a monogenic recessive gene, designated *en*. Gene *en* was tightly linked to gene *a-2* and loosely linked to gene *yg-7*.

Salam and Downey (1978)
See Morphological traits/Leaf/Shape/*Brassica napus*.

Klein Geltink (1983)
In the crosses between turnip rape [= subsp. *oleifera*] cv. Goldwalze (entire leaves) x cvs. Krasnaja Samarkandskaja and Tsutsui (cut leaves), and in crosses between cv. Teutonengold x KL 1 (entire

leaves) and cv. Krasnaja Samarkandskaja (cut leaf), the F_1 plants had entire leaves. F_2 progenies segregated in a 3:1 ratio of plants with entire leaves to plants with cut leaves, indicating a single dominant gene. In the cross KL 1 x cv. Krasnaja Samarkandskaja, a digenic inheritance was obtained for the F_2 population, *i.e.* 15:1 plants with entire leaves to plants with cut leaves. The genotypes for the cultivars were postulated as being $E_1E_1e_2\ e_2$ or $e_1e_1E_2\ E_2$ for cvs. Goldwalze and Teutonengold, $E_1E_1E_2e_2$ or $E_1e_1E_2E_2$ for cv. KL1, and $e_1e_1e_2e_2$ for cvs. Tsutsui and Krasnaja Samarkandskaja.

Leaf/Shape/*Raphanus sativus*

Makarova and Ivanova (1983)
Lyrate leaves were dominant over entire leaves. F_1 hybrids uniformly produced lyrate leaves; the 3:1 ratio of lyrate to entire leaves in the F_2 generation indicated monogenic inheritance.

Leaf/Size/*Brassica juncea*

Singh *et al.* (1968)
The segregation ratios of F_1, F_2, and BC generations of crosses between Indian mustard lines 259 (small leaves) x 260 (large leaves) were consistent with a monogenic model of inheritance, with large leaf being dominant to small leaf.

Chaudhary and Sharma (1982)
Two distinct parental lines and their F_1, F_2, and F_3 generations were evaluated for days to flower, leaf length, number of primary branches per plant, plant height, length of the main fruiting branch, silique length and diameter, and number of seeds per silique. Significant positive heterosis was shown for days to flower, number of primary branches per plant, and plant height; significant negative heterosis was shown for length of main fruiting branch and silique length. High heritability was shown for days to flower, leaf length, number of primary branches per plant, plant height, length of main fruiting branches, and silique length. Dominant gene action was indicated for leaf length, number of primary branches per plant, plant height, and length of main fruiting branch. Additive gene effects made a significant contribution to days to flower as well as to plant height, and length of main fruiting branches.

Mehan and Labana (1983)
The inheritance of leaf length and width was studied in an eight parent diallel set of crosses. Leaf length was measured on the fourth leaf of each plant. A model with six parameters was adopted. The additive component was significant in 17 cross combinations; dominance effects were significant in 13 crosses. Duplicate type of non-allelic interaction was shown in 16 crosses; two crosses showed complementary epistasis.

Leaf/Size/*Brassica napus*

Paul (1992a)
See Morphological traits/Leaf/Area/*Brassica napus*.

Leaf/Size/*Brassica oleracea*

Pease (1926)
In crosses between cabbage [= var. *capitata*] x kohlrabi [= var. *gongylodes*], the broad leaf of the cabbage was dominant over the narrow leaf of the kohlrabi. The trait was controlled by a single gene, designated *W*.

Pal and Swarup (1966)
See Morphological traits/Leaf/Number/*Brassica oleracea*.

Leaf/Size/*Brassica rapa*

Song *et al.* (1995)
See Morphological traits/Leaf/Lobe number/*Brassica rapa*.

Leaf/Size/*Raphanus raphanistrum*

Conner and Via (1993)
See Morphological traits/Anther/Filament length/*Raphanus raphanistrum*.

Leaf/Size/*Raphanus sativus*

Prasad and Prasad (1978)
See Morphological traits/Leaf/Number/*Raphanus sativus*.

Leaf/Trichomes/Number/*Brassica rapa*

Ågren and Schemske (1992)
See Morphological traits/Flower/Number/*Brassica rapa*.

Ågren and Schemske (1994)
See Morphological traits/Flower/Number/*Brassica rapa*.

Leaf/Trichomes/Pubescence/glabrous/*Brassica bourgeaui*

Kianian and Quiros (1992a)
The presence of leaf pubescence was dominant in interspecific crosses between glabrous species *Brassica oleracea*, wild kale, kohlrabi [= *Brassica oleracea* var. *gongylodes*], broccoli [= *Brassica oleracea* var. *italica*], Chinese kale [= *Brassica oleracea* var. *alboglabra*], and *Brassica bourgeaui* x pubescent species *Brassica incana*. Segregation for this characteristic in F_2 populations was polygenic.

Leaf/Trichomes/Pubescence/glabrous/*Brassica incana*

Kianian and Quiros (1992a)
See Morphological traits/Leaf/Trichomes/Pubescence/glabrous/*Brassica bourgeaui*.

Leaf/Trichomes/Pubescence/glabrous/*Brassica juncea*

Singh (1958)
Hairiness was dominant over glabrousness in Indian mustard and controlled by a single gene.

Pokhriyal *et al.* (1964)
The inheritance of leaf and stem pubescence was studied in crosses between rai genotypes Cream Rye (glabrous) x T_3E_4-1 (pubescent). The F_1 plants were pubescent. The F_2 segregation ratios were consistent with pubescence being governed by two complementary genes. There was variation in the number of trichomes, indicating the presence of minor genes.

Singh *et al.* (1968)
The segregation ratios of F_1, F_2, and BC generations of crosses between Indian mustard line 257(glabrous leaves) x line 259 (pubescent leaves) were consistent with a monogenic model of inheritance, with the trait pubescent leaf being dominant over the trait glabrous leaf.

Dixit and Singh (1973)
F_2 and BC segregation ratios of crosses between pubescent and glabrous rai [= *B. juncea*] accessions were consistent with two independent genes with dominance for pubescence.

Leaf/Trichomes/Pubescence/glabrous/*Brassica napus*

Salam and Downey (1978)
See Morphological traits/Leaf/Shape/*Brassica napus*.

Leaf/Trichomes/Pubescence/glabrous/*Brassica oleracea*

Thompson (1956)
Hairiness of the first leaf was found to be dominant in marrowstem kale [= var. *acephala*].

Sampson (1967b)
A gene for hairy first leaf margins from curly kale, designated *Hr-1*, was found to be linked with gene *pg-2* for pale green seedlings. Recombination frequency between the genes averaged 13.15 ± 0.68%. Gene *Hr-1* was unlinked to genes *Wh* (white petals), *gl -1* (glossy foliage), *ps* (persistent petals), *cr* (cream petals), A^{ck} (purple stems and ovaries), *ms-1* and *ms-4* (male sterility), and *pg-1* (pale green seedling).

Wills and Smith (1972)
See Morphological traits/Anther/Tip colour/*Brassica oleracea*.

Wills and Smith (1974)
See Morphological traits/Cotyledon/Number (polycotyledony)/*Brassica oleracea*.

Sampson (1978b)
A dominant gene for heavy pubescence, designated *Hr-2*, from curly kale [= var. *acephala*] acted in an additive manner with gene *Hr-1* (hairy leaf margins) to produce relatively long hairs on leaves, petioles and stems. Linkage (group 4) with 39.9 ± 0.7% recombination between the two genes was tentatively proposed. Incomplete penetrance of *Hr-2* in an *hr-1hr-1* background was also considered. Gene *Hr-2* was linked to gene *le* (leaf excrescence) with 10.4 ± 0.6% recombination.

Kianian and Quiros (1992a)
See Morphological traits/Leaf/Trichomes/Pubescence/glabrous/*Brassica bourgeaui*.

Leaf/Trichomes/Pubescence/glabrous/*Brassica rapa*

Mohammad and Sikka (1937)
Pubescence was dominant over glabrousness with a 3:1 ratio, indicating single gene control.

Mohammad *et al.* (1942)
Hairiness was found to be inherited independently from reddish brown seed coat colour (gene Br_2) in a cross between strain C. 19 (red brown-seeded, hairy) x strain L. 5 (yellow-seeded, glabrous). Hairiness was controlled by a single, dominant gene, designated *H*.

Shibutani and Okamura (1957)
The F_1 generation of crosses between turnips [= subsp. *rapifera*] with pubescent vs. glabrous leaves showed dominance of pubescent over glabrous leaves. No F_2 segregation ratios were provided.

Salam and Downey (1978)
See Morphological traits/Leaf/Shape/*Brassica napus*.

Teutonico and Osborn (1994)
Each of the traits yellow seed coat colour, low erucic acid content, and leaf pubescence mapped to a single locus on three different linkage groups on a RFLP linkage map constructed for turnip rape [= subsp. *oleifera*] using anonymous genomic DNA and cDNA clones from *Brassica* species and *Arabidopsis thaliana*.

Song *et al.* (1995)
See Morphological traits/Leaf/Lobe number/*Brassica rapa*.

Leaf/Trichomes/Pubescence/glabrous/*Crambe abyssinica*

Meier and Lessman (1973a)
Reciprocal interspecific crosses were made between USDA Plant Introductions of glabrous *Crambe abyssinica* (PI 247310) and pubescent *Crambe hispanica* (PI 279346). F_1 seedlings were glabrous, although the glabrous allele was not completely dominant in the heterozygous condition, as some of the F_1 seedlings had hairs along the edge and tip of older leaves. Segregation analyses of

6,229 F_2 seedlings indicated a 3:1 ratio (4,712 glabrous: 1,517 pubescent). Leaf pubescence was under the control of a single, recessive gene, designated *p*, with diploid inheritance.

Leaf/Trichomes/Pubescence/glabrous/*Crambe hispanica*

Meier and Lessman (1973a)
See Leaf/Trichomes/Pubescence/glabrous/*Crambe abyssinica*.

Beck *et al.* (1975)
The inheritance of glabrous vs. pubescent leaf type in *Crambe hispanica* USDA Plant Introduction PI 279346 was studied. Two glabrous genotypes were found in this normally pubescent accession. One genotype segregated with respect to leaf type and a second one produced all glabrous leaves. Six individuals from the former plant were self-pollinated. Selected plants were paired randomly with other *C. hispanica* types and crossed reciprocally. Combined segregation ratios in 44 F_2 families involving 4,004 seedlings (3,037 glabrous: 967 pubescent) indicated that the glabrous trait was controlled by a single gene, *P*. Plants with glabrous leaves were postulated to have the dominant allele *P* and plants with pubescent leaves, the recessive allele *p*.

Results were verified in 155 F_3 generation populations (derived from selfing of randomly selected glabrous F_2 plants) which fitted the expected 1:2 ratio (54:101); all 44 pubescent F_2s produced pubescent F_3s.

Leaf/Trichomes/Pubescence/glabrous/*Raphanus sativus*

Madzharova (1975)
F_1 hybrids between radish cv. Perla, with glabrous leaves and white roots, and six other cultivars, with hairy tops and red roots, showed dominance of hairy over the glabrous leaf blade, with red colour, large size and firmness of roots dominant over the white colour. The F_2 segregated into a nearly 3:1 ratio of hairy to glabrous progeny. In all cases plants with glabrous leaves had white roots. Crosses between white-root cultivars with hairy and glabrous leaves gave F_1 plants producing violet roots and F_2 plants producing white roots and glabrous leaves, suggesting complementary action of two allelomorphic pairs *AA* and *BB*.

Bonnet (1979)
The F_1, F_2, and BC_1 generations of a cross between cv. Biser round white radish, with glabrous leaves and yellow seeds [also studied in Madzharova (1975)] and a line of round radish which was red and white, with hairy leaves and brown seeds were studied. The traits red root and hairy leaf showed complete linkage as in Madzharova (1975), and were also linked to stem and seed coat colour. Segregation data suggested a simple monogenic dominant determinism for the group of traits (red root, hairy leaf, red stem, brown seed). F_1 plants had a red root with small white tip; the F_2 and BC_1 plants had only two classes: white and red with small white tip.

Leaf/Waxiness (glossy)/*Brassica carinata*

Jambhulkar and Raut (1995)
Waxy leaves were observed in synthesized *B. carinata*. True breeding lines for waxy vs. glossy leaves were crossed reciprocally. F_1 progeny showed intermediate expression, while F_2 segregation showed a 1:2:1 ratio (72:155:76 progeny), confirming monogenic inheritance with incomplete dominance.

Leaf/Waxiness (glossy)/*Brassica incana*

Kianian and Quiros (1992a)
An interspecific cross was made between a kohlrabi [= *Brassica oleracea* var. *gongylodes*] cultivar with glossy foliage and *Brassica incana* (waxy). Glossy foliage was dominant in the F_1 progeny; the segregating F_2 progeny best fitted a dihybrid ratio with complementary gene action.

Leaf/Waxiness (glossy)/*Brassica juncea*

Yadav *et al.* (1985)
Segregation data of crosses between glossy mutant RC-1425 x wild-type cv. Prakash were consistent with the action of a single recessive gene.

Angadi *et al.* (1987)
The inheritance of a glossy mutation in Indian mustard was studied in crosses between waxy cultivars T-6342, RLM-514, Seeta, PR-18 and TM-7 x a glossy mutant of cultivar B-85. F_2 and BC segregation ratios were consistent with a single dominant gene for glossiness, designated *Wl*.

Leaf/Waxiness (glossy)/*Brassica napus*

Thompson (1972)
Winter rape crosses in which cv. Bronowski [= subsp. *oleifera*] was the male parent showed a high proportion of male sterile plants in the F_2 generation. The male sterile plants were homozygous for a recessive allele *rf*; pollen fertile plants were *RfRf* or *Rfrf*, with a single locus determining pollen sterility or fertility. Cultivar Bronowski therefore had a fertile cytoplasm (F) for pollen fertility and a nuclear genome *rfrf*. The female parental lines had a male sterile cytoplasm (S) and a nuclear genome *RfRf*. The expression of male sterility was modified by other factors including environment. Spring rape crosses with cv. Bronowski as the male parent segregated for pollen sterility and fertility and for a glossy leaf trait which showed incomplete dominance. Plants homozygous for the glossy leaf gene *GG* had glossy leaves and stems in the field and could be distinguished from the heterozygote *Gg*. The proportion of *Gg* to *gg* plants in the F_2 fitted a 2:1 ratio with a deficiency of *GG* plants which supported a semi-lethal effect of the homozygous *GG* plants after fertilization. There was a strong association between glossy leaves and male fertility, non-glossy and male sterility, supporting linkage of allele *g* with allele *rf*, with a low recombination frequency.

Heyn (1977)
Two genes were described. Gene Gl_D was postulated for a glossy trait (no wax on leaves, small amounts of wax on stems) that was dominant to wild-type waxy. The F_2 progeny segregated 3 glossy

plants to 1 waxy plant. Gene gl_R was postulated for a glossy trait that was recessive to wild-type waxy. The F_2 progeny segregated 15 waxy plants to 1 glossy plant (duplicate gene loci with dominance of both loci).

Mo *et al.* (1992)
A waxless mutant (waxless leaves, stems, etc.) was identified in a F_2 population derived from the cross (Canadian rape x Tower) F_3 x 82B031-3-3 [= subsp. *oleifera*]. The segregation ratios of the F_2 and BC_1 generations were 3:1 waxless to waxy plants, and 1:1 waxless to waxy plants, respectively, indicating a single dominant gene for waxlessness, designated *Wl*; the wild-type allele was designated *Nwl* (waxy).

Mo *et al.* (1995)
Reciprocal crosses were made between a waxless (low wax) line of oilseed rape [= subsp. *oleifera*] cv. Nilla and two wild-type cultivars of Chinese origin, Zhong You 821 and T9103 [= subsp. *oleifera*]. The waxless trait was found to be recessive. F_2 and BC segregation data were consistent with a digenic mode of inheritance.

Leaf/Waxiness (glossy)/*Brassica oleracea*

Anstey and Moore (1954)
Studies were made between a glossy (waxless) mutant of broccoli [= var. *italica*] cv. Italian Green Sprouting (accession Puyallup 123) x normal waxy plants. Segregation analyses of F_1 (all normal), F_2, F_3, and BC generations indicated that glossy foliage was controlled by a single recessive gene, designated *gl*.

Anstey (1955)
Studies demonstrated linkage between glossy gene *gl* and a white petal colour gene, *Wh* in broccoli [= var. *italica*].

North and Priestly (1962)
A waxless mutation in brussels sprouts [= var. *gemmifera*] cv. The Cluseed was controlled by a single recessive gene, which was assumed to be the same as gene *gl* described in var. *italica* by Anstey and Moore (1954).

Priestly and Wills (1966)
The inheritance of a waxless mutant found in collards [= var. *sabauda*] cv. Green Glaze was due to an incompletely dominant gene, *Go*.

Sampson (1966b)
The glossy foliage gene, *gl*, designated as *gl-1* in the present paper, was shown to be linked with the white petal gene *Wh*, with 23.8±1.5% recombination.

Priestly (1967)
The inheritance of a waxless trait in brussels sprouts [= var. *gemmifera*] cv. Irish Elegance was found to be controlled by a single recessive gene. Progeny of the cross between waxless genotypes of cv. Irish Elegance and cv. The Cluseed described by North and Priestly (1962) consisted of waxy plants only, indicating that the two recessive genes were non-allelic.

Wills and Smith (1972)
See Morphological traits/Anther/Tip colour/*Brassica oleracea*.

Wills and Smith (1973)
See Morphological traits/Anther/Tip colour/*Brassica oleracea*.

Wills and Smith (1974)
See Morphological traits/Cotyledon/Number (polycotyledony)/*Brassica oleracea*.

Tatlioglu (1989)
Genetic analysis of selfed progenies and reciprocal F_1, F_2, and BC_1 populations of crosses of a waxless mutant and three waxy kohlrabi [= var. *gongylodes*] plants indicated that waxlessness was controlled by two independent, recessive genes, *a* (glossy waxless) and *b* (dull waxless). To be able to form a wax layer, a plant required a dominant allele at both genes (*A_B_*).

Kianian and Quiros (1992a)
See Morphological traits/Leaf/Waxiness (glossy)/*Brassica incana*.

Leaf/Waxiness (glossy)/*Brassica rapa*

Singh (1954)
An inheritance study of a bloomless (waxless) mutant of yellow sarson [= subsp. *trilocularis*] indicated that the waxless trait was monogenic recessive. The gene was designated *b* (waxless plants).

Singh *et al.* (1969)
The inheritance of a bloomless (waxless) trait in self-fertile Varanasi toria [= *B. campestris* var. *sarson*] was controlled by a single recessive gene.

Stringam (1976)
The inheritance of two bloomless mutants derived from ethylene imine-treated seed of yellow sarson [= subsp. *trilocularis*] was examined in crosses with a wild-type genotype of yellow sarson. The mutants were also crossed to determine allelism. The trait was determined to be controlled by two single recessive genes, *b-2* and *b-3*.

Ovary colour/*Brassica oleracea*

Sampson (1967a)
See Morphological traits/Anther/Tip colour/*Brassica oleracea*.

Wills and Smith (1972)
See Morphological traits/Anther/Tip colour/*Brassica oleracea*.

Ovule number/*Raphanus raphanistrum*

Mazer (1987)
A half-sib breeding design was used to estimate paternal genetic effects on, or when possible, narrow-sense heritability of, quantitative traits influencing male reproductive success in wild radish. In all cases, differences among maternal plants in the proportion of ovules fertilized, early ovule growth, number of seeds per silique, and mean individual seed weight per silique far exceeded differences among pollen donors. There was no significant additive genetic variance in male performance with respect to these traits.

Mazer and Schick (1991)
The effects of planting density on phenotype and heritability estimates for parameters for life-history and floral traits were examined in wild radish. Phenotypic correlations and estimated narrow-sense and broad-sense heritabilities were made for the traits days to germination, days to flowering, petal area, ovule number/flower, pollen production/ flower, and modal pollen grain volume. The results indicated that seeds in high-density plots germinated significantly faster than seeds sown in medium- or low-density plots, but the plants flowered significantly later. Fewer ovules per flower were found in plants in high-density plots than in medium- and low-density plots. There were no significant differences between petal area and pollen traits among planting densities. Analysis of variance to detect additive genetic variance of each trait in each planting density revealed significant paternal effects on days to flowering and modal pollen grain volume at low density; the traits days to germination, days to flowering, and ovule number/flower exhibited significant paternal effects in medium-density plots; only modal pollen grain volume differed among paternal sibships in high-density plots. Narrow-sense heritability estimates for days to germination, days to flowering, ovule number/flower, and modal pollen grain volume differed markedly among planting density treatments.

Petal/Colour/Bicoloured/*Brassica rapa*

Pandey and Singh (1971)
A plant with bicoloured petals (the proximal part of the petal was light yellow while the distal part of the petal was white) was identified in a brown sarson accession [= var. *dichotoma*]. The trait was true-breeding. F_1 plants from crosses between the variant and wild-type plants had yellow petals. F_2 and BC_1 segregation ratios indicated a monogenic recessive inheritance.

Cours (1977)
The inheritance of striped petals (cream petals with a yellow stripe down the middle) was studied in a genotype of *B. rapa*. The trait was maternally inherited. The gene for striped petals was designated *sp.*

Petal/Colour/Cream/*Brassica carinata*

Getinet *et al.* (1993)
Reciprocal crosses were made between line PGRC/Ethiopia 21224 (cream petals) and true-breeding yellow-petalled line Awassa selection 67 to produce F_1, F_2, and BC_1 generations. All F_1 reciprocal hybrids (151 hybrids) and backcrosses to the yellow-petalled parent (1,195 plants) had yellow petals, indicating dominance of yellow over cream. Backcrosses to the cream-petalled parent segregated in

a 1:1 ratio (418 yellow: 398 cream). The F_2 generation segregated in a 3:1 ratio (349 yellow: 135 cream), indicating monogenic control, with the yellow petal allele dominant over the recessive cream petal allele.

Petal/Colour/Cream/*Brassica juncea*

Sun (1945)
The inheritance of a cream-petalled genotype was reported to be conditioned by two genes, designated Y_1 and Y_2.

Singh *et al.* (1964)
A mutant with light cream petals was identified in a rai genotype. The trait was recessive to yellow and controlled by two genes, designated Y_1 and Y_2, Y_1 being epistatic to Y_2.

Bhuiyan (1986)
Segregation data of a cross between cv. Rai 5 (yellow petals) and line E 115-1 (creamy white petals) indicated that yellow colour was dominant and that the trait was controlled by two duplicate genes, designated Y_1 and Y_2.

Petal/Colour/Cream/*Brassica napus*

Morice (1960)
Monohybrid segregations were obtained in crosses between plants of oilseed rape [= subsp. *oleifera*] with lemon-yellow petals (wild-type) x plants with orange petals, and plants with lemon-yellow petals x plants with pale yellow petals. The results confirmed those reported by Sylvén (1927). The inheritance of cream petal colour was studied in crosses with plants bearing petals that were lemon-yellow, pale yellow, orange, and pale orange. Postulated genotypes were *A_B_C_* (lemon-yellow), *A_bbC_* (orange), *aaB_C_* (pale yellow), *aabbC_* (pale orange), and *aaB_ cc* (cream).

Heyn (1977)
Cream petals were found to be recessive to yellow petals. All F_1 plants had yellow petals.

Petal/Colour/Cream/*Brassica oleracea*

Anstey and Moore (1954)
Studies were made between a cream-petalled mutant from broccoli [= var. *italica*] cv. De Cicco Italian Green Sprouting (accession Puyallup 145) x normal yellow-petalled plants. Segregation analyses of F_1 (all normal), F_2, and BC generations indicated that cream petal colour was controlled by a single recessive gene, designated *cr*.

Sampson (1966b)
The cream petal gene *cr* was determined to be linked to gene *pg-1*, a gene for pale green foliage in broccoli [= var. *italica*].

Petal/Colour/Cream/*Brassica rapa*

Cours (1977)
The inheritance of cream petals was studied in USDA introduction PI 175054. Segregation ratios were consistent with monogenic inheritance and a recessive allele, designated *cr.* Allele *cr* was found to be epistatic to alleles *ly* (light yellow petals), *dy* (dark yellow petals), and *o* (pale orange petals).

James and Williams (1980)
The inheritance of the trait "cream corolla" observed in a *B. campestris* strain derived from USDA PI 175054 was found to be monogenic. The trait was conditioned by a recessive allele, designated *cr*. Linkage studies between *cr* and genes *Pb2* and *Pb3* (clubroot resistance to race 6) provided no evidence for linkage.

Orakwue and Crowder (1983)
Variegated mutants were identified in self-progenies of normal *B. campestris* or in natural populations in the *B. campestris* genetics program at the Department of Plant Breeding, Cornell University, Ithaca, U.S.A. The variegation (white and pinkish-purple on the foliage, stems, and siliques) was most evident at the peak of foliage development. The trait was recessive and linked to cream petal colour. Penetrance of the trait was complete, but its expressivity was variable.

Petal/Colour/Cream-yellow/*Brassica juncea*

Rawat and Anand (1986)
A mutant with cream-yellow petals was crossed reciprocally to yellow-petalled plants of cvs. Pusa Bold, Varuna, and RLM 198. The F_1 plants of all crosses had yellow petals. The F_2 segregation data indicated a two gene inheritance with dominant epistatic action (12:3:1). Postulated genotypes were *Y_ _ _* (yellow), *yyCr_* (cream-yellow), and *yycrcr* (white).

Petal/Colour/Cream-yellow/*Brassica napus*

Heyn (1977)
Cream-yellow petals were found to be recessive to yellow petals. All F_1 plants had yellow petals.

Petal/Colour/Dark yellow/*Brassica rapa*

Cours (1977)
The inheritance of dark yellow petals was studied in USDA introduction PI 175054. The trait required high light intensity for full expression. Segregation ratios were consistent with monogenic inheritance and a recessive gene, designated *dy.*

Petal/Colour/Lemon-yellow/*Brassica napus*

Sylvén (1927)
Monohybrid segregations were obtained in crosses between plants of oilseed rape [= subsp. *oleifera*] with lemon-yellow petals (wild-type) x plants with orange petals, and plants with lemon-yellow petals

(wild-type) x plants with pale yellow-petals. Postulated genotypes were *AABB* (lemon-yellow), *AAbb* (orange), *aaBB* (pale yellow), and *aabb* (pale orange).

Morice (1960)
See Morphological traits/Petal/Colour/Cream/*Brassica napus*.

Séguin-Swartz (1988)
The inheritance of light or pale petal colour in cv. Westar [= subsp. *oleifera*] was determined in reciprocal crosses between a doubled haploid line with pale yellow petals and a doubled haploid line with lemon-yellow petals (wild-type). F_1, F_2, and BC to pale yellow segregation data were consistent with monogenic inheritance, pale yellow being recessive to lemon-yellow.

Petal/Colour/Light yellow/*Brassica juncea*

Alam and Aziz (1954)
The inheritance of petal colour was investigated in several rai [= *B. juncea*], brown sarson [= *B. rapa* subsp. *dichotoma*], and yellow sarson [= *B. rapa* subsp. *trilocularis*] crosses. Yellow petals were dominant in F_1 progenies in both species. In the sarson crosses, petal colour was conditioned by two genes, designated Y_1 and Y_2, with recessive epistasis (F_2 ratio: 9 yellow: 3 light yellow: 4 white). In rai, petal colour was conditioned by two genes, designated Y_1 and Y_3, with dominant epistasis (F_2 ratio: 12 yellow: 3 light yellow: 1 white).

Singh (1958)
Yellow pigmentation of petals was due to the presence of two dominant genes Y_1 and Y_2. The genotypes were postulated as being $Y_1\_Y_2\_$ (yellow petals), $Y_1\_\ y_2y_2$ (light yellow petals), and $y_1y_1Y_2\_$ or $y_1y_1y_2y_2$ (white petals).

Petal/Colour/Light yellow/*Brassica rapa*

Alam and Aziz (1954)
See Morphological traits/Petal/Colour/Light yellow/*Brassica juncea*.

Cours (1977)
The inheritance of light yellow petals was studied in USDA introduction PI 175079. The trait required high light intensity for full expression. Segregation ratios were consistent with monogenic inheritance and a recessive gene, designated *ly.* Allele *ly* was epistatic to allele *dy* (dark yellow petals).

Petal/Colour/Light yellow/*Sinapis alba*

McGrath (1988)
F_2 segregation ratios of crosses between plants with light yellow (pale yellow) petals and plants with bright yellow petals (wild-type) indicated monogenic recessiveness for the pale yellow colour. The gene was designated *py*.

Petal/Colour/Ochre/*Brassica napus*

Heyn (1977)
Ochre petals were found to be recessive to yellow petals. All F_1 plants had yellow petals. The F_2 segregation of a cross between yellow-petalled plants and ochre-petalled plants was in most cases 15 yellow-petalled plants to 1 ochre-petalled plant, indicative of duplicate gene loci with dominance of both loci.

Petal/Colour/Orange/*Brassica napus*

Sylvén (1927)
See Morphological traits/Petal/Colour/Lemon-yellow/*Brassica napus*.

Morice (1960)
See Morphological traits/Petal/Colour/Cream/*Brassica napus*.

Heyn (1977)
Orange petals were found to be recessive to yellow petals. All F_1 plants had yellow petals. The F_2 segregation of a cross between yellow-petalled plants and orange-petalled plants was 15 yellow-petalled plants to 1 orange-petalled plant (duplicate gene loci with dominance of both loci) and 3 yellow-petalled plants to 1 orange-petalled plant (one single dominant gene for yellow colour).

Petal/Colour/Orange/*Brassica rapa*

Cours (1977)
The inheritance of orange (light orange) petals was studied in a yellow sarson [= subsp. *trilocularis*] genetic stock (G.R. Stringam, University of Alberta, Canada) treated with the mutagen ethyleneimine. Segregation ratios were consistent with monogenic inheritance and a recessive allele, designated *o.*

Petal/Colour/Pale orange/*Brassica napus*

Sylvén (1927)
See Morphological traits/Petal/Colour/Lemon-yellow/*Brassica napus*.

Morice (1960)
See Morphological traits/Petal/Colour/Cream/*Brassica napus*.

Petal/Colour/Pale yellow/*Brassica napus*

Sylvén (1927)
See Morphological traits/Petal/Colour/Lemon-yellow/*Brassica napus*.

Morice (1960)
See Morphological traits/Petal/Colour/Cream/*Brassica napus*.

Séguin-Swartz (1988)
See Morphological traits/Petal/Colour/Lemon-yellow/*Brassica napus*.

Petal/Colour/White/*Brassica carinata*

Jambhulkar and Raut (1995)
White flower colour was observed in synthesized *B. carinata*. True breeding lines for yellow vs. white flowers were crossed reciprocally. F_1 progeny showed intermediate expression, *i.e.* cream-colour, while F_2 segregation showed a 1:2:1 ratio (166:323:152 progeny), confirming monogenic inheritance with incomplete dominance.

Petal/Colour/White/*Brassica cretica*

Snogerup *et al.* (1990)
The inheritance of white petal colour was studied in interspecific crossing experiments. White-petalled populations of *Brassica cretica* subsp. *cretica*, *Brassica insularis*, *Brassica incana*, and Chinese kale [= *Brassica oleracea* var. *alboglabra*] were crossed with yellow-petalled populations of various taxa for a total of 72 crossing combinations. F_1 hybrids in crosses with *B. cretica* were intermediate in petal colour, while all F_1 plants of crosses with *B. insularis* and var. *alboglabra* were white-petalled. In general, gene(s) determining white petal colour were dominant to gene(s) for yellow petal colour.

White-petalled populations of different taxa were also crossed with each other in order to test for gene homology. Crossing combinations included *B. cretica* x *B. insularis*, *B. cretica* x *B. incana*, *B. cretica* x *B. oleracea* var. *alboglabra*, *B. insularis* x *B. incana*, *B. insularis* x *B. oleracea* var. *alboglabra*, and *B. insularis* x *B. insularis*. In all but one cross (*B. cretica* x *B. incana*), petals of F_1 plants were pure white. Different F_2 segregation patterns were observed. The three crosses with *B. cretica* segregated for white-petalled, intermediate, and yellow-petalled types. In the crosses between *B. insularis*, *B. incana*, and *B. oleracea* var. *alboglabra*, all F_2 plants had white petals. The data suggested that the gene(s) determining petal colour in *B. cretica* was (were) situated at a different locus compared to the other species.

Petal/Colour/White/*Brassica incana*

Snogerup *et al.* (1990)
See Morphological traits/Petal/Colour/White/*Brassica cretica*.

Petal/Colour/White/*Brassica insularis*

Snogerup *et al.* (1990)
See Morphological traits/Petal/Colour/White/*Brassica cretica*.

Petal/Colour/White/*Brassica juncea*

Sun (1945)
Digenic inheritance for the control of petal colour (yellow dominant) was observed. Double recessives had white petals. Postulated genotypes were $Y_1Y_1\_\_$ (yellow); $y_1y_1Y_2Y_2$ (light yellow), and $y_1y_1y_2y_2$ (white).

Sun (1946)
Digenic inheritance (12 yellow: 3 light yellow: 1 white) was described for the control of petal colour in Meitan da-yu-tsai [= *B. juncea* subsp. *gracilis*].

Alam and Aziz (1954)
See Morphological traits/Petal/Colour/Light yellow/*Brassica juncea*.

Anand and Mishra (1985)
A mutant with white petals and protruding stigmas was described. Reciprocal crosses between the mutant and the wild-type (yellow petals and non-protruding stigmas) indicated dominance of the yellow petal colour and non-protruding stigmas over white petal colour and protruding stigmas.

Brar *et al.* (1991)
Yellow-petalled Indian cvs. RH-30, Pusa Bold, Varuna, DIR-202 and PR-18 were crossed with white-petalled Indian cv. Rai B-85. F_1 plants in all crosses were yellow-petalled, indicating dominance of yellow over white. The F_2 segregation ratios (12:3:1) were consistent with control by two epistatic genes, designated Y_1 and Y_2, Y_1 being epistatic to Y_2.

Petal/Colour/White/*Brassica napus*

Heyn (1977)
A white-petalled trait introgressed from a *Raphanobrassica* hybrid by B.R. Stefansson, University of Manitoba, Canada, was found to be dominant over white and controlled by two genes with complementary gene action (F_2 segregation: 9 yellow-petalled plants: 7 white-petalled plants).

Chen and Jönsson (1987)
Monogenic dominance was described in crosses between a resynthesized *B. napus* and yellow-petaled oilseed rape [= subsp. *oleifera*] cvs. Topas and Global and line Sv28053. The resynthesized *B. napus* orginated from a cross between turnip rape [= subsp. *oleifera*] line Sv38301 (yellow petals) x line No4003 of *B. oleracea* var. *alboglabra* (white petals).

Chen *et al.* (1988a)
In a newly resynthesized *B. napus* rape form (*Brassica oleracea* var. *alboglabra* x *Brassica campestris* subsp. *oleifera*), the white petal trait of var. *alboglabra* was partially epistatic over the yellow petal of *B. campestris*.
Quazi (1988)
The inheritance of petal colour was investigated in a cross between F_4 generation plants of line OL418 (yellow-petalled), derived from an interspecific cross between oilseed rape [= *Brassica napus* subsp. *oleifera*] cv. Tower x kale [= *Brassica oleracea* var. *acephala*] cv. Rawara, and F_5 generation plants of line 15 (white petalled), derived from an interspecific cross between cv. Tower x broccoli [=

Brassica oleracea var. *italica*] line G1117B. The F_2 segregation ratios were consistent with a single dominant gene for white petal. The gene was found to segregate independently from a gene for coronal scales.

Chen and Heneen (1990)
Crosses were made between male fertility restored yellow-petalled lines Sv84-28053 and Sv02372 and white/pale-petalled resynthesized line No7076 containing a monogenic dominant white/pale petal gene from *Brassica oleracea* var. *alboglabra*. The segregation data indicated that white petal colour was dominant over yellow. Petal colour was inherited independently from male fertility restoration.

Crosses were also made between yellow-petalled line Sv84-28053 and yellow-petalled *Brassica rapa* yellow sarson line K-151 [= subsp. *trilocularis*]. The segregation data for the trigenomic (AAC) progeny indicated a monogenic dominant gene for white/pale petal colour and independent inheritance of petal colour and male fertility restoration. The following genotypes were postulated: $w_C w_C(S)Ms_A Ms_A ms_C ms_C$ or $w_C w_C(S)ms_A ms_A Ms_C Ms_C$ for line Sv84-28053, $w_C w_C(S)Ms_A Ms_A ms_C ms_C$ or $w_C w_C(S)\ ms_A ms_A Ms_C Ms_C$ for line Sv02372, $W_C W_C(N)ms_A ms_A ms_C ms_C$ for line No7076, and $w_C w_C(N)ms_A ms_A$ for line K-151.

Petal/Colour/White/*Brassica oleracea*

Pearson (1929)
Several white-petalled plants were identified in cabbage [= var. *capitata*]. White petal colour was controlled by one dominant gene, designated *Wh*.

Kakizaki (1930a)
Monogenic dominant inheritance was described for white petals in cabbage [= var. *capitata*].

Anstey (1955)
White petal colour found in broccoli [= var. *italica*] cv. Medium was controlled by one dominant gene, designated *W* [later referred to as *Wh* by Sampson (1966a)]. Gene *W* was linked to gene *gl* (glossy foliage).

Sampson (1966b)
The linkage between the white petal gene *Wh* and the glossy foliage gene *gl* in broccoli [= var. *italica*], designated as *gl-1* in the present paper, was confirmed (23.8±1.5% recombination).

Wills and Smith (1972)
See Morphological traits/Anther/Tip colour/*Brassica oleracea*.

Snogerup *et al.* (1990)
See Morphological traits/Petal/Colour/White/*Brassica cretica*.

Kianian and Quiros (1992a)
Segregation ratios in a F_2 population (45:15 plants) derived from reciprocal F_1 hybrids of crosses between white-petalled (B479) and yellow-petalled (B478) Chinese commercial accessions of Chinese kale [= var. *alboglabra*] fitted a dominant monogenic model, with white dominant over yellow.

Petal/ColourWhite/*Brassica rapa*

Mohammad *et al.* (1942)
White petal colour was found to be inherited independently from reddish brown seed coat colour (gene Br_2) in a cross between strain C. 19 (red brown-seeded, yellow petals) x strain L. 5 (yellow-seeded, white petals). White petal colour was controlled by a single, recessive gene, designated *y*.

Sun (1946)
Monogenic or digenic inheritance was observed in crosses between a white-petalled genotype and a yellow-petalled genotype of pak choi [= subsp. *chinensis*]. The yellow-petal trait was dominant.

Alam and Aziz (1954)
See Morphological traits/Petal/Colour/Light yellow/*Brassica juncea*.

Petal/Colour/White/*Brassicoraphanus*

Kato and Tokumasu (1976)
Studies were conducted on the genetics of petal colour in *Brassicoraphanus* [amphidiploids derived from *B. japonica* (= *B. rapa* subsp. *japonica*) and *R. sativus*] and its possible linkage to a gene that affects embryo development and ultimately seed fertility.

The petal colour of various F_1 and F_2 hybrids between white-flowered *Raphanus* and yellow-flowered *Brassica* was reported to be generally pure white or white with a purplish tinge on veins, suggesting that white petal colour was controlled by a single dominant (or epistatic) gene.

Petal/Colour/White/*Raphanus raphanistrum*

Stanton *et al.* (1986)
Crosses were performed between homozygous white- and yellow-petalled lines established from a wild population originating from Connecticut, U.S.A. The inheritance pattern was indicative of a single gene with white petals being dominant over yellow petals.

Petal/Colour/White/*Raphanus sativus*

Trouard Riolle (1920)
In interspecific crosses between wild radish [= *Raphanus raphanistrum*] and radish [= *Raphanus sativus*], the white or rose-tinged white petal colour of radish was dominant to the yellow petal colour of wild radish. White petal colour was dominant to rose-tinged white petal colour and lavender petal colour.

Fukushima (1929)
In intergeneric crosses between cabbage [= *Brassica oleracea* var. *capitata*] x radish [= *Raphanus sativus*], the yellow petal colour of cabbage was recessive to the white petal colour of radish.
Kato and Tokumasu (1976)
White petal colour was controlled by a single dominant gene.

Petal/Colour/Yellow/*Brassica juncea*

Chen and Tong (1985)
See Morphological traits/Leaf/Colour/Purple pigmentation/*Brassica juncea*.

Petal/Colour/Yellow/*Brassica napus*

Davey (1931)
In swedes [= *B. napus* subsp. *rapifera*], bright lemon-yellow petal colour and dull or matt, buff yellow petal colour (Naples yellow) were conditioned by genes controlling white flesh and yellow flesh colour, respectively, or by closely linked genes. Similarly, in turnips [= *B. rapa* subsp. *rapifera*], bright lemon-yellow petal colour and matt, buff yellow petal colour were conditioned by genes controlling white flesh and yellow flesh colour, respectively, or by closely linked genes.

Petal/Colour/Yellow/*Brassica oleracea*

Fukushima (1929)
In intergeneric crosses between cabbage [= *Brassica oleracea* var. *capitata*] x radish [= *Raphanus sativus*], the yellow petal colour of cabbage was recessive to the white petal colour of radish.

Petal/Colour/Yellow/*Brassica rapa*

Davey (1931)
See Morphological traits/Petal/Colour/Yellow/*Brassica napus*.

Petal/Colour/Yellow/*Raphanus raphanistrum*

Trouard-Riolle (1920)
In interspecific crosses between wild radish [= *Raphanus raphanistrum*] and radish [= *Raphanus sativus*], the white or rose-tinged white petal colour of radish was dominant to the yellow petal colour of wild radish.

Petal/Coronal scales/*Brassica napus*

Quazi (1988)
The inheritance of petal colour was investigated in a cross between F_4 generation plants of line OL418 (yellow-petalled), derived from an interspecific cross between oilseed rape [= *Brassica napus* subsp. *oleifera*] cv. Tower x kale [= *Brassica oleracea* var. *acephala*] cv. Rawara, and F_5 generation plants of line 15 (white petalled), derived from an interspecific cross between cv. Tower x broccoli [= *Brassica oleracea* var. *italica*] line G1117B. The F_2 segregation ratios were consistent with a single dominant gene for white petal. The gene was found to segregate independently from a gene for coronal scales.

Petal/Margin colour/*Brassica rapa*

Cours (1977)
The inheritance of red petal margins (presumably due to the presence of anthocyanin) was studied in the progeny of crosses between USDA introductions PI 175079 and 175054. The trait was preferentially, though not exclusively, inherited maternally. The gene for red petal margins was designated *rpm.*

Petal/Number/Apetalous/*Brassica carinata*

Rana (1984)
Reciprocal crosses between apetalous and petalous plants resulted in F_1s resembling the petalled parent. Studies of the F_2 and F_3 progenies from these crosses and the F_1 and F_2 testcross progenies indicated that the development of petals was controlled by two major nuclear genes. The occurrence of variable numbers of partially petalled plants in the segregating populations suggested the action of a number of modifying genes. No true-breeding, partially petalled plants were found, which was attributed to the heterozygosity and environmental sensitivity of such types. An environmental influence on petal development was indicated by the presence of apetalous flowers on petalled plants and petalous flowers on apetalous plants, and by the frequent presence of rudimentary petals in apetalous types.

Petal/Number/Apetalous/*Brassica juncea*

Singh *et al.* (1991)
The inheritance of the apetalous trait in Indian mustard line RC 199 was studied in reciprocal crosses with wild-type line RH 30 and cv. Varuna. The trait was recessive and controlled by two duplicate genes (15:1 F_2 segregation ratio and 3:1 BC_1 segregation ratio to apetalous parent). The postulated genotype of apetalous line RC 199 was $p_1p_1p_2p_2$.

Petal/Number/Apetalous/*Brassica napus*

Buzza (1983)
Reciprocal crosses were made between oilseed rape [= subsp. *oleifera*] apetalous line PL and normal line RU6. Petal number was determined on the first 25 flowers to open. Plants of the F_1 generations were normal except for an occasional missing petal. Petal number of the F_2 plants ranged widely with a few plants being apetalous and more than half being nearly completely petalled; about 25% of the plants had 10 to 80% petals. BC segregation data indicated about a 1:2:1 segregation of apetalous, intermediate, and mostly petalled plants, respectively.

The data indicated a two gene control with four alleles. The absence of dominant alleles would give rise to an apetalous plant, one to two dominant alleles to intermediate types, and four dominant alleles to fully petalled plants. The genotypes *PPPP* (fully petalled plants) and *pppp* (apetalous plants) were postulated.

Fu *et al.* (1990)
Reciprocal crosses were made between oilseed rape [= subsp. *oleifera*] apetalous line APL-0256 and normal line DL. The flowers of F_1 progenies were normal, indicating that the apetalous trait was recessive. F_2 plants varied widely. The F_2 (255:1) and BC_1 (15:1) ratios indicated that the trait was controlled by four nuclear genes. The same results were obtained from crosses of line APL-0256 and other normal lines. The genotypes $P_1P_1P_2P_2P_3P_3P_4P_4$ (normal flowers) and $p_1p_1p_2p_2p_3p_3p_4p_4$ (apetalous flowers) were postulated.

Ratios for a cross between apetalous line APL-0256 and line AL, a small petalled MI-cytoplamic male sterile line, indicated a two gene inheritance. The genotypes $P_1P_1P_2P_2p_3p_3p_4p_4$ (line AL) and $p_1p_1p_2p_2p_3p_3p_4p_4$ (line APL-0256) were postulated.

Kelly *et al.* (1995)
RFLP analysis was used to identify the genes which control flower morphology in three distinct petalless variants of oilseed rape [= subsp. *oleifera*] and silique angle in two additional variants. One petalless phenotype “stap” had petals which developed into stamen-like structures, with an associated effect on leaf morphology of reduced size and shriveling. The stap phenotype was determined by an epistatic interaction between recessive alleles at a pair of homoeologous loci on the C and A genomes. Changes in floral and leaf morphology were completely linked as pleiotropic effects of the same gene. Another petalless type “apet” was controlled by an interaction between alleles at three loci, *apet-1*, *apet-2*, and *apet-3*. Genes *apet-1* and *apet-2* were major loci with *apet-3* a modified locus. The third variant “npet” produced completely petalless flowers with no obvious pleiotropic effects. Between four and six loci were required for the expression of *npet*, *npet-1*, and *npet-2* as major loci with up to four modified loci *npet-3* to *npet-6* with additive effects on expression of the trait. Alleles for upright siliques were dominant over alleles for horizontal siliques and the additive interactions between the two loci could be shown.

Petal/Number/Apetalous/*Brassica rapa*

Ramanujam (1940)
A true-breeding apetalous mutant was controlled by a nuclear recessive gene, on the basis of segregating progenies of reciprocal crosses.

Singh (1961b)
An apetalous mutant was observed in brown sarson [= var. *dichotoma*]. Most apetalous flowers had four stamens; the remaining flowers had five or six stamens of more or less equal length. Silique development and seed set were normal. The apetalous trait was found to be recessive and controlled by a single gene. The variable stamen number trait appeared to be linked to the apetalous trait.

Cours (1977)
The inheritance of apetalous flowers (all or nearly all petals lacking) was studied in the progeny of crosses between USDA introductions PI 183395 and 175079. Segregation ratios were consistent with monogenic inheritance with a recessive allele, designated *pl.*

Petal/Number/Polypetalous/*Brassica rapa*

Singh (1961c)
A mutant with increased petal number (five to six petals) was observed in brown sarson [= var. *dichotoma*]. Penetrance was 65.5%. Following continued inbreeding and selection, lines with complete penetrance and an average expressivity of 0.87 were developed. In these lines, flowers had generally five to eight petals; up to 13 petals were observed. Although F_2 segregation data from reciprocal crosses between a selected mutant line and a wild-type line did not fit Mendelian ratios, it was concluded that a major gene with recessive expression controlled the trait and that its expressivity was conditioned by at least three genes.

Cours (1977)
The inheritance of polypetalous flowers (more than 4 petals, usually 5-8 petals) was studied in the progeny of a cross between USDA introductions 175079 and PI 175054. Polypetalousness appeared to be dominant, but was strongly influenced by the environment. The trait was designated as *Pp*.

Petal/Shape/Creased/*Brassica napus*

Luczkiewicz (1995)
Seed irradiation of winter rapeseed [= subsp. *oleifera*] cvs. Jet Neuf (France) and Brink (Sweden), and Polish cvs. Wipol and Janpol produced three floral mutations: creased petals, dispersed petals (long and narrow petals) in the corolla, and split pistil-stigma. The creased petal phenotype was recessive and controlled by a single gene locus. The dispersed petal phenotype was also recessive and segregation in the F_2 fitted a two gene model. The split pistil-stigma phenotype was associated with an increase in shattering and lower fertility. The trait was recessive and determined to be controlled by two genes.

Petal/Shape/Crinkly/*Brassica oleracea*

Wills and Smith (1972)
See Morphological traits/Anther/Tip colour/*Brassica oleracea*.

Wills and Smith (1973)
See Morphological traits/Anther/Tip colour/*Brassica oleracea*.

Petal/Shape/Cupped/*Brassica rapa*

Cours (1977)
The inheritance of cupped petals (petal edges turned upward, giving the petals a cupped appearance) was studied in USDA introduction PI 175079. The trait required high light intensity for full expression. Segregation ratios were consistent with monogenic inheritance with a recessive allele, designated *cup.*

Petal/Shape/Dispersed/*Brassica napus*

Luczkiewicz (1995)
See Morphological traits/Petal/Shape/Creased/*Brassica napus*.

Petal/Shape/Folded/*Brassica nigra*

Delwiche and Williams (1981)
Folded petals (petals folded back upon themselves before and after bud opening) observed in USDA Plant Introduction PI 193758, were found in testcross and F_2 segregation studies to be controlled by single recessive gene, designated *fp*.

Petal/Shape/Jagged/*Brassica rapa*

Hawk and Crowder (1978)
A mutant with jagged petal margins (irregular margins as opposed to entire margins) was isolated in the S_1 generation of plants of *B. campestris* introduction 175054 or 175079 from the Regional Plant Introduction Station, Ames, Iowa, U.S.A. F_2 and testcross segregation data indicated a single recessive gene, designated *jp*. The trait was associated with a wrinkled and thickened leaf characteristic, allowing detection of the mutant at the first true leaf stage.

Hawk (1982b)
Tight linkage was identified between two seedling mutants isolated from early flowering plants of USDA Plant Introductions PI 175054 and PI 175079. A green hypocotyl mutant allelic to previously reported gene *a-2* (Stringam, 1971) was found to be linked to a mutant with wrinkled leaves and jagged petal margins (gene *jp*). Genes *a-2* and *jp* were assigned to linkage group I.

Petal/Shape/Rolled margins/*Brassica rapa*

Cours (1977)
The inheritance of rolled petal margins (lateral sides of petals upturned) was studied in USDA introduction PI 175054. The trait required high light intensity for full expression and was conditioned by a single dominant gene, designated *Ropm.*

Petal/Shape/Split/*Brassica napus*

Palmer (1958)
Crosses were made between plants of swede [= subsp. *rapifera*] cv. Calder with split petals (petals divided near their base) x cv. Grandmaster (wild-type). Segregation ratios were consistent with the split petal trait being under the control of one dominant gene with varying penetrance rates in the homozygous and the heterozygous condition.

Petal/Shape/Tucked/*Brassica rapa*

Hawk and Crowder (1978)
A mutant with tucked petals (curled downward) was isolated in the S_1 generation of plants of *B. campestris* introduction 175054 or 175079 from the Regional Plant Introduction Station, Ames, Iowa, U.S.A. F_2 and testcross segregation data indicated a single recessive gene, designated *tu*.

Petal/Size/*Brassica juncea*

Pokhriyal *et al.* (1964)
The inheritance of petal width was studied in crosses between a rai mutant with narrow petals x a wild-type rai cv. Laha 101. The narrow petal trait was recessive to the wild-type and controlled by two genes.

Petal/Size/*Raphanus raphanistrum*

Mazer and Schick (1991)
See Morphological traits/Ovule number/*Raphanus raphanistrum*.

Conner and Via (1993)
See Morphological traits/Anther/Filament length/*Raphanus raphanistrum*.

Petiole/Colour/*Brassica oleracea*

Sampson (1967a)
See Morphological traits/Anther/Tip colour/*Brassica oleracea*.

Petiole/Colour/*Brassica rapa*

Shibutani and Okamura (1957)
The F_1 generation of crosses between turnips [= subsp. *rapifera*] with purplish red (cyanin) vs. clear red (pelargonin) petioles showed dominance of purplish red over clear red petioles. No F_2 segregation ratios were provided.

Petiole/Necrosis/*Brassica oleracea*

Pound and Walker (1953)
Leaf necrosis (spotting) in cabbage [= var. *capitata*] was found to be recessive and conditioned by a number of genes. Petiole necrosis was also recessive, but appeared to be controlled by a different set of genes.

Petiole/Size/*Brassica rapa*

McCammon and Honma (1984)
Petiole width in pak-choi [= subsp. *chinensis*] was reported to be simply inherited, with narrow petioles dominant over wide petioles. No segregation ratios were presented.

Song *et al.* (1995)
See Morphological traits/Leaf/Lobe number/*Brassica rapa*.

Petiole/Thickness/*Brassica rapa*

McCammon and Honma (1984)
Petiole thickness in pak-choi [= subsp. *chinensis*] was found to be under the control of two partially dominant genes, with thick petioles being dominant over thin petioles. Additive effects were also found to be significant. A complementary gene model (9:7) best explained the observed segregations.

Song *et al.* (1995)
See Morphological traits/Leaf/Lobe number/*Brassica rapa*.

Pistil/Length/*Raphanus raphanistrum*

Conner and Via (1993)
See Morphological traits/Anther/Filament length/*Raphanus raphanistrum*.

Pistil/Protruding stigma/*Brassica juncea*

Anand and Mishra (1985)
A mutant with white petals and protruding stigmas was described. Reciprocal crosses between the mutant and the wild-type (yellow petals and non-protruding stigmas) indicated dominance of the yellow petal colour and non-protruding stigmas over white petal colour and protruding stigmas.

Pistil/Split stigma/*Brassica napus*

Luczkiewicz (1995)
See Morphological traits/Petal/Shape/Creased/*Brassica napus*.

Pistil/Style tip colour/*Brassica rapa*

Cours (1977)
The inheritance of non-pigmented style tip (probably due to the absence of anthocyanin) was studied in USDA introduction PI 175079. The trait was conditioned by a single recessive gene, designated *as*. Gene *as* was linked to gene *aa* (anthocyaninless anther tip).

Plant/Branch number/*Brassica carinata*

Subudhi and Raut (1994a)
The inheritance of a number of traits was studied in parental, F_1, F_2, and F_3 generations of interspecific crosses between *Brassica juncea* and *Brassica carinata*. Additive gene action predominated for the number of primary branches, number of secondary branches, length of the main branch, number of siliques on the main branch, number of seeds per silique, 1,000 seed weight, and seed yield.

Plant/Branch number/*Brassica juncea*

Paul (1978)
The F_1 and F_2 populations of five crosses between the mustard strains Varuna, Laha 101, KB2, Rai5, Rai7, and Rai Monipuri were assessed on an individual plant basis for number of primary and secondary branches, number of siliques per plant, number of seeds per silique, 1,000 seed weight, and seed yield per plant. Both additive and dominant components were significant for these traits. Degrees of dominance were variable. The estimates of broad-sense heritability and genetic advance were moderate to high. None of the F_1 hybrids showed heterosis above the high parent Laha 101.

Paul (1979)
The F_1 and F_2 populations of four crosses between the mustard strains Varuna, Laha 101, KB2, Rai5, Rai7, and Rai Monipuri were assessed on an individual plant basis for number of primary and secondary branches, number of siliques per plant, number of seeds per silique, 1,000 seed weight, and seed yield per plant. The genetic control of seed yield and yield components was determined to be under both additive and dominant gene action. Broad-sense heritability estimates between 0.65 and 0.78 were shown for yield components. Estimates of genetic advance were high for seed size, seed per silique, and number of primary branches, indicating that these traits were mainly determined by additive gene effects.

Chaudhary and Sharma (1982)
See Morphological traits/Leaf/Size/*Brassica juncea*.

Govil *et al.* (1984)
A diallel cross among ten strains of mustard was studied to estimate gene effects on yield, yield components, and oil content. Both additive and dominance gene action were significant for days to flower, plant height, number of primary branches, number of secondary branches, number of siliques on the main raceme, number of days to maturity, number of seeds per silique, 1,000 seed weight, yield per plant, and oil content.

Labana *et al.* (1984)
The inheritance of plant height, number of secondary branches, and number of siliques on the main branch was determined in a diallel cross with 16 genotypes of Indian mustard. Both additive and non-additive genetic effects were important for the three traits. Dominance estimates indicated partial dominance for plant height and overdominance for the number of secondary branches and the number of siliques on the main branch.

Thakral *et al.* (1986)
Three crosses of Indian mustard were analyzed for the inheritance of seed yield and its components (plant height, number of primary branches, number of secondary branches, length of the main raceme, number of siliques on the main raceme, silique length, and number of seeds per silique). Significant reciprocal differences were evident in all traits except for the number of primary branches and seeds per silique. The additive genetic component was significant for most traits with few traits showing a significant dominance component, e.g. in one cross, number of secondary branches, length of main raceme, and seed yield. Partial dominance was noted for plant height, number of primary branches, number of siliques on the main raceme, silique length, and number of seeds per silique, and over-dominance for seed yield, number of secondary branches, and length of the main raceme.

Sachan and Singh (1988)
Twenty generations of the cross Pant Rai 5 X BRR 63 were assessed for quantitative inheritance of plant height, length of the main branch, number of siliques on the main branch, number of primary branches per plant, and harvest index of individual plants. Oil content was assessed on a pooled seed sample from each generation. Additive genetic effects were significant for all traits; dominant effects contributed to plant height, length of the main branch, oil content, number of siliques on the main branch, and harvest index. Four genetic models, additive dominance, digenic interactions, trigenic interactions, and linked digenics were fitted for all traits. Duplicate epistasis was recorded for all the traits except number of primary branches per plant.

Subudhi and Raut (1994a)
See Morphological traits/Plant/Branch number/*Brassica carinata*.

Plant/Branch number/*Brassica napus*

Malik *et al.* (1995)
A 7 x 7 diallel cross (one-way) was performed using oilseed rape [= subsp. *oleifera*] genotypes. Non-additive gene effects were prevalent for all traits, whereas additive gene effect was important for plant height, number of primary and secondary branches, and number of siliques on the main branch. High heritability estimates were obtained for the number of primary and secondary branches and oil content. Low heritability estimates were obtained for seed yield and other traits.

Plant/Branch number/*Brassica rapa*

Rao (1977)
Nine strains and accessions of brown sarson [= subsp. *dichotoma*] were crossed in a 36 cross half diallel and genetic parameters for eleven quantitative traits were assessed. Oil content and number of secondary branches showed poor heritability while number of primary branches and number of seeds per silique showed moderate heritability. The other seven traits were days to flowering, plant height, branching type, silique set, silique length, beak length, and seed size. Branching type, days to flowering, beak length, silique length, and seed size showed high heritability estimates and high genetic advance. Heterosis was shown for most of the traits with variable estimates in the different crosses. Seed size, plant height, and number of primary branches had a significant effect on oil content. Ten of the eleven traits showed dominance for expression; plant height had additive gene action.

Paul (1978-1979)
The F_1 and F_2 populations of four crosses between four strains of *Brassica campestris* subsp*. oleifera*, Assam Local, Pusa Kalyani, Saphala, and T 9, were assessed on an individual plant basis for number of primary and secondary branches, number of siliques per plant, number of seeds per silique, 1,000 seed weight, and seed yield/plant. Both additive and dominance gene effects were significant for these traits. Degree of dominance was variable depending on the cross. Broad-sense heritabilities were high for all traits. The hybrid Assam Local x Pusa Kalyani showed high parent heterosis for seed yield, outyielding the best cultivar.

Yadava *et al.* (1985)
Thirty-nine genotypes of brown sarson [= subsp. *dichotoma*] were assessed for ten agronomic and quality traits. Significant variation was shown for plant height, total number of siliques per plant, number of siliques on the main shoot, number of secondary branches per plant, and seed yield. Oil content and 1,000 seed weight showed low variation. Heritability estimates were highest for total number of siliques per plant (48.46%) and lowest for oil content (15.90%).

Plant/Branch number/*Eruca vesicaria* subsp*. sativa*

Yadav and Kumar (1984)
Eleven yield-related traits were studied in 50 strains of eruca [= *E. sativa*] from India, selected on the basis of geographical diversity of origin and morphological variability. Compared with the other traits, estimates of heritability and genotypic and phenotypic coefficients of variation were higher (h_2 >90%) for primary (93.2%) and secondary branches per plant (95.2%), silique length (90.0%), number of siliques per plant (93.8%), 1,000 seed weight (94.2%), and number of seeds per silique (97.2%). Seed yield had an heritability of 88.2%. In both early-sown and late-sown crops, seed yield was significantly, positively correlated with the number of siliques on the main shoot (r = 0.45 to 0.57) and the number of siliques per plant (r = 0.51 to 0.62).

Plant/Branching habit/*Brassica juncea*

Singh *et al.* (1968)
The segregation ratios of F_1, F_2, and BC generations of crosses between Indian mustard lines 259 (basal branching habit) x 260 (high branching habit) were consistent with a monogenic model of inheritance, with the trait basal branching habit being dominant to the trait high branching habit.

Chen and Tong (1985)
See Morphological traits/Leaf/Colour/Purple pigmentation/*Brassica juncea*.

Yadav (1988)
The segregation ratios of crosses between wild-type x true-breeding lines that branched at the base, had adaxial leaf hairs, and produced clumped inflorescences were determined. Basal branching was controlled by two duplicate recessive genes. Adaxial leaf hairiness was dominant and controlled by a single gene. Clumping flowering was controlled by two duplicate recessive genes.

Plant/Branching habit/*Brassica napus*

Liu and Liu (1987a)
Forty-two and 50 true-breeding oilseed rape [= subsp. *oleifera*] lines from seven countries were investigated in 1982-83 and 1983-84, respectively. Heritabilities of days to flower, silique length, 1,000 seed weight, and length of the main raceme were found to be high, while heritabilities of the number of siliques per plant, seed yield per plant, silique density, branching height, and seed density were low. Days to flower was negatively correlated with the erucic acid content, while the length of the main raceme and the number of siliques on the main raceme were positively correlated with the erucic acid content of the lines.

Plant/Branching habit/*Brassica oleracea*

Keyes and Honma (1986)
Reciprocal crosses between a sister line of broccoli [= var. *italica*] cv. Solohead x cv. Spartan Early indicated that lateral suppression was dominant over non-suppression. The observed F_2 ratio (9:7) suggested a complementary two gene model. Genes Ns_1 and Ns_2 conditioned lateral suppression.

Plant/Branching habit/*Brassica rapa*

Shibutani and Okamura (1957)
The F_1 generation of crosses between turnips [= subsp. *rapifera*] with spreading vs. upright habit showed dominance of spreading over upright habit. No F_2 segregation ratios were provided.

Rao (1977)
See Morphological traits/Plant/Branch number/*Brassica rapa*.

Plant/Colour/Green (anthocyanin-free)/*Brassica oleracea*

Sampson (1966a)
Linkage was observed between male sterility gene *ms-1* of green sprouting broccoli [= var. *italica*] and gene *c* (anthocyanin-free plant with bright green hypocotyl) of curly kale [= var. *acephala*] and variegated ornamental kale.

Plant/Colour/Pink/*Raphanus sativus*

Humaydan and Williams (1976)
Crosses were made between a true-breeding line for uniformly pink roots, stems, and leaves selected from cv. China Rose Winter and nonpigmented cv. White Spike plants. Segregation data from F_1 (all pink) and F_2 generations (218 pink: 68 non-pigmented) indicated that pink pigmentation was controlled by a single gene, designated *Pi*, with dominance for pink expression.

In cv. China Rose Winter, gene *Pi* was linked to gene *Ac1* (resistance to white rust race 1) with a recombination value of 3.28%.

Plant/Colour/Purple pigmentation/*Brassica oleracea*

Sampson (1967a)
See Morphological traits/Anther/Tip colour/*Brassica oleracea*.

Wills and Smith (1972)
See Morphological traits/Anther/Tip colour/*Brassica oleracea*.

Plant/Colour/Yellow-green/*Brassica nigra*

Delwiche and Williams (1981)
Yellow-green plant, where plants are yellow-green throughout their life, was observed in USDA Plant Introduction PI 197401. The trait was found in testcross and F_2 segregation studies to be controlled by a single recessive gene, designated *yg1*.

Plant/Diameter/*Brassica rapa*

Tan *et al.* (1982)
See Morphological traits/Head/Diameter/*Brassica rapa*.

Plant/Height/*Brassica juncea*

Chaudhary and Sharma (1982)
See Morphological traits/Leaf/Size/*Brassica juncea*.

Govil *et al.* (1984)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Labana *et al.* (1984)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Thakral *et al.* (1986)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Acharya (1988)
A survey of genetic stocks showed a wide range of genetic variation in physiological traits. The highest heritability (95.8%) was recorded for seed weight, days to flower, plant height, length of flowering period, and silique length. High heritability with high genetic advance as a percentage of the mean was observed for seed weight, plant height and days to flowering, suggesting additive gene action controlling these traits.

Sachan and Singh (1988)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Plant/Height/*Brassica napus*

Lefort-Buson and Dattée (1982a)
See Morphological traits/Leaf/Number/*Brassica napus*.

Lefort-Buson and Dattée (1982b)
See Morphological traits/Leaf/Number/*Brassica napus*.
Grant and Beversdorf (1985)
The F_1 hybrids from a diallel between spring oilseed rape [= subsp. *oleifera*] cultivars showed positive heterosis for seed yield (up to 72%) over the higher yielding parent. Heterosis for 1,000 seed weight, percent oil, plant height and lodging resistance was non-significant while protein content showed negative heterosis. Hybrids were intermediate to their parents in flowering data and physiological maturity. Specific combining ability (SCA) was more important than general combining ability (GCA) for seed yield, percent oil, percent protein, plant height, and lodging resistance, suggesting non-additive gene effects controlling these traits. SCA was equally important as GCA for 1,000 seed weight and physiological maturity suggesting both additive and non-additive gene effects controlling these traits. The best specific combinations for seed yield heterosis were cv. Westar x cv. Hanna, cv. Regent x cv. Liné, cv. Regent x line D-1 produced average high parent heterosis values of 50, 38 and 30% respectively. Cultivar Topas was the best general combiner for seed yield.

Ringdahl *et al.* (1986)
See Morphological traits/Leaf/Number/*Brassica napus*.

Lefort-Buson *et al.* (1987a)
S6 lines from cultivars of European (E) and Asiatic (A) origin were crossed to establish three groups of F_1 hybrids E x E, A x A, and E x A. Four traits were recorded: plant height at flowering, seed yield, yield per silique, and 1,000 seed weight. Heterosis was demonstrated for plant height, seed yield, and yield per silique in one year. The E x A group had higher levels of heterosis than either the E x E or A x A group. Response to environment was similar for all groups. General combining ability (GCA) exceeded specific combining ability (SCA) in both E and A groups. In the E x A, SCA were significant and equal to GCA.

Knaak and Ecke (1995)
Genetic distance between 64 oilseed rape cultivars was estimated using RFLP analysis. Seven divergent groups were shown within the winter types using cluster analysis. Seed yield performance of 22 experimental hybrids significantly exceeded the yield of their parents by an average of 16.9% with a range from -3.9% to 27.4%. Similar values were determined for oil-yield (g oil/m^2) and plant height. The correlation between heterosis of F_1 hybrids and the genetic distance of their parental lines was significant and ranged from $r = 0.71$ for oil-yield to $r = 0.73$ for plant height.

Malik *et al.* (1995)
See Morphological traits/Plant/Branch number/*Brassica napus*.

Plant/Height/*Brassica oleracea*

Pease (1926)
In crosses between brussels sprouts [= var. *gemmifera*] and cabbage [= var. *capitata*], the tall growth habit of brussels sprouts was dominant over the sessile growth habit of cabbage. The trait was controlled by a single gene, designated *T*.

Kwan (1934)
See Morphological traits/Leaf/Colour/Purple pigmentation/*Brassica oleracea*.

Yarnell (1953)
A dwarf phenotype in cabbage [= var. *capitata*] was reported to be recessive to the wild-type phenotype.
Dickson (1968)
The inheritance of plant height in broccoli [= var. *italica*] was studied in crosses between broccoli (tall) x cauliflower [= var. *botrytis*] accessions USDA PI 204767 and PI 217934 (short). The tall trait was conditioned by a single dominant gene, designated *T*.

Plant/Height/*Brassica rapa*

Joarder and Eunus (1970)
The inheritance of four quantitative traits: plant height at heading, plant height at ripening, length of vegetative period, length of reproductive period, was studied in the progeny of two crosses between white mustard and red mustard [= *B. campestris*]. Plant height at heading time was found to be controlled by dominant alleles. The heritability of all four traits was high: 81 to 84% for sowing to heading (the length of the vegetative period, 79 to 87% for heading to ripening (the length of the reproductive period), 49 to 71% for plant height at heading (flowering), and 79 to 94% for plant height at ripening (maturity). Seed coat colour was found to be controlled by a single pair of major genes with red (*R_*) dominant to white (*rr*). The four traits were highly correlated with yield. The length of the reproductive period was inherited independently of the gene for seed coat colour.

Rao (1977)
See Morphological traits/Plant/Branch number/*Brassica rapa*.

Hawk and Crowder (1978)
A dwarf mutant was isolated in the S_1 generation of *B. campestris* introduction 175054 or 175079 from the Regional Plant Introduction Station, Ames, Iowa, U.S.A. The plants were darker green than the wild-type plants. Pollen production and seed set were reduced under high temperature (about 32° C). F_2 and testcross segregation data indicated a single recessive gene, designated *dw*.

James and Williams (1980)
The inheritance of the trait “rosette” (internodal elongation absent) observed in a *B. campestris* strain derived from a cross between USDA PI 183395 x PI 175079 was found to be monogenic. The trait was conditioned by a recessive allele, designated *ro*. Linkage studies between *ro* and genes *Pb1* and *Pb2* (clubroot resistance to race 6) provided evidence of loose linkage between *ro* and *Pb2* (recombination: 0.46).

Tan *et al.* (1982)
See Morphological traits/Head/Diameter/*Brassica rapa*.

Yadava *et al.* (1985)
See Morphological traits/Plant/Branch number/*Brassica rapa*.

Prasad (1993)
See Morphological traits/Cotyledon/Size/*Brassica rapa*.

Plant/Height/*Crambe abyssinica*

Meier and Lessman (1973b)
The heritability of nine agronomic traits was determined for the interspecific cross *Crambe abyssinica* (USDA Plant Introduction PI 247310) x *Crambe hispanica* (PI 279346). Heritability for percentage of oil could not be estimated since there were no significant differences among progeny. Heritability estimates for the remaining eight traits were 42% for maturity, 42% for test weight, 48% for seed yield, 62% for seed size, 71% for 95% bloom, 72% for plant height, 75% for seedling emergence, and 76% for days to first flower. Evidence of heterosis was detected for seed yield, test weight, and oil percent.

Lessman (1975)
Broad-sense heritability estimates were made on the basis of 162 crambe lines selected from USDA accessions PI 247310 and PI 279345. Broad-sense heritability estimates were 22% for percent glucosinolates, 24% for percent oil by NMR, 45% for seed yield, 70% for percent oil, 76% for plant height, 78% for days to bloom, and 88% for test weight. Test weight was positively correlated with percent seed oil (0.97), shorter stature (0.99), and earlier maturity (1.0).

Plant/Height/*Crambe hispanica*

Meier and Lessman (1973b)
See Morphological traits/Plant/Height/*Crambe abyssinica*.

Plant/Height/*Raphanus sativus*

Kubka *et al.* (1974)
See Morphological traits/Cotyledon/Size/*Raphanus sativus*.

Pandey *et al.* (1981)
See Morphological traits/Leaf/Number/*Raphanus sativus*.

Khan *et al.* (1983)
Plant yield and 14 related traits were studied in 33 radish cultivars. High phenotypic and genotypic coefficients of variation were observed for foliage weight, percent forked roots, and percent cracked roots. Root length and foliage weight were highly heritable. Foliage weight was positively correlated to foliage height and root weight. Root length and weight were negatively correlated to percent root dry matter.

Plant/Main branch length/*Brassica carinata*

Subudhi and Raut (1994a)
See Morphological traits/Plant/Branch number/*Brassica carinata*.

Plant/Main branch length/*Brassica juncea*

Thakral *et al.* (1986)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Sachan and Singh (1988)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Subudhi and Raut (1994a)
See Morphological traits/Plant/Branch number/*Brassica carinata*.

Plant/Main branch length/*Brassica napus*

Liu and Liu (1987a)
See Morphological traits/Plant/Branching habit/*Brassica napus*.

Plant/Trichomes (pubescence/glabrous)/*Brassica nigra*

Delwiche and Williams (1981)
Glabrousness (entire plant nearly free of trichomes) was observed in USDA Plant Introduction PI 193758. The trait was found in testcross and F_2 segregation studies to be controlled by a single recessive gene, designated *glb*.

Pollen/Abortive/*Brassica oleracea*

Wills and Smith (1972)
See Morphological traits/Anther/Tip colour/*Brassica oleracea*.

Pollen/Colour/*Brassica nigra*

Delwiche and Williams (1981)
Cream-coloured pollen, observed in an accession collected from the Welsh Plant Breeding Station, Aberystwyth, UK, was found in testcross and F_2 segregation studies to be controlled by a single recessive gene, designated *cp*.

Pollen/Colour/*Raphanus sativus*

Humaydan and Williams (1976)
The inheritance of a cream-coloured pollen mutant in Wisconsin breeding line 1735 was studied in a cross to genotypes with normal bright yellow pollen. Segregation data of F_1 and F_2 generations indicated that cream pollen colour was controlled by a single recessive gene, designated *cp*.

Pollen/Production per flower/*Raphanus raphanistrum*

Mazer and Schick (1991)
See Morphological traits/Ovule number/*Raphanus raphanistrum*.

Pollen/Production per flower/*Raphanus sativus*

Young *et al.* (1994)
See Morphological traits/Corolla width/*Raphanus sativus*.

Pollen/Size/*Raphanus raphanistrum*

Mazer and Schick (1991)
See Morphological traits/Ovule number/*Raphanus raphanistrum*.

Pollen/Size/*Raphanus sativus*

Young *et al.* (1994)
See Morphological traits/Corolla width/*Raphanus sativus*.

Root/Colour/*Brassica napus*

Kajanus (1912)
The inheritance of the colour of the root above ground in swede [= subsp. *rapifera*], *i.e.* the 'top', was ascribed to two genes, designated P_1 (red-green, dominant to green) and P_2 (red, dominant to both red-green and green).

Kajanus (1913)
In swede [= subsp. *rapifera*], the light purple pigmentation of the underground portion of the root was under the control of a factor, designated P_1; the dark purple pigmentation of the entire root was under the control of a second factor, designated P_2. In the absence of both factors, the roots were green.

Hallqvist (1915)
The inheritance of white flesh colour in swedes [= subsp. *rapifera*] was controlled by two dominant genes, designated M_1 and M_2.

Davey (1931)
Inheritance studies of flesh colour in swedes [= subsp. *rapifera*] indicated a digenic or monogenic model of inheritance with white flesh being dominant to yellow flesh. It was also observed that bright yellow and dull yellow petal colours were conditioned by either the same genes or by closely related genes for white flesh and yellow flesh colour, respectively, in both swedes and turnips [= *B. rapa* subsp. *rapifera*].

Davey (1932)
The inheritance of the trait "purple neck" in yellow-fleshed swedes [= subsp. *rapifera*] was controlled by a single dominant gene, designated N_1. A second gene for purple neck, designated N_2, was identified in a white-fleshed strain. There was no linkage between genes N_1 and N_2 and genes M_1 and M_2 for flesh colour.

Sterling (1951)
The inheritance of yellow flesh colour in swede [= subsp. *rapifera*] was studied in crosses between white flesh cv. Danish Giant and yellow flesh cv. Ditmars Bronze Top. Yellow flesh was controlled by two recessive duplicate genes. No linkage was observed between flesh colour and resistance to clubroot.

Root/Colour/*Brassica rapa*

Kajanus (1913)
In turnip [= subsp. *rapifera*], the pigmentation of the flesh was controlled by a factor for white flesh, designated *M*, which inhibited the production of yellow pigment. The pigmentation of the skin was controlled by two factors, designated *V* (green skin) and *P* (red skin). Gene *P* was dominant over gene *V*; both genes were unlinked and unlinked to gene *M.* Genotypes were: *PVM* (red skin, white flesh), *Pvm* (red skin, yellow flesh), *PvM* (red skin, white flesh), *pVM* (green skin, white flesh), *Pvm* (red skin, yellow flesh), *pVm* (green skin, yellow flesh), *pvM* (yellow skin, white flesh), and *pvm* (yellow skin, yellow flesh).

Davey (1931)
In both turnips [= subsp. *rapifera*] and swedes [= *B. napus* subsp. *rapifera*], bright yellow and dull yellow petal colours were conditioned by either genes controlling white flesh and yellow flesh colour, respectively, or by closely linked genes.

Tedin (1932)
The inheritance of clubroot resistance was determined in crosses between turnip [= subsp. *rapifera*] Danish cultivars Majnaepe and Marienlyst V (flat root, upper portion of root green or light red, white flesh, resistant or nearly clubroot immune) x Swedish cultivars Weibulls Pedigree Bortfelder (long, narrow root, upper portion of root yellow-green, yellow flesh, highly clubroot susceptible) and Weibulls Rödtoppig Bortfelder (long, narrow root, upper portion of root dark red, yellow flesh, highly clubroot susceptible). In F_2 progenies, flesh colour segregated 3 white flesh: 1 yellow flesh, the red colour of the upper portion of the root was conditioned by at least two genes, and root shape and clubroot resistance were under polygenic control.

Shibutani and Okamura (1957)
The F_1 generation of crosses between turnips [= subsp. *rapifera*] with different root colours showed dominance of green vs. white pigmentation of the root above ground and dominance of purplish red (cyanin) vs. clear red (pelargonin) pigmentation of the underground portion of the root. No F_2 segregation ratios were provided.

Brar *et al.* (1969)
See Morphological traits/Leaf/Shape/*Brassica rapa*.

Aoba (1970)
The inheritance of seed coat colour (brown, orange) and root colour (purple, red, white) was investigated in turnip [= subsp. *rapifera*]. Seed coat colour and root colour were conditioned by two genes, designated *P* and *C*. Postulated genotypes were *C_P_* (purple root and brown seed), *C_ pp* (red root and orange seed), *ccP_* (white root and brown seed), and *ccpp* (white root and orange seed).

Hoshi (1975)
Inheritance studies in turnip [= subsp. *rapifera*] varieties with red, purple, and white roots suggested control by two genes with recessive epistasis (F_2 segregation ratios in a red- x white-rooted cross were 9 purple-rooted plants: 3 red-rooted plants: 4 white-rooted plants). The genes were designated *R* and *E*.

Prasad (1993)
See Morphological traits/Cotyledon/Size/*Brassica rapa*.

Root/Colour/*Raphanus raphanistrum*

Frost (1923)
In interspecific crosses between radish [= *Raphanus sativus*] and wild radish [= *Raphanus raphanistrum*], purple root colour was found to be dominant to red root colour and conditioned by a single gene, designated *R*. Root diameter was found to be linked to purple root colour in progeny of interspecific crosses between radish x wild radish.

Root/Colour/*Raphanus sativus*

Malinovski (1916)
Yellow root colour was found to be dominant to white root colour, and conditioned by a single gene.

Frost (1923)
See Morphological traits/Root/Colour/*Raphanus raphanistrum*.

Uphof (1924)
Crosses were made between cv. Long Red (red roots) x cv. Icicle (white roots). The F_1 plants had violet roots. A single gene determined root colour in these cultivars.

Yellow radish cv. Round Yellow was crossed to white radishes (cvs. Round White, Early White, and Icicle). Yellow root colour was found to be dominant to white root colour. The trait was controlled by a single gene.

Tatebe (1936)
The inheritance of root colour in radish was investigated in a series of paired crosses among white-, red-, purple-, and yellow-rooted types. Red, purple, and yellow were dominant to white and the F_2 progenies segregated 3:1 in each cross. Gene *R*, for red colour, was epistatic over gene *Y*, for yellow colour. In the yellow x purple cross, gene R^p, for purple colour, was epistatic over gene *Y*; the F_2 segregated 12 purple-rooted plants: 3 yellow-rooted plants: 1 white-rooted plant. In the red x purple cross, the F_1 was purple and the F_2 segregated 3 purple-rooted plants: 1 red-rooted plant. The author suggested that purple root colour was determined by a set of multiple allelomorphs with two factors for red and white, the allelomorphic series being $R^p>R>r$. Postulated genotypes were R^pR^pyy (purple-rooted plants), *RRyy* (red-rooted plants), *rrYY* (yellow-rooted plants), and *rryy* (white-rooted plants).

Tatebe (1937a)
The inheritance of root colour in radish was determined. Postulated genotypes for exterior root colour were *R_ yy* (red roots), R^p_ *yy* (purple roots), *rrY_* (yellow roots), and *rryy* (white roots). Pale green neck or hypocotyl was conditioned by gene *G*. White neck was conditioned by gene *vg*. Red striping was conditioned by gene R^S.

Tatebe (1938)
The allelic series *R*, R^p, R^s, and *r* was proposed to describe the inheritance of root colour in radish.

Okuno (1943)
Root colour in radish was conditioned by three genes, designated R_2, R_3, and *C*. Postulated genotypes were R_2_R_3_*cc* (red roots), R_2_r_3r_3C_ or $r_2r_2R_3$_*C*_ (purple roots), and $r_2r_2r_3r_3Cc$ (white). Genes R_2 and R_3 were lethal in the homozygous state.

Harborne and Paxman (1964)
Crosses were made between red (cv. Red Turnip) and white forms (cvs. Carter's Icicle and White Turnip) of radish. Results were consistent with one gene, designated *H*, for the control of hydroxylation of pelargonidin to cyanin (*hh*: red forms). Pigment distribution was independent of the *H* locus.

Madzharova (1975)
F_1 hybrids between radish cv. Perla, with glabrous leaves and white roots, and six other cultivars, with hairy tops and red roots, showed dominance of hairy over the glabrous leaf blade, with red colour, large size and firmness of roots dominant over the white colour. The F_2 segregated into a nearly 3:1 ratio of hairy to glabrous progeny. In all cases plants with glabrous leaves had white roots. Crosses between white-root cultivars with hairy and glabrous leaves gave F_1 plants producing violet roots and F_2 plants producing white roots and glabrous leaves, suggesting complementary action of two allelomorphic pairs *AA* and *BB* which in either single or double state condition the violet colour.

Bonnet (1979)
The F_1, F_2, and BC_1 generations of a cross between cv. Biser round white radish, with glabrous leaves and yellow seeds [also studied in Madzharova (1975)] and a line of round radish which was red and white, with hairy leaves and brown seeds were studied. The traits red root and hairy leaf showed complete linkage as in Madzharova (1975), and were also linked to stem and seed coat colour. Segregation data suggested a simple monogenic dominant determinism for the group of traits (red

root, hairy leaf, red stem, brown seed). F_1 plants had a red root with small white tip; the F_2 and BC_1 plants had only two classes: white and red with small white tip.

Makarova and Ignatova (1981)
Root colour was controlled by two genes, one conditioning the presence or absence of colour (*A*) and the other gene conditioning the type of colour (*B*).

Dayal (1983)
A cross was made between European cv. Scarlet Globe with coloured roots and Indian cv. Newar with white roots. The F_1 hybrids all had coloured roots. F_2 segregation data (262 coloured: 82 white) revealed that root colour was governed by a single colour gene, designated *C*, with the allele for colour being completely dominant to the recessive allele, *c* (white).
Gene *C* segregated independently of a gene for root shape, *L*.

Makarova and Ivanova (1983)
Segregation data from a cross between glabrous-leaved cvs. Salatnyi (round, red roots) x Salatnaya Kitaiskaya (long, white roots) indicated that anthocyanin colouration of the roots was controlled by recessive epistatic genes, with purple: red: white roots segregating in the ratio 9:3:4. The studies further suggested that one gene, *A*, was responsible for the presence/absence of colouration and another gene, *B*, was responsible for the type of colouration, recessive *a* being epistatic to *B*, *i.e.* blocking the expression of colour irrespective of whether it was purple (*BB*, *Bb*) or red (*bb*). Evidence was examined for the existence of a series of *A* genes, one responsible for colouration of the whole plant (*Apl*) and one for colouration of the root (*Ar*).

Ahmed and Tanki (1994)
The inheritance of root colour in turnip [= subsp. *rapifera*] was studied in nine crosses involving five parents. Purple root colour was dominant over pink, partially purple, and white root colour, and was under the control of two genes *P* and *C*. These two genes in double dominant state produce purple roots. The genotype of purple parent was tentatively designated as *PPCC*. The pink and partially purple root colours were dominant over white and they were under the control of single dominant genes *P* and *C*, respectively. Postulated genotypes were *PPCC* (purple), *PPcc* (pink), *ppCC* (partially purple), and *ppcc* (white). Root shape was studied in two crosses involving parents with either round or flat round roots. Round root shape was dominant to flat round root shape in the F_1 generation and was under the control of a single gene, designated *R*.

Root/Percent cracked roots/*Raphanus sativus*

Khan *et al.* (1983)
See Morphological traits/Plant/Height/*Raphanus sativus*.

Root/Percent forked roots/*Raphanus sativus*

Khan *et al.* (1983)
See Morphological traits/Plant/Height/*Raphanus sativus*.

Root/Shape/*Brassica juncea*

Chen and Tong (1985)
See Morphological traits/Leaf/Colour/Purple pigmentation/*Brassica juncea*.

Root/Shape/*Brassica rapa*

Ragionieri (1920)
The trait “fleshy root” was conditioned by a single recessive gene in reciprocal crosses between turnip [= subsp. *rapifera*] x Pe-tsai [= subsp. *pekinensis*].

Tedin (1932)
See Morphological traits/Root/Colour/*Brassica rapa*.

Shaw (1936)
The inheritance of root shape was studied in crosses between thin-rooted yellow sarson [= subsp. *trilocularis*] line 60-1-5 and a thick-rooted turnip [= subsp. *rapifera*]. F_1 plants had roots that were intermediate in thickness. The ratio of thin-rooted plants to intermediate, turnip-like plants was 1:3.
Shibutani and Okamura (1957)
The F_1 generation of crosses between turnips [= subsp. *rapifera*] with different root shapes (long, round) had intermediate root shapes. No F_2 segregation ratios were provided.

Brar *et al.* (1969)
See Morphological traits/Leaf/Shape/*Brassica rapa*.

Root/Shape/*Raphanus raphanistrum*

Panestos and Baker (1968)
Interspecific crosses were made between plants from two wild populations of *Raphanus raphanistrum* from central California, U.S.A., and radish [= *Raphanus sativus*] cv. Cincinnati Market and radish plants from one wild population from central California, U.S.A. F_1 and F_2 segregation data indicated that the swollen root trait characteristic of *R. sativus* and slender, well-branched root of *R. raphanistrum* were oligogenically determined, probably by two major genes with a number of modifiers, with genes for swollen root recessive to the genes for slender, well-branched root. All F_1 plants had a slender, well-branched root.

Root/Shape/*Raphanus sativus*

Malinovski (1916)
The inheritance of root shape was studied in a cross between a long-rooted x a round-rooted radish cultivars. Long-rootedness was conditioned by two unlinked, dominant genes.

Uphof (1924)
Monogenic inheritance was observed for root shape in radish (F_2 ratio: 1 round-rooted plant: 2: intermediate: 1 long-rooted plant).

Tatebe (1937b)
The inheritance of root shape was investigated in crosses between radishes with long roots and with round roots. The root shape of the F_1 plants was intermediate; the F_2 generation segregated 1 plant with long roots: 2 plants intermediate for root shape: 1 plant with round roots, suggesting one gene and incomplete dominance.

Panestos and Baker (1968)
See Morphological traits/Root/Shape/*Raphanus raphanistrum*.

Dayal (1983)
A cross was made between the European cv. Scarlet Globe with round roots and Indian cv. Newar with long roots. The F_1 hybrids all had oval roots. F_2 segregation data (72 round: 178 oval: 94 long) revealed that root shape was governed by a single gene, designated *L*, with the allele for long root shape being partially dominant to the recessive allele, *l* (round), which in heterozygous condition gave oval roots.
Gene *L* segregated independently of a gene for root colour, *C*.

Makarova and Ivanova (1983)
Analysis of a cross between radish cvs. Salatnyi (round red roots) x Salatnaya Kitaiskaya (long white roots), indicated that the F_1 hybrids combined the long roots of one parent with the root diameter of the round-rooted parent.

Ahmed and Tanki (1994)
The inheritance of root colour in turnip [= subsp. *rapifera*] was studied in nine crosses involving five parents. Purple root colour was dominant over pink, partially purple, and white root colour, and was under the control of two genes *P* and *C*. These two genes in double dominant state produce purple roots. The genotype of purple parent was tentatively designated as *PPCC*. The pink and partially purple root colours were dominant over white and they were under the control of single dominant genes *P* and *C*, respectively. Postulated genotypes were *PPCC* (purple), *PPcc* (pink), *ppCC* (partially purple), and *ppcc* (white). Root shape was studied in two crosses involving parents with either round or flat round roots. Round root shape was dominant to flat round root shape in the F_1 generation and was under the control of a single gene, designated *R*.

Root/Size/*Brassica carinata*

Thakral and Singh (1995a)
Seeds of six parents and 15 F_1 hybrids were germinated on filter paper containing 0, 125, and 175 meq/L chloride salt solutions. Seedling vigour was correlated with germination percentage, rate of germination, root length, seedling fresh weight, seedling dry weight. No correlations were found between these traits and seed yield.

Root/Size/*Brassica rapa*

Kajanus (1913)
In turnip [= subsp. *rapifera*], root length was controlled by two genes, designated L_1 and L_2.

Root/Size/*Raphanus raphanistrum*

Frost (1923)
Root diameter was found to be linked to purple root colour in progeny of interspecific crosses between radish [= *Raphanus sativus*] x wild radish [= *Raphanus raphanistrum*].

Root/Size/*Raphanus sativus*

Frost (1923)
See Morphological traits/Root/Size/*Raphanus raphanistrum*.

Prasad and Prasad (1978)
See Morphological traits/Leaf/Number/*Raphanus sativus*.

Gospodarek and Hulewicz (1979)
The effect of 1,000 seed weight on productive traits and their correlations were studied in large- and small-seeded progenies of radish. Plant weight, root weight and diameter, and the number of productive roots were positively correlated with 1,000 seed weight. The seed position effect was also highly significant.

Pandey *et al.* (1981)
See Morphological traits/Leaf/Number/*Raphanus sativus*.

Khan *et al.* (1983)
See Morphological traits/Plant/Height/*Raphanus sativus*.

Shattuck (1985)
Rutabaga [= subsp. *rapifera*] cvs. Altrasweet, American Purple Top, Bangholm, Danestone, Laurentian, Niko, Vige, Wilhelmsburger, and Wye were evaluated for agronomic traits. Root yield was highly correlated with the biological yield and foliage weight. The accumulation of root dry matter per unit area was highly correlated with the soluble sugar concentration in the root juice (r = 0.77). Percent dry matter, foliage weight, root diameter, and root length accounted for 86% of the variability for dry root weight.

Ling *et al.* (1986)
See Morphological traits/Leaf/Area/*Raphanus sativus*.

Root/Texture/*Brassica rapa*

Shibutani and Okamura (1957)
The F_1 generation of crosses between turnips [= subsp. *rapifera*] with different root textures had intermediate root textures. No F_2 segregation ratios were provided.

Root/Texture/*Raphanus sativus*

Uphof (1924)
The trait “corky epidermal layer” in winter radish cultivars (black) was dominant to the “smooth epidermis” of spring and summer varieties.

Seed/Coat colour (testa colour)/*Brassica carinata*

Getinet *et al.* (1987)
Reciprocal crosses were made between a yellow-seeded line PGRC/Ethiopia 1972-83 and true-breeding brown-seeded cv. S-67 to produce F_1, F_2, and BC_1 generations. All F_1 reciprocal crosses (the heterozygous condition) and backcrosses to the yellow-seeded parent produced yellow seed with a slight tinge of brown (yellow-brown-seeded), indicating incomplete dominance (semidominance) of brown over yellow. Backcrosses to the brown-seeded parent segregated in a 1:1 ratio (805 brown-seeded: 811 yellow-brown-seeded); the F_2 generation segregated in a 3:1 ratio (877 yellow-seeded and yellow-brown-seeded: 296 brown-seeded), indicating monogenic control with incomplete dominance (semidominance) of brown over yellow. The homozygous recessive condition resulted in yellow seed.

Singh *et al.* (1995)
The inheritance of seed coat colour was studied in crosses between true-breeding dark brown-seeded x yellow-seeded lines of Ethiopian mustard. F_2 progenies segregated 1 dark dull yellow brown-seeded plant: 4 brown-seeded plants: 6 dull brown-seeded plants: 4 dull yellow-seeded plants: 1 bright yellow-seeded plant, indicating control by two incompletely dominant genes.

Seed/Coat colour (testa colour)/*Brassica juncea*

Nayar and George (1970)
The F_2 segregation data for a cross between a yellow-seeded mutant of cv. Rai 5 (mutant YSM_2) and black-seeded cv. Rai 5 indicated a monogenic recessive inheritance. Mutant YSM_2 was obtained following irradiation with ß-rays.
Singh and Srivastava (1974)
The inheritance of seed coat colour was investigated in a cross between a yellow-seeded rai accession (App-3) x brown-seeded rai (T.11). F_1 plants had brown seed. The F_2 segregation ratio was consistent with a single recessive gene for yellow seed coat colour.

Vera *et al.* (1979)
The inheritance of seed coat colour was studied in crosses between brown-seeded Canadian cv. Blaze, European cv. Ekla, Canadian landrace Commercial Brown, and yellow-seeded Canadian cv. Domo. Brown seed coat colour (*R*) was dominant to yellow seed coat colour (*r*). Segregation patterns for F_2 and BC_1 generations were either brown or yellow and were consistent with a digenic model of inheritance. Postulated genotypes were $R_1\_r_2r_2$ and $R_1\_R_2\_$ for brown-seeded plants and $r_1r_1r_2r_2$ for yellow-seeded plants.

Vera and Woods (1982)
The digenic inheritance of seed coat colour was confirmed.

Aslam and Bechyne (1983a)
Seed coat colour in *Brassica juncea* was controlled by two independently inherited genes. Brown seed coat was dominant over yellow seed coat.

Dhillon *et al.* (1986)
The segregation pattern of the progeny of a cross between strains PR-15 (black-brown-seeded) and Lear (yellow-seeded) provided evidence for a two gene system with epistatic action (segregation ratio: 12 black seeds: 3 light brown seeds: 1 yellow seed). The following genotypes were postulated: *A*_ _ _ (brown-seeded), *aaB*_ (light brown-seeded), and *aabb* (yellow-seeded).

Chauhan and Kumar (1987)
Digenic segregation (15:1) was observed for seed coat colour in F_2 progenies of crosses between brown-seeded cultivars and lines Varuna, T 6342, Sekhar, PR 34, and RW 75-123-2, and yellow-seeded lines TM 9, K 1, and YSRL 1. Brown seed was dominant over yellow seed.

Singh and Aruna (1994)
Digenic inheritance with duplicate gene action was determined in crosses between brown-seeded cvs. RCC 15, Kranti, and Khrisna, and yellow-seeded cvs. DIRA 313, DIRA 326, and RW 3/86.

Seed/Coat colour (testa colour)/*Brassica napus*

Henderson and Pauls (1982)
The seed coat colour of 99 doubled haploid lines were derived from cultured F_1 microspores of a cross between a yellow-seeded rapeseed [= subsp. *oleifera*] line and dark-seeded canola [= subsp. *oleifera*] line G231 and cv. Topas was examined. The frequency of the yellow-seeded doubled haploid lines was consistent with a model based on six genes with recessive alleles for yellow seed coat colour.

Shirzadegan (1986)
Reciprocal crosses between yellow-, partially yellow-, and light brown-seeded lines x black-seeded oilseed rape [= subsp. *oleifera*] cv. Quinta were made. F_2 segregation data indicated that seed coat colour was controlled by three genes, designated Bl_1, Bl_2, and Bl_3. Yellow seed occurred when all alleles at the three loci were recessive.

Chen *et al.* (1988a)
Brassica napus was resynthesized from crosses between Chinese kale [= *Brassica oleracea* var. *alboglabra*] x turnip rape [= *Brassica campestris* subsp. *oleifera*]. For the crosses, a black-seeded accession and a light brown-seeded accession of Chinese kale and one brown-seeded accession and ten yellow-seeded accessions of turnip rape were used. The black-seeded trait of Chinese kale and the brown-seeded trait of turnip rape were completely epistatic over the yellow-seeded trait of turnip rape and the light brown-seeded trait of Chinese kale.

Ruecker (1991)
Crosses were made between five genotypes of winter oilseed rape [= subsp. *oleifera*]: line A (black-seeded), line B (brown-seeded), lines C, D, and E (yellow-brown-seeded). Black seed coat colour was completely dominant over the other colours. Two or three factors were postulated; yellow-brown was considered to represent a fully recessive genotype.

Wang and Liu (1991)
Genetic analysis of mutable gene(s) in Chinese yellow-seeded *B. napus* [= subsp. *oleifera*] line Ly84-24. Line Ly84-24 was the S_1 progeny of a yellow seeded plant (2178-25) derived from seven generations of selfing of a yellow-seeded mutant plant discovered in 1976 by H.L. Liu, Huazhong Agricultural University, Wuhan, China.

Progeny of line Ly84-24 showed yellow, heavily dotted (HD) yellow, lightly dotted (LD) yellow, and black seeds. Dark spots were traced to the palisade layer of the seed coat or the aleurone layer of the endosperm. The segregation of HD and LD yellow seeds was 3HD: 1LD, indicating that one allele was involved in the degree of dotting. HD was dominant over LD. The dotting gene was designated *Al1** for aleurone 1* (the * denoting a mutable allele); the recessive allele was designated *al1*.

A black palisade gene, designated *Bl1*, was found to be unstable. Allele *Bl1** represented the variegated form of gene *Bl1*. The following genotypes were postulated: *bl1*/bl1**, *al1*/al1** (highly dotted yellow seeds), *bl1*/bl1**, *al1*/al1* (highly and lightly dotted yellow seeds), *bl1*/bl1**, *al1/al1* (lightly dotted yellow seeds), and *Bl1*/–,–/– (black seeds).

Another allele for completely yellow seeds was identified and designated as *r-bl1* for recessive allele *bl1*.

The mutable allele *Bl1** was associated with a transposable element, designated *Tbn1* (Transposon *Brassica napus* 1).

Seed/Coat colour (testa colour)/*Brassica rapa*

Shaw (1934)
Crosses were made between yellow-seeded yellow sarson [= subsp. *trilocularis*] x red-seeded toria [= subsp. *dichotoma*] and black sarson [= subsp. *oleifera*]. The F_1 plants were all red-seeded. In the F_2, the frequency of yellow-seeded plants was lower than the expected 3:1 ratio of red-seeded to yellow-seeded plants. The presence of a lethal factor in yellow-seeded plants was postulated.

Shaw (1936)
Crosses were made between yellow-seeded yellow sarson [= subsp. *trilocularis*] x red-seeded toria [= subsp. *dichotoma*] and black sarson [= subsp. *oleifera*]. Seed coat colour was controlled by a single gene, red being dominant over yellow.

Mohammad *et al.* (1942)
The inheritance of seed coat colour in crosses among strains with various seed coat colours originally derived from yellow sarson [= subsp. *trilocularis*] and toria crosses was studied. The strains were: strain H. 4 (dark red brown-seeded), strain H. 12 (red brown-seeded), strain H. 16 (yellow brown-seeded), and strain H. 20 (yellow-seeded). Seed coat colour was controlled by three genes, designated Br_1 (dark reddish brown), Br_2 (reddish brown), and Br_3 (yellowish brown); yellow seeds were produced when none of the seed coat colour factors were present. The existence of modifying genes that caused the occurrence of various shades of brown in the F_2 generations was suggested. The postulated genotypes were given as $Br_1Br_1br_2br_2Br_3Br_3$ and $Br_1Br_1br_2br_2br_3br_3$ (dark reddish brown), $br_1br_1Br_2Br_2Br_3Br_3$ and $br_1br_1Br_2Br_2br_3br_3$ (reddish brown), $br_1br_1br_2br_2Br_3Br_3$ (yellowish brown), and $br_1br_1br_2br_2br_3br_3$ (yellow).

Reddish brown seed coat colour (gene Br_2) was found to be inherited independently from white petal colour (gene *y*) in a cross between strain C. 19 (red brown-seeded, yellow petals) x strain L. 5 (yellow-seeded, white petals). Gene Br_2 was also inherited independently from a gene for hairiness (gene *H*) and a gene for number of valves in the siliques (gene *V*).

Aoba (1970)
The inheritance of seed coat colour (brown, orange) and root colour (purple, red, white) was investigated in turnip [= subsp. *rapifera*]. Seed coat colour and root colour were conditioned by two genes, designated *P* and *C*. Postulated genotypes were *C_P_* (purple root and brown seed), *C_ pp* (red root and orange seed), *ccP_* (white root and brown seed), and *ccpp* (white root and orange seed).

Joarder and Eunus (1970)
See Morphological traits/Plant/Height/*Brassica rapa*.

Ahmed and Zuberi (1971)
The inheritance of seed coat colour was studied in toria [= subsp. *oleifera*] cvs. Toria-A (reddish-brown-seeded), Toria-BP (yellow-seeded), Toria-TP (yellow-seeded), and Toria-7 (reddish-brown-seeded). The segregation of the F_1, F_2, and both BC generations indicated that the trait was controlled by a single gene; reddish brown was completely dominant over yellow.

Jönsson (1975)
Inheritance studies in turnip rape [= subsp. *oleifera*] indicated that yellow seed coat colour was controlled by a minimum of three genes.

Stringam (1980)
The inheritance of seed coat colour was studied in crosses between brown-seeded Swedish spring cv. Arlo [= subsp. *oleifera*] x yellow-seeded Indian spring land race yellow sarson [= subsp. *trilocularis*], and Canadian brown-seeded spring cvs. Echo, Polar, and Torch [= subsp. *oleifera*] and the yellow sarson landrace. In general, the F_2 and testcross segregation data indicated a two, unlinked, dominant gene model. The genes were designated *Br1* and *Br3*. Dominance at the *Br1* locus resulted in brown seed, while dominance at the *Br3* locus, and with recessive alleles at the *Br1* locus, resulted in yellow-brown seed; homozygous recessive alleles at both loci resulted in yellow seed.

Hawk (1982a)
Crosses were made between a green hypocotyl, yellow-seeded selection of *B. campestris* x an early-flowering wild-type line and cv. Torch [= subsp. *oleifera*]. Segregation ratios were consistent with a single recessive gene which controlled both green hypocotyl colour and yellow seed coat colour. The gene for green hypocotyl colour was epistatic to the dominant alleles at the Br_1 and Br_3 seed coat colour loci.

Schwetka (1982)
Seed coat colour in turnip rape [= subsp. *oleifera*] was controlled by one or two genes with epistatic action. Two genes with epistatic action, designated Br_1 and Br_6 and four genes with hypostatic action, designated Br_3, Br_4, Br_5, and Br_7 were described. Two alleles, designated br^1_1 and br^21 (yellow seed coat colour) were found at the Br_1 locus. One allele, designated br^1_6 (yellow seed coat colour) and a second allele, designated br^2_6 (light hilum colour), were found at the Br_6 locus. The genes for seed coat colour were inherited independently from a gene for hilum colour, designated Br_8.

Barcikowska (1983)
Yellow seed coat colour in F_5 progeny of hybrids between Chinese cabbage [= subsp. *pekinensis*] and a genotype of yellow sarson [= subsp. *trilocularis*] was controlled by a single recessive gene.

Chen and Heneen (1992)
The inheritance of seed coat colour was studied in four Indian yellow-seeded yellow sarson accessions (K-151, K-88, T-42, RS-24), one yellow-seeded Swedish accession (Sv85-38301), and a black-seeded

accession (cv. Kova). Diallel crosses among the yellow-seeded accessions indicated that the Indian accessions had the same genotype and were different from the Swedish accession.

Black seed coat colour was found to be dominant over yellow seed coat colour. The segregation patterns for seed coat colour in the F_2 generation (including reciprocals) and the BC_1 generation (BC to the yellow-seeded parent) indicated that black seed coat colour was controlled by a single dominant gene, although distorted segregation patterns were observed in some generations. Seed coat colour was controlled mainly by the maternal genotype, but could be influenced by the genotypes of the endosperm and embryo.

Chauhan *et al.* (1995)
A carmel (= caramel) seed coat colour mutant was isolated in yellow sarson [= subsp. *trilocularis*] strain YSIK 4 treated with 50 kR. Progenies (F_1, F_2, BC_1, and BC_2) of crosses between the mutant x wild-type strain NDYS 1 (yellow-seeded) indicated that the caramel colour was dominant over the wild-type colour and controlled by a single gene.

Teutonico and Osborn (1994)
See Morphological traits/Leaf/Trichomes/Pubescence/glabrous/*Brassica rapa*.

Seed/Coat colour (testa colour)/*Raphanus sativus*

Bonnet (1979)
The F_1, F_2, and BC_1 generations of a cross between cv. Biser round white radish, with glabrous leaves and yellow seeds [also studied in Madzharova (1975)] and a line of round radish which was red and white, with hairy leaves and brown seeds were studied. The traits red root and hairy leaf showed complete linkage as in Madzharova (1975), and were also linked to stem and seed coat colour. Segregation data suggested a simple monogenic dominant determinism for the group of traits (red root, hairy leaf, red stem, brown seed). F_1 plants had a red root with small white tip; the F_2 and BC_1 plants had only two classes: white and red with small white tip.

Seed/Epidermis type/*Brassica rapa*

Shibutani and Okamura (1957)
The F_1 generation of crosses between turnips [= subsp. *rapifera*] with different types of epidermis showed that type A (distinct cell layers, cells swelling upon imbibition) was dominant over type B (indistinct epidermal layer). No F_2 segregation ratios were provided.

Seed/Hilum colour/*Brassica rapa*

Schwetka (1982)
Seed coat colour in turnip rape [= subsp. *oleifera*] was controlled by one or two genes with epistatic action. Two genes with epistatic action, designated Br_1 and Br_6 and four genes with hypostatic action, designated Br_3, Br_4, Br_5, and Br_7 were described. Two alleles, designated br^1_1 and br^21 (yellow seed coat colour) were found at the Br_1 locus. One allele, designated br^1_6 (yellow seed coat colour) and a second allele, designated br^2_6 (light hilum colour), were found at the Br_6 locus. The genes for seed coat colour were inherited independently from a gene for hilum colour, designated Br_8.

Seed/Mucilage/*Brassica rapa*

King *et al.* (1982)
The inheritance of the presence or absence of seed mucilage was determined from F_1 segregation data from crosses of mucilaginous lines of Canadian spring cv. Candle [= subsp. *oleifera*] and from testcross segregation data from the F_1 progenies x Canadian spring cv. Torch (non mucilaginous). The presence or absence of mucilage in the seed coat was determined by the genotype of the maternal parent. The mucilage production trait was dominant. The segregation data were consistent with a model involving two genes with dominance epistasis. The genes were designated *M1* and *M2*.

Seed/Number/*Brassica carinata*

Subudhi and Raut (1994a)
See Morphological traits/Plant/Branch number/*Brassica carinata*.

Seed/Number/*Brassica juncea*

Paul (1978)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Paul (1979)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Chaudhary and Sharma (1982)
See Morphological traits/Leaf/Size/*Brassica juncea*.

Govil *et al.* (1984)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Thakral *et al.* (1986)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Subudhi and Raut (1994a)
See Morphological traits/Plant/Branch number/*Brassica carinata*.

Seed/Number/*Brassica napus*

Lefort-Buson and Dattée (1982a)
See Morphological traits/Leaf/Number/*Brassica napus*.

Lefort-Buson and Dattée (1982b)
See Morphological traits/Leaf/Number/*Brassica napus*.

Lefort-Buson *et al.* (1987a)
See Morphological traits/Plant/Height/*Brassica napus*.

Sharaan (1987)
Quantitative genetic analysis of data collected from a two-year field test of oilseed rape [= subsp. *oleifera*] German cv. AD201 and French cvs. Crésor, Brutor, BRO, BRIO, and Orpal indicated that the number of seeds per silique, early flowering, and seed weight per plant were highly heritable.

Seed/Number/*Brassica rapa*

Rao (1977)
See Morphological traits/Plant/Branch number/*Brassica rapa*.

Paul (1978-1979)
See Morphological traits/Plant/Branch number/*Brassica rapa*.

Seed/Number/*Eruca vesicaria* subsp. *sativa*

Yadav and Kumar (1984)
See Morphological traits/Plant/Branch number/*Eruca vesicaria* subsp. *sativa*.

Seed/Number/*Raphanus raphanistrum*

Mazer (1987)
See Morphological traits/Ovule number/*Raphanus raphanistrum*.

Seed/Row number/*Brassica rapa*

Aslam and Bechyne (1983b)
Inheritance studies indicated that siliques with two rows of seed were dominant over siliques with four rows of seed. The trait was controlled by a single dominant gene. Two-row plants in the progeny of four-row plants were observed in rare cases.

Seed/Set/*Brassica juncea*

Tripathi *et al.* (1980)
Crosses were made between Alternaria black spot resistant line RC 781 and alternaria black spot susceptible cultivars Prakash, RH 30, RL 18, and T 59. F_2 segregation ratios indicated that Alternaria black spot resistance was dominant and monogenic. Resistance to Alternaria black spot was linked to reduced silique length, seed set, and 1,000 seed weight.

Seed/Size/*Brassica juncea*

Paul (1978)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Paul (1979)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Govil *et al.* (1984)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Badwal and Labana (1987)
Nine mustard cultivars were studied in a one way 36 single crosses in a half diallel mating system. Both general and specific combining ability (SCA) were significant for seed size and protein content. Only SCA was significant for oil content. Additive and non-additive genetic control was identified for seed size and protein content. Only non-additive effects were observed for oil content.

Seed/Size/*Brassica napus*

Lefort-Buson and Dattée (1982a)
See Morphological traits/Leaf/Number/*Brassica napus*.

Lefort-Buson *et al.* (1987a)
See Morphological traits/Plant/Height/*Brassica napus*.

Seed/Size/*Brassica rapa*

Rao (1977)
See Morphological traits/Plant/Branch number/*Brassica rapa*.

Paul (1978-1979)
See Morphological traits/Plant/Branch number/*Brassica rapa*.

Seed/Size/*Crambe abyssinica*

Meier and Lessman (1973b)
See Morphological traits/Plant/Height/*Crambe abyssinica*.

Seed/Size/*Crambe hispanica*

Meier and Lessman (1973b)
See Morphological traits/Plant/Height/*Crambe abyssinica*.

Seedling colour/*Raphanus sativus*

Uphof (1924)
The inheritance of the trait “reddish cortex” was determined to be conditioned by two genes with duplicate dominant alleles for red colour (F_2 ratio: 15 seedlings with red cortex: 1 seedling with white cortex). The genes were designated R_1 and R_2.

Tatebe (1938)
The cross between cv. Cincinnati Market (segregating for green seedlings) x cv. Golden Ball (green seedlings) produced F_1 green seedlings. The F_2 generation produced true-breeding green plants and plants segregating in an approximate ratio of 3 green: 1 yellow seedlings. Factor x_a (yellow seedlings) was postulated.

Sepal/Persistence/*Brassica oleracea*

Sampson (1958a)
Sepal persistence in green sprouting broccoli [= var. *italica*] was controlled by a single recessive gene, designated *ps*.
Sampson (1966b)
The sepal persistence gene *ps* in green sprouting broccoli [= var. *italica*] was shown to be linked to the self-incompatibility locus and to gene *A* (anthocyanin production), with 22.8±0.7% recombination.

Wills and Smith (1972)
See Morphological traits/Anther/Tip colour/*Brassica oleracea*.

Sepal/Tip colour/*Brassica rapa*

Cours (1977)
The absence of purple pigmentation (presumably anthocyanin) on the tip of sepals in young flower buds was studied in USDA introduction PI 175079. The trait was conditioned by a single recessive gene, designated *ab.*

Sepal/Width/*Brassica rapa*

James and Williams (1980)
The inheritance of the trait “narrow sepals” (sepals involute in mature buds giving a narrow tubular appearance to the bud) observed in a *B. campestris* strain derived from a cross between USDA PI 183395 x PI 175079 was found to be monogenic. The trait was conditioned by a recessive allele, designated *nsep*. Linkage studies between *nsep* and gene *Pb3* for resistance to clubroot race 6 in Chinese cabbage [= subsp. *pekinensis*] cv. Michihili and turnip [= subsp. *rapifera*] lines ECD 02 and ECD 03 provided no evidence of linkage.

Silique/Beak length/*Brassica rapa*

Rao (1977)
See Morphological traits/Plant/Branch number/*Brassica rapa*.

Silique/Colour/*Raphanus sativus*

Humaydan and Williams (1976)
Inheritance studies of purple vs. green pigmentation in the siliques of radish USDA Plant Introduction PI 179982 [= var. *caudatus*], based on F_1 and F_2 generations, indicated that purple pigmentation was controlled by a single dominant gene, designated *Pu*. Modifying genes were also suggested by the increased variation observed in the F_2 progenies compared with the F_1.

Silique/Inner silique mutant/*Brassica rapa*

Pathak and Singh (1949)
The occurrence of plant mutants where one to two extra siliques were observed inside the normal silique was described. The inner siliques appeared to be normal and contained a few seeds that matured. The trait appeared to be controlled by a single recessive gene.

Silique/Length/*Brassica juncea*

Tripathi *et al.* (1980)
See Morphological traits/Seed/Set/*Brassica juncea*.

Chaudhary and Sharma (1982)
See Morphological traits/Leaf/Size/*Brassica juncea*.

Thakral *et al.* (1986)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Acharya (1988)
See Morphological traits/Plant/Height/*Brassica juncea*.

Silique/Length/*Brassica napus*

Chay (1985)
The presence of relatively few genes with major effects was suggested for a cross between spring oilseed rape [= subsp. *oleifera*] inbred line TB 42 (short siliques) and long podded selection from cv. China A '555553'. Silique length was little affected by environment. Segregation in the F_2 fitted a 9:7 ratio. A two gene-two allele system with complete or nearly complete dominance was proposed for the trait. It was postulated that long siliques were produced when at least one dominant allele was present at both loci. The genotypes $L_1\_L_2\_$ (long siliques) and $L_1\_l_2l_2$, $l_1l_1L_2\_$, and $l_1l_1l_2l_2$ (short siliques) were postulated.

Liu and Liu (1987a)
See Morphological traits/Plant/Branching habit/*Brassica napus*.

Chay and Thurling (1989)
The inheritance of silique length was studied in a cross between spring oilseed rape [= subsp. *oleifera*] line TB42 (short siliques) and line CA553, a long podded selection from cv. China A. The mean length of the F_1 plants was intermediate between those of the parents, but slightly greater than the mid-parent value. The F_2 distribution was bimodal with a 9:7 ratio. Much of the variation was attributed to two major, complementary genes, designated L_1/l_1 and L_2/l_2; minor modifier genes were also postulated.

Silique/Length/*Brassica rapa*

Rao (1977)
See Morphological traits/Plant/Branch number/*Brassica rapa*.

Silique/Length/*Eruca vesicaria* subsp. *sativa*

Yadav and Kumar (1984)
See Morphological traits/Plant/Branch number/*Eruca vesicaria* subsp. *sativa*.

Silique/Number/*Brassica carinata*

Subudhi and Raut (1994a)
See Morphological traits/Plant/Branch number/*Brassica carinata*.

Silique/Number/*Eruca vesicaria* subsp. *sativa*

Yadav and Kumar (1984)
See Morphological traits/Plant/Branch number/*Eruca vesicaria* subsp. *sativa*.

Seed/Number/*Brassica juncea*

Paul (1978)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Paul (1979)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Govil *et al.* (1984)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Labana *et al.* (1984)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Thakral *et al.* (1986)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Sachan and Singh (1988)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Subudhi and Raut (1994a)
See Morphological traits/Plant/Branch number/*Brassica carinata*.

Silique/Number/*Brassica napus*

Richards and Thurling (1979)
Heritability of silique number per plant was found to be low.

Lefort-Buson and Dattée (1982a)
See Morphological traits/Leaf/Number/*Brassica napus*.

Lefort-Buson and Dattée (1982b)
See Morphological traits/Leaf/Number/*Brassica napus*.

Malik *et al.* (1995)
See Morphological traits/Plant/Branch number/*Brassica napus*.

Wu *et al.* (1995)
A mutant with two to three pistils and 10-18 stamens in each flower was obtained from the progeny of an interspecific cross between oilseed rape [= *Brassica napus* subsp. *oleifera*] and turnip rape [= *Brassica rapa* subsp. *oleifera*]. Reciprocal crosses were made between multiple silique *B. napus* and single silique *B. napus* and *B. rapa* cultivars. The multiple silique trait was recessive with no reciprocal effects in the intervarietal crosses within *B. napus*. The trait was also recessive in the interspecific crosses when *B. rapa* was the female parent. When the multiple silique *B. napus* was used as the female parent in the interspecific crosses, a high percentage (78.3 to 98.21%) of the F_1 hybrid plants had multiple siliques, indicating cytoplasmic influence on the trait.

Silique/Number/*Brassica rapa*

Rao (1977)
See Morphological traits/Plant/Branch number/*Brassica rapa*.

Paul (1978-1979)
See Morphological traits/Plant/Branch number/*Brassica rapa*.

Yadava *et al.* (1985)
See Morphological traits/Plant/Branch number/*Brassica rapa*.

Falk *et al.* (1995)
Canadian cultivars Echo, Torch, and Tobin and the Swedish strain SV8236580 were reciprocally hand crossed by bud-pollination in a complete diallel. Six of the 12 hybrids exhibited mid-parent heterosis with values of 35% for the Tobin x Torch hybrid and 14% for the reciprocal Torch x Tobin hybrid. Strong positive correlations were found between number of siliques per m^2 and seed yield ($r = 0.81$) and between number of siliques per m^2 and number of siliques per plant ($r = 0.68$). Hybrids produced 12% higher plants per plot and 9% more siliques per m^2 on average than the parental cultivars.

Wu *et al.* (1995)
See Morphological traits/Silique/Number/*Brassica napus*.

Silique/Orientation/*Brassica juncea*

Pokhriyal *et al.* (1964)
The appressed silique trait (3-10 degree angle) found in a rai mutant was dominant to opened silique arrangement (50-60 degree angle) and controlled by a single gene.

Nayar and George (1970)
The F_2 segregation data for a cross between a mutant with appressed siliques (mutant *APM*) and cv. Rai 5 (opened silique arrangement) indicated a monogenic recessive inheritance. Mutant *APM* was obtained following irradiation with X-rays. The silique arrangement of *APM* resembled that of *Brassica nigra*.

Brar *et al.* (1991)
The inheritance of appressed siliques was examined in the progeny of a cross between lines RC-781 and UVR-4. The F_2 segregation fitted a 9:7 distribution, indicative of two complementary genes.

Silique/Orientation/*Brassica napus*
Kelly *et al.* (1995)
Alleles for upright siliques were dominant over alleles for horizontal siliques, based on RFLP analysis. Additive interactions between two loci were identified.

Silique/Valve number/*Brassica rapa*

Mohammad *et al.* (1942)
The trait 2-valved siliques was found to be dominant over the trait 4-valved siliques in the F_2 progeny of a cross between strain C. 19 (red brown-seeded, 2-valved siliques) x strain L. 5 (yellow-seeded, 4-valved siliques). The gene for 2-valved siliques was designated as *V*; gene *V* was inherited independently from gene Br_2 (reddish brown seed).

Kadkol *et al.* (1986a)
The inheritance of multivalved siliques was studied in the following crosses: Canadian spring cv. Torch [= subsp. *oleifera*] (2-valved siliques) x yellow sarson [= subsp. *trilocularis*] line IB-5 (4-valved siliques) and yellow sarson line B-46 (4-valved siliques) x Canadian spring cv. Torch (2-valved siliques). F_2 segregation data indicated that the multivalve trait was controlled by three genes, two of which being

epistatic over the third gene when they were recessive (54:10 ratio). The multivalve trait and four traits used to assess silique strength (bending moment, energy, bending moment per silique length, and energy per silique length) showed linkage.

Segregation data for the F_2 generation of a cross between brown sarson line DS-17-D (2-valved siliques) x yellow sarson line IB-5 (4-valved siliques) indicated a two gene control with dominant epistatic action (12:3:1 ratio for 2-valved: 3-valved: 4-valved siliques).

Stem/Colour/*Brassica oleracea*

Sampson (1967a)
See Morphological traits/Anther/Tip colour/*Brassica oleracea*.

Stem/Colour/*Raphanus sativus*

Bonnet (1979)
The F_1, F_2, and BC_1 generations of a cross between cv. Biser round white radish, with glabrous leaves and yellow seeds [also studied in Madzharova (1975)] and a line of round radish which was red and white, with hairy leaves and brown seeds were studied. The traits red root and hairy leaf showed complete linkage as in Madzharova (1975), and were also linked to stem and seed coat colour. Segregation data suggested a simple monogenic dominant determinism for the group of traits (red root, hairy leaf, red stem, brown seed). F_1 plants had a red root with small white tip; the F_2 and BC_1 plants had only two classes: white and red with small white tip.

Stem/Enlarged/*Brassica incana*

Kianian and Quiros (1992a)
Segregation ratios in a F_2 population (36:16 plants) derived from reciprocal F_1 hybrids of crosses between kohlrabi [= *Brassica oleracea* var. *gongylodes*] with enlarged stem and *B. incana* fitted a dominant monogenic model, with enlarged stem (bulb) being dominant. The size of bulbs, however, behaved as a polygenic trait.

Stem/Enlarged/*Brassica oleracea*

Pease (1927)
The inheritance of bulb formation in kohlrabi [= var. *gongylodes*] was studied in crosses between kohlrabi x cabbage [= var. *capitata*], curly kale [= var. *acephala*], thousand-head kale [= var. *fruticosa*], savoy cabbage [= var. *sabauda*] and brussels sprouts [= var. *gemmifera*]. Bulb formation was dominant and conditioned by three genes, designated B_1, B_2, and B_3. Gene B_1 or gene B_2 was linked to gene *D* for purple leaves in cabbage.

Allgayer (1928)
A dominant gene, designated *B*, conditioned stem thickness in tree kale [= var. *acephala*]. Symbol *B* was superseded by symbol *Br* (Yarnell, 1956).

Kianian and Quiros (1992a)
See Morphological traits/Stem/Enlarged/*Brassica incana*.

Stem/Node number/*Brassica oleracea*

Hodgkin (1981)
The inheritance of node number and rate of node production was investigated in brussels sprouts [= var. *gemmifera*] using 10 F_1 cultivars (Leonore, King Arthur, Peer Gynt, Parsifal, Jade E, Perfect Line, Achilles, Kadina, Gleneagles, and Nelson) and 45 progenies derived from intercrossing and selfing. A close correlation was observed between total node number and rate of node production, as well as between total node number and number of harvested sprouts.

Stem/Trichomes (pubescence)/*Brassica juncea*

Pokhriyal *et al.* (1964)
The inheritance of leaf and stem pubescence was studied in crosses between rai genotypes Cream rye (glabrous) x T_3E_4-1 (pubescent). The F_1 plants were pubescent. The F_2 segregation ratios were consistent with pubescence being governed by two complementary genes. There was variation in the number of trichomes, indicating the presence of minor genes.

Stomates/Guard cell length/*Brassica napus*

Paul (1992b)
The inheritance of stomatal frequency, guard cell length, stomatal pore length, and leaf diffusion resistance of forage rape [= subsp. *oleifera*] was studied in a 5 x 5 diallel cross. Significant additive and dominance effects were observed for all traits except leaf diffusion resistance of the lower surface in one of the two years of the test. Low narrow-sense heritability was observed for leaf diffusion resistance and pore length. Leaf diffusion resistance was negatively correlated with stomatal frequency and pore length. Stomatal frequency and pore length were also negatively correlated.

Stomates/Number/*Brassica napus*

Paul (1992b)
See Morphological traits/Stomates/Guard cell length/*Brassica napus*.

Stomates/Stomatal pore length/*Brassica napus*

Paul (1992b)
See Morphological traits/Stomates/Guard cell length/*Brassica napus*.

PHENOLOGICAL TRAITS

Days to flower (see Earliness/Maturity)

Days to 95% bloom (see Earliness/Maturity)

Earliness/Maturity/*Brassica carinata*

Zaman (1989)
The inheritance of days to flower and maturity in the interspecific crosses *Brassica napus* x *Brassica rapa, B. napus x Brassica juncea*, *B. napus* x *Brassica oleracea* var. *alboglabra*, and *B. napus* x *Brassica carinata* were determined to be under polygenic control.

Earliness/Maturity/*Brassica juncea*

Chaudhary and Sharma (1982)
See Morphological traits/Leaf/Size/*Brassica juncea*.

Govil *et al.* (1984)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Acharya (1988)
See Morphological traits/Plant/Height/*Brassica juncea*.

Zaman (1989)
See Phenological traits/Earliness/Maturity/*Brassica carinata*.

Earliness/Maturity/*Brassica napus*

Campbell and Kondra (1978)
Analysis of single plants in parental, F_1, and F_2 populations of three crosses of oilseed rape [= subsp. *oleifera*] showed reciprocal differences indicating cytoplasmic effects for most of the observed traits. The types of gene action shown in the F_1 included dominance for early flowering and early maturity, additive effects and heterosis for yield and yield components. The oilseed rape cvs. Nugget, Oro, and Target were chosen to represent a range of maturity. Heritabilites were generally low for the traits observed, with the exception of days to first flower as an indicator of maturity.

Singh and Yadav (1980)
A 9 X 9 diallel of nine inbreds of rapeseed [= subsp. *oleifera*] Sangram, T9, ITSA, TH 14, TH 17, Fd 60, 146-1, YSM, and Laha T 36, was assessed for days to 50% flower, maturity, and seed yield, and the genetic components of variation were estimated. Overdominance was shown for flowering, maturity, and seed yield. The estimates of narrow-sense heritability were low for flowering and seed yield and moderate for maturity. Both general combining ability (GCA) and specific combining ability

(SCA) variances were significant for flowering and seed yield, whereas only the SCA variance was significant for maturity. The F_1 hybrids of parents from genetically divergent groups for flowering and maturity showed high SCA effects. Significant SCA effects were also found for seed yield, suggesting non-additive gene action in the expression of these traits.

Lefort-Buson and Dattée (1982b)

See Morphological traits/Leaf/Number/*Brassica napus*.

Sernyk and Stefansson (1983)

F_1 hybrids produced by hand crossing seven and four cultivars of *B. napus* [= subsp. *oleifera*] were assessed for agronomic and quality traits. Days to first flowering and days to maturity indicated a partial dominance of earliness in all hybrids. Tall stature was partially dominant. Significant heterosis for seed yield was observed. The heterosis for seed yield in summer rape hybrids cv. Marnoo x cv. Regent and cv. Karat x cv. Regent exceeded those of cv. Regent by 38 and 43%, respectively. Heterosis for total dry matter production was also significant in the three highest yielding hybrids. Correlations among seed yield, total dry matter production and apparent harvest index were positive and highly significant. Seed oil content, seed protein content, and 1,000 seed weight were comparable to those for cv. Regent.

Ringdahl *et al.* (1986)

See Morphological traits/Leaf/Number/*Brassica napus*.

Liu and Liu (1987a)

See Morphological traits/Plant/Branching habit/*Brassica napus*.

Sharaan (1987)

See Morphological traits/Seed/Number/*Brassica napus*.

Thukral and Singh (1987)

A diallel cross between nine oilseed rape [= subsp. *oleifera*] lines was analysed for combining ability. Maturity and seed yield were largely governed by non-additive gene effects. Flowering was influenced by non-additive gene effects. The best parents for inheritance of earliness, both at flowering and maturity were cv. Tower and N 20-4; for seed yield, cv. Midas and DBO15. Crosses between early and high yielding parents provided the best opportunity for producing improved seed yield in an early maturing background.

Brandle and McVetty (1989a)

Seven groups of inbred lines were derived from summer oilseed rape [= subsp. *oleifera*] cvs. Westar, Regent, Lergo, Marnoo, Ariel, Karat, and R83-11 by single seed descent for three generations followed by selfing. The lines were assessed for agronomic traits and seed oil and protein concentrations. The low levels of inbreeding depression for days to flower and maturity, assessed as the difference between the mean of the inbred lines and the mean of their respective source cultivars, led to the conclusion that there were few segregating loci for earliness in the cultivars and recessive alleles at these loci were at a very low frequency. No significant inbreeding depression was found for earliness in cvs. Lergo or Regent, implying additive genetic effects.

Zaman (1989)

See Phenological traits/Earliness/Maturity/*Brassica carinata*.

Thurling and Kaveeta (1992)
Two sources of early flowering genes were *Brassica napus* breeding line RU2 and *Brassica rapa* population Chinoli C42, which flowered significantly earlier than the commercial cv. Wesbrook independent of vernalization or photoperiod. In a cross between RU2 and cv. Wesbrook, flowering time in the F_2 was highly heritable, with transgressive segregation for earliness in the F_2 and BC_1F_2. After several BC generations and selfing, early flowering lines were selected. Variation in flowering time was primarily due to differences in growth rate. F_2 plants of the interspecific cross between Chinoli C42 and Wesbrook varied in chromosome number and flowering time. Two BC generations followed by selfing without selection produced euploid *B. napus* lines, all flowering significantly earlier than cv. Wesbrook. The earliest flowering line was equal to the Chinoli C42 parent.

Earliness/Maturity/*Brassica oleracea*

Swarup *et al.* (1963)
Analysis of a diallel cross with six lines of cabbage [= var. *capitata*] indicated dominance for the number of marketable heads, large head weight, and early maturity.

Watts (1964)
Diallel crosses were made in autumn cauliflower [= var. *botrytis*] between eight cultivars (Veitch's Autumn Giant, Autumn Queen, Lucifer, All Saints, Veitch's self-protecting, October Giant, Moneymaker, and Tremendous) and in early summer cauliflower between six inbred lines of cv. Cambridge 5. In autumn cauliflower, the inheritance of curding periods was additive with no evidence of gene interaction. Mostly dominant polygenes were found in most cultivars with early to mid maturity, while late maturity was determined by recessive polygenes. In the early summer cauliflower inbred lines, diallel analysis indicated a higher degree of dominance of the early curding trait and more specific combining ability than in the autumn cauliflower cultivars. In the early summer cauliflower lines, low number of leaves produced before curding was positively associated with early curding.

Swarup and Pal (1966)
See Morphological traits/Curd/Size/*Brassica oleracea*.

Dickson (1968)
The inheritance of earliness was studied in crosses between early broccoli [= var. *italica*] cv. Coastal and accession USDA PI 189028 x late summer cauliflower [= var. *botrytis*] accessions USDA PI 241621, PI 250218, PI 217934, and PI 269311. Earliness in the broccoli parents was controlled by a single dominant gene, designated *Ea*.

Chiang (1969)
See Morphological traits/Head/Core length/*Brassica oleracea*.

Summers and Honma (1980)
Crosses were made between single plant selections of cabbage [= var. *capitata*]. Segregating populations from crosses between smooth green cabbage cultivars showed dominance for early maturity, large head weight, low weight of non-wrapper leaves, and low stalk weight. Opposite dominance effects were observed in red x green cabbage crosses.

Zaman (1989)
See Phenological traits/Earliness/Maturity/*Brassica carinata*.

Earliness/Maturity/*Brassica rapa*

Joarder and Eunus (1970)
See Morphological traits/Plant/Height/*Brassica rapa*.

Rao (1977)
See Morphological traits/Plant/Branch number/*Brassica rapa*.

Zaman (1989)
See Phenological traits/Earliness/Maturity/*Brassica carinata*.

Ågren and Schemske (1992)
See Morphological traits/Flower/Number/*Brassica rapa*.

Thurling and Kaveeta (1992)
See Phenological traits/Earliness/Maturity/*Brassica napus*.

Prasad (1993)
See Morphological traits/Cotyledon/Size/*Brassica rapa*.

Ågren and Schemske (1994)
See Morphological traits/Flower/Number/*Brassica rapa*.

Song *et al.* (1995)
See Morphological traits/Leaf/Lobe number/*Brassica rapa*.

Earliness/Maturity/*Crambe abyssinica*

Meier and Lessman (1973b)
See Morphological traits/Plant/Height/*Crambe abyssinica*.

Lessman (1975)
See Morphological traits/Plant/Height/*Crambe abyssinica*.

Earliness/Maturity/*Crambe hispanica*

Meier and Lessman (1973b)
See Morphological traits/Plant/Height/*Crambe abyssinica*.

Earliness/Maturity/*Raphanus raphanistrum*

Panestos and Baker (1968)
Interspecific crosses were made between plants from two wild populations of *Raphanus raphanistrum* from central California, U.S.A., x radish [= *Raphanus sativus*] cv. Cincinnati Market and radish plants from one wild population from central California, U.S.A. F_1 and F_2 segregation data indicated that the late time to flowering characteristic of *R. sativus* and the early flowering time of *R. raphanistrum* were polygenically controlled, although three distinct groups (early, medium, late) with the ratios of 5:10:3 in the F_2 generation were recognized. F_1 hybrids were almost intermediate between the parents.

Conner (1993)
Major genes affecting quantitative traits within a single natural population of wild radish [= *R. raphanistrum*] from Binghamton, New York, U.S.A., were tested using an indirect method based on the patterns of family means and within and between family variances for traits. This method determined whether or not a single major locus was responsible for most of the variability in the trait, but could not be used to provide an estimate of the number of genes segregating for a trait. From 350 plants grown from field-collected seed (parental generation), 50 plants were selected as pollen donors and used to pollinate six randomly selected dams or pollen recipients in order to create 300 full-sibling families, with a final sample size of 289 full-sib families and 1,125 offspring. Major (single) gene effects were found for emergence time and flowering time.

Mazer and Schick (1991)
See Morphological traits/Ovule number/*Raphanus raphanistrum*.

Conner and Via (1993)
See Morphological traits/Anther/Filament length/*Raphanus raphanistrum*.

Earliness/Maturity/*Raphanus sativus*

Panestos and Baker (1968)
See Phenological traits/ Earliness/Maturity/*Raphanus raphanistrum*.

Vahidy and Hartmann (1971)
Individual plant selections were performed in cv. Chinese half long (daikon) for late flowering (six generations) and early flowering (four generations). The response to selection was gradual with no appreciable decrease of variability. Realized heritability of mean flowering time in the first four generations of selection averaged 37.4%. Realized heritability in more advanced generations averaged 33%.

Vahidy and Hartmann (1972a)
Reciprocal crosses were made between ten early and ten late flowering lines of radish cv. Daikon. No significant differences between the crosses and their reciprocals were found for days to flower. F_1 hybrids showed intermediate values between those of the parental lines. The heritability estimate, calculated from the variances of F_1 and F_2 generations, was 34.9%. This estimate was similar to that obtained by two other methods (Vahidy and Hartmann 1971, 1972b). Frequency distributions of the

F_1 and F_2 generations showed no dominance for the time of flowering and indicated polygenic control of flowering time, *i.e.* greater than two pairs of genes.

Earliness/Maturity/*Thlaspi arvense*

McIntyre and Best (1978)
Crosses were made between early-flowering and late-flowering strains of *T. arvense* from Saskatchewan, Canada. All of the F_1 plants had the late-flowering phenotype. The F_2 generation and BC to the early-flowering parent gave segregation rations of 3:1 and 1:1 late-flowering to early-flowering phenotypes, respectively, suggesting control by a single gene with complete dominance of the late-flowering allele.

Seed germination/*Brassica carinata*

Thakral and Singh (1995a)
Seeds of six parents and 15 F_1 hybrids were germinated on filter paper containing 0, 125, and 175 meq/L chloride salt solutions. Seedling vigour was correlated with germination percentage, rate of germination, root length, seedling fresh weight, seedling dry weight. No correlations were found between these traits and seed yield.

Seed germination/*Brassica juncea*

Verma and Lal (1991)
Fifteen lines were crossed to tester lines DIR-313 and TM-22 and to the F_1 hybrid DIR-313 X TM-22, and the hybrids were analysed for germination percent, seedling dry weight and electrical conductance of seed leachate. Both additive and dominance components were important with additive effects predominant for all traits.

Seed germination/*Brassica napus*

Acharya *et al.* (1983)
Heritability estimates of germinability and growth at different temperatures (5, 7.5, 10, 20, and 25° C) of Canadian spring oilseed rape [= *B. napus* subsp. *oleifera*] cvs. Midas and Regent, and line DI-820, and turnip rape [= *B. rapa* subsp. *oleifera*] cvs. Torch and Candle indicated a complex inheritance (possibly polygenic) which was very strongly influenced by the environment. Broad-sense heritability values were about 60% for *B. napus* and 90% for *B. rapa*.

Seed germination/*Brassica oleracea*

Chiang and Jacob (1992)
The inheritance of precocious seed germination in cabbage was studied in reciprocal crosses between breeding line 87-19-5 (with precocious seed germination) x cv. Little Rock (without precocious seed

germination). The F_2 and BC segregation ratios were consistent with a single dominant gene for precocious seed germination.

Seed germination/*Brassica rapa*

Acharya *et al.* (1983)
See Phenological traits/Seed germination/*Brassica napus*.

Prasad (1993)
See Morphological traits/Cotyledon/Size/*Brassica rapa*.

Seed germination/*Raphanus raphanistrum*

Mazer and Schick (1991)
See Morphological traits/Ovule number/*Raphanus raphanistrum*.

Seed germination/*Raphanus sativus*

Prasad and Prasad (1978)
See Morphological traits/Leaf/Number/*Raphanus sativus*.

Seedling/Emergence/*Crambe abyssinica*

Meier and Lessman (1973b)
See Morphological traits/Plant/Height/*Crambe abyssinica*.

Seedling/Emergence/*Crambe hispanica*

Meier and Lessman (1973b)
See Morphological traits/Plant/Height/*Crambe abyssinica*.

Seedling/Emergence/*Raphanus raphanistrum*

Conner (1993)
See Phenological traits/Earliness/Maturity/*Raphanus raphanistrum*.

Conner and Via (1993)
See Morphological traits/Anther/Filament length/*Raphanus raphanistrum*.

Seedling/Vigour/*Brassica carinata*

Thakral and Singh (1995a)
Seeds of six parents and 15 F_1 hybrids were germinated on filter paper containing 0, 125, and 175 meq/L chloride salt solutions. Seedling vigour was correlated with germination percentage, rate of germination, root length, seedling fresh weight, seedling dry weight. No correlations were found between these traits and seed yield.

YIELD AND QUALITY TRAITS

Head firmness/*Brassica rapa*

Tan *et al.* (1982)
See Morphological traits/Head/Diameter/*Brassica rapa*.

Seed fatty acids/Eicosenoic acid (C20:1)/*Brassica carinata*

Rahman (1976)
The inheritance of fatty acid contents was investigated in the F_1, F_2, and BCF_1 populations derived from an interspecific cross between *Brassica juncea* and *Brassica carinata* (5th and 6th generation inbred lines from stocks from the Oleiferous *Brassica* Breeding Program of the Agricultural University, Prague, Czechoslovakia). Erucic acid content was governed by a single gene, with additive action. Eicosenoic acid content was conditioned by the same gene as erucic acid. Linolenic acid and linoleic acid contents were controlled by different single genes, which showed dominance and additive gene action, respectively. The inheritance of oleic acid content could not be determined. Environment influenced the contents of some fatty acids, particularly when their content was high.

Seed fatty acids/Eicosenoic acid (C20:1)/*Brassica juncea*

Rahman (1976)
See Yield and quality traits/Seed fatty acids/Eicosenoic acid (C20:1)/*Brassica carinata*.

Seed fatty acids/Eicosenoic acid (C20:1)/*Brassica napus*

Kondra and Stefansson (1965)
Three strains of rapeseed [= subsp. *oleifera*] were used in this study, zero erucic acid line Liho-Z (0.2-0.8%) isolated from cv. Liho, zero erucic acid line Bud-Z from Budapest, and high erucic acid line Nug-E from Canadian cv. Nugget. The F_1 from diallel crosses between the three parents, the six BCF_1 populations and the parental lines were grown in the field. Erucic acid and eicosenoic acid content were determined by the genotype of the embryo. The segregation of erucic acid content of the seed oil from the BCF_1 populations fitted a 1:2:1 model, indicating the influence of two genes with additive gene action. The zero erucic acid genotypes were assigned the genotype *e1e1e2e2* and the high erucic acid genotype *E1E1E2E2*. Each *E1* and *E2* allele contributed one-quarter of the erucic acid level of the high

erucic acid parent. The seed from the crosses and BCF_1 populations between the two zero erucic acid lines Bud-Z and Liho-Z had zero erucic acid levels, establishing the presence of two common gene loci in the two strains. The inheritance of eicosenoic acid content was determined to be controlled by two gene action with high expression dominant to low. The association between low levels of eicosenoic acid and zero erucic acid content established that the same two genes controlled the expression of the two long chain fatty acids.

Krzymanski and Downey (1969)
The inheritance of eicosenoic acid content was studied in conjunction with that of erucic acid in crosses between Polish spring cv. Bronowski [= subsp. *oleifera*] (11-20% eicosenoic acid and 5-10% erucic acid) and winter cv. Qulzower Olequell (high erucic acid content) and between Polish winter cv. Wazarski (high erucic acid content) and Canadian spring line SZ61-1 (0.5-2% eicosenoic acid and zero erucic acid). Segregation patterns indicated one gene pair with each allele acting additively and contributing about 6% eicosenoic acid and about 3.5% erucic acid. The genotypes *ee* (0-2% eicosenoic acid, zero erucic acid), E^de (7-12% eicosenoic acid, 2-4% erucic acid), and E^dE^d (13-17% eicosenoic acid, 4-13% erucic acid) were postulated.

Rahman and Bechyne (1975)
Interspecific crosses were made between oilseed rape [= *Brassica napus* subsp. *oleifera*] and turnip rape [= *Brassica rapa* subsp. *oleifera*] with different contents of erucic acid, linoleic acid, and linolenic acid. The frequency distribution in the F_2 generation showed three groups of segregants ranging from 0 to 42% erucic acid which fitted a 1:2:1 single gene ratio. The genotypes *aa*, *Aa*, and *AA* were proposed, with each *A* allele contributing 15-17% erucic acid to the seed oil. The segregation of eicosenoic acid supported the segregation of a single gene with dominance for eicosenoic acid values above 4%. A single gene with dominance for high expression (above 11%) was also proposed for the control of linolenic acid in the crosses. Similarly, the segregation for linoleic acid suggested a single gene control although the average parental values were relatively close, 18.8 and 22.2% for *B. napus* and *B. rapa*, respectively. A strong environmental influence was evident in the wide variation for linoleic acid content in the F_2.

Chen and Heneen (1989)
Inheritance studies of the seed oil fatty acid composition of four resynthesized oilseed rape [= subsp. *oleifera*] lines indicated that low palmitic acid content was partially epistatic to high palmitic acid content. High oleic acid content was either partially hypostatic or transgressively epistatic to low oleic acid content, depending on the erucic acid content of the parents. Low linoleic acid content was controlled by epistatic gene action in two crosses and additive gene action in the other two crosses. Low linolenic acid content was under the control of partial or transgressive epistasis. In general, high eicosenoic acid content was epistatic to low eicosenoic acid content. In three crosses, partial epistasis was detected for high erucic acid content, whereas in the fourth cross, hypostasis was observed. Two genes, one residing in the genome of *B. rapa* and the second gene residing in the genome of *B. oleracea*, controlled erucic acid production in *B. napus*.

Liu and Liu (1990)
The inheritance of erucic and eicosenoic acid were studied in the F_1, F_2, BC_1, and BC_2 of crosses between four genotypes of oilseed rape [= subsp. *oleifera*]. The additive-dominance model was adequate for erucic acid inheritance, with predominant additive effects at two loci with an equal effect on erucic acid content of 13.0 to 14.5. The dominance effects were less than 1.0. The inheritance of eicosenoic acid was complex. One locus showed incomplete dominance in the F_1 for the alleles increasing the eicosenoic value. When the parents differed at two loci, there was overdominance for

high expression, indicating non-allelic interactions. The two loci difference showed additive by additive and additive by dominance effects.

Seed fatty acids/Eicosenoic acid (C20:1)/*Brassica rapa*

Rahman and Bechyne (1975)
See Yield and quality traits/Seed fatty acids/Eicosenoic acid (C20:1)/*Brassica napus*.

Seed fatty acids/Eicosenoic acid (C20:1)/*Sinapis alba*

Ecker and Yaniv (1993)
Inheritance of fatty acid composition was studied in F_1 diallel crosses in the accessions Tel-Maabarot and Bet-Dagan from Israel, 44-873 from St. Petersburg, Russia, and Mustang and 3568 from Idaho, U.S.A. Crosses were made among accessions having contrasting amounts of oleic acid and erucic acid; concentrations of oleic acid, linoleic acid, eicosenoic acid, and erucic acid were determined. Genetic analysis confirmed that the composition of the fatty acids was controlled mainly by the nuclear genes of the embryo. Additive gene action with partial dominance for the reducing alleles was noted for oleic acid and linoleic acid, while erucic acid showed an additive mode of inheritance with partial dominance for the enhancing alleles. Positive heterosis was demonstrated for eicosenoic acid. Erucic acid content was strongly negatively correlated with oleic acid (r = -0.97) and linoleic acid (r = -0.93) contents, suggesting a genetic interdependence between these fatty acids. Broad-sense and narrow-sense heritability estimates were consistently high for oleic acid (0.96 vs. 0.82), linoleic acid (0.92 vs. 0.70), and erucic acid (0.97 vs. 0.90), but were divergent for eicosenoic acid (0.94 vs. 0.46).

Seed fatty acids/Erucic acid (C22:1)/*Brassica carinata*

Liu and Liu (1987b)
A new gene system was proposed to identify the various alleles that condition erucic acid production. The new symbols consist of the letter *E* for erucic acid, a subscripted letter to represent the genome, *i.e.* E_A (*B. rapa*), E_B (*B. nigra*), E_C (*B. oleracea*), E_AE_C (*B. napus*), E_AE_B (*B. juncea*), and E_BE_C (*B. carinata*), and a superscripted figure to indicate the allele at the locus, for example E_C^1.

Fernandez-Escobar *et al.* (1988)
Reciprocal interspecific crosses between *Brassica carinata* and low erucic acid oilseed rape [= *Brassica napus* subsp. *oleifera*] cv. Duplo were performed. Segregation ratios of F_2 and BC generations to *B. carinata* indicated that erucic acid content was controlled by two additive genes.

Getinet *et al.* (1994)
Zero erucic acid Ethiopian mustard [= *Brassica carinata*] was developed through an interspecific cross with zero erucic acid Oriental mustard (*Brassica juncea*). The interspecific cross between Ethiopian mustard cv. S-67 and Zem 2336 was followed by four backcrosses to cv. Dodolla, a yellow-seeded *B. carinata* with high seed oil content. Each BC generation was selfed and the BCF_2 seed analyzed for fatty acid composition by half-seed method. Zero erucic acid seed were identified in the BCF_2 seed generation. The zero erucic acid allele had been introgressed from the A genome of Zem *B. juncea*

into the C genome of *B. carinata*. Two gene control of erucic acid content in *B. carinata* with additive gene action was indicated.

Getinet *et al.* (1997)
The inheritance of erucic acid was studied in progeny of crosses between Ethiopian mustard [= *Brassica carinata*] cultivars Dodolla and S-67 (high erucic acid) x line C90-14 (zero erucic acid). The erucic acid of the F_1 seed was intermediate to that of the parents. F_2 and testcross ratios were consistent with control by two genes acting additively with each locus contributing about 10% erucic acid.

Seed fatty acids/Erucic acid (C22:1)/*Brassica juncea*

Rahman (1976)
See Yield and quality traits/Seed fatty acids/Eicosenoic acid (C20:1)/*Brassica carinata*.

Kirk and Hurlstone (1983)
Segregation data of crosses between the low erucic acid lines Zem1 and Zem2 and European and Indian cultivars with a high erucic acic content indicated that erucic acid content was controlled by two genes, one in each genome, and three alleles, E_0, E_1, and E_2, conferring 1, ~12, and ~20% erucic acid, respectively.

Liu and Liu (1987b)
See Yield and quality traits/Seed fatty acids/Erucic acid (C22:1)/*Brassica carinata*.

Wang and Li (1990)
The inheritance of erucic acid content was determined in the progeny of crosses between low erucic acid cv. Zem 2 x high erucic acid cvs. Yilihuang, 707, 624, 548, 556, and Xinyou No. 1. Erucic acid content was conditioned by two incompletely dominant genes.

Khalatkar *et al.* (1991)
Crosses were made between Indian mustard cv. Pusa Bold as the BC parent with line ZYR-4 with the objective of adding white rust resistance, yellow seed coat colour, and low erucic acid content in the seed oil. Zero erucic acid F_2 plants were tested for resistance to white rust. The F_2 segregation fitted a 15:1 ratio of high to zero erucic acid plants, indicating digenic control. The preselected F_2 plants segregated in a 3:1 ratio for resistance, indicating monogenic control with dominance for resistance to white rust.

Getinet *et al.* (1994)
See Yield and quality traits/Seed fatty acids/Erucic acid (C22:1)/*Brassica carinata*.

Seed fatty acids/Erucic acid (C22:1)/*Brassica napus*

Craig (1961)
Analysis of six rapeseed (*B. napus* subsp. *oleifera* and *B. rapa* subsp. *oleifera*) cvs. Argentine, Arlo, Golden, Gute, Polish and Regina II over 22 stations using gas liquid phase chromatography of seed oils identified significant effects of location on each fatty acid except linolenic acid (C18:3). The majority

of the variation was in oleic acid (C18:1), linoleic acid (C18:2), and erucic acid (C22:1). The inverse relation between oleic acid and erucic acid had a correlation coefficient of -0.975.

Downey and Craig (1964)
Genetic analysis of oilseed rape [= subsp. *oleifera*] genotypes segregating for erucic acid content indicated control by two additive genes.

Harvey and Downey (1964)
Genetic analysis of F_2, F_3, and BC generations of a cross between a zero erucic acid line of cv. Liho [= subsp. *oleifera*] and high erucic acid cv. Golden [= subsp. *oleifera*] (41.3% erucic acid) provided evidence for a two gene model and additive gene action.

Stefansson and Hougen (1964)
Seed from 125 strains from three *Brassica* species, *B. napus* [= subsp. *oleifera*], *B. rapa* [= subsp. *oleifera*], and *B. juncea*, were screened for erucic acid content. The range in *B. napus* strains was 28-42%, *B. rapa* 23-55%, and *B. juncea* 21-41%. Analysis of 127 single plant selections from cv. Liho, a rapeseed cultivar from Limburger Hof, Germany, showed a range of erucic acid content from 6 to 50%. Four generations of selection in cv. Budapest produced successively lower levels of erucic acid to a level of 0.3%. The levels of oleic acid in these low erucic acid selections increased to 70% and were accompanied by a decrease in eicosenoic acid levels to less than 3%. Transfer of the zero erucic acid trait to improved germplasm was accomplished through crosses and selection. Analysis of the F_2 progeny supported the two gene model with additive gene action for the control of erucic acid levels.

Kondra and Stefansson (1965)
See Yield and quality traits/Seed fatty acids/Eicosenoic acid (C20:1)/*Brassica napus*.

Krzymanski and Downey (1969)
See Yield and quality traits/Seed fatty acids/Eicosenoic acid (C20:1)/*Brassica napus*.

Krzymanski (1970)
It was determined in crosses between oilseed rape [= subsp. *oleifera*] winter cultivars x a low erucic acid selection of spring cv. Bronowski that erucic acid content was controlled by one or two nuclear genes. There were a number of alleles or pseudoalleles acting in an additive manner.

Rahman and Bechyne (1975)
See Yield and quality traits/Seed fatty acids/Eicosenoic acid (C20:1)/*Brassica napus*.

Shiga (1978)
Germplasm screening was used to identify sources of low erucic acid content among Asian cultivars. No low erucic acid levels were found so reciprocal crosses were made between Japanese cvs. Chisaya-natane, Norin 16, and Asahi-natane x a zero erucic acid line introduced from Canada. Reciprocal differences were noted in the F_1 hybrids. When a Japanese cultivar was used as the female parent, the F_1 hybrids were shorter with better resistance to lodging. Zero erucic acid types were selected in the F_2 generation with the segregation ratio fitting a 1:15 low vs. high erucic acid types, supporting a two gene model for control of erucic acid with additive gene action. One line produced from the cross Norin 16 x zero-erucic F5-37 contained only 3% linolenic acid.

Anand and Downey (1981)
The five alleles *e*, *Ea*, *Eb*, *Ec*, and *Ed* were identified as influencing erucic acid content with each controlling the synthesis of 0, 10, 15, 30, and 35% of the erucic acid content. Selected plants with erucic acid contents of 7-8%, genotype *EdEdee*, were reciprocally crossed to plants with the genotype *Eaeee* and 10% erucic acid. The alleles *Ea*, *Ed*, and *e* were established to be in the same genome and at the same locus, probably on the *B. oleracea* genome.

Tang and Yang (1986)
Correlation and regression analysis of the major fatty acids, oil and protein content, glucosinolate content, and the sum of oleic and linoleic acid and the sum of oil and protein were investigated in 51 strains with low erucic acid (<3.5%). Linoleic acid had a negative correlation with oleic acid (r = -0.8046) and a positive correlation with linolenic acid (r = 0.5258). Erucic acid and glucosinolate content were not correlated with the other traits. Oil content was negatively correlated with protein content (r = -0.5357).

Liu and Liu (1987a)
See Morphological traits/Plant/Branching habit/*Brassica napus*.

Liu and Liu (1987b)
See Yield and quality traits/Seed fatty acids/Erucic acid (C22:1)/*Brassica carinata*.

Li and Qiu (1987)
Erucic acid synthesis in 22 swede [= subsp. *rapifera*] inbred lines was controlled by additive genes.

Chen *et al.* (1988b)
Crosses were made between synthetic *B. napus* line No7076 (pale-petalled, 25.8% erucic acid) x line Sv84-28053 (yellow-petalled, zero erucic acid). A single additive gene in the C genome controlled synthesis of erucic acid. There was no linkage between the gene for erucic acid and flower colour.

Fernandez-Escobar *et al.* (1988)
See Yield and quality traits/Seed fatty acids/Erucic acid (C22:1)/*Brassica carinata*.

Chen and Heneen (1989)
See Yield and quality traits/Seed fatty acids/Eicosenoic acid (C20:1)/*Brassica napus*.

Siebel and Pauls (1989a)
Microspore-derived spontaneous doubled haploid lines were developed from the F_1 generation of crosses between low (cv. Regent, 0.1%) and high (cv. Golden, 42%) erucic acid cultivars [= subsp. *oleifera*]. The fatty acid analysis of the doubled haploid lines confirmed the genetic control of erucic acid content by two genes with additive genetic interaction. Transgressive segregation occurrred both above the high parent and below the low parent. The levels of erucic acid were negatively correlated with the levels of palmitic acid (C16:0), oleic acid (C18:1), and linoleic acid (C18:2). Both negative and positive correlations were found between erucic acid and linolenic acid (C18:3).

Chen and Beversdorf (1990a)
Three microspore-derived populations of spring rapeseed [= subsp. *oleifera*] were derived from crosses between parental lines with contrasting fatty acid composition differing in amounts of erucic acid (C22:1, 0 to 42.3%), oleic acid (C18:1, 20.2 to 69.1%), linoleic acid (C18:2, 11.1 to 22.8%), and linolenic acid (C18:3, 2.6 to 11.3%) acid. The same two loci influenced the accumulation of erucic acid

and oleic acid, controlling the chain elongation step between oleic acid and erucic acid. Erucic acid was confirmed to be controlled by two major loci, each with two alleles with additive effects. At least two additional loci involving the control of the desaturation step from oleic acid to linoleic acid influenced the amount of oleic acid although to a lesser degree than the genes controlling the chain elongation step of oleic acid to erucic acid. In zero erucic acid populations, linoleic acid was determined to be under two gene control while the accumulation of linolenic acid was determined to be influenced by three gene loci with additive gene action.

Chen and Beversdorf (1990b)
Two populations were developed using microspore culture and single-seed descent from each of four crosses between parental oilseed rape [= subsp. *oleifera*] lines with contrasting seed oil profiles for erucic acid, oleic acid, linoleic acid, and linolenic acid. The means, ranges, and distribution patterns of the seed oil fatty acid profiles were comparable between the two populations within each cross. Linolenic acid, erucic acid, and linoleic acid contents were highly variable within both the microspore-derived and the single-seed descent populations in the four crosses. The results confirmed the random nature of the gametic arrays from microspore sampling of F_1 plants for fatty acid profiles examined. Differences between the two populations were assumed to be the result of residual heterozygosity within the single-seed descent population.

Liu and Liu (1990)
See Yield and quality traits/Seed fatty acids/Eicosenoic acid (C20:1)/*Brassica napus*.

Lühs and Friedt (1995)
In order to study the inheritance of erucic acid in resynthesized high erucic acid rapeseed (*Brassica napus*), double-low spring oilseed cultivars were crossed to resynthesized high erucic genotypes with 55 to 60% C22:1. The observed segregation ratio in the F_2 progeny supported the control of erucic acid synthesis in resynthesized *B. napus* by two genes acting in an additive manner. A single effective allele, designated *E*, contributed 16 to 17% C22:1.

Seed fatty acids/Erucic acid (C22:1)/*Brassica rapa*

Craig (1961)
See Yield and quality traits/Seed fatty acids/Erucic acid (C22:1)/*Brassica napus*.

Dorrell and Downey (1964)
The segregation ratios for F_2, F_3, and BC populations of crosses between a zero erucic acid line derived from cv. Polish [= subsp. *oleifera*] (25-30% erucic acid) and the high erucic acid (59%) Indian cvs. yellow sarson [= subsp. *trilocularis*] and Brown Sarson [= subsp. *dichotoma*] indicated a single gene, acting in an additive manner.

Rahman and Bechyne (1975)
See Yield and quality traits/Seed fatty acids/Eicosenoic acid (C20:1)/*Brassica napus*.

Liu and Liu (1987b)
See Yield and quality traits/Seed fatty acids/Erucic acid (C22:1)/*Brassica carinata*.

Cheng *et al.* (1993)
The inheritance of erucic acid content was determined in crosses between a nucleolar trisomic line (No. 2891) x Chinese landrace Wu Chang Bei You Cai and a non-nucleolar trisomic line (No. 2881) x Chinese landrace Xi Shui You Cai Bei. Both trisomic lines were derived from a *B. rapa-B. alboglabra* monosomic addition line in which the gene for erucic acid content was located on the alien chromosome. In both crosses, F_2 progenies derived from the trisomic F_1 plants showed a disomic inheritance pattern, indicating that the extra chromosome in No. 2891 and No. 2881 did not carry the erucic acid gene.

Rahman *et al.* (1994)
F_2 segregation of a cross between a white-petalled, high erucic acid yellow sarson accession [= subsp. *trilocularis*] and the yellow-petalled, low erucic acid Canadian canola cv. Tobin [= subsp. *oleifera*] indicated that erucic acid content was controlled by a single gene with additive action (1:2:1 ratio).

F_2 segregation of a cross between a yellow-petalled yellow sarson accession and the Canadian canola cv. Tobin (yellow-petalled) deviated significantly from expectation when the plants were grown in Bangladesh instead of Denmark, suggesting that the results could be due to male gamete selection.

Teutonico and Osborn (1994)
See Morphological traits/Leaf/Trichomes/Pubescence/glabrous/*Brassica rapa*.

Seed fatty acids/Erucic acid (C22:1)/*Brassica oleracea*

Liu and Liu (1987b)
See Yield and quality traits/Seed fatty acids/Erucic acid (C22:1)/*Brassica carinata*.

Seed fatty acids/Erucic acid (C22:1)/*Sinapis alba*

Ecker and Yaniv (1993)
See Yield and quality traits/Seed fatty acids/Eicosenoic acid (C20:1)/*Sinapis alba*.

Seed fatty acids/Erucic acid (C22:1)/*Sinapis arvensis*

Chen *et al.* (1995)
Wild Brassiceae material collected from Xianjiang Autonomous region, northwest China, referred to as Xianjiang wild rape, was concluded to be in the same cytodeme as *Sinapis arvensis* (genomes SS, 2*n* =18). Low erucic seeds were identified (10-11% erucic acid) and the segregation pattern fitted a monogenic additive mode of inheritance, *i.e.* 1 *EE* (18-22% erucic acid): 2 *Ee* (9-14% erucic acid): 1 *ee* (<1% erucic acid).

Seed fatty acids/Linoleic acid (C18:2)/*Brassica carinata*

Rahman (1976)
See Yield and quality traits/Seed fatty acids/Eicosenoic acid (C20:1)/*Brassica carinata*.

Seed fatty acids/Linoleic acid (C18:2)/*Brassica juncea*

Rahman (1976)
See Yield and quality traits/Seed fatty acids/Eicosenoic acid (C20:1)/*Brassica carinata*.

Seed fatty acids/Linoleic acid (C18:2)/*Brassica napus*

Craig (1961)
See Yield and quality traits/Seed fatty acids/Erucic acid (C22:1)/*Brassica napus*.

Rahman and Bechyne (1975)
See Yield and quality traits/Seed fatty acids/Eicosenoic acid (C20:1)/*Brassica napus*.

Bartkowiak-Broda and Krzymanski (1983)
Diallel crosses were made between seven inbred lines of zero erucic winter oilseed rape [= subsp. *oleifera*] which were significantly different in the distribution of the C18 fatty acids oleic acid (C18:1, 47.7 to 64%), linoleic acid (C18:2, 16:0 to 25.9%), and linolenic acid (C18:3, 12.6 to 17.1%). Comparisons were made of fatty acid composition of the parental lines and hybrids on the basis of seed harvested from field trials. Linolenic acid and oleic acid contents were determined by the maternal plant genotype, while linoleic acid content was predominantly controlled by the maternal plant, with some degree of influence from the embryo genotype. The implication for selection lay in the requirement to analyze seed from the second generation of the hybrid because of the maternal influence. The environment during seed development had a strong influence on the C18 fatty acid composition.

Tang and Yang (1986)
See Yield and quality traits/Seed fatty acids/Erucic acid (C22:1)/*Brassica napus*.

Chen and Heneen (1989)
See Yield and quality traits/Seed fatty acids/Eicosenoic acid (C20:1)/*Brassica napus*.

Siebel and Pauls (1989a)
See Yield and quality traits/Seed fatty acids/Erucic acid (C22:1)/*Brassica napus*.

Siebel *et al.* (1989a)
Oleic acid content was found to be negatively correlated with erucic acid content in seeds of microspore-derived spontaneous doubled haploid plants from crosses between low and high erucic acid parents.

Chen and Beversdorf (1990a)
See Yield and quality traits/Seed fatty acids/Erucic acid (C22:1)/*Brassica napus*.

Seed fatty acids/Linoleic acid (C18:2)/*Brassica rapa*

Craig (1961)
See Yield and quality traits/Seed fatty acids/Erucic acid (C22:1)/*Brassica napus*.

Rahman and Bechyne (1975)
See Yield and quality traits/Seed fatty acids/Eicosenoic acid (C20:1)/*Brassica napus*.

Seed fatty acids/Linoleic acid (C18:2)/*Sinapis alba*

Ecker and Yaniv (1993)
See Yield and quality traits/Seed fatty acids/Eicosenoic acid (C20:1)/*Sinapis alba*.

Seed fatty acids/Linolenic acid (C18:3)/*Brassica carinata*

Rahman (1976)
See Yield and quality traits/Seed fatty acids/Eicosenoic acid (C20:1)/*Brassica carinata*.

Seed fatty acids/Linolenic acid (C18:3)/*Brassica juncea*

Rahman (1976)
See Yield and quality traits/Seed fatty acids/Eicosenoic acid (C20:1)/*Brassica carinata*.

Roy and Tarr (1985)
A selection from the F_2 generation of the interspecific cross oilseed rape [= *Brassica napus* subsp. *oleifera*] cv. Tower x *Brassica juncea* with low levels of linolenic acid (C18:3) combined with high linoleic acid (C18:2) designated IXLIN was compared to the Oro mutant (Röbbelen and Nitsch, 1975) with high linoleic acid: low linolenic acid content. The inheritance of the IXLIN source of low levels of linolenic acid was determined to be recessive or additive. Selection for low levels of linolenic acid was also approached through the ratio of linoleic acid: linolenic acid.

Seed fatty acids/Linolenic acid (C18:3)/*Brassica napus*

Rahman and Bechyne (1975)
See Yield and quality traits/Seed fatty acids/Eicosenoic acid (C20:1)/*Brassica napus*.

Rakow and McGregor (1975)
Two lines developed from mutation treatment of low erucic acid rapeseed were selected for contrasting linolenic acid content (line M57: 5%, line M364: 20%) to determine whether the altered linolenic acid was associated with significant changes in the remainder of the seed oil fatty acid profile and other seed quality characteristics. Seed maturation and seed oil accumulation under controlled environment conditions were not affected by the altered linolenic acid levels. Significant differences in fatty acid profile were limited to reciprocal differences in the levels of oleic acid and linolenic acid when expressed on a percentage basis in the two lines. Differences in the rate of accumulation of oleic acid and linolenic acid were presumed to be the cause of the different accumulation patterns in the two lines. Chlorophyll content was not affected by the linolenic acid content, in contrast to a previous report linking high linolenic acid content with higher chlorophyll levels in the seed.

Röbbelen and Nitsch (1975)
Seed from the first low linolenic mutation line M57 originally derived from the zero erucic cv. Oro [= subsp. *oleifera*] was used for the study. The M3 and M4 generation of seeds treated with the mutagen EMS were selected for reduction in levels of linolenic acid. Plants with 39% linoleic acid and 4.3% linoleic acid and with 30% linoleic acid and 3.2% linolenic acid were selected. Crosses between mutant lines were made to identify complementary mutations which would result in further improvements. On average, the progeny showed intermediate levels of linoleic acid and linolenic acid contents. Single plants were selected with improved fatty acid profiles. No physiological limitation was associated with the low linolenic acid mutant lines.

Bartkowiak-Broda and Krzymanski (1983)
See Yield and quality traits/Seed fatty acids/Linoleic acid (C18:2)/*Brassica napus*.

Jönsson and Persson (1983)
A selection program for increased linoleic acid (C18:2) in winter oilseed rape [= subsp. *oleifera*] at Svalöv produced a line with 35% linoleic acid and 8-10% linolenic acid (C18:3) and a line with 22% linoleic acid and less than 5% linolenic acid in the seed oil. These lines were crossed to the low linolenic acid material produced by mutation (Röbbelen and Nitsch, 1975). The genetic control of both linoleic acid and linolenic was determined to be one or two genes with no dominance. The influence of the environment was low. An increase in palmitic acid (C16:0) was noted in the segregating generations. Using single plant and single seed selection in summer turnip rape, linoleic acid contents of 51%, linolenic acid contents of 3% and oleic acid + stearic acid (C18:0) contents of 80% were found. Material with very high levels of palmitic acid (12%) was found to be stable under different environments.

Roy and Tarr (1985)
See Yield and quality traits/Seed fatty acids/Linolenic acid (C18:3)/*Brassica juncea*.

Roy and Tarr (1986)
A cross between the interspecific source of low linolenic acid content in *Brassica napus* subsp. *oleifera* designated IXLIN and the Oro low linolenic mutant (Röbbelen and Nitsch, 1975) provided the source of lines with very low levels of linolenic acid (C18:3, 1.6 to 1.8%) in combination with high levels of linoleic acid (C18:2, 30%). The seed oil quality of the line is stable and no adverse affect was noted on seed development and yield.

Tang and Yang (1986)
See Yield and quality traits/Seed fatty acids/Erucic acid (C22:1)/*Brassica napus*.

Brunklaus-Jung and Röbbelen (1987)
Fourteen mutant lines of oilseed rape [= subsp. *oleifera*] with high linolenic acid (C18:2) and low linolenic acid (C18:3) contents were characterized for the inheritance of altered fatty acid composition. One recessive allele was identified as conferring the low linolenic acid trait of six mutants. Two mutants were identified with one incomplete dominant allele. Six mutant lines carried two independent alleles with additive gene action; three mutant lines showed partial dominance over alleles increasing linolenic acid content. Performance (yield, oil content) of the mutant lines was improved by backcrosses of the mutant lines to adapted cultivars. There was no linkage between the low linolenic acid trait and yield depression.

Diepenbrock (1987)
The mutation lines in this study were M43 with a linolenic acid (C18:3) content of 3% and M364 with 14% linolenic acid (Röbbelen and Nitsch, 1975). Reciprocal crosses, F_1, and BC_1F_1 generations were developed to determine the mode of inheritance of linolenic acid. The C18:3 concentration in the triacylglycerol at 50 days after flowering was influenced by the genotype of the embryo while the C18:3 concentration in the monogalactosyl-diacylglycerol at 30 days after flowering was determined by the maternal parent, probably a cytoplasmic influence. The switch from maternal to embryonic influence was explained by the pattern of C18:3 synthesis over the course of seed development, with the diacylgycerol transferred to the chloroplast envelope from the endoplasmic reticulum followed by C18:3 synthesis.

Diepenbrock and Wilson (1987)
Two mutant lines M43 and M364 (Röbbelen and Nitsch, 1975) were crossed reciprocally. The concentration of linolenic acid in the triacylgycerol was influenced by nuclear and cytoplasmic interaction while the concentration of linolenic acid in the monogalactosyl-diacylglycerol was determined by maternal (cytoplasmic) factors.

Roy and Tarr (1987)
The material used in the study was derived from crosses between the low linolenic acid mutant of cv. Oro [= subsp. *oleifera*] (Röbbelen and Nitsch, 1975), low linolenic acid material selected from interspecific crosses between *Brassica napus*, *Brassica juncea*, and *Brassica carinata* 'IXLIN'. Selections from the crosses showed variation for high oleic acid (C18:1, 69%), high linoleic acid (C18:2, 35%), and low linolenic acid (C18:3, 2%). Stability and viability of the lines with very low levels of linolenic acid (1.5%) were good.

Pleines and Friedt (1988)
Selection for low linolenic acid content in the seed oil of zero erucic acid rapeseed produced twelve lines with modified C18 fatty acid composition. The heritability of all C18 fatty acids was low at the single seed level. Significant genotype, environment, and genotype x environment interactions were found for palmitic acid (C16:0), oleic acid (C18:1), linoleic acid (C18:2), and linolenic acid (C18:3). Correlations between the C18 fatty acids were negative between C18:1: C18:2 and C18:1: C18:3, while C18:2: C18:3 were positively correlated. Formulas for calculating enzyme activities during C18 fatty acid biosynthesis proved to be useful for selection and development of low C18:3 material.

Chen and Heneen (1989)
See Yield and quality traits/Seed fatty acids/Eicosenoic acid (C20:1)/*Brassica napus*.

Pleines and Friedt (1989)
Two spring oilseed [= subsp. *oleifera*] rape lines differing for linolenic acid content were reciprocally crossed. The low linolenic acid line was derived from interspecific crosses (Roy and Tarr, 1987). The high linolenic acid line was developed by selection after three generations of inbreeding. Parental lines and reciprocal F_1s, F_2s, BC_1, and BC_2 were grown under two temperature regimes (warm 24.5/18.0° C and cold 14.5/8.0° C) and the mature seed was analyzed for fatty acid composition. The F_1 seed from the cross with the low linolenic acid line as the female showed significantly lower linolenic acid content, while the reciprocal F_1 did not differ from the mid-parent value, indicating maternal effects in the low linolenic acid line. Temperature had a significant effect on the expression of linolenic acid and the degree of maternal influence.

Siebel and Pauls (1989a)
See Yield and quality traits/Seed fatty acids/Erucic acid (C22:1)/*Brassica napus*.

Chen and Beversdorf (1990a)
See Yield and quality traits/Seed fatty acids/Erucic acid (C22:1)/*Brassica napus*.

Jourdren *et al.* (1996)
The pollen fatty acid composition was determined on 80 doubled haploid plants derived from a single F_1 hybrid from a cross between Canadian cv. Stellar (low C18:3, LDR or low desaturation ratio) and French cv. Drakkar (high C18:3). The low linolenic acid content and LDR traits from cv. Stellar were expressed in both pollen and seed, with a positive correlation ($r = 0.88$). The inheritance of low linolenic acid content and LDR was controlled by two major genes with additive effects, both in seed and pollen. Minor genes also appeared to be expressed in both pollen and seed.

Seed fatty acids/Linolenic acid (C18:3)/*Brassica rapa*

Rahman and Bechyne (1975)
See Yield and quality traits/Seed fatty acids/Eicosenoic acid (C20:1)/*Brassica napus*.

Seed fatty acids/Linolenic acid (C18:3)/*Sinapis alba*

Ecker and Yaniv (1993)
See Yield and quality traits/Seed fatty acids/Eicosenoic acid (C20:1)/*Sinapis alba*.

Seed fatty acids/Low desaturation ratio/*Brassica napus*

Jourdren *et al.* (1996)
See Yield and quality traits/Seed fatty acids/Linolenic acid (C18:3)/*Brassica napus*.

Seed fatty acids/Maternal effect/*Brassica napus*

Kondra and Stefansson (1970a)
The fatty acid composition of seed oils was determined from reciprocally crossed and self-pollinationed parental strains which differed for oleic acid and linoleic acid content to determine the maternal effects on oil quality. There were significant differences in the fatty acid composition of reciprocally crossed seed which is genetically the same constitution, indicating a maternal influence. The oleic acid and linoleic acid values for cross-pollinated seed differed from the values for maternal self-pollinated seed. Therefore the genotype of the embryo also influences fatty acid composition.

Thomas and Kondra (1973)
Three strains of zero erucic acid rapeseed [= subsp. *oleifera*] were selected for variation in the C18 fatty acids, oleic acid, linoleic acid, and linolenic acid. Analysis of selfed seed from parental lines and F_1 hybrids from reciprocal crosses showed a significant maternal effect for the C18 fatty acids but the

influence of the embryonic genotype was also significant. A strong environmental influence was identified with greater expression in the field environment compared to the greenhouse results.

Seed fatty acids/Oleic acid (C18:1)/*Brassica napus*

Craig (1961)
See Yield and quality traits/Seed fatty acids/Erucic acid (C22:1)/*Brassica napus*.
Bartkowiak-Broda and Krzymanski (1983)
See Yield and quality traits/Seed fatty acids/Linoleic acid (C18:2)/*Brassica napus*.

Tang and Yang (1986)
See Yield and quality traits/Seed fatty acids/Erucic acid (C22:1)/*Brassica napus*.

Chen and Heneen (1989)
See Yield and quality traits/Seed fatty acids/Eicosenoic acid (C20:1)/*Brassica napus*.

Siebel and Pauls (1989a)
See Yield and quality traits/Seed fatty acids/Erucic acid (C22:1)/*Brassica napus*.

Siebel *et al.* (1989a)
Oleic acid content was found to be negatively correlated with erucic acid content in seeds of microspore-derived spontaneous doubled haploid plants from crosses between low and high erucic acid parents.

Chen and Beversdorf (1990a)
See Yield and quality traits/Seed fatty acids/Erucic acid (C22:1)/*Brassica napus*.

Seed fatty acids/Oleic acid (C18:1)/*Brassica rapa*

Craig (1961)
See Yield and quality traits/Seed fatty acids/Erucic acid (C22:1)/*Brassica napus*.

Seed fatty acids/Oleic acid (C18:1)/*Sinapis alba*

Ecker and Yaniv (1993)
See Yield and quality traits/Seed fatty acids/Eicosenoic acid (C20:1)/*Sinapis alba*.

Seed fatty acids/Palmitic acid (C16:0)/*Brassica napus*

Chen and Heneen (1989)
See Yield and quality traits/Seed fatty acids/Eicosenoic acid (C20:1)/*Brassica napus*.

Siebel and Pauls (1989a)
See Yield and quality traits/Seed fatty acids/Erucic acid (C22:1)/*Brassica napus*.

Seed glucosinolates/*Brassica juncea*

Love (1988)
The inheritance of seed glucosinolate content was studied in *B. campestris* crosses between cv. R500 (high glucosinolate content) x strain CZY (low glucosinolate content), *B. napus* crosses between cvs. York and Midas (high glucosinolate content) x cvs. Egra and Westar (low glucosinolate content), and *B. juncea* crosses between strain 60143 containing 3-butenyl glucosinolate x cvs. ZEM and Domo containing 2-propenyl glucosinolate. In *B. campestris* and *B. napus*, F_2 and BC segregration ratios were consistent with control by three genes with dominance for high glucosinolate content. In both species, C4 to C5 amino acid precursor elongation was controlled by a dominant gene, designated *EL3*. In *B. campestris*, glucosinolate maturation and hydroxylation in both C4 and C5 pathways were controlled by the dominant genes *MT* and *HY*. Genes *EL3*, *MT*, and *HY* were unlinked in *B. campestris*. Glucosinolate production in *B. juncea* was controlled by more than one gene.

Love *et al.* (1990)
Inheritance of glucosinolate composition was examined in crosses between cv. Domo and line Zem 84-2293 (2-propenyl glucosinolate) and the Indian line 60143 (3-butenyl glucosinolate). Glucosinolate composition was controlled by more than one locus with multiple additive alleles.

Stringam and Thiagarajah (1995)
Inheritance of the alkenyl glucosinolates was determined in F_2, BC_1 and F_1-derived doubled haploid (DH) populations in a cross between high glucosinolate East Indian cv. RLM 514 and a low glucosinolate *B. juncea* breeding line from the University of Alberta, Edmonton, Canada. At least four genes were identified with recessive alleles at each locus required for the expression of low alkenyl glucosinolate levels. No reciprocal effects or maternal plant influences were identified. Partial or overdominance for the expression of high glucosinolate levels was shown in the DH population mean and distribution. Segregation ratios in the DH lines fitted both a 1:31 and 1:255 ratio, indicating that 5 to 8 recessive alleles controlled the complete absence of alkenyl glucosinolates in *B. juncea*. The BC progeny ratios suggested 6 to 9 recessive alleles. A ratio of 1:7 with three recessive alleles at three loci controlled low propenyl levels in both the DH and BC populations. The BC progeny ratios fitted a two gene control of 3-butenyl glucosinolate content, with two recessive alleles required for absence of expression.

Seed glucosinolates/*Brassica napus*

Kondra and Stefansson (1970b)
Glucosinolate content of rapeseed meal was investigated in crosses between oilseed rape [= subsp. *oleifera*] Polish cv. Bronowski (low glucosinolate content) and Canadian cv. Target (high glucosinolate content). The gluconapin, glucobrassicanapin, and progoitrin content was determined by the genotype of the maternal parent. The studies indicated that higher gluconapin values were partially dominant to lower values. Complete absence of gluconapin was controlled by three recessive alleles. Higher gluconapin values were overdominant to lower values and four or five recessive alleles controlled the absence of gluconapin. Higher values of progoitrin were partially dominant to the absence of progoitrin; the absence of progoitrin was controlled by four recessive alleles. There was linkage between the gene systems controlling the three glucosinolates.

Krzymanski (1970)
It was determined in crosses between oilseed rape [= subsp. *oleifera*] winter cultivars (high glucosinolate conent) x spring cv. Bronowski (low glucosinolate content) that glucosinolate content was controlled maternally. Heterosis was observed for pentenyl isothiocyanate. Incomplete dominance was observed for oxazolidinethiones.

Lein (1972)
Low glucosinolate content was found to be determined by two to three recessive or partially recessive genes in crosses between oilseed [= subsp. *oleifera*] cvs. Bronowski (low glucosinolate content) and Oro (high glucosinolate content). Low glucosinolate content was inherited independently from low erucic acid content.

Anand (1978)
The inheritance of the seed glucosinolates gluconapin, glucobrassicanapin and progoitrin was studied using a diallel cross involving 10 cultivars. Glucosinolate content was found to be under maternal control. Additive gene action was found for gluconapin, while partial to complete dominance was observed for glucobrassicanapin and progoitrin.

Salam and Downey (1978)
The inheritance of 3-butenyl isothiocyanate, 4-pentenyl isothiocyanate, and 5-vinyl-2-oxazolidinethione was determined in an interspecific cross between oilseed rape [= *Brassica napus* subsp. *oleifera*] cv. Bronowski (low seed glucosinolate content) x turnip rape [= *Brassica rapa* subsp. *oleifera*] cv. Polish (high seed glucosinolate content). The F_2 segregation ratios were consistent with single gene control for 3-butenyl isothiocyanate and 4-pentenyl isothiocyanate and digenic control for 5-vinyl-2-oxazolidinethione.

Busch and Röbbelen (1981)
Digenic inheritance was observed, with dominance of high values for total glucosinolate content.

Olivieri *et al.* (1982)
The inheritance of seed glucosinolate content was determined in a diallel cross between ten rapeseed [= subsp. *oleifera*] cultivars (Brink, Crésor, Dolora, Eurora, Midas, Primor, Ramsès O, Status, Vanda) and experimental line 51/74. Additivity and dominance were the main genetic components. Broad-sense heritability was 0.77 and narrow-sense heritability was 0.59.

Bartkowiak-Broda *et al.* (1983)
Diallel crosses between seven inbred lines with different contents and profiles of glucosinolates indicated that low glucosinolate content was controlled by recessive genes. Environmental effects were significant.

Gland (1985)
The inheritance of glucocosinolates was studied in crosses between resynthesized *B. napus* forms and natural genotypes [= subsp. *oleifera*]. Two dominant genes controlled high glucosinolate content, assuming that the second gene expressed overdominance over the first gene. Three dominant genes controlled the absence of sinigrin in progeny of the cross R 49 (high) x cv. Emerald (low).

Olivieri and Parrini (1986)
Genes for total glucosinolate content were found to be pleiotropic or linked to genes controlling the filling stage, as total glucosinolate content was correlated with the 1,000 seed weight.

Paul *et al.* (1986a)
The inheritance of thiocyanate and (+)S-methyl-L-cysteine sulphoxide content was studied in a diallel cross involving five cultivars of forage rape. Both additive and dominance components were significant for the two traits; the additive gene effect was greater than the dominance effect. Non-allelic gene interaction was detected for thiocyanate content. Narrow-sense heritability was relatively high for both traits. Thiocyanate and (+)S-methyl-L-cysteine sulphoxide contents were positively correlated; they were not correlated with dry matter yield and its components.

Tang and Yang (1986)
See Yield and quality traits/Seed fatty acids/Erucic acid (C22:1)/*Brassica napus*.
Zhou and Liu (1987)
Inheritance of glucosinolate content was studied in crosses between Canadian canola [= subsp. *oleifera*] cv. Altex x high glucosinolate Chinese rapeseed [= subsp. *oleifera*] cv. Huayou 8 and swede [= subsp. *rapifera*] line YG81-33. High seed glucosinolate content was partially dominant over low glucosinolate content and conditioned by three major genes.

Hu (1988)
A diallel between five inbred lines of rapeseed [= subsp. *oleifera*] was analyzed for oil, protein and total glucosinolate content. The additive-dominant model was adequate to explain the inheritance of all traits, with partial dominance tending to increase oil and protein content. Narrow-sense heritability estimates were 59.6% for oil content, 87.4% for glucosinolates, and 42.4% for protein content. Oil content was negatively correlated with protein content and total glucosinolate content was positively correlated with protein content.

Love (1988)
See Yield and quality traits/Seed glucosinolates/*Brassica juncea*.

Mou and Liu (1988)
Inheritance studies of total glucosinolate content in oilseed rape [= subsp. *oleifera*] cultivars indicated a three gene control in reciprocal crosses between Chinese cv. Huayou No. 16 x Australian cv. Marnoo and Chinese cv. Huayou No. 13 x Australian cv. Wesroona, and a two gene control in a cross between Chinese cv. 71-39 x Canadian cv. Andor. A digenic interaction model was adequate for total glucosinolate content in four crosses, with dominant and dominant x dominant effects important for cv. Huayou No. 16 and cv. Marnoo. There was no dominant effects for cv. 71-39 and cv. Andor.

Siebel and Pauls (1989b)
Inheritance studies were performed in oilseed rape [= subsp. *oleifera*] using crosses between doubled haploid plants of cv. Golden (high seed glucosinolate content) and cv. Regent (low seed glucosinolate content). Polygenic control was observed.

Mou and Liu (1990)
The inheritance of the total content of seed glucosinolates in oilseed rape [= subsp. *oleifera*] was studied in the crosses Huayou No. 16 (high) x Marnoo (low), Huayou No. 13 (high) x Wesroona (low), and 71-39 (high) x Andor (low). High glucosinolate content was partially dominant over low glucosinolate content. Three genes conditioned glucosinolate content in the crosses Huayou No. 16

x Marnoo and Huayou No. 13 x Wesroona, and two genes in the cross 71-39 x Andor. Glucosinolate content inheritance fitted a digenic interaction model, with additive and dominant effects, and epistasis.

Kräling *et al.* (1991)
Heritability of sinapoyl esters in seed of 42 lines and 98 synthetic lines was estimated at $h^2 = 0.6$ ($r^2 = 0.57$).

Rücker and Rudloff (1991)
The inheritance of seed glucosinolate content in winter oilseed rape [= subsp. *oleifera*] was studied in reciprocal crosses between doubled haploid lines A633 (low seed glucosinolate content) x A13 (high seed glucosinolate content) and in a complete diallel cross with eight doubled haploid lines ranging in seed glucosinolate content. The results of the A633 x A13 crosses indicated four to five genes with two to three of the genes being dominant. Broad-sense and narrow-sense heritabilities were high (0.95 and 0.87, respectively.
Mithen and Magrath (1992)
The inheritance of resistance to blackleg isolate RFMLM11 was examined in synthetic *B. napus* lines, line 235 (highly resistant) and line 233 (highly susceptible). F_1 hybrids (lines 235 x 233) had intermediate size lesions relative to the parental lines, indicating that resistance and susceptibility were codominant. Lesion size within F_2 progeny segregated in a continuous manner, suggesting that resistance was determined by a polygenic system. Resistance to blackleg was inherited independently from leaf glucosinolate content.

Magrath *et al.* (1993)
Six unlinked loci determined the inheritance of aliphatic glucosinolates in progeny of crosses between synthetic oilseed rape [= subsp. *oleifera*] lines and cultivars. One locus conditioned the presence/absence of propyl glucosinolates. One locus conditioned the expression of pentyl glucosinolates. Two loci controlled the production of alkenyl glucosinolates. Two loci controlled the hydroxylation of both butenyl and pentenyl glucosinolates.

Magrath *et al.* (1994)
Genetic studies of aliphatic glucosinolates within segregating populations of recombinant lines of oilseed rape [= *B. napus* subsp. *oleifera*] and *Arabidopsis thaliana* derived from crosses between parental lines with contrasting glucosinolate phenotypes. In *B. napus*, alleles at a single locus (*Gsl-pro*) regulated the presence or absence of propyl glucosinolates and those at two other loci (*Gsl-elong-C* and *Gsl-elong-A*; from genomes C and A, respectively) regulated side chain elongation of the amino acid derivative which results in the production of butyl and pentyl glucosinolates. Alleles at a single locus in *A. thaliana* (*Gsl-elong-Ar*) regulated side chain elongation of aliphatic glucosinolates in this species. It was suggested that the *Gsl-elong-Ar* gene was homologous to *Gsl-elong* genes in *B. napus*.

Parkin *et al.* (1994)
Segregation studies of the degree of hydroxylation in recombinant lines derived from crosses between oilseed rape [= subsp. *oleifera*] cultivars and synthetic *B. napus* lines indicated that two loci regulate hydroxylation of butenyl and pentenyl glucosinolates in both leaves and seeds. Alleles at a locus on linkage group 13 (*Gsl-oh-C*) have a major effect while alleles at a homoeologous locus on group 3 (*Gsl-oh-A*) have a minor effect.

Ruecker and Röbbelen (1994)
The inheritance of total glucosinolate content was studied with a complete F_1 diallel mating of eight doubled haploid oilseed rape [= subsp. *oleifera*] lines that differed in total content of individual glucosinolates, as well as in their profile, and with the segregating populations of two crosses between doubled haploid lines. Most of the genetic variability was caused by effects due to general combining ability; heterosis was unimportant. Broad-sense and narrow-sense heritabilities of glucosinolate content were high, 0.95 and 0.87, respectively. For glucosinolate content below 20 μmol/g seed, broad-sense and narrow-sense heritabilities were 0.69 and 0.66, respectively. Low total glucosinolate content was found to be controlled by four to five recessive genes with additive gene action. The alkenyl glucosinolate profiles of F_2 plants of resynthesized rapeseed lines were determined by four loci, two that were responsible for the elongation of butenyl glucosinolate to pentenyl glucosinolate and two that were responsible for hydroxylation of alkenyl glucosinolates.
Initial genetic studies of indolyl glucosinolate contents (0.1-4.5 μmol/g seed) indicated that two or three genes could be involved. The frequency distribution of F_2 phenotypes was virtually continuous. Genotypes with low alkenyl and low indolyl glucosinolate contents were selected after crossing parents with low alkenyl/high indolyl and high alkenyl/low indolyl glucosinolate contents.

Lethenborg *et al.* (1995)
Reciprocal crosses were made between a double low spring rape cultivar and an artificially synthesized *B. napus* generated by crossing *B. oleracea* var. *alboglabra* and a cultivar of yellow sarson [= *B. rapa* subsp. *trilocularis*]. Analysis of basic generations (F_1, F_2, BC_1, BC_2) for progoitrin and total glucosinolates fitted an additive-dominance model to explain the accumulation of progoitrin in the seeds. The inheritance of total glucosinolates was more complex with epistatic effects detected.

Seed glucosinolates/*Brassica oleracea*

Hill *et al.* (1984)
Heritability of total glucosinolate (GS) content was estimated in eight parents of *B. oleracea* reciprocally crossed in all combinations (four with high GS, 275-418 ppm, and four with low GS, 39-49 ppm). Regression of offspring on the parents estimated narrow-sense heritability at 0.32.

Chiang *et al.* (1986)
The inheritance of three glucosinolate components (goitrin, volatile isothiocyanates and the thiocyanate ion) was studied in cabbage [= var. *capitata*]. Results indicated that: all three components showed a strong heterosis towards lower concentrations, the maternal effect in inheritance was observed for goitrin only, lower concentrations of goitrin and volatile isothiocyanates were controlled by four to six genes, and the inheritance of thiocyanate ion was governed by only two to three loci.

Seed glucosinolates/*Brassica rapa*

Salam and Downey (1978)
See Yield and quality traits/Seed glucosinolates/*Brassica napus*.

Love (1988)
See Yield and quality traits/Seed glucosinolates/*Brassica juncea*.

Seed glucosinolates/*Crambe abyssinica*

Lessman (1975)
See Morphological traits/Plant/Height/*Crambe abyssinica*.

Seed proteins/Cruciferin/*Brassica oleracea*

Kianian and Quiros (1992b)
Sequences homologous to rRNA, napin, cruciferin, self-incompatibility, isocitrate lyase and malate synthase were mapped to the *B. oleracea* genome. Four segregating F_2 populations were examined: three intraspecific F_1 hybrids of collards [= var. *sabauda*] (B115) x cauliflower [= var. *botrytis*] (B 265); collards (B165) x broccoli [= var. *italica*] (B008), and wild kale from the USSR (B1661) x cauliflower (B265), and a fourth population derived from kohlrabi [= var. *gongylodes*] (B255) x *B. insularis* (B364). Ribosomal RNA (rRNA) mapped to three unlinked loci, designated *NOR-1*, *-2*, and *-3*; napin to five linked loci (*pN2-1*, *-2*, *-3*, *-4*, *-5*, and *-6*), the self-incompatibility trait to three linked loci (*pBOS5-1*, *-2*, and *-3*), isocitrate lyase to two linked loci (*pBSIL9-1* and *-3*), malate synthase to two independent loci (*pBSMS-1* and *-2*), and cruciferin to two independent loci (*pC1-1* and *pC1-2*).

Seed proteins/Napin/*Brassica oleracea*

Kianian and Quiros (1992b)
See Yield and quality traits/Seed glucosinolates/*Brassica oleracea*.

Soluble sugar/*Brassica napus*

Shattuck (1985)
See Morphological traits/ Root/Size/*Raphanus sativus*.

Yield/Curd/*Brassica oleracea*

Pal and Swarup (1966)
See Morphological traits/Leaf/Number/*Brassica oleracea*.

Yield/Foliage/*Brassica napus*

Shattuck (1985)
See Morphological traits/ Root/Size/*Raphanus sativus*.

Paul *et al.* (1986b)
The inheritance of yield was investigated in forage oilseed rape [= subsp. *oleifera*]. The general analysis of the data indicated that additive effects were predominant for all traits. Analysis using a six parameter model, with the epistatic variation separated, indicated that dominance effects were more

important than additive effects. Non-allelic gene interactions were present for all traits except the number of leaves. Additive x additive epistatic effects were important.

Yield/Foliage/*Brassica oleracea*

Johnston (1968)
See Morphological traits/Leaf/Number/*Brassica oleracea*.

Yield/Foliage/*Raphanus sativus*

Brar *et al.* (1972)
The inheritance of plant, root, and leaf weight was studied in diallel crosses of three European radish cultivars (Scarlet-Long, Sparkler, and Rapid-Red) and three Asiatic cultivars (Japanese-White, Desi-White, and Nadauni). Complementary epistasis was found for all three traits. The European cultivars had a larger number of dominant genes than the Asiatic cultivars. Light weight was dominant over heavy weight for all three traits. The ratios of positive to negative alleles were 1:3, 1:1, and 1:5 per plant, root, and leaf weights, respectively, and were inherited by 0.7, 0.3, and 3.7 factors, respectively.

Prasad and Prasad (1978)
See Morphological traits/Leaf/Number/*Raphanus sativus*.

Pandey *et al.* (1981)
See Morphological traits/Leaf/Number/*Raphanus sativus*.

Khan *et al.* (1983)
See Morphological traits/Plant/Height/*Raphanus sativus*.

Parthasarathy and Medhi (1983)
Genetic correlations for root length, root diameter, top weight, root: top ratio, and root weight were studied in nine Asiatic cultivars of radish (Pusa Desi, Pusa Himani, Pusa Reshmi, Pusa Chetki, Punjab Safed, Kalyanpur, Japanese White, HR 1, and Meghalaya Selection). Root length followed by top weight were closely associated with root weight, with root length/root weight and top weight/root weight genotypic correlation values of 0.758 for both, co-heritability values of 0.814 and 0.725, and coefficient of genetic prediction values of 0.584 and 0.444, respectively, for each pair of traits.

Ling *et al.* (1986)
See Morphological traits/Leaf/Area/*Raphanus sativus*.

Yield/Head/*Brassica oleracea*

Kwan (1934)
See Morphological traits/Leaf/Colour/Purple pigmentation/*Brassica oleracea*.

Swarup *et al.* (1963)
See Phenological traits/Earliness/Maturity/*Brassica oleracea*.

Chiang (1969)
See Morphological traits/Head/Core length/*Brassica oleracea*.

Summers and Honma (1980)
See Phenological traits/Earliness/Maturity/*Brassica oleracea*.

Yield/Head/*Brassica rapa*

Tan *et al.* (1982)
See Morphological traits/Head/Diameter/*Brassica rapa*.

Yield/Oil*Brassica juncea*

Rawat and Anand (1981)
The F_1 and F_2 populations of all possible crosses between twelve strains of Indian mustard were sampled for oil content. Additive and non-additive gene action for oil content was shown in the F_1 generation. The parents BIC 1562 and BIC 1692 were the best general combiners for oil content. Four crosses showed positive significant specific combining ability effects. Oil content was concluded to be governed by both additive and non-additive genetic effects.

Govil *et al.* (1984)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Dhari and Yadava (1985)
The segregating and BC generations of five crosses between diverse mustard germplasm were studied to determine the gene effects of oil content. Dominance effects were significant for all crosses and additive effects were shown in two crosses. The presence of epistatic interactions was shown for all crosses.

Pal and Singh (1986)
Six generations of two crosses between a high yielding Russian line EC 126743 and Indian cvs. Varuna and Prakash were analysed for oil content. A simple additive dominance model was adequate for describing the inheritance of oil content in two environments.

Badwal and Labana (1987)
See Morphological traits/Seed/Size/*Brassica juncea*.

Sachan and Singh (1988)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Dhillon *et al.* (1991)
Both additive and non-additive genetic effects were found for seed yield, oil yield, 1,000 seed weight, and number of siliques on the main raceme. Estimates of general combining ability (GCA) identified the parental cv. Varuna as having high GCA for seed yield and oil yield, and cv. Pusa Bold as having high GCA for seed yield, oil yield, and 1,000 seed weight.

Thakral and Singh (1995b)
Diallel crosses were made between relatively salt tolerant Indian mustard lines RH 7859, RH 7846, and RH 781 x salt sensitive lines RH 8315, RWH 1, and RH 8113. The 15 F_1 progenies with the parental lines were grown in a saline stress environment and a control environment. The additive and dominant components were significant for seed yield and oil content in both environments. One major gene group was indicated in the control of seed yield and of oil content under stress environments.

Chauhan *et al.* (1996)
The genetics of oil content were examined in crosses between yellow-seeded Indian mustard lines NDYR8 x NQR 9301 and NDYR10 x NQR 9301. The scaling test indicated epistasis in both crosses. In the cross NDYR8 x NQR 9301, additive gene effects and additive x dominance gene interactions were predominant. In the cross NDYR10 x NQR 9301, both additive and dominance gene effects, and the three types of epistasis (i, j, and l) controlled the inheritance of oil content.

Yield/Oil/*Brassica napus*

Grami and Stefansson (1977)
The F_1, F_2, and BC generations of a cross between the spring oilseed rape [= subsp. *oleifera*] cvs. Midas and Tower were studied for the genetic control of percent protein, percent oil, and sum of oil and protein as a percentage of seed. All three traits were found to be controlled by additive gene action. The sum of oil and protein was shown to be more effective than selection for either protein or oil alone.

Grami *et al.* (1977)
Estimates of broad-sense heritability in the F_2 generations of a cross between the oilseed summer rape [= subsp. *oleifera*] cvs. Midas and Tower was 0.26 for each of percent protein and percent oil and 0.33 for the sum of oil and protein. The average phenotypic and genotypic correlations between protein and oil content were 0.81 and 0.71, respectively.

Grant and Beversdorf (1985)
See Morphological traits/Plant/Height/*Brassica napus*.

Tang and Yang (1986)
See Yield and quality traits/Seed fatty acids/Erucic acid (C22:1)/*Brassica napus*.

Gupta and Labana (1988)
Oil content was assessed on the hybrids and parental lines of a half-diallel between eight diverse genotypes of *B. napus*. General combining ability was significant indicating only additive gene action.

Hu (1988)
See Yield and quality traits/Seed glucosinolates/*Brassica napus*.

Knaak and Ecke (1995)
See Morphological traits/Plant/Height/*Brassica napus*.

Yield/Oil/*Brassica rapa*

Rao (1970)
Nine cultivars of Brown Sarson were used to produce 36 F_1 hybrids, which were evaluated for seed oil content. Additive and dominant genetic effects were shown. Heterosis for both increased and decreased oil contents was noted in different hybrids. The variation in the dominance-recessive expression may be related to the diverse origin of the parental cultivars: four self-compatible, one partially self-incompatible, and four self-incompatible types.

Rao (1977)
See Morphological traits/Plant/Branch number/*Brassica rapa*.

Yadava *et al.* (1985)
See Morphological traits/Plant/Branch number/*Brassica rapa*.

Yield/Oil/*Crambe abyssinica*

Lessman (1975)
See Morphological traits/Plant/Height/*Crambe abyssinica*.

Yield/Protein/*Brassica juncea*

Badwal and Labana (1987)
See Morphological traits/Seed/Size/*Brassica juncea*.

Yield/Protein/*Brassica napus*

Grami and Stefansson (1977)
See Yield and quality traits/Yield/Oil/*Brassica napus*.

Grami *et al.* (1977)
See Yield and quality traits/Yield/Oil/*Brassica napus*.

Grant and Beversdorf (1985)
See Morphological traits/Plant/Height/*Brassica napus*.

Tang and Yang (1986)
See Yield and quality traits/Seed fatty acids/Erucic acid (C22:1)/*Brassica napus*.

Hu (1988)
See Yield and quality traits/Seed glucosinolates/*Brassica napus*.

Wang and Qiu (1990)
The inheritance of seed protein content was investigated in a half-diallel with six cultivars of oilseed rape [= subsp. *oleifera*]. Seed protein content was controlled by both additive and dominant genes.

There was no epistasis. Broad-sense and narrow-sense heritabilities were 74.77% and 57.24%, respectively. Protein content was significantly negatively correlated with oil content. There was a positive correlation between seed protein content and nitrate reductase activity in the leaves of young plants and in plants at the beginning of flowering.

Yield/Root/*Brassica napus*

Shattuck (1985)
See Morphological traits/ Root/Size/*Raphanus sativus*.

Ramsay *et al.* (1994a)
Analysis of a complete diallel with 11 inbred lines of swedes [= subsp. *rapifera*] revealed both additive and non-additive genetic variation for dry matter yield and other quantitative traits. The data did not fit a simple additive-dominance model with independence of action and distribution of the genes.

Ramsay *et al.* (1994b)
Augmented triple test crosses between inbred lines of swede (= subsp. *rapifera*] derived from cvs. Criffel, Marian, and Bagholm Wilby, were assessed in field trials for the components of dry weight yield. Dry matter percentage was under additive genetic control while fresh weight yield was under additive x dominance control. Dry weight yield also showed additive and dominance effects. Large reciprocal differences were identified for fresh and dry weight yield in the cross between inbred lines from Criffel and Marian. In both crosses, the F_1 outyielded the better parent by 14 and 12%. Twelve and 2% of the recombinant inbred lines from the two crosses were predicted to outyield the F_1.

Yield/Root/*Raphanus sativus*

Brar *et al.* (1972)
See Yield and quality traits/Yield/Foliage/*Raphanus sativus*.

Kubka *et al.* (1974)
See Morphological traits/Cotyledon/Size/*Raphanus sativus*.

Singh *et al.* (1977)
Heritability estimates in 22 strains of radish for seven quantitative traits were root length (30%), root width (41%), skin width (88%), number of leaves/root (91%), top ratio (23%), root ratio (27%), and plant yield (64%). Yield was positively correlated with all traits except root length and root ratio; root and top ratios were negatively correlated (-1.0). Genotypic correlations were higher than phenotypic correlations.

Prasad and Prasad (1978)
See Morphological traits/Leaf/Number/*Raphanus sativus*.

Gospodarek and Hulewicz (1979)
See Morphological traits/Root/Size/*Raphanus sativus*.

Pandey *et al.* (1981)
See Morphological traits/Leaf/Number/*Raphanus sativus*.

Khan *et al.* (1983)
See Morphological traits/Plant/Height/*Raphanus sativus*.

Parthasarathy and Medhi (1983)
See Yield and quality traits/Yield/Foliage/*Raphanus sativus*.

Ling *et al.* (1986)
See Morphological traits/Leaf/Area/*Raphanus sativus*.

Yield/Seed/*Brassica carinata*

Subudhi and Raut (1994a)
See Morphological traits/Plant/Branch number/*Brassica carinata*.

Thakral and Singh (1995a)
Seeds of six parents and 15 F_1 hybrids were germinated on filter paper containing 0, 125, and 175 meq/L chloride salt solutions. Seedling vigour was correlated with germination percentage, rate of germination, root length, seedling fresh weight, seedling dry weight. No correlations were found between these traits and seed yield.

Yield/Seed/*Brassica juncea*

Paul (1978)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Paul (1979)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Tripathi *et al.* (1980)
See Morphological traits/Seed/Set/*Brassica juncea*.

Govil *et al.* (1984)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Thakral *et al.* (1986)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Dhillon *et al.* (1991)
See Yield and quality traits/Yield/Oil/*Brassica juncea*.

Subudhi and Raut (1994a)
See Morphological traits/Plant/Branch number/*Brassica carinata*.

Thakral and Singh (1995b)
See Yield and quality traits/Yield/Oil/*Brassica juncea*.

Bhajan *et al.* (1997)
The heritability of shattering resistance and seed yield under salt stress was investigated in a diallel cross with seven parents (cv. Varuna, cv. Kranti, RCC 15, DIRA 313, DIRA 326, RK 8702, and RW 29-6). Narrow-sense heritability was 23.0% for silique shattering and 43.6% for seed yield.

Yield/Seed/*Brassica napus*

Campbell and Kondra (1978)
See Phenological traits/Earliness/Maturity/*Brassica napus*.

Singh and Yadav (1980)
See Phenological traits/Earliness/Maturity/*Brassica napus*.

Lefort-Buson and Dattée (1982a)
See Morphological traits/Leaf/Number/*Brassica napus*.

Lefort-Buson and Dattée (1982b)
See Morphological traits/Leaf/Number/*Brassica napus*.

Sernyk and Stefansson (1983)
See Phenological traits/Earliness/Maturity/*Brassica napus*.

Grant and Beversdorf (1985)
See Morphological traits/Plant/Height/*Brassica napus*.

Lefort-Buson *et al.* (1987a)
See Morphological traits/Plant/Height/*Brassica napus*.

Liu and Liu (1987a)
See Morphological traits/Plant/Branching habit/*Brassica napus*.

Brandle and McVetty (1989b)
Yields of inbred line derived hybrids were compared to their respective cultivar derived hybrids. Some inbred line derived hybrids were significantly higher and some lower yielding. There were differences in general combining ability (GCA) effects among inbred lines. Yield was controlled predominantly by additive genetic effects. Parental GCA was found to be more effective that the mid-parent value in predicting expected hybrid yield. The regression of expected using parental GCA vs. observed hybrid yield was significant with an r^2 value of 0.88.

Malik *et al.* (1995)
See Morphological traits/Plant/Branch number/*Brassica napus*.

Yield/Seed/*Brassica rapa*

Manner (1959)
Seed yield components and seed yield, days to flower, and plant height were studied in the progeny of crosses of turnip rape [= subsp. *oleifera*] between winter cvs. Gruber, Rapido, Storrybs, and Sprengel x spring cv. Mette. On average, the F_1 hybrids were later maturing than cv. Mette and the hybrids were taller than the parents. The number of flowering hybrids varied with the cross. On average, seed yield per hybrid plant was higher than for cv. Mette.

F_2 progenies were generally later than cv. Mette and flowering was delayed. F_2 plants were taller than cv. Mette. Seed weight per silique was higher than in cv. Mette (30.1 mg), ranging from 36.5 to 44.0 mg. Seed weight of the F_2 progenies was higher than that of cv. Mette (2.2.mg), ranging from 2.7 to 3.2 mg. On average, the mean length of siliques and the number of seeds per silique were similar in the F_2 progenies and cv. Mette.

Paul (1978-1979)
See Morphological traits/Plant/Branch number/*Brassica rapa*.

Yadava *et al.* (1985)
See Morphological traits/Plant/Branch number/*Brassica rapa*.

Falk *et al.* (1995)
See Morphological traits/Silique/Number/*Brassica rapa*.

Yield/Seed/*Crambe abyssinica*

Meier and Lessman (1973b)
See Morphological traits/Plant/Height/*Crambe abyssinica*.

Lessman (1975)
See Morphological traits/Plant/Height/*Crambe abyssinica*.

Yield/Seed/*Crambe hispanica*

Meier and Lessman (1973b)
See Morphological traits/Plant/Height/*Crambe abyssinica*.

Yield/Seed/*Eruca vesicaria* subsp. *sativa*

Yadav and Kumar (1984)
See Morphological traits/Plant/Branch number/*Eruca vesicaria* subsp. *sativa*.

Kumar and Yadav (1986)
The genetics of seven yield component traits (seed yield per plant, 1,000 seed weight, silique length, number of siliques, number of seeds per silique, main shoot length, and plant height)were studied in a 10-parent diallel cross utilizing lines RTM 2, Ldh Comp 1, and TMC 13, 25, 27, 50, 74, 82, 84, 86 of

eruca (as *E. sativa*]. Narrow-sense heritability was high for silique length (330%), main shoot length (139.9%), 1,000 seed weight (83.9%), plant height (65.9%), number of siliques per plant (45.8%), and number of seeds per silique (37.3%), and low for seed yield (24.1%). Dominance was found to be significant for all traits except silique length for which an additive component was important. Dominant genes were in excess of recessive genes for all traits except 1,000 seed weight and seed yield per plant.

Yield/Seed/*Raphanus raphanistrum*

Mazer (1987)
See Morphological traits/Ovule number/*Raphanus raphanistrum*.

Yield/Seed/*Raphanus sativus*

Kubka *et al.* (1974)
See Morphological traits/Cotyledon/Size/*Raphanus sativus*.

Gospodarek and Hulewicz (1979)
See Morphological traits/Root/Size/*Raphanus sativus*.

Mazer and Wolfe (1992)
The results of studies designed to study the effects of planting density, genotype, and their interaction on plant seed production in wild accessions of *R. sativus* indicated that planting density had a strong effect on mean seed set. Planting density influenced the magnitude of maternal effects on progeny phenotype. Seed set was also influenced by genotype x density interactions.

DISEASE AND PEST RESISTANCE TRAITS

Disease resistance/Alternaria black spot (*Alternaria brassicae*)/*Brassica juncea*

Tripathi *et al.* (1980)
See Morphological traits/Seed/Set/*Brassica juncea*.

Disease resistance/Alternaria black spot (*Alternaria brassicae*)/*Brassica rapa*

Zhang *et al.* (1996)
Diallel crosses were made in Chinese cabbage [= subsp. *pekinensis*] between Alternaria black spot resistant strains 94-217 and 94-231 x Alternaria black spot susceptible strains 94-219 and 94-273. The results indicated that resistance to Alternaria black spot in seedlings was dominant and mainly controlled by additive genes. Broad-sense and narrow-sense heritabilities were 0.845 and 0.814, respectively.

Disease resistance/Alternaria leaf spot (*Alternaria brassicicola*)/*Brassica napus*

Ahmad *et al.* (1991)
In vitro selection for resistance to Alternaria leaf spot and the herbicide chlorsulfuron in rapid cycling *B. napus* resulted in the generation of heritable resistance to the pathogen and resistance to the herbicide.

Disease resistance/Alternaria leaf spot (*Alternaria brassicicola*)/*Brassica oleracea*

King and Dickson (1994)
A diallel cross was made between 12 parents (9 Alternaria leaf spot resistant accessions of *B. oleracea* and one susceptible accession each of cauliflower [= var. *botrytis*], broccoli [= var. *italica*], and cabbage [= var. *capitata*]. Both additive gene action and dominance played a role in resistance, with partial dominance being the most significant. Heritability estimates for a cross between red cabbage accession USDA Plant Introduction no. PI 291998 (leaf spot resistant) and a susceptible Chinese kale [= var. *alboglabra*] were H^2= 86% and h^2= 53%. There was no linkage between plant colour (red or green) and leaf spot resistance.

Disease resistance/Black root (*Aphanomyces raphani*)/*Raphanus sativus*

Barham *et al.* (1983)
Twelve commercial and experimental radish cultivars were evaluated in seven field trials in Florida, Ohio, Minnesota, and California, U.S.A. Combined analysis of data from the field trials gave heritability estimates for resistance to various fungi ranging from 0.19 for *Aphanomyces raphani* to 0.65 for *Rhizoctonia solani*.

Disease resistance/Black rot (*Xanthomonas campestris* pv. *campestris*)/*Brassica napus*

Guo *et al.* (1991a)
Intraspecific and interspecific crosses between *Brassica napus* and *Brassica rapa* indicated that the high resistance of accessions of *B. napus* was completely dominant in F_1 progenies in both intraspecific and interspecific crosses. Segregation ratios in BC progenies were consistent with a single dominant gene for resistance in the highly resistant *B. napus* accessions. In a cross between a moderately resistant accession (USDA Plant Introduction PI 273640) x a black rot susceptible accession (CC55), the F_2 segregated 1 medium black rot resistant plant to 3 susceptible plants, suggesting that medium resistance was conditioned by a homozygous recessive modifier gene. The symbol *Br* was assigned to the gene for high black rot resistance and the symbol *bm* was assigned to the modifier gene. Postulated genotypes were *Br_ _ _* (high resistance to black rot), *brbrbmbm* (moderate resistance to black rot), and *brbrBm_* (susceptibility to black rot).

Guo *et al.* (1991b)
High level of resistance to black rot in *B. napus* was conditioned by a single dominant gene. Quantitative inheritance for moderate black rot resistance was observed in two accessions of Chinese cabbage [= *B. rapa* subsp. *pekinensis*].

Disease resistance/Black rot (*Xanthomonas campestris* pv. *campestris*)/*Brassica oleracea*

Bain (1955)
Resistance in a black rot resistant selection of cabbage [= var. *capitata*] cv. Huguenot was controlled by one or more dominant genes.

Sharma *et al.* (1972)
Dominant polygenic inheritance was observed for black rot resistance in cauliflower [= var. *botrytis*].

Williams *et al.* (1972)
Segregation ratios for F_1, F_2, and BC populations of crosses between black rot resistant Japanese cabbage [= var. *capitata*] cv. Early Fuji x black rot susceptible cultivars were consistent with control by one major gene, designated *f*, for resistance to black rot. In the heterozygous condition, gene *f* was influenced by one recessive modifier gene, designated *a*, and one dominant modifier gene, designated *B*.

Dickson and Hunter (1987)
Juvenile inheritance to black rot Wisconsin strain PHW117 in Chinese accession USDA PI 436606 of cabbage [= var. *capitata*] was controlled by one recessive gene. One or two modifier genes for tolerance to black rot were identified in an unrelated cabbage line.

Disease resistance/Black rot (*Xanthomonas campestris* pv. *campestris*)/*Brassica rapa*

Guo *et al.* (1991b)
Quantitative inheritance for moderate black rot resistance was observed in two accessions of Chinese cabbage [= *B. rapa* subsp. *pekinensis*]. High level of resistance to black rot in *B. napus* was conditioned by a single dominant gene.

Disease resistance/Blackleg (*Leptosphaeria maculans*)/*Brassica insularis*

Mithen and Lewis (1988)
An interspecific cross was made between Chinese kale [= *Brassica oleracea* var. *alboglabra*] (highly susceptible to blackleg) and an accession of wild *Brassica insularis* from Sardinia, Italy, which showed a hypersensitive resistance to isolate Lm 10 of *L. maculans*. Hypersensitive resistance was dominant in the F_1 progeny. Analyses of F_1 and F_2 progenies suggested that resistance was determined by two dominant, independently-segregating genes.

Disease resistance/Blackleg (*Leptosphaeria maculans*)/*Brassica juncea*

Roy (1984)
Complete resistance to *L. maculans* was transferred from *Brassica juncea* to *Brassica napus* through interspecific hybridization. Mustard-type resistance appeared to be inherited as a major gene or genes. Segregation for resistance and susceptibility continued to occur during later generations of selection of resistant progeny.

Keri *et al.* (1990)
Reciprocal crosses were made between lines UM3021, UM3043, and UM3323 (blackleg resistant) and UM3132 (blackleg susceptible) from the University of Manitoba, Winnipeg, Canada. Segregation data indicated that the resistance was controlled by two nuclear genes with dominant recessive epistatic action. This conclusion was based on the observation that some F_3 lines derived from blackleg susceptible F_2 plants segregated for resistance in a 1:3 ratio.

Hill (1991)
F_2 segregation data for progeny of a cross between a blackleg susceptible line and a blackleg resistant line of cv. Domo inoculated with isolate Lm1192 indicated that blackleg resistance of seedlings was controlled by two dominant genes. The resistance was expressed as a hypersensitive response.

Disease resistance/Blackleg (*Leptosphaeria maculans*)/*Brassica napus*

Delwiche (1980)
Specific blackleg resistance in seedlings of oilseed rape [= subsp. *oleifera*] line R39 and cv. Girita was controlled by single dominant genes, designated, *Lm1* and *Lm2*, respectively.

Roy (1984)
See Disease and pest resistance traits/Disease resistance/Blackleg (*Leptosphaeria maculans*)/ *Brassica juncea*.

Hill (1991)
The inheritance of blackleg resistance in seedlings was examined in several crosses between true-breeding oilseed rape [= subsp. *oleifera*] that were either blackleg susceptible or blackleg resistant. In the cross cv. Bingo (susceptible) x cv. Topas (resistant), a single recessive gene controlled resistance to isolate Lm1190. Two complementary dominant genes were found in cv. Topas that interacted with isolate Lm1190. In the cross cv. Westar (susceptible) x cv. Cyclone (resistant), it was found that cv. Cyclone plants possessed one or two recessive resistance genes that interacted with isolate Lm1192.

Sippel *et al.* (1991)
The inheritance of resistance to virulent isolate LM26 collected in Manitoba, Canada, was examined in the progeny of crosses representing combinations of susceptibility and resistance between doubled haploid plants of oilseed rape [= subsp. *oleifera*] cvs. Global, Karat, Marnoo, Regent, Topas, and Westar, and lines A0087 and MR. Plants were inoculated at the crown and measurements of the length of lesions were made. Disease resistance was found to be polygenic and primarily recessive.

Mithen and Magrath (1992)
See Yield and quality traits/Seed glucosinolates/*Brassica napus*.

Stringam *et al.* (1992)
Blackleg resistance of the Australian oilseed rape [= subsp. *oleifera*] cvs. Maluka and Shiralee was controlled by a single dominant gene.

Dion *et al.* (1995)
Gene *LmFr1* controlled adult plant resistance to blackleg in the French spring rapeseed [= subsp. *oleifera*] cv. Crésor. QTL mapping suggested that a single chromosomal region was involved in the

resistance. Mendelian analysis also confirmed the presence of a single major blackleg resistance gene. A second minor QTL for blackleg resistance was identified from the data set originating from one of four year-site assays.

Ansan-Melayah (1996)
Specific blackleg resistance in seedlings of oilseed rape [= subsp. *oleifera*] cvs. Quinta and Glacier was controlled by single dominant genes, designated, *Rlm1* and *Rlm2*, respectively.

Pang and Halloran (1996a)
The inheritance of adult plant resistance from *B. juncea* into *B. napus* was determined in the F_2 and F_3 progenies of a cross between blackleg resistant oilseed rape [= subsp. *oleifera*] line 579NO48-109-DG-1589, designated R13, and blackleg susceptible Canadian cv. Tower. F_2 segregation ratios were bimodal, indicating that the resistance was controlled by major genes. F_3 segregation ratios were consistent with the involvement of three nuclear genes, designated Bl_1, Bl_2, and Bl_3, which interacted in a complex manner (Bl_1 epistatic to Bl_2 and Bl_3; Bl_2 and Bl_3 complementary gene action).

Pang and Halloran (1996b)
The inheritance of adult plant resistance to blackleg isolate MB2 was studied in the F_2 and BC_1 populations of a cross between oilseed rape [= subsp. *oleifera*] cvs. Maluka (resistant) x Niklas (highly susceptible). Blackleg resistance was dominant and likely controlled by a single, incompletely dominant major gene.

Pang and Halloran (1996c)
The inheritance of seedling and adult plant resistance to blackleg isolate MB2 was studied in 49 families derived by intercrosses of 14 randomly chosen F_2 plants of a cross between oilseed rape [= subsp. *oleifera*] cvs. Maluka (blackleg resistant) x Niklas (highly blackleg susceptible). Significant non-additive genetic variances were observed for all measures of disease severity, indicating strong dominance/epistasis at loci controlling blackleg resistance. The highest ratio of additive to non-additive genetic variance was found for crown-canker development, after stem wound-inoculation. The disease reaction of seedlings and stems was not correlated.

Mayerhofer *et al.* (1997)
Bulked segregant analysis was used to identify RAPD and RFLP markers associated with blackleg resistance in oilseed rape [= subsp. *oleifera*] cv. Shiralee. The results suggested that blackleg resistance was controlled by a single major gene, designated *LmR1*.

Disease resistance/Blackleg (*Leptosphaeria maculans*)/*Brassica oleracea*

Mithen and Lewis (1988)
See Disease and pest resistance traits/Disease resistance/Blackleg (*Leptosphaeria maculans*)/ *Brassica insularis.*

Disease resistance/Blackleg (*Leptosphaeria maculans*)/*Brassica rapa*

Mitchell-Olds *et al.* (1995)
The results of artificial selection on seedlings for multiple disease resistance to the pathogens *Leptosphaeria maculans*, *Peronospora parasitica*, and *Albugo candida*, indicated heritable genetic variation for resistance to each pathogen and a positive correlation between resistance to *L. maculans* and *P. parasitica*.

Disease resistance/Cauliflower mosaic virus/*Brassica oleracea*

Pound and Walker (1951)
Resistance to turnip virus 1 (virus A) and cauliflower virus 1 (virus B) in cabbage [= var. *capitata*] was found to be partially dominant and probably conditioned by several genes. Resistance genes to the two viruses may be linked.

Disease resistance/Clubroot (*Plasmodiophora brassicae*)/*Brassica napus*

Sterling (1951)
Clubroot resistance in swede [= subsp. *rapifera*] was conditioned by two partially dominant genes. Two partially dominant genes also conditioned clubroot susceptibility.

Lammerink (1967)
Resistance to clubroot races B and C was controlled by single dominant genes in New Zealand Clubroot Resistant Rape [= subsp. *oleifera*] and swede [= subsp. *rapifera*] cv. New Zealand Wilhemsburger.

Johnston (1970)
Resistance to clubroot race N4 in New Zealand Clubroot Resistant Giant Rape [= subsp. *oleifera*] was controlled by a major dominant gene.

Ayers and Lelacheur (1972)
Crosses were made between clubroot resistant rutabaga [= subsp. *rapifera*] cvs. York and Wilhemsburger x clubroot susceptible cv. Laurentian. Resistance to clubroot was dominant. One major gene and two major genes determined resistance to clubroot race 2 in cvs. York and Wilhemsburger, respectively. One major gene determined resistance to clubroot race 3 in both cultivars.

Crute *et al.* (1983)
Clubroot resistance in *B. napus* and *B. rapa* was likely controlled by a small number of genes.

Gustafsson and Fält (1986)
On the basis of segregation ratios obtained from crosses between clubroot susceptible and clubroot resistant genotypes of oilseed rape [= subsp. *oleifera*] and swede [= subsp. *rapifera*], up to three unlinked dominant resistance genes were identified.

Disease resistance/Clubroot (*Plasmodiophora brassicae*)/*Brassica oleracea*

Walker and Larson (1951)
Clubroot resistance in cabbage [= var. *capitata*] was recessive and polygenic.

Gallegly (1956)
Segregation data of a cross between clubroot resistant cabbage [= var. *capitata*] accession 93-595s x clubroot susceptible cultivars of broccoli [= var. *italica*] and cauliflower [= var. *botrytis*] indicated polygenic resistance.

Weisaeth (1961)
Polygenic inheritance to clubroot in cabbage [= var. *capitata*] was described.

Chiang and Crête (1970)
Crosses between clubroot susceptible cabbage [= var. *capitata*] Red Acre and Golden Acre x clubroot resistant cabbage line 8-41 indicated that clubroot resistance was recessive and controlled by duplicate genes. The clubroot resistance genes were designated pb_1 and pb_2.

Chiang and Crête (1976)
The results of a 4 x 4 diallel cross involving clubroot resistant (race 6) cabbage [= var. *capitata*] cv. Badger Shipper and inbred line 8-41 and clubroot susceptible cvs. Baby Head and Storage Green, indicated significant additive effects.

Chiang and Crête (1983)
Resistance to clubroot race 2 was transferred from *B. napus* to cabbage [= var. *capitata*]. The resistance to race 2 in BC_3 and BC_4 generations was determined to be under the control of a single, dominant gene. The gene for clubroot resistance was inferred to be located on the A genome.

Voorrips and Visser (1991)
Segregation ratios obtained in F_1 and self-progenies of crosses between cabbage [= var. *capitata*] cultivars indicated recessive resistance to clubroot.

Laurens and Thomas (1993)
The inheritance of clubroot resistance and tolerance in marrowstem and green curly kale [= var. *acephala*] was investigated in diallel crosses. Genetic control of resistance to clubroot in juvenile and adult kale plants was polygenic and dominant. Broad-sense heritability values greater than 0.8 were obtained. There was no correlation between phenotypic and genetic values for resistance to clubroot and those for tolerance to the pathogen.

Voorrips (1995)
In general, clubroot resistance in *B. oleracea* appears to be partly recessive and partly additive, and controlled by a few major genes.

Grandclément and Thomas (1996)
Complete diallel crosses were made between kale [= var. *acephala*] lines R1 and R2 which were very resistant to clubroot x cauliflower [= var. *botrytis*] lines S1, S2, and S3 which were susceptible to clubroot, and between a kale line (I1) with ‘intermediate’ clubroot resistance x the three cauliflower lines. In both diallels, Griffing’s analysis indicated that general combining ability was greater than

specific combining ability, indicating predominance of additive effects. The results of Hayman's analysis indicated that in the very resistant lines clubroot resistance was controlled by dominant alleles. In contrast, in line I1 (intermediate clubroot resistance), resistance was controlled by recessive alleles.

Disease resistance/Clubroot (*Plasmodiophora brassicae*)/*Brassica rapa*

Tedin (1932)
See Morphological traits/Root/Colour/*Brassica rapa*.

Sterling (1951)
The inheritance of clubroot resistance was studied in crosses between highly clubroot resistant S4 plants of swede [= *B. campestris* var. *napobrassica*] cv. Danish Giant and highly clubroot susceptible plants of cv. Ditmars Bronze Top. Four major gene pairs conditioned resistance and susceptibility to clubroot in the material. Susceptibility was partially dominant in some parents, while resistance was partially dominant in others. No linkage was observed between clubroot resistance and flesh colour.

Wit (1965)
Crosses were made between homozygous clubroot resistant and homozygous clubroot susceptible turnip [= subsp. *rapifera*] lines. F_1 progenies were completely healthy. F_2 progenies segregated in 3:1, 9:7, and 27:37 ratios, indicating that resistance was due to at least three dominant genes, designated *A*, *B*, and *C*.

Strandberg and Williams (1967)
A clubroot resistant selection of Chinese cabbage [= subsp. *pekinensis*] cv. Michihli was crossed with the wild-type parent. Resistance to races 6 and 7 was conditioned by a single dominant gene.

James *et al.* (1978)
The inheritance of clubroot resistance was investigated in crosses using two clubroot resistant lines from the European Clubroot Differential host series and one commercial cultivar. The resistance to clubroot race 6 of the commercial cultivar was conditioned by a single dominant gene, designated *Pb1*. The resistance of the lines was conditioned by more than one independent dominant gene. Two single dominant genes for clubroot resistance, designated *Pb2* and *Pb3*, were identified.

James and Williams (1980)
On the basis of F_2 and testcross segregation data, a single dominant gene, designated *Pb1*, conditioned resistance to clubroot race 6 in Chinese cabbage [= subsp. *pekinensis*] cv. Michihili. Resistance to race 6 was controlled by single dominant genes, designated *Pb2* and *Pb3*, in turnip [= subsp. *rapifera*] stocks ECD 02 and ECD 03. Genes *Pb1*, *Pb2*, and *Pb3* were unlinked. No linkage was observed between genes *Pb2* or *Pb3* and *cr* (cream petals), or between gene *Pb3* and *nsep* (narrow sepals). Gene *Pb2* was loosely linked to *ro* (rosette).

Crute *et al.* (1983)
Clubroot resistance in *B. rapa* and *B. napus* was mainly differential and likely controlled by a small number of genes.

Disease resistance/Downy mildew (*Peronospora parasitica*)/*Brassica napus*

Nashaat *et al.* (1995)
Resistance to isolate P003 was conditioned by a single dominant gene in oilseed rape [= subsp. *oleifera*] line RES-26, a selection from cv. Janetezkis, and by two unlinked dominant genes in line RES-02, a selection from cv. Komet.

Disease resistance/Downy mildew (*Peronospora parasitica*)/*Brassica oleracea*

Natti *et al.* (1967)
The resistance to crucifer downy mildew at the cotyledon stage in *Brassica oleracea* was determined to be race specific and controlled by a single dominant gene.

Hoser-Krauze *et al.* (1995)
Studies showed that the resistance to downy mildew in broccoli [= var. *italica*] was governed by three or four dominant complementary genes. The number of genes varied depending on the resistant parent which was used in the crosses.

Mahajan *et al.* (1995)
The inheritance of downy mildew resistance in three resistant x susceptible crosses (cc x HR 5-4, 3-5-1-1 x 244, and cc x 244), one susceptible x susceptible cross (244 x 267-6-9), and one resistant x resistant cross (cc x 3-5-1-1) was studied in Indian cauliflower [= var. *botrytis*] over 1990 and 1991. Downy mildew resistance in the crosses cc x HR 5-4 and 3-5-1-1 x 244 was governed by a single dominant gene, designated *PPA3*. Recessive epistasis was observed in the cross cc x 244.

Carvalho and Monteiro (1996)
Crosses were made in tronchuda cabbage [= var. *tronchuda*] between downy mildew resistant plants of cv. Algarvia (ISA 207) x downy mildew susceptible plants of cv. Penca de Chaves (ISA 19). Preliminary results (F_1 and S_1) indicated that cotyledon resistance was controlled by two dominant complementary genes, designated *R1* and *R2*.

Disease resistance/Downy mildew (*Peronospora parasitica*)/*Brassica rapa*

Niu *et al.* (1983)
Forty-six lines (open pollinated cultivars, inbreds, and F_1 hybrids) of Chinese cabbage [= subsp. *pekinensis*] were screened for reaction to downy mildew (isolate PHW 640). Resistance to downy mildew on cotyledons was found to be dominant. The segregation ratios of F_2 and testcross progenies suggested a monogenic, dominant type of inheritance for most of the selfed families that were examined.

Mitchell-Olds *et al.* (1995)
See Disease and pest resistance traits/Disease resistance/Blackleg (*Leptosphaeria maculans*)/*Brassica rapa*.

Disease resistance/ Fusarium yellows or wilt (*Fusarium oxysporum* f. sp. *conglutinans*/ *Brassica oleracea*

Walker (1926)
Resistance to Fusarium yellows in cabbage [= var. *capitata*] was conditioned by a single, dominant gene.

Walker (1930)
Resistance to Fusarium yellows in cabbage [= var. *capitata*] cv. Jersey Wakefield, cv. Copenhagen Market, and a wild accession from England was conditioned by a single, dominant gene.

Anderson (1933)
Polygenic resistance to Fusarium yellows was reported in cabbage [= var. *capitata*] cv. Wisconsin Hollander.

Blank and Walker (1933)
A dominant gene for Fusarium wilt was present in brussels sprouts [= var. *gemmifera*] and kohlrabi [= var. *gongylodes*].

Blank (1937)
Two types of resistance to Fusarium yellows were reported in cabbage [= var. *capitata*] cv. Wisconsin All Seasons. Type A resistance, which was effective at relatively high soil temperatures of about 24° C, was controlled by a single dominant gene; type B resistance, which was effective at lower soil temperatures and ineffective at higher soil temperatures of about 24° C, was polygenically controlled and similar to that described for cv. Wisconsin Hollander (Anderson, 1933).

Disease resistance/Fusarium yellows (*Fusarium oxysporum* f. sp. *conglutinans*)/ *Raphanus sativus*

Peterson and Pound (1960)
Crosses were made between susceptible cv. Early Scarlet Globe and cv. Red Prince which is resistant to *F. oxysporum* f. sp. *conglutinans* race 2. F_1 progenies showed intermediate levels of resistance, while F_2 and BC progenies showed resistance of about 15%. These ratios suggested that resistance was polygenic in nature.
Williams and Pound (1967)
The inheritance of resistance to *F. oxysporum* f. sp. *conglutinans* race 2 in resistant cv. White Spike was reported to be under polygenic control.

Hida and Ashizawa (1985)
The inheritance of resistance to *F. oxysporum* f. sp. *conglutinans* was studied in the following crosses: cv. Red Prince x cv. Long Scarlet, cv. Kotabe x cv. Aokubi Miyashige Marujiri, and cv. Red Prince x cv. Aokubi Miyashige Marujiri. The degree of resistance (high to low) of the cultivars was Red Prince > Kotabe > Long Scarlet > Aokubi Miyashige Marujiri. Analyses of F_1, F_2, BC_1, and BC_2 generations supported a polygenic model for resistance to the fungus, but the observed selection effects suggested that several major genes might be involved. Resistance was related to root colour, red-rooted cultivars being more resistant than white-rooted cultivars, and purple-rooted cultivars being intermediate between red- and white-rooted cultivars.

Disease resistance/Powdery mildew (*Erysiphe polygoni*)/*Brassica oleracea*

Walker and Williams (1965)
The resistance to powdery mildew of cabbage [= var. *capitata*] cv. Globelle was controlled by a single dominant gene, whose expression was influenced by modifying genes.

Disease resistance/*Pseudomonas* leaf blight (*Pseudomonas syringae* pv. *maculicola*)/ *Brassica juncea*

Oram *et al.* (1985)
F_2 segregation data from crosses between *Pseudomonas* leaf blight resistant and susceptible genotypes suggested that the bacterial resistance was controlled by a partially dominant allele at a single locus.

Disease resistance/Rhizoctonia bottom rot (*Rhizoctonia solani*)/*Brassica oleracea*

Williams and Walker (1966)
The inheritance of resistance to rhizoctonia bottom rot in cabbage [= var. *capitata*] was investigated in crosses between breeding lines 3564R (resistant) x 517S (susceptible). F_2 and testcross segregation ratios were consistent with control by a single dominant gene for resistance.

Disease resistance/Rhizoctonia root rot (*Rhizoctonia solani*)/*Raphanus sativus*

Barham *et al.* (1983)
See Disease and pest resistance traits/Disease resistance/Black root (*Aphanomyces raphani*)/ *Raphanus sativus*.

Disease resistance/Sclerotinia stem rot, stalk rot (*Sclerotinia sclerotiorum*) /*Brassica napus*

Liu *et al.* (1991)
The sclerotinia stem rot tolerance of various Chinese, Australian and Swedish cultivars and breeding lines was examined. Differences among lines were observed under laboratory and field conditions. Tolerance to stem rot was found to be heritable.

Disease resistance/Sclerotinia stem rot, stalk rot (*Sclerotinia sclerotiorum*)/ *Brassica oleracea*

Baswana *et al.* (1991)
The inheritance of resistance in cauliflower [= var. *botrytis*] to stalk rot was investigated in a population from six generations of six crosses. Parents included cvs. Janavon and Early White Adams White which are resistant and moderately resistant sources from Katrain and U.S.A., respectively, and the highly stalk rot susceptible commercial cvs. Pusa Snowball-I and K-1. Disease incidence was recorded

on parental, F_1, F_2, and backcrossed plants. Resistance was found to be polygenic, under the control of recessive genes and due primarily to additive gene action. Narrow-sense heritability estimates ranged from 35 to 58%.

Dickson and Petzoldt (1994)
Results of a cross between stem rot resistant collards [= var. *sabellica*] accession 8204 x susceptible cabbage [= var. *capitata*] accession 8063 indicated that the resistance was conditioned by a major recessive gene. Results of a cross between stem rot resistant Savoy cabbage [= var. *sabauda*] accession 8246 x susceptible cabbage accession R UP indicated that the resistance was recessive and possibly conditioned by more than a single gene.

Disease resistance/Turnip mosaic virus/*Brassica napus*

Shattuck and Stobbs (1987)
The inheritance of resistance to turnip mosaic virus (TuMV) was studied in crosses between rutabaga [= subsp. *rapifera*] cv. Laurentian (TuMV susceptible) x rutabage Line 165 (TuMV resistant) and triazine-resistant cv. Laurentian (TuMV susceptible) x Line 165. TuMV resistance was conditioned by a single dominant gene.

Walsh (1989)
Immunity to an isolate of turnip mosaic virus from the United Kingdom was studied in lines selected from cv. Rafal. Segregation F_2 ratios of crosses between uniformly immune Rafal lines and susceptible cultivars Mikado and Yeoman indicated control by a single dominant gene.

Disease resistance/Turnip mosaic virus/*Brassica oleracea*

Pound and Walker (1951)
Resistance to turnip virus 1 (virus A) and cauliflower virus 1 (virus B) in cabbage [= var. *capitata*] was found to be partially dominant and probably conditioned by several genes. Resistance genes to the two viruses may be linked.

Disease resistance/Turnip mosaic virus/*Brassica rapa*

Niu *et al.* (1983)
Thirty-seven lines (open pollinated cultivars, inbreds, and F_1 hybrids) of Chinese cabbage [= subsp. *pekinensis*] were screened for reaction to turnip mosaic virus (isolate PHW 645). Resistance of cotyledons to TuMV was expressed as a hypersensitive response. Segregation ratios of progenies from a cross between accession PHW64701 (homozygous TuMV resistant) and accession PHW64708 (TuMV susceptible) were consistent with a two dominant gene model.

Yoon *et al.* (1993)
Segregation ratios obtained by visual observation of progenies of crosses between Chinese cabbage [= subsp. *pekinensis*] resistant line 0-2 and susceptible lines E-7, E-9 and FL-9, inoculated with TuMV strains TuMV-C4 and TuMV-C5, indicated that two recessive genes conferred resistance to both strains.

Suh *et al.* (1995)
The inheritance of resistance to turnip mosaic virus strains TuMV-C1, TuMV-C2, TuMV-C3, TuMV-C4, and TuMV-C5 in Chinese cabbage [= subsp. *pekinensis*] was determined using monoclonal antibodies. Crosses were made between resistant line 0-2 and the susceptible lines Seoul, SSD31, Cheongbang, and Yaki 1 ho. Resistance to TuMV was controlled by a single dominant gene or double dominant genes depending on the strain and cross. A single dominant gene was involved in the SSD31 x 0-2 cross and double dominant genes were involved in the Seoul x 0-2 cross tested against strains TuMV-C3 and TuMV-C5. ELISA tests using inoculated and non-inoculated leaves of the same plant suggested that the dominant resistance genes inhibited virus movement rather than virus multiplication.

Disease resistance/White rust (*Albugo candida*)/*Brassica carinata*

Delwiche and Williams (1974)
Monogenic dominant resistance to race 2 was found in Ethiopian mustard.

Singh and Singh (1988)
Inheritance of white rust resistance in P_1, P_2, F_1, F_2, and BC generations of five interspecific crosses between *Brassica juncea* (susceptible) x *Brassica carinata* (resistant) revealed that one gene with complete dominance conferred resistance to white rust. This gene was located in the C genome of *B. oleracea*, which is one of the two diploid progenitors of *B. carinata*.

Disease resistance/White rust (*Albugo candida*)/*Brassica juncea*

Thukral and Singh (1986)
Crosses were made between white rust resistant Indian line EC 12749 and white rust susceptible Indian cvs. Parkash and Varuna. Segregation ratios indicated that white rust resistance was controlled by dominant alleles and additive genes.

Singh and Singh (1987)
Resistance to white rust was studied in the F_3 progeny of the complex cross [/ RH30 x Domo / RIK78-6 x RH30 / x / RIK78-6 x Prakash / x / Varuna x TM2 /], where cv. Domo, RIK-7806, and TM2 possessed a moderate to a high degree of white rust resistance and RH-30, Prakash, and Varuna were susceptible to the disease. Significant additive variance and, to a lesser degree significant dominance variance was observed. The average degree of dominance indicated overdominance. Narrow-sense heritability was 52.2%.

Singh and Singh (1988)
Inheritance of white rust resistance in P_1, P_2, F_1, F_2, and BC generations of five interspecific crosses between *Brassica juncea* (susceptible) x *Brassica carinata* (resistant) revealed that one gene with complete dominance conferred resistance to white rust. This gene was located in the C genome of *B. oleracea*, which is one of the two diploid progenitors of *B. carinata*.

Tiwari *et al.* (1988)
Segregation data of reciprocal crosses between Soviet white rust resistant cv. Vniimk-405 and Canadian susceptible cv. Blaze fitted a single dominant gene for resistance.

Gulati *et al.* (1991)
Segregation ratios of F_2 and BC_1 generations of a cross between Dira 335 (susceptible to white rust) and Dira 313-6 (resistant to white rust) were consistent with monogenic dominant resistance.

Khalatkar *et al.* (1991)
See Yield and quality traits/Seed fatty acids/Erucic acid (C22:1)/*Brassica juncea*.

Rao and Raut (1994)
The inheritance of white rust resistance was investigated in an interspecific cross between white rust susceptible Indian mustard [= *Brassica juncea*] cv. Varuna x white rust resistant *Brassica napus* synthetic line Indian Synthetic Napus 706. Reciprocal F_2 and BC segregation ratios were consistent with digenic inheritance with dominant and recessive gene interaction (F_2 ratios: 13 resistant plants: 3 susceptible plants). Genes ac_1 and Ac_2 were proposed for white rust susceptibility.

Subudhi and Raut (1994b)
The inheritance of white rust resistance was studied in interspecific crosses between *Brassica juncea* cv. Pusa Barani (white rust susceptible) x *Brassica napus* strains N-368, N-576, and N-606 (white rust resistant). The F_1 plants were completely immune to white rust. F_2 segregation ratios indicated monogenic inheritance (3:1 ratio) or digenic inheritance with epistatic gene interaction (13:3 ratio).

Sachan *et al.* (1995)
Crosses were made between white rust resistant Canadian cvs. Domo and Cutlass and white rust susceptible Indian cvs. Kranti and Varuna. Resistance was conditioned by a single dominant gene in the Canadian cultivars.

Disease resistance/White rust (*Albugo candida*)/*Brassica napus*

Fan *et al.* (1983)
The inheritance of white rust resistance (race 7) was studied in reciprocal crosses between Canadian spring oilseed rape [= subsp. *oleifera*] cv. Regent (resistant to white rust) and Chinese winter oilseed rape lines Green Cup Leaf and 2282-9 (susceptible to white rust race 7). F_1 progenies were resistant to white rust indicating that the resistance was a dominant trait and nuclearly encoded. F_2 segregation data were consistent with a three independent gene model; the presence of a dominant allele at either one of the genes resulted in resistance. The genes were designated *Ac7-1*, *Ac7-2*, and *Ac7-3*.

Liu *et al.* (1987)
Segregation data in progeny of a cross between white rust susceptible line 2282-9 and white rust resistant cv. Regent [= subsp. *oleifera*] were consistent with a model of digenic inheritance.

Verma and Bhomik (1989)
The inheritance of resistance to race 2 of white rust (*B. juncea* race) was studied in a cross between a white rust resistant *B. napus* line (BN-Sel.) x a white rust susceptible line (BN-38 Sel.). The F_1 plants were resistant to the disease. The F_2 and testcross segregation ratios were consistent with a digenic model with duplicate gene action (15: 1 and 3:1 ratios, respectively).

Liu and Rimmer (1991)
The inheritance of resistance to a white rust isolate recovered from *B. carinata* was controlled by a single dominant gene for resistance.

Rao and Raut (1994)
The inheritance of white rust resistance was investigated in an interspecific cross between white rust susceptible Indian mustard [= *Brassica juncea*] cv. Varuna x white rust resistant *Brassica napus* synthetic line Indian Synthetic Napus 706. Reciprocal F_2 and BC segregation ratios were consistent with digenic inheritance with dominant and recessive gene interaction (F_2 ratios: 13 white rust resistant plants: 3 white rust susceptible plants). Genes ac_1 and Ac_2 were proposed for white rust susceptibility.

Subudhi and Raut (1994b)
See Disease and pest resistance traits/Disease resistance/White rust (*Albugo candida*)/*Brassica juncea*.

Disease resistance/White rust (*Albugo candida*)/*Brassica nigra*

Delwiche and Williams (1974)
Monogenic dominant resistance to race 2 was found in black mustard.

Delwiche and Williams (1981)
The inheritance of a naturally resistant variant to white rust race 2, originally detected in plants grown from seed from a wild *B. nigra* from Madison, Wisconsin, U.S.A. (W3) was studied in testcross and F_3 generations. Resistance to white rust race 2 was controlled by a single dominant gene, designated *Ac2*.

Disease resistance/White rust (*Albugo candida*)/*Brassica rapa*

Delwiche and Williams (1974)
Monogenic dominant resistance to race 2 was found in *B. campestris* [*= B. rapa*].

Edwards and Williams (1987)
Three cycles of selection for minor genes for resistance to white rust race 2 were conducted in a rapid cycling turnip rape genotype devoid of major white rust resistance genes. The mode of inheritance appeared to be polygenic.

Mitchell-Olds *et al.* (1995)
See Disease and pest resistance traits/Disease resistance/Blackleg (*Leptosphaeria maculans*)/*Brassica rapa.*

Disease resistance/White rust (*Albugo candida*)/*Raphanus sativus*

Williams and Pound (1963)
The inheritance of resistance to *A. candida* race 1 at the cotyledonary stage in cvs. China Rose Winter and Round Black Spanish was controlled by a single dominant gene.

Humaydan and Williams (1976)
Segregation data from F_1 (all resistant) and F_2 generations (105 resistant: 40 susceptible progeny) indicated that inheritance of resistance to *A. candida* race 1 in cv. China Rose Winter was controlled by a single dominant gene, *R*, later renamed *Ac1*. Linkage between *Ac1* and *Pi*, a gene for uniform pink pigmentation of the plant, was also demonstrated.

Pest resistance/Cabbage aphid (*Brevicoryne brassicae*)/*Brassica napus*

Quazi (1988)
F_2 segregation data in interspecific crosses between oilseed rape [= *Brassica napus* subsp. *oleifera*] cv. Tower (cabbage aphid susceptible) and kale [= *Brassica oleracea* var. *acephala*] cv. Rawara (cabbage aphid resistant) suggested genetic control by a single dominant gene. BC ratios to susceptible cvs. Tower and Rangi (fodder rape) were consistent with a single dominant gene model of inheritance.

Pest resistance/Cabbage aphid (*Brevicoryne brassicae*)/*Brassica oleracea*

Quazi (1988)
See Disease and pest resistance traits/Pest resistance/Cabage aphid (*Brevicoryne brassicae*)/ *Brassica napus*.

Pest resistance/Flea beetle (*Phyllotreta cruciferae*)/*Brassica napus*

Lamb *et al.* (1993)
The inheritance of antixenosis resistance to the flea beetle (*Phyllotreta cruciferae*) was studied in reciprocal crosses between oilseed rape [= subsp. *oleifera*] lines L19 and M12. Line L19 was less susceptible to flea beetles than line M12. The authors postulated control by two or more genes.

Pest resistance/Mustard aphid (*Lipaphis erysimi*)/*Brassica juncea*

Goomber and Labana (1983)
The inheritance of aphid resistance in brown mustard was studied in a diallel cross with four moderately resistant parents (T6342, RLM198, RL18, and RLM514) and three susceptible parents (KB_1, KB_2, and Varuna). An additive-dominance model was fitted only for the T6342 x RLM514 cross (resistant x resistant) and showed additive gene effects. A digenic-epistatic model revealed the importance of both additive and dominance components and predominance of non-additive gene effects. The cross KB_1 x KB_2 (susceptible x susceptible) showed complementary gene action and four other crosses showed duplicate epistasis for the number of aphids per plant.

Pest resistance/Onion thrips (*Thrips tabaci*)/*Brassica oleracea*

Stoner *et al.* (1986)
On the basis of F_1, F_2, and BC_1 segregation data, resistance to onion thrips in cabbage [= var. *capitata*] was quantitatively inherited, with susceptibility dominant. Epistasis was suspected.

PHYSIOLOGICAL TRAITS

Ascorbic acid content/*Brassica oleracea*

Walker and Foster (1946)
The inheritance of ascorbic acid content was studied in crosses between cabbage [= var. *capitata*] lines with high or low ascorbic acid content. The ascorbic acid content of F_1 plants was intermediate between that of the parents, while the values for the F_2 plants were normally distributed, suggesting polygenic control.

Asynaptic mutants/*Brassica rapa*

Stringam (1970)
The inheritance of three asynaptic mutants was determined. Mutants 566-1B and 597 originated from seed of yellow sarson [= subsp. *trilocularis*] treated with ethyleneimine; mutant 818 originated from the F_1 progeny of a cross between yellow sarson x a Polish [= subsp. *oleifera*] strain. Mutants 566-1B, 597, and 818 were conditioned by single recessive genes, designated *as*, as_2, and as_3, respectively.

Bolting/*Brassica napus*

Mero and Honma (1984a)
The inheritance of bolting in Chinese cabbage [= *B. rapa* subsp. *pekinensis*] was investigated by hybridizing Chinese cabbage with *B. napus*. Segregation data suggested that bolting response was conditioned by a few major genes and that the percentage of bolting plants was dependent on the Chinese cabbage cultivar used. The observed segregation ratios appeared to have resulted from variable ploidy and random assortment of chromosomes carrying genes for vernalization requirement.

Bolting/*Brassica oleracea*

Sutton (1924)
The F_2 segregation ratios of a cross in cabbage [= var. *capitata*] between Red Pickling Cabbage (tendency to bolt) x a green heading cabbage suggested that the traits “tendency to bolt” and “green leaf colour” were conditioned by unlinked, single recessive genes.

Malinovski (1928)
In crosses between bolting and non-bolting types of cabbage [= var. *capitata*], the F_1 plants were non-bolting. F_2 segregation ratios were consistent with a single dominant gene for non-bolting.

Samson (1930)
Non-bolting in cabbage [= var. *capitata*] was conditioned by a single dominant gene.

Bouwkamp and Honma (1969)
F_2 segregation ratios of crosses between broccoli [= var. *italica*] inbred lines with different flowering response (bolting) and frost resistance indicated two dominant epistatic genes for frost resistance (ratio: 9 resistant: 7 sensitive) and polygenic control for bolting. The traits were unlinked.

Bolting/*Brassica rapa*

Shibutani and Okamura (1957)
The F_1 generation of crosses between turnips [= subsp. *rapifera*] with different bolting habits had an intermediate bolting habit. No F_2 segregation ratios were provided.

Mero and Honma (1984a)
See Physiological traits/Bolting/*Brassica napus*.

Mero and Honma (1984b)
The inheritance of bolting in Chinese cabbage [= *B. rapa* subsp. *pekinensis*] was investigated by hybridization with chikale (*B. rapa* subsp. *pekinensis* x *B. napus*). Two Chikale lines were developed by hybridizing Chinese cabbage cv. Mandarin with kale cv. Siberian (*B. napus*). Chikale line QB-2 bolted after one week of vernalization while Chikale line LB-7 bolted after four weeks of vernalization. Segregation data for bolting response from reciprocal crosses between Chinese cabbage cv. Wong Bok and lines QB-2 and LB-7 indicated two major additive genes with modifiers.

Mero and Honma (1985)
Segregation for bolting resistance in an interspecific cross between Chinese cabbage [= *Brassica rapa* subsp. *pekinensis*] and turnip [= *Brassica rapa* subsp. *rapifera*] was conditioned by two major additive genes. There was a progressive increase in bolting with increased vernalization. The nuclear genome of the parent affected the segregation in subsequent generations.

Chlorophyll synthesis suppressor mutant/*Brassica rapa*

Stringam (1978)
A mutant suppressing chlorophyll synthesis of plants carrying the *yg-6* gene (Stringam, 1973) was identified in yellow sarson [= subsp. *trilocularis*]. Repression of chlorophyll synthesis at the *yg-6* locus was controlled by a partially dominant gene, designated *r*.

Drought tolerance/*Brassica juncea*

Chaudhari *et al.* (1989)
Drought adaptation was studied in the F_1, BC_1, and BC_2 generations of the crosses Varuna x RH7513, Domo x RC781, Domo x RIK, RC781 x RIK, and Varuna x Blaze. Scaling tests and joint scaling tests indicated digenic interaction for leaf water potential, relative water content, osmotic potential, and leaf diffusive conductance. In the cross RC781 x RIK, the component traits leaf water potential, relative water content, osmotic potential, and leaf diffusive conductance had significant digenic interactions, whereas the overall effect traits osmotic adjustment and transpirational cooling fitted a simple additive and dominance model.

Fertility/*Brassica rapa*

Brune (1949b)
Fertility in intraspecific hybrids of turnip [= subsp. *rapifera*] x Chinese cabbage [= subsp. *pekinensis*] and pak-choi [= subsp. *chinensis*] was conditioned by three dominant genes, two from the turnip parent and the other one from the Chinese cabbage or pak-choi parent.

Freezing tolerance/*Brassica rapa*

Teutonico *et al.* (1995)
F_3 families from 85 F_2 plants derived by selfing a single F_1 plant from the cross cv. Per (biennial) x cv. R500 (annual) [= subsp. *trilocularis*] were used for RFLP analysis and assayed for freezing tolerance (acclimated freezing tolerance and acclimation ability). The results indicated polygenic inheritance. The most complete genetic model included four QTLs on linkage groups 2 (10.6% of the variation), 4 (4.2%), 5 (7.8%), and 7 (26.5%).

Frost resistance/*Brassica oleracea*

Bouwkamp and Honma (1969)
See Physiological traits/Bolting/*Brassica oleracea*.

Gibberellic acid content/*Brassica napus*

Zhang and Guan (1993)
The GA_3 content in the apex of oilseed rape [= subsp. *oleifera*] genotypes was under genetic control, with dominance or overdominant heterosis. No maternal effects were detected. Environmental effects were important.

Growth habit and vernalization/*Brassica incana*

Kianian and Quiros (1992a)
Segregation ratios in a F_2 population (41:11 plants) obtained from a cross between an annual kohlrabi [= var. *gongylodes*] genotype and a perennial genotype of *B. incana* best fitted a monohybrid ratio. The annual habit was dominant.

Growth habit and vernalization/*Brassica napus*

Thurling and Das (1979a)
Substantial genotypic variation for the duration of the pre-anthesis stage was observed in the spring rape [= subsp. *oleifera*] cvs. Target, Oro, Masoweicki, Bronowski, Norin 16, and Isuzu, and their F_1 hybrids grown under controlled environment. Variation in the pre-anthesis growth stage, particularly the stem elongation phase, was attributed mainly to additive effects. However, intermediate duration of the stem elongation phase was dominant over the prolonged period which was dominant over the short phase. A breeding scheme for modifying flowering time in short growing season areas was proposed with the combination of a short vegetative period, a longer period for stem elongation and optimal flowering time. The genetic variation required could be obtained from crossing three parents with different geographical origins followed by screening under non-vernalizing conditions of 25° C and continuous light.

Thurling and Das (1979b)
A 10 x 10 complete diallel cross of spring rape cultivars was analyzed for length of the vegetative period and leaf number at initiation of flowering. The vernalization requirement of *B. napus* was determined by recessive alleles. The Japanese cv. Isuzu had a significant response to vernalization under controlled environment, with the response due to one or few major genes.

Thurling and Das (1979c)
Crosses between spring oilseed rape cvs. Target, Bronowski, and Isuzu were analyzed for the duration of the vegetative stage under controlled environment. Four loci with two alleles at each were defined which accounted for the quantitative response to vernalization; the alleles were distinguished by the delay caused in flowering under unvernalized conditions and the length of the vernalization treatment required to satisfy the response. The allele *v1* caused significant delay in flowering under unvernalized conditions but the response was satisfied after four weeks of vernalization; *v2* short delay, *v3* moderate delay satisfied by four weeks of vernalization, and *v4* slight delay not expressed after four weeks of vernalization. Winter habit was conferred by the presence of two recessive alleles. The genotypes of the parents were defined as cv. Target *V1V1V2V2V3V3V4V4*; cv. Isuzu *v1v1v2v2V3V3 V4V4*; and cv. Bronowski *V1V1V2V2v3v3v4v4*.

Van Deynze and Pauls (1994)
Doubled haploid and F_2 populations were derived from the F_1 of a cross between spring and winter *B. napus* [= subsp. *oleifera*]. Spring habit was dominant to winter habit and the requirement for vernalization was controlled by one major gene and one minor gene, designated *A* and *B*, respectively. The presence of gene *A* was sufficient to allow flowering in less than 62 days without vernalization. Gene *B* allowed plants to flower in between 62 and 77 days. Plants with the double recessive genotypes required more than 77 days to flower in the absence of vernalization.
Ferreira *et al.* (1995)

The study used doubled haploid lines derived from the F_1 of a cross between cvs. Major (biennial) and Stellar (annual) and mapped the loci controlling the vernalization requirement. The results confirmed that the vernalization response was recessive to non-response. A major locus of linkage group 9 or closely linked loci was identified as affecting flowering time through vernalization requirement.

Growth habit and vernalization/*Brassica oleracea*

Kristofferson (1921)
The inheritance of annual plants recovered in the progeny of a cross between cabbage [= var. *capitata*] x kale [= var. *acephala*] was controlled by a single recessive factor.

Horovitz and Perlaska (1954)
The inheritance of a mutant annual cabbage [= var. *capitata*] in biennial cv. Wisconsin All Season was determined in a cross between biennal Savoy cabbage [= var. *sabauda*] cv. Crespo x the Wisconsin All Season mutant. On the basis of the F_1 and BC generations, the annual habit was found to be under the control of a recessive gene, designated *t*, for “tropic”.

Wellensiek (1960)
In crosses between annual and biennial brussels sprouts [= var. *italica*], the annual habit was monogenic and dominant. The annual plant was a naturally occurring variant found in a field of brussels sprouts.

Walkof (1963)
The inheritance of annual flowering habit in a mutant of cabbage [= var. *capitata*] cv. Morden Midget was conditioned by a single dominant gene. Some of the mutant annual plants resembled green sprouting broccoli.

Kianian and Quiros (1992a)
See Physiological traits/Growth habit and vernalization/*Brassica incana*.

Growth habit and vernalization/*Brassica rapa*

Teutonico and Osborn (1995)
The F_2 single plants from a cross between biennial cv. Per and annual oilseed cv. R500 [= subsp. *trilocularis*] were self-pollinated to produce F_3 families. RFLP analysis and map construction were used, including eight loci detected by cold-induced genes from *B. napus* and *Arabidopsis thaliana*. Days to flower were recorded under non-vernalized and vernalized conditions. More than one major gene was involved in the response of *B. rapa* to vernalization and the requirement for vernalization was dominant as the F_1 did not flower without vernalization. Comparison of linkage maps between the *B. rapa* population and a previous study in *B. napus* (Ferreira *et al.*, 1994) using RFLP markers identified some common linkage groups.

Growth rate /*Brassica napus*

Paul (1992a)
See Morphological traits/Leaf/Area/*Brassica napus*.

Harvest index/*Brassica juncea*

Sachan and Singh (1988)
See Morphological traits/Plant/Branch number/*Brassica juncea*.

Herbicide resistance/Atrazine/*Brassica napus*

Beversdorf *et al.* (1980)
Resistance to triazine herbicides (atrazine, cyanazine, and metribuzin) was transferred to cv. Tower [= subsp. *oleifera*] from *B. rapa* cvs. Torch and Candle by backcrossing. The resistance was determined to be maternally inherited.

Herbicide resistance/Atrazine/*Brassica rapa*

Machado *et al.* (1978)
The inheritance of the triazine herbicide atrazine was studied in reciprocal crosses between resistant and susceptible wild biotypes [= subsp. *sylvestris*]. The F_1 progeny of the atrazine resistant x atrazine susceptible cross was resistant to the herbicide, whereas the progeny of the atrazine susceptible x atrazine resistant cross was susceptible to the herbicide, indicating maternal inheritance.

Herbicide resistance/Chlorsulfuron/*Brassica napus*

Swanson *et al.* (1988)
The inheritance of chlorsulfuron tolerance was studied in reciprocal crosses between progeny of a microspore-derived, chlorosulfuron tolerant mutant (M-37) of cv. Topas [= subsp. *oleifera*] and cv. Topas. The segregation ratios were consistent with a single nuclear gene with incomplete dominance.

Ahmad *et al.* (1991)
In vitro selection for resistance to Alternaria leaf spot and the herbicide chlorsulfuron in rapid cycling *B. napus* resulted in the generation of heritable resistance to the pathogen and resistance to the herbicide.

Herbicide resistance/Dicamba/*Sinapis arvensis*

Jasieniuk *et al.* (1995)
Inheritance studies of the resistance of wild mustard to the auxinic herbicide dicamba indicated that the trait was controlled by a single, dominant nuclear gene. Three reciprocal crosses were made between herbicide resistant and herbicide susceptible (wild-type) plants. F_1 progenies were resistant

to the herbicide (50, 200, and 400 g active ingredients per hectare); F_2 progenies segregated in a 3:1 ratio of resistant to susceptible plants. BC progenies segregated in a 1:1 ratio.

Herbicide resistance/Simazine/*Brassica napus*

Karim and Bradshaw (1968)
Nuclear genetic control of variation in response to simazine was detected in oilseed *Brassica* species.

Bradshaw *et al.* (1978)
The simazine resistance of oilseed rape [= subsp. *oleifera*] appeared to be polygenically inherited and tolerance could be significantly improved by recurrent selection.

McGuire and Thurling (1992a)
Genetic analyses of variation in simazine tolerance in populations derived from crosses among cultivars of *B. napus*, representative of the range of tolerance (more tolerant parents Haya, Target, Tower, Wesbrook, and Gulle) and less tolerant cultivars (Chisaya and Bronowski), indicated that the narrow-sense heritability of tolerance equalled 0.61-0.69 in value.

McGuire and Thurling (1992b)
Interspecific crosses between *Brassica rapa* plants selected for improved simazine tolerance and plants of the *Brassica napus* Australian canola cv. Wesbrook [= subsp. *oleifera*] showed that the introgression of genes from *B. rapa* could significantly improve the simazine tolerance of the *B. napus* recipient parent.

Herbicide resistance/Simazine/*Brassica rapa*

McGuire and Thurling (1992b)
Substantial variation in two measures of simazine tolerance was observed in a controlled environment among half-sib families of *B. rapa* obtained from a highly variable cross-composite population of *B. rapa*. Narrow-sense heritability estimates were 0.57 for simazine tolerance index and 0.53 for seedling survival at 15 days after sowing.

Interspecific crosses between *Brassica rapa* plants selected for improved simazine tolerance and plants of the *Brassica napus* Australian canola cv. Wesbrook [= subsp. *oleifera*] showed that the introgression of genes from *B. rapa* could significantly improve the simazine tolerance of the *B. napus* recipient parent.

Heterosis/*Brassica napus*

Lefort-Buson *et al.* (1987b)
The genetic variability of manually produced crosses between European or Asiatic oilseed rape [= subsp. *oleifera*] lines was mainly additive. Specific effects similar to those observed in the parents were obtained for F_1 hybrids of crosses between lines of different origin, *i.e.* European vs. Asiatic.

Knaak and Ecke (1995)
See Morphological traits/Plant/Height/*Brassica napus*.

Heterosis/*Brassica rapa*

Schuler *et al.* (1992)
Mid-parent heterosis in hand-crossed F_1 hybrids between turnip rape [= subsp. *oleifera*] cv. Tobin and 19 Canadian and European strains averaged 18% for seed yield, -1.0% for percent oil content, 17% for oil yield, -0.7% for days to maturity, and 7.0% for plant height. There was no heterosis for days to flower or average single seed weight.

Falk *et al.* (1995)
See Morphological traits/Silique/Number/*Brassica rapa*.

Leaf canopy/*Brassica napus*

Lefort-Buson and Dattée (1982b)
See Morphological traits/Leaf/Number/*Brassica napus*.

Leaf differentiation rate/*Brassica rapa*

Tan *et al.* (1982)
See Morphological traits/Head/Diameter/*Brassica rapa*.

Leaf diffusion resistance/*Brassica napus*

Paul (1992b)
See Morphological traits/Stomates/Guard cell length/*Brassica napus*.

Lodging/*Brassica napus*

Lefort-Buson and Dattée (1982b)
See Morphological traits/Leaf/Number/*Brassica napus*.

Grant and Beversdorf (1985)
See Morphological traits/Plant/Height/*Brassica napus*.

Male sterility/Cytoplasmic/*Brassica juncea*

Banga and Labana (1985)
Male sterile plants were identified in the F_2 generation of the cross Indian line RLM-198 x European line EJ-33. The inheritance pattern was studied in the F_1, F_2, F_3, and BC generations. The sterility occurred when the cytoplasm of RLM-198 ('S' for sterility-inducing cytoplasm) interacted with recessive nuclear genes of EJ-33; EJ-33 possessed a male fertile cytoplasm (F). The following genotypes were

postulated (S)*RFRF* for RLM-198, (F)*rfrf* for EJ-33, and (S)*rfrf* for the male sterile plants. The CMS system was designated MS-4.

Male sterility/Cytoplasmic/*Brassica napus*

Thompson (1972)
See Morphological traits/Leaf/Waxiness (glossy)/*Brassica napus*.

Shiga (1976)
Cytoplasmic male sterility was identified in the F_2 generation of a cross between Chisaya-natane as a female and Hokuriku 23 as a pollen parent. Male sterility was maintained by backcrossing to the original male parent Hokuriku 23. 131 Japanese cultivars were classified into three groups by fertility indices of the hybrids: 23 fertility restoring, 79 partially restoring, and 29 non-restoring cultivars. The fertility restoring gene(s) determined seed set in the hybrid and the relative position of the anther to the stigma. Rapeseed cultivars could be classified into two groups 'S' with male sterile-inducing cytoplasm and 'N' with non-male sterile-inducing cytoplasm. A classification is proposed dividing the S group into six classes and the N group into three classes according to the number and action of the fertility restorer genes. High parent heterosis for seed yield in winter oilseed rape was approximately 50%. Seed yields of 108 hybrids were found to be equal or greater than the pollen parents.

Shiga *et al.* (1978)
The expression of male sterility in hybrids was studied in reciprocal interspecific crosses between male sterile (MS) lines of *B. napus* and the AA genome species *Brassica chinensis*, *Brassica narinosa*, *Brassica parachinensis*, *Brassica pekinensis*, and *Brassica rapa*. The male sterility line was also crossed with the F_1 hybrids of artificially synthesized *B. napus* CC x AA Kyabusai and Murasaki-natane *B. napus* which has a normal cytoplasm and lacks restorer alleles. All but one of the AA genome cultivars had normal cytoplasm (N) with weak restorer alleles *rf* resulting in full or partial male sterility in the hybrids between MS line (female) and the AA genome cultivars (S*rfrf* or S*Rfrf*) and full male fertility in the reciprocal cross (N*rfrf*, N*Rfrf*). The results for artificially synthesized *B. napus* AACC were similar to the AA genome crosses; the Kyabusai had S cytoplasm which could result from the CC genome species.

Yang and Fu (1990)
The inheritance of polima cytoplasmic male sterility was studied in oilseed rape [= subsp. *oleifera*]. The restorer plants were found to have one pair of fertility-restoring genes (*Rf*) and several temperature-sensitive genes (*Ts*). The *Rf* genes were found to be allelic.

Celis and Jourdan (1993)
The inheritance of a partial male fertile trait was studied in backcrosses between an oilseed rape [= subsp. *oleifera*] cybrid plant with a novel mitochondrial genome x cv. Triton. The results suggested that the partial male sterility trait was controlled by the mitochondrial genome.

Male sterility/Cytoplasmic/*Brassica oleracea*

Pearson (1972)
In cytoplasmic male sterile cabbage [= var. *capitata*] carrying black mustard [= *Brassica nigra*] cytoplasm, a petaloid sterility (stamens transformed into petals or carpels with absence of nectaries) was controlled by a single gene, designated *p*.

Male sterility/Cytoplasmic/*Brassica rapa*

Ohkawa (1983)
The inheritance of male sterile cytoplasm in *B. rapa* line I-4 and its use in F_1 seed production in *B. rapa* and *B. napus* was studied in reciprocal crosses between I-4 and 33 other cultivars of *B. rapa* subsp. *rapifera* (17), *pekinensis* (7), *oleifera* (4), *nipposinica* (2), *chinensis* (1), *trilocularis* (1), and one unknown line. Male sterility was shown to be cytoplasmically controlled in I-4 which has fertility restorer nuclear genes. Male sterile plants were obtained from the F_2 and BC_1 populations of the hybrids between I-4 line as female and the cultivars having no fertility restorer genes. Male sterility could be maintained by the maintainers for the cytoplasmic male sterility in *B. napus*, and restored by the restorers for male sterility in *B. napus*.

Male sterility/Cytoplasmic/*Raphanus sativus*

Ogura (1968)
Male sterility in a Japanese radish type was governed by a cytoplasmic factor and by one recessive gene, *ms*.

Male sterility/Fertility restoration/*Brassica juncea*

Anand *et al.* (1986)
The inheritance of male fertility restoration in cytoplasmic male sterile *B. juncea* plants was conditioned by two complementary genes, designated Rf_1 and Rf_2 in *B. nigra* and Rf_1' and Rf_2' in *B. rapa*.

Male sterility/Fertility restoration/*Brassica napus*

Shiga (1976)
See Physiological traits/Male sterility/Cytoplasmic/*Brassica napus*.

Shiga *et al.* (1977)
Four genes were reported to condition male fertility restoration in male sterile lines of *B. napus*.

Fang and McVetty (1987)
Crosses were made between *pol* cms lines of Swedish spring canola [= subsp. *oleifera*] cv. Karat x Australian spring canola cv. Marnoo and winter rapeseed strain Italy and line UM2353 from the University of Manitoba, Winnipeg, Canada. Segregation data indicated that both Italy and UM2353 contained a single dominant gene for male fertility restoration.

Fang and McVetty (1989)
The inheritance of male fertility restoration for the polima cytoplasmic male sterility (CMS) system in summer oilseed rape [= subsp. *oleifera*] was studied in crosses between two polima CMS lines and the male fertility restorers Italy and UM2353. Segregation ratios were consistent with control by a single dominant gene in each restorer, gene *Rfp1* in Italy and gene *Rfp2* in line UM2353. Genes *Rfp1* and *Rfp2* were non-allelic.

Chen and Heneen (1990)
Crosses were made between male fertility restored yellow-petalled lines Sv84-28053 and Sv02372 and white/pale-petalled resynthesized line No7076 containing a monogenic dominant white/pale petal colour gene from *B. alboglabra*. The segregation data indicated that male fertility restoration was under monogenic control and independent of the petal colour gene.

Crosses were also made between line Sv84-28053 and yellow-petalled *B. rapa* yellow sarson line K-151. The segregation data for the trigenomic (AAC) progeny indicated that male fertility restoration was independently inherited from white/pale petal colour. The following genotypes were postulated: $w_C w_C(S)Ms_A Ms_A ms_C ms_C$ or $w_C w_C(S)ms_A ms_A Ms_C Ms_C$ for line Sv84-28053, $w_C w_C(S)\ Ms_A Ms_A ms_C ms_C$ or $w_C w_C(S)ms_A ms_A Ms_C Ms_C$ for line Sv02372, $W_C W_C\ (N)ms_A ms_A ms_C msC$ for line No7076, and $w_C w_C(N)ms_A ms_A$ for line K-151.

Sodhi *et al.* (1994)
The inheritance of fertility restoration for the 'tour' cytoplasmic male sterility in oilseed rape [= subsp. *oleifera*] was determined in crosses between plants of the male sterile line BO15 and plants of restoring cultivars Mangun and Yudal. F_1 and F_2 segregation ratios were consistent with control by a single dominant gene.

Zhou and Bai (1994)
The inheritance of fertility restoration was studied in crosses between plants carrying the dominant *Ms* gene for male sterility and fertility-restoring plants. Fertility restoration was controlled a single dominant gene.

Male sterility/Genic/*Brassica bourgeaui*

Kianian and Quiros (1992a)
Interspecific crosses of *Brassica bourgeaui* with *Brassica alboglabra*, *Brassica oleracea*, and *Brassica cretica* indicated that male sterility was recessive.

Male sterility/Genic/*Brassica cretica*

Kianian and Quiros (1992a)
See Physiological traits/Male sterility/Genic/*Brassica bourgeaui*.

Male sterility/Genic/*Brassica juncea*

Banga and Labana (1983)
The inheritance of male sterility in the progenies of crosses between a male sterile mutant (identified in an open-pollinated population of German line EJ-32) x male fertile plants of the same line and lines RLM 198 and BS 119, indicated that the trait was recessive and controlled by a single gene.

Male sterility/Genic/*Brassica napus*

Takagi (1970)
The inheritance of a mutation for male sterility induced by gamma-irradiation in Japanese cv. Murasaki-natane was studied in crosses between the mutant and the parent cultivar. The trait was controlled by a single recessive gene.

Heyn (1977)
Digenic inheritance was observed for a male sterility trait. F_2 segregation data were 15:1 and 3:1 male fertile plants to male sterile plants. The genotype of the male sterile plants was $ms_1ms_1ms_2ms_2$.

Mathias (1985)
A male sterile line was isolated in Polish winter cv. Janpol [= subsp. *oleifera*]. Male sterile and male fertile flowers were phenotypically very similar; stamens of sterile flowers were almost as long as male fertile stamens, but somewhat narrower, and they were brown and without visible pollen. The trait was controlled by a dominant nuclear gene designated Ms_j. The genotypes ms_jms_j (male fertile plants) and Ms_jms_j (male sterile plants) were postulated. Dominant homozygotes were missing.

Li *et al.* (1988)
The inheritance of a genetic male sterility system was studied in the Chinese male sterile line No. 23. The segregation data were consistent with a two gene control with dominant epistasis. The genotypes $Ms_1Ms_1ms_2ms_2$ and $Ms_1ms_1ms_2ms_2$ for male sterile plants were postulated, with all other genotypes giving rise to male fertile plants.

Mariani *et al.* (1991)
The development of a male sterility system was described in cv. Drakkar [= subsp. *oleifera*]. The system consisted of the barnase gene causing male sterility and the Barstar gene coding for a protein inhibitor of the barnase gene, and hence fertility restoration. Plants carrying the barnase and the barstar genes were fully fertile.

Theis (1991)
The inheritance of male sterility in synthetic *B. napus* (*B. oleracea* x *B. chinensis*) was determined in crosses between the synthetic line x French winter oilseed rape cv. Jet Neuf. The F_1 plants were male fertile. Segregation ratios of the F_2 generation (265 male fertile to 69 male sterile plants) and the BC_1 generation (male sterile line x F_1 plants) (192 male fertile to 181 male sterile plants) indicated that male sterility was conditioned by a single recessive gene.

Pan *et al.* (1993)
The inheritance of a genetic male sterility trait in oilseed rape [= subsp. *oleifera*] line 79.7 was determined to be under the control of two recessive, duplicate genes.

Male sterility/Genic/*Brassica oleracea*

Jensma (1957)
Male sterility in cauliflower [= var. *botrytis*] was suggested to be controlled by a single recessive gene, designated *ms*.

Johnson (1958)
Male sterility in brussels sprouts [= var. *gemmifera*] was conditioned by a single recessive gene. Dominance of male fertility was imperfect, with heterozygotes producing some male sterile flowers. Heterozygous plants produced more male sterile flowers at warm temperature (70° F) than at cool temperature (55° F).

Cole (1959)
A natural male sterile mutation in green sprouting broccoli [= var. *italica*] was conditioned by a single recessive gene, designated *ms*. The male sterile mutant plant was also glossy. Genes *ms* and *gl* were unlinked.

Nieuwhof (1961)
Male sterility in cauliflower [= var. *botrytis*] was conditioned by a single recessive gene, designated *ms.* Male sterility in brussels sprouts [= var. *gemmifera*] cv. Roodnerf was conditioned by a number of recessive factors.

Rundfeldt (1961)
A temperature sensitive strain of cabbage is described. The plants were male sterile in summer and male fertile in winter.

Borchers (1966)
Male sterility in an inbred line of purple cauliflower [= var. *botrytis*] cv. Early Purple Head was conditioned by a single recessive gene, designated ms_4. Gene ms_4 was not allelic to genes ms_1 (Cole 1959) or ms_2 (Johnson 1958).

Sampson (1966a)
Linkage was observed between male sterility gene *ms-1* of green sprouting broccoli [= var. *italica*] and gene *c* (anthocyanin-free plant with bright green hypocotyl) of curly kale [= var. *acephala*] and variegated ornamental kale.

Sampson (1966b)
Male sterility was controlled by a recessive gene, *ms-1*, in sprouting broccoli [= var. *italica*], and was distinct from gene *ms-2* described in brussels sprouts [= var. *gemmifera*], and gene *ms-4*, found in cauliflower [= var. *botrytis*] cv. Purple Head.

Nieuwhof (1968)
Allelic tests for male sterility genes ms_B from brussels sprouts [= var. *gemmifera*] and ms_c from cauliflower [= var. *botrytis*] indicated that the genes were different. The results of other crosses indicated that the genes acted independently.

Dickson (1970)
A broccoli [= var. *italica*] temperature sensitive male sterility gene designated ms_6 was inherited in a recessive manner. Gene ms_6 was non-allelic to the male sterility genes ms_1, ms_2, ms_4, and ms_5. Male sterile plants produced pollen following exposure to low temperature.

Dunemann and Grunewaldt (1991)
Inheritance of male sterility was studied in backcrosses between a chemically-induced male sterile mutant (No. 210) of broccoli [= var. *italica*] cv. Providence x cvs. Prominence and Skiff and genotypes of cabbage [= var. *capitata*], savoy cabbage [= var. *sabauda*], and kohlrabi [= var. *gongylodes*]. In all cases, the ratio of male sterile plants to male fertile plants was 1:1, indicating a single gene for male sterility. The male sterility gene was dominant.

Kianian and Quiros (1992a)
See Physiological traits/Male sterility/Genic/*Brassica bourgeaui*.

Ruffio-Chable *et al.* (1993)
A monogenic dominant gene conditioning male sterility in cauliflower [= var. *botrytis*] was used to develop F_1 hybrids. Male sterility was incompletely expressed at low temperature.

Male sterility/Genic/*Brassica rapa*

Das and Pandey (1961)
Crosses were made between plants of brown sarson [= subsp. *dichotoma*] cv. M-18 heterogeneous for male sterility. Anthers of male sterile progeny contained no pollen or a small amount of sterile pollen. Male sterile plants had smaller petals than male fertile plants. The segregation data indicated a single recessive gene for genic male sterility.

Das and Chowdhury (1963)
Male sterile plants were recovered in the progeny of a cross between brown sarson [= subsp. *dichotoma*] cvs. M-18 and A. The male sterile plants had normal, but indehiscent, anthers containing viable pollen grains. The F_2 segregation data indicated that functional male sterility was controlled by a single recessive gene.

Chowdhury and Das (1966)
Male sterility in yellow sarson [= subsp. *trilocularis*] was controlled by a single recessive gene.

Chowdhury and Das (1967)
The inheritance of male sterility was studied in the progenies of crosses between plants of self-incompatible cvs. Russ Rai A-6/3 and Lotani Kurja-3, and self-compatible cultivars 4505 and 5004-2. The results indicated that genes for male sterility in self-compatible and self-incompatible cultivars were non-allelic. Homozygosity of recessive alleles resulted in male sterility.

Hawk and Crowder (1978)
A male sterile mutant was isolated in the S_1 generation of *B. campestris* introduction 175054 or 175079 from the Regional Plant Introduction Station, Ames, Iowa, U.S.A. The anthers of the male sterile mutant were small, pointed, white, and devoid of pollen. F_2 and testcross segregation data indicated a single recessive gene, designated *ms*.

van der Meer (1986)
Male sterile plants were found in the BC progeny of a Chinese cabbage [= subsp. *pekinensis*] x pak choi [= subsp. *chinensis*] hybrid to Chinese cabbage. The trait was controlled by a single dominant gene.

van der Meer (1987)
Male sterile plants were recovered in the BC progeny of a Chinese cabbage [= subsp. *pekinensis*] cv. Granaat x pak choi [= subsp. *chinensis*] hybrid x Chinese cabbage cv. Monument. Inheritance studies indicated that male sterility was conditioned by a single dominant gene.

Bhajan *et al.* (1993)
Male sterile plants were identified in an Indian collection of yellow sarson [= subsp. *trilocularis*] lines. Male sterile plants had smaller sepals and petals than male fertile plants, a longer gynoecium, small, narrow, and pointed stamens, and empty anthers on shorter filaments. The inheritance of male sterility was observed to be monogenic recessive.

Male sterility/Genic/*Raphanus sativus*

Tokumasu (1951)
A gene for male sterility, designated *ms*, was reported in Japanese radish.

Ogura (1968)
Male sterility in a Japanese radish type was governed by a cytoplasmic factor and by one recessive gene, *ms*.

Humaydan and Williams (1976)
The inheritance of male sterility in plants of cv. Early Scarlet Globe was found to be controlled by a single recessive gene, designated *ms1*, pending allelic tests with gene *ms*.

Nieuwhof (1990)
Crosses were made between male sterile and male fertile plants of Japanese radish. Studies of segregation for male sterility in full-sib families and BC generations indicated that male sterility was probably determined by one dominant and two recessive genes acting independently, with evidence that minor genes could be involved. Since the three genes acted independently, they did not need to be present in male sterile material, which could account for the monogenic inheritance reported by Ogura (1968) and Humaydan and Williams (1976). Expression of male sterility was affected by temperature. In some populations, a reversible temperature effect was found, most male sterile plants occurring at 10, 14 and 26° C and most male fertile plants occurring at 17 and 20° C.

Meristem mutant (blind)/*Brassica oleracea*

Dickson (1968)
The trait “blind” (lacking a growing point) in broccoli [= var. *italica*] was determined to be conditioned by a single recessive gene, designated *bl*.

Nitrogen uptake and utilization/*Brassica napus*

Yau and Thurling (1987)
Significant genetic variation in nitrogen uptake and utilization was observed in an F_2 population of spring oilseed rape [= subsp. *oleifera*] under field or controlled environment conditions. Narrow-sense heritabilities for these traits were consistently low.

Node production/*Brassica oleracea*

Hodgkin (1981)
The inheritance of node number and rate of node production was investigated in brussels sprouts [= var. *gemmifera*] using 10 F_1 cultivars (Leonore, King Arthur, Peer Gynt, Parsifal, Jade E, Perfect Line, Achilles, Kadina, Gleneagles, and Nelson) and 45 progenies derived from intercrossing and selfing. A close correlation was observed between total node number and rate of node production, as well as between total node number and number of harvested sprouts.

Nodule formation/*Brassica napus*

Trinick and Hadobas (1995)
The formation of nodule-like structure on roots of *Arabidopsis* and *B. napus* by strains of *Bradyrhizobium* was found to be heritable.

Organelle transmission/Chloroplast/*Arabis albida*

Corriveau and Coleman (1988)
Maternal inheritance of plastid DNA was confirmed for *Arabidopsis thaliana*, *Arabis albida*, *Brassica campestris* [*= B. rapa*], *B. napus*, *B. oleracea*, *Lepidium virginicum*, and *Raphanus sativus*.

Organelle transmission/Chloroplast/*Brassica napus*

Corriveau and Coleman (1988)
See Physiological traits/Organelle transmission/Chloroplast/*Arabis albida*.

Organelle transmission/Chloroplast/*Brassica oleracea*

Corriveau and Coleman (1988)
See Physiological traits/Organelle transmission/Chloroplast/*Arabis albida*.

Heath and Earle (1995)
The inheritance of chloroplasts in protoplast-derived somatic hybrids between cauliflower [= var. *botrytis*] and turnip rape [= *B. rapa* subsp. *oleifera*] was observed to be biased towards the turnip rape genome.

Organelle transmission/Chloroplast/*Brassica rapa*

Corriveau and Coleman (1988)
See Physiological traits/Organelle transmission/Chloroplast/*Arabis albida*.

Heath and Earle (1995)
See Physiological traits/Organelle transmission/Chloroplast/*Brassica oleracea*.

Organelle transmission/Chloroplast/*Lepidium virginicum*

Corriveau and Coleman (1988)
See Physiological traits/Organelle transmission/Chloroplast/*Arabis albida*.

Organelle transmission/Chloroplast/*Raphanus sativus*

Corriveau and Coleman (1988)
See Physiological traits/Organelle transmission/Chloroplast/*Arabis albida*.

Organelle transmission/Mitochondrion/*Brassica napus*

Kemble at al. (1988)
In protoplast-derived cybrids of oilseed rape [= subsp. *oleifera*], mitochondrial DNA plasmids from one parent were either lost or transferred to the mitochondria of the other parent. Mitochondria harbouring these plasmids became dominant in the regenerated plants and were inherited maternally through successive sexual generations.

Erickson and Kemble (1990)
Paternal inheritance of mitochondria was observed in about 10% of F_1 progeny from crosses between triazine tolerant male fertile *B. napus* plants and polima male sterile plants carrying a male fertility restorer gene on an extra chromosome.

Erickson and Kemble (1993)
Paternal transmission of mitochondria was observed in a cross between a female line and a male fertile line carrying the polima cytoplasm.

Stiewe and Röbbelen (1994)
The inheritance of a recombined *B. rapa- B. tournefourtii* mitochondrial genome in a cytoplasmic male sterile line of oilseed rape [= subsp. *oleifera*] cv. Duplo derived via protoplast fusion was found to be stable.

Pollen/Fatty acids/*Brassica napus*

Jourdren *et al.* (1996)
See Yield and quality traits/Seed fatty acids/Linolenic acid (C18:3)/*Brassica napus*.

Pollen/Fertility/*Brassica carinata*

Subudhi and Raut (1995)
Seed and pollen fertility were studied in the early generations of the interspecific crosses *Brassica juncea* x *Brassica napus* and *B. juncea* x *Brassica carinata*. High heritability and genetic advance for seed and pollen fertility were noticed in several cross combinations.

P**ollen fertility/*Brassica juncea***

Subudhi and Raut (1995)
See Physiological traits/Pollen fertility/*Brassica carinata*.

Pollen fertility/*Brassica napus*

Subudhi and Raut (1995)
See Physiological traits/Pollen fertility/*Brassica carinata*.

Regenerative ability (tissue culture)/*Raphanus sativus*

Lutova and Verzina (1984)
Inheritance of the capacity for callus and root formation in isolated radish cotyledons cultured *in vitro* indicated that the interline F_1 hybrids showed dominance for callogenesis and root development. Segregation for root formation in the F_2 was in the monohybrid or dihybrid ratio, and reciprocal differences were evident, while callogenesis appeared to be controlled by a single gene, designated *c*. The genes for root development were designated *rs* and *rl*. The three genes were independently inherited.

Respiration rate/*Brassica napus*

Paul (1992c)
The inheritance of the rate of dark respiration was studied in leaves of forage rape [= subsp. *oleifera*] in a 5 x 5 diallel cross. Additive and dominance effects were detected. Broad-sense heritability was quite high; narrow-sense heritability was moderate. Non-allelic gene interactions were observed in both years of the study. A significantly lower respiration rate than that of the parents was observed in some of the F_1 hybrids.

Root growth/*Brassica rapa*

Shibutani and Okamura (1957)
The F_1 generation of crosses between turnips [= subsp. *rapifera*] with different root growth rates had an intermediate rate of growth. No F_2 segregation ratios were provided.

Salt tolerance/*Brassica napus*

Ashraf *et al.* (1987)
The genetic variation for NaCl tolerance of forage rape at the seedling stage was assessed in nutrient solution culture. Shoot growth was severely inhibited after two weeks of growth in 200, 225, and 250 mmol/l NaCl, but there was considerable variability between seedlings. Ten thousand seeds were screened for shoot growth at high NaCl concentrations. A selection intensity of less than 1% was achieved. Selected plants in two polycrossed populations of each species allowed the estimation of realized heritability (0.62) and narrow-sense heritability (0.74).

Seed dormancy/*Sinapis arvensis*

Garbutt and Witcombe (1986)
Crosses between dormant and non-dormant lines established from a natural population from Nottingham, UK, clearly showed both a maternal and an embryonic component of seed dormancy. The maternal component of dormancy was shown to be controlled by a single locus, with two alleles, the dormant allele *I*, being dominant to the non-dormant allele *i*. Genetic control of the embryonic component was not clear.

Seed leachate (electrical conductance)/*Brassica juncea*

Verma and Lal (1991)
Fifteen lines were crossed to tester lines DIR-313 and TM-22 and to the F_1 hybrid DIR-313 X TM-22, and the hybrids were analysed for germination percent, seedling dry weight and electrical conductance of seed leachate. Both additive and dominance components were important with additive effects predominant for all traits.

Self-compatibility/*Brassica napus*

Thompson (1978)
One dominant gene determined self-compatibility in a cross between a self-incompatible line and a wild-type line.

An *et al.* (1991)
On the basis of results of genetic analyses involving four generations for four crosses and six generations for three crosses, self-compatibility in *B. napus* was controlled by a minimum of two genes. Heritability of the trait was about or less than 50%.

Self-compatibility/*Brassica oleracea*

Wallace and Nasrallah (1968)
A self-compatible cabbage mutant was identified in a self-incompatible inbred line of cabbage [= var. *capitata*] homozygous for an S-allele. The self-compatibility trait was determined by a dominant gene unrelated to the self-incompatibility S-allele system.

Thompson and Taylor (1971)
Self-compatibility was determined in two inbred lines of kale (marrowstem and curled kale) [= var. *acephala*] by a single dominant gene, independent of the self-incompatibility S locus; the self-compatibility gene was expressed only in the absence of S-alleles high in the dominance series. Partial self-compatibility occurred in plants homozygous for recessive S-alleles and active for the dominant self-compatibility gene. The modification from complete to partial self-compatibility was suggested to be due to modifier genes.

Hodgkin (1978)
The inheritance of partial self-compatibility was studied in 15 progenies of a half-diallel cross with selfs from two purple sprouting broccoli [= var. *italica*] inbreds, two brussels sprouts [= var. *gemmifera*] inbreds, and one marrowstem kale [= var. *acephala*] inbred homozygous for highly recessive S-allele S_{15}. Significant amounts of additive gene action were observed on cross-pollinated inflorescences for seed set per flowering site and its components, seeded siliques per flower and number of seeds per seeded silique. There was also considerable heterosis and gene interaction. Complex gene interactions were postulated for seed production on self-pollinated inflorescences.

Hodgkin (1980a)
The inheritance of partial self-compatibility was studied in a half-diallel with seven brussels sprouts [= var. *gemmifera*] inbreds and one cabbage [= var. *capitata*] inbred. Differences for both self- and outcross seed production were mainly due to general combining ability effects. Heterosis was also important for cross-pollinated inflorescences. There was no evidence of increased self-compatibility in specific S-allele heterozygotes (mutual weakening).

Hodgkin (1980b)
The inheritance of partial self-compatibility was studied in a half-diallel with six brussels sprouts [= var. *gemmifera*] plants homozygous for moderately recessive S-allele S_{45}. Significant amounts of additive gene action were found for seed set per flower for both self- and cross-pollinated inflorescences. This was also the case for seeded siliques per flower and seeds per seeded silique on cross-pollinated inflorescences and for seeded silique production on self-pollinated inflorescences.

Self-compatibility/*Brassica rapa*

Shaw (1934)
Reciprocal crosses were made between self-compatible yellow sarson [= subsp. *trilocularis*] x self-incompatible toria [= subsp. *dichotoma*] and black sarson [= subsp. *oleifera*]. The F_1 plants were self-compatible. The F_2 segregation ratios were somewhat close to a 3:1 ratio of self-compatible to self-incompatible plants; control by a single gene was postulated.

Brune (1949b)
A dominant gene for self-compatibility was reported in crosses between Chinese cabbage [= subsp. *pekinensis*] and turnip [= subsp. *rapifera*].

Zuberi *et al.* (1981)
A self-compatible allele s_c was found in a population of self-incompatible plants of var. toria. Allele s_c was recessive to two self-incompatibility alleles (*s* alleles) in pollen and the pistil and was dominant in the pollen and recessive in the pistil to the *s* allele lowest in the dominance series.

Hinata *et al.* (1983)
An epistatic recessive gene, designated *m*, which suppressed the action of *S*-alleles in yellow sarson [= subsp. *trilocularis*] was described.

Nou *et al.* (1993a)
Self-compatible strain C635 contained stigmatic *S*-glycoproteins that were expressed developmentally in a similar way as the *S*-glycoproteins of self-incompatible strain S-23. The *S*-glycoproteins co-segregated with the self-compatibility phenotype in F_2 progeny. Testcross data indicated that self-compatibility was the result of the action of a modifier gene, designated *mod*, which was located outside the S-locus. The recessive *mod* allele suppressed the expression of *S*-alleles in the pistil but not in the pollen.

Self-compatibility/*Iberis amara*

Bateman (1954)
Parental material was from two garden sources, the Helsinki Botanic Garden, Finland, and the Poznan Botanic Garden, Poland. In the first population, self-fertility was due to a recessive gene independent of the *S* locus, whereas in the second population the self-fertility gene was a mutant at the *S* locus and was recessive to some incompatibility alleles but dominant to others.

Self-compatibility (Pseudo-)/*Brassica napus*

Chen *et al.* (1988a)
In a newly resynthesized rape form (*B. oleracea* var. *alboglabra* x *B. campestris* subsp. *oleifera*), the self-incompatibility trait of *B. campestris* was epistatic to the self-compatibility trait of var. *alboglabra*.

Self-compatibility (Pseudo-)/*Raphanus sativus*

Litzow and Ascher (1983)
Inheritance of pseudo-self compatibility (PSC) was examined in crosses among low, medium, and high PSC plants from radish cvs. Sparkler, White Icicle, Comet, and Mr. Big “r” Sparkler. PSC resulted in plants with a functional sporophytic incompatibility system and which were capable of producing seeds from self or incompatible cross pollinations in amounts ranging from less than 1% to 100% of a compatible outcrossing. Modification of the expression of S-alleles permitting PSC was controlled by a modifying polygenic complex, which was independent of the S locus and which appeared to have a threshold effect. Plants that did not possess PSC when used as male or female could produce progeny with increased PSC levels. This suggested that specific combinations and numbers of genes influenced PSC. Once high PSC levels were attained, epistatic gene action predominated.

Self-incompatibility/*Brassica juncea*

Singh (1959)
The inheritance of self-incompatibility in rai was investigated in a cross between a self-incompatible mutant of cv. R.T. 11 and cv. R.T. 11 (self-compatible). The self-incompatibility trait was conditioned by a single recessive gene.

Self-incompatibility/*Brassica napus*

Ayotte *et al.* (1985)
The inheritance of self-incompatibility in two lines (R, Z) of rutabaga [= subsp. *rapifera*] was determined. In line Z, silique set data for the F_2 generation showed a 3:1 ratio of self-incompatible to self-compatible plants, indicating one dominant gene. The presence in line R of a dominant modifier gene, interacting only with S-allele heterozygotes, was postulated to explain a 10:6 ratio of self-compatible to self-incompatible plants in this line.

Self-incompatibility/*Brassica oleracea*

Detjen (1927)
Four types of incompatibility were described in cabbage [= var. *capitata*]: Type *A*: cross-compatible and slightly self-incompatible; type *B*: fully cross-compatible and strongly self-incompatible; type *C*: highly cross-incompatible and self-incompatible; and type *D*: similar to type *A*, but with an increased degree of cross-compatibility and self-incompatibility. Evidence based on the phenotype of F_1 plants indicated that type *B* incompatibility was inheritable and dominant over type *A* and that type *C* incompatibility was dominant over type *B*.

Kakizaki (1930b)
Self-incompatibility in cabbage [= var. *capitata*] was controlled by three 'oppositional' alleles (*S1*, *S2*, *S3*) and two 'sympathetic' alleles (*T1* and *T2*). In the style, gene *T* was epistatic to gene *S*. Plants heterozygous for *S* alleles were self-incompatible unless they were homozygous for a *T* allele. Plants homozygous for *S* alleles were always self-incompatible.

Mizushima and Katsuo (1954)
Self-incompatibility in cabbage [= var. *capitata*] was controlled by a sporophytic system, with two or more loci, designated S_p and S_q, with up to three alleles, designated S_{p1}, S_{p2}, S_{p3}, S_{q1}, S_{q2}, S_{q3}.

Sampson (1957a)
Studies on cv. Calabrese Green Sprouting broccoli [= var. *italica*] indicated a sporophytic system with one locus and multiple S-alleles. Four alleles were identified, three were independent and one was recessive to the others in the pollen and incompletely recessive in the stigma (modifier genes).

Thompson and Taylor (1965)
Close linkage was observed in marrowstem kale [= var. *acephala*] between *S* alleles and hypocotyl pigmentation, stem pigmentation, anther reddish-purple terminal spot, sepal purple tip pigmentation, and silique pigmentation (purple line around all or part of each valve). Purple hypocotyl, purple stem,

purple anther spot, purple sepal tip, and purple markings on siliques were all dominant to the absence of purple. Purple anther spot was usually dominant over the absence of a purple anther spot.

Wills and Smith (1972)
See Morphological traits/Anther/Tip colour/*Brassica oleracea*

Nasrallah (1974)
The inheritance of quantitative differences in stigmatic proteins of a self-incompatible cabbage [= var. *capitata*] and a self-compatible mutant derived from the self-incompatible line was conditioned by a single gene with dosage effects.

Hoser-Krauze (1981)
Investigations of F_1, F_2, BC_1, and BC_2 of crosses between four homozygous self-incompatible lines of Indian cauliflower [= var. *botrytis*] cv. Pusa Katki having different *S* alleles: *Sa*, *Sb*, *Sc*, *Sd*, and self-compatible lines of the summer cvs. Rapid, Master, Idol, Early Abundance, and Super Snowball, showed that self-compatibility and self-incompatibility were determined by the same locus, *S*. *Sb* and *Sd* alleles showed high activity and dominance in pollen over *Sa* and *Sc* alleles. The F_1 of crosses between homozygous self-incompatible lines *SbSb*,*SdSd* x male self-compatible lines was 100% self-incompatible, and the F_2 generation segregated 3 self-incompatible to 1 self-compatible lines. BC_1 and BC_2 to self-compatible father lines segregated in a 1:1 ratio. For recessive pollen alleles *Sa* and *Sc*, the F_1 was 100% self-compatible, the F_2 segregated 1:3, and BC_1 was 100% self-compatible.

Ockendon (1982)
Self-incompatibility was determined by a single locus with at least 50 naturally occurring alleles.

Kianian and Quiros (1992b)
See Yield and quality traits/Seed glucosinolates/*Brassica oleracea*.

Self-incompatibility/*Brassica rapa*

Bateman (1955)
Self-incompatibility in turnip [= subsp. *rapifera*] was controlled by a single multiallelic gene, designated *S.*

Richards and Thurling (1973)
Self-incompatibility in cv. Arlo [= subsp. *oleifera*] was controlled by a single locus sporophytic system with several alleles (codominant in the stigma and with various levels of dominance in the pollen).

Sareen and Kakar (1975)
Self-incompatibility in brown sarson [= subsp. *dichotoma*] cv. Kanpur Lotani was controlled by a single locus *S*, with four alleles, S_1, S_2, S_3, and S_4. Allele S_3 was dominant over allele S_2 in the pollen. The other alleles acted independently.

Zuberi *et al.* (1981)
A single gene with sporophytic action was identified in var. toria. Five *s* alleles were found in two small samples of toria. A self-compatibility allele s_c was also found. Allele s_c was recessive to two *s* alleles in pollen and pistil and was dominant in the pollen and recessive in the pistil to the *s* allele lowest in the dominance series.

Zuberi and Lewis (1988)
Self-incompatibility in *B. rapa* (family 6/79 studied in a series of bud-self and sib-crosses) was controlled by two complementary genes, the long-established *S* gene with sporophytic action on the pollen and a pollen-gametophytically active gene, *G*, which is complementary to *S* and is oppositional in its action in that both *S* and *G* alleles must be matched to give an incompatible reaction. The *G* genes in *B. rapa* and *Raphanus sativus* were closely similar; both genes had a low number of alleles, were fully expressed only in some *S* allele combinations, and were linked to *S*.

Nou *et al.* (1991)
Variation of *S*-alleles and self-incompatibility was studied in a naturalized population growing in Oguni-machi, Japan. Of 58 plants collected from the population, 45 were self-incompatible and eight were self-compatible. Progenies from 30 of the 32 selfed families investigated showed segregation data consistent with a one locus *S*-allele model of sporophytic self-incompatibility. Sixteen different *S*-alleles were identified and the total number of *S*-alleles in the population was estimated at 20-30. The genetic control of associated major and minor S-glycoproteins was assumed to be by S-like DNA sequences that were closely linked to the *S*-locus.

Nou *et al.* (1993a)
Self-compatible strain C635 contained stigmatic *S*-glycoproteins that were expressed developmentally in a similar way as the *S*-glycoproteins of self-incompatible strain S-23. The *S*-glycoproteins co-segregated with the self-compatibility phenotype in F_2 progeny. Testcross data indicated that self-compatibility was the result of the action of a modifier gene, designated *mod*, which was located outside the S-locus. The recessive *mod* allele suppressed the expression of *S*-alleles in the pistil but not in the pollen.

Nou *et al.* (1993b)
S-alleles of self-incompatibility were isolated from a wild population growing at Balcesme, Turkey. Out of 88 plants observed, 73 were self-incompatible and four were self-compatible. In certain families, selfed progenies from a self-incompatible plant segregated into fewer than three incompatibility classes, which was consistent with a one-locus sporophytic genetic control of self-incompatibility. Eighteen independent S-alleles were identified and the total number of S-alleles in the population was estimated to be more than 30. Out of 25 combinations of S-alleles tested, dominance interactions were observed in six combinations on the pollen side and in five combinations on the stigma side.

Nou *et al.* (1994)
SRA-glycoproteins in *Brassica* species were found only in stigmas and showed a high degree of structural homology to the S-locus glycoproteins associated with self-incompatibility. An SRA-allele was found to be inherited independently of S-glycoprotein alleles. Segregation data of the F_2 progenies supported the S-glycoprotein allele model for pollen tube behaviour, but not SRA-alleles. The results indicated dominance relationships between SRA-alleles.

Self-incompatibility/*Capsella grandiflora*

Riley (1936)
Self-incompatibility in *C. grandiflora* was controlled by a sporophytic system in both pollen and style, with dominance.

Bateman (1955)
Self-incompatibility was controlled by a single-locus sporophytic system, with multiple *S*-alleles, in both pollen and style, with at least three alleles (*S1*, *S2*, *S3*) showing dominance.

Self-incompatibility/*Cardamine pratensis*

Correns (1912)
Self-incompatibility in *C. pratensis* was controlled by a digenic dominant sporophytic system in both pollen and style. Genes *B* and *G* were postulated. Parental genotypes in the crosses were *Bb* and *Gg.* Genotypes of F_2 progeny were: *BG* (incompatible with both parents), *Bg* (incompatible with *Bb* plants only), *bG* (incompatible with *Gg* plants only), and *bg* (self-incompatible, compatible with both parents).

Lawrence (1930)
Correns's (1912) results were re-examined and explained by assuming tetraploidy and several *S* alleles. The parental genotypes were postulated as $S_1S_1Z_1Z_2$ and $S_3S_3Z_3Z_4$.

Self-incompatibility/*Eruca vesicaria* subsp. *sativa*

Lewis (1977)
Studies of F_1, F_2, and F_3 generations identified a sporophytic incompatibilty system with three (perhaps four) complementary genes in Eruca [= *E. sativa*]. Codominance among allelic pairs was distributed approximately evenly between pollen and style.

Verma *et al.* (1977)
In material derived from a local market cultivar in India, the sporophytic system was controlled by more than one gene (at least three genes were implicated). The alleles exhibited both dominance and codominance depending on the alleles in both pollen and stigma.

Verma *et al.* (1985)
Results from a diallel mating matrix of bud-selfed families of *Eruca sativa* [= *E. vesicaria* subsp. *sativa*] were consistent with multigenic control of self-incompatibility.

Self-incompatibility/*Iberis amara*

Bateman (1954)
The parental material was from the Helsinki Botanic Garden, Finland, the Poznan Botanic Garden, Poland, and from a natural population from Hertfordshire, UK. Results indicated single locus, multiple allelic sporophytic control, with simultaneous existence of dominance and independence between S-alleles in both style and pollen. Alleles could be arranged in a linear order of dominance. In the wild population, the number of S-alleles was estimated at more than 22 alleles.

Self-incompatibility/*Leavenworthia crassa*

Lloyd (1967)
Studies conducted on seed from a natural population from Alabama, U.S.A., indicated a single-locus, multi-allelic, sporophytic system. At least 12 S-alleles were observed. Allelic interactions in the pollen grains and stigma were of two types, independent action of both alleles and dominance of one allele over the other.

Self-incompatibility/*Lesquerella densipila*

Sampson (1958b)
Incompatibility was controlled by a series of multiple *S*-alleles at one locus. The pollen phenotype was determined sporophytically. A minimum of eight *S*-alleles was obtained from *L. densipila* and two from *L. lescurii*. Both gene independence and dominance were found among the fully analyzed heterozygotes. Dominance was restricted to the pollen controlling part of the alleles and two levels of potency were established.

Self-incompatibility/*Lesquerella lescurii*

Sampson (1958b)
Incompatibility was controlled by a series of multiple *S*-alleles at one locus. The pollen phenotype was determined sporophytically. A minimum of eight *S*-alleles was obtained from *L. densipila* and two from *L. lescurii*. Both gene independence and dominance were found among the fully analyzed heterozygotes. Dominance was restricted to the pollen controlling part of the alleles and two levels of potency were established.

Self-incompatibility/*Raphanus raphanistrum*

Kroh (1956)
Self-incompatibility in wild radish was controlled by a sporophytic system, with two or more loci with multiple alleles.

Sampson (1964)
A single-locus sporophytic system was observed in two populations from Nova Scotia, Canada, and one population from Poland. Interactions of eight *S*-alleles included dominance in the stigma in four of the possible 28 heterozygotes, whereas dominance in the pollen was found in 18 of the 28 heterozygotes. The stigma dominance order was non-linear, whereas a linear sequence with four levels of activity occurred in the pollen.

Sampson (1967c)
The study presented the first estimate of the total number of *S*-alleles occurring in a wild cruciferous species. The estimate of 25-34 *S*-alleles at the single-locus was based on theoretical calculations based on data from two populations from Nova Scotia, Canada, one population from New Brunswick, Canada, and two populations from Poland.

Verma *et al.* (1991a)
In genetic studies of self-incompatibility in a wild population of *R. raphanistrum* from Davis, California, U.S.A., the observation of semi-compatibility between sibs in a bud-selfed family was consistent with the two gene gametophytic (gene *G*)-sporophytic (gene S) system described in Lewis *et al.* (1988) for *Raphanus sativus*.

Self-incompatibility/*Raphanus sativus*

Bateman (1955)
Self-incompatibility in radish was controlled by a single multiallelic gene, designated *S.*

Tatebe (1956)
The inheritance of self-incompatibility in radish cvs. Tokinashi and Nerima indicated two allelomorphic genes, designated *S* and *I*. Gene *S* was believed to be epistatic to gene *I*, except when heterozygous.

Sampson (1957b)
A single-locus sporophytic system was observed in cv. Scarlet Globe. Multiple allelic control was observed. The reaction of the pollen was sporophytically determined. Five *S*-alleles were recovered from three plants. Four *S*-alleles acted fully and independently of each other in heterozygotes. The fifth *S*-allele was recessive in the pollen and incompletely recessive in the stigmas when tested in heterozygotes with two of the active alleles.

Putrament (1960)
Self-incompatibility in radish [= var. *radicula*] was controlled by a sporophytic system, with two loci with multiple alleles.

Lewis (1979)
Sporophytic self-incompatibility was controlled by more than one locus (the exact number of loci could not be specified).

Lewis *et al.* (1988)
Studies in select plants of *R. sativus* var. *radicula* (Polish cv. Rzodkiewka Gruntowa Würzburska) indicated that incompatibility was controlled by a gametophytic-sporophytic system. Six alleles (S_1 to S_6) were found for the *S* gene which typically in the Cruciferae has sporophytic control of the pollen and is multiallelic with dominant and codominant alleles in both pollen-mother cells and in styles. An additional gene was identified, gene *G*, which was gametophytic in its action in the pollen and complemented the *S* gene. Two alleles, G_1 and G_2, were identified. *G* and *S* were linked. Both *S* and *G* alleles must be matched to give an incompatible reaction. However in some *S* allelic combinations, the difference between the two *G* alleles was not expressed. Gene *G* was an essential part of the incompatibility recognition process but not used for multiple allelic variation of the incompatibility system.

Verma *et al.* (1991b)
In genetic studies of self-incompatability in Japanese radish cv. Tokinashi, the observation of semi-compatibility between sibs was consistent with the two gene gametophytic-sporophytic system described in Lewis *et al.* (1988) for a Polish cultivar of radish.

Self-incompatibility/*Sinapis arvensis*

Ford and Kay (1985)
Studies of the genetics of incompatibility in a wild population from South Wales, UK, confirmed a single-locus, multi-allelic sporophytic incompatibility system similar to that found in other crucifers. Fourteen different *S*-alleles were found in a sample of ten plants collected from a single field, which would give a minimum estimate (Paxman's maximum likelihood estimate) of 24 *S*-alleles in the population. Both dominance and independent action of alleles occurred in the pollen and stigma.

Stevens and Kay (1988)
Analyses were conducted on diallel crosses within F_1 and F_2 families derived from crosses between plants from geographically remote populations (Crete x Lincolnshire, UK) and (Crete x South Wales, UK) and within self families derived from the parental plants. Control by a single locus was established. The expression of individual *S*-alleles could be modified, as shown by incomplete dominance in a selfed family and mutual weakening in a F_1 family.

Selfing rate/*Brassica napus*

Damgaard and Loeschcke (1994)
The broad-sense heritability value for selfing rate in Swedish oilseed rape [= subsp. *oleifera*] cv. Topas was 0.80. The narrow-sense heritability value was 0.41.

Shattering resistance/*Brassica juncea*

Bhajan *et al.* (1997)
See Yield and quality traits/Yield/Seed/*Brassica juncea*.

Shattering resistance/*Brassica rapa*

Kadkol *et al.* (1985)
In crosses between yellow sarson [= subsp. *trilocularis*] and brown sarson [= subsp. *dichotoma*] lines, high silique strength was detemined to be controlled by two to three recessive genes interacting in a dominant epistatic manner.

Kadkol *et al.* (1986a)
The inheritance of four measures of silique strength (bending moment, energy, bending moment per silique length, and energy per silique length) was determined from the segregation data obtained from reciprocal crosses between Canadian spring cv. Torch [= subsp. *oleifera*] (shattering susceptible) x brown sarson [= subsp. *dichotoma*] line DS-17-D and yellow sarson [= subsp. *trilocularis*] line IB-5 (both shattering resistant), and from the cross Torch x yellow sarson line B-46 (shattering resistant). Silique strength was found to be recessive in all crosses. In general, the segregation data for the measures of silique strength, except “bending moment per silique length” indicated recessive inheritance at three loci in the yellow sarson lines and at two loci in the brown sarson line; gene interaction was dominant epistasis. The trait “bending moment per silique length” appeared to be quantitatively inherited.

In the cross with the yellow sarson lines, the four measures of silique strength showed linkage with a multivalved silique trait.

Kadkol *et al.* (1986b)
Quantitative genetic analysis of silique strength in the progeny of a cross between Canadian spring cv. Torch [= subsp. *oleifera*] (shattering susceptible) x brown sarson [= subsp. *dichotoma*] line DS-17-D (shattering resistant) indicated a high degree of non-additive genetic variance. A high broad-sense heritability were obtained for four measures of silique strength (bending moment, energy, bending moment per silique length, and energy per silique length), indicating a small number of epistatic genes controlling silique strength in this cross.

Transgenes/*Brassica napus*

Fry *et al.* (1987)
Inheritance of the T-DNA was studied in self-progeny of 13 transgenic plants and backcrosses to wild-type of four transgenic plants, using a nopaline assay. Seven of the 13 transgenic plants contained multiple functional inserts of the T-DNA.

Guerche *et al.* (1987)
The transformed root phenotype conferred by transformation with *Agrobacterium rhizogenes*, *i.e.* rapid growth, reduced apical dominance and plagiotropism, was inherited in a Mendelian fashion. Evidence for the insertion of T-DNA into two independent loci in the same plant was provided.

Radke *et al.* (1988)
The segregation of the *NPT II* gene in the T2 generation of plants of cv. Westar [= subsp. *oleifera*] transformed with *Agrobacterium tumefaciens* was determined. In the progeny of plant 767-4a, out of 88 seedlings, 67 were tolerant to kanamycin, suggesting a 3:1 ratio and a single integration site. All progeny of plant 767-1a (58 seedlings) and plant 767-2a (83 seedlings) were tolerant to the antibiotic, suggesting multiple integration events.

Dusbabkova *et al.* (1992)
The inheritance of a transgene (TL- and TR-DNA of agropine plasmid pRi of *Agrobacterium rhizogenes* 15834) was studied in a transformant of spring oilseed rape [= subsp. *oleifera*] cv. HM-81. In self-progenies (R1, R2, and R3), the plants mostly expressed the transformed phenotype. In crosses with a non-transformed line, the transgene acted as a dominant trait. F_2 progeny segregated 3 transgenic plants to 1 normal plant. The results suggested that the TL-DNA was introgressed at two loci on a pair of homologous chromosomes. Recombination frequency was estimated as 12% in the pollen, and 6% in the pollen and the ovules. In some crosses, the transgene appeared to be maternally inherited.

Kohno-Murase *et al.* (1994)
A heritable change in fatty acid profile (reduction in 18:1 content and increase in 18:2 content) was observed in oilseed rape plants expressing a seed-specific napin antisense gene.

Schröder *et al.* (1994)
The inheritance of the marker genes *aadA* and *nptII* in the T2 generation of 37 plants of cv. Hanna [= subsp. *oleifera*] transformed with *Agrobacterium tumefaciens* was determined. Eight plants segregated as a single locus for both genes and 17 plants segregated as a single locus for at least one of the

genes. Comparisons of the Southern blot analysis of the T1 generation and the segregation patterns of the T2 generation did not fit the expected Mendelian ratio when the plants has more than two copies of the T-DNA. These plants had a 3:1 segregation ratio regardless of the number of inserted copies.

Transgenes/*Brassica rapa*

Jun *et al.* (1995)
The inheritance of a nopaline synthase/neomycin phosphotransferase II (nptII) chimeric gene for kanamycin resistance and a coat protein gene from tobacco mosaic virus L was investigated in the progeny of transformed plants of Chinese cabbage [= subsp. *pekinensis*] cv. Spring Flavor and found to be stable.

ISOZYMES AND MOLECULAR TRAITS

Isozymes

AAT (Aspartate aminotransferase, EC 2.6.1.1)/*Brassica oleracea*

Arús and Orton (1983)
The inheritance and linkage relationships of eight allozyme loci (*Pgm-1*, *Pgm-2*, *Pgi-2*, *Lap-1*, *Adh-2*, *Aps-1*, *Aps-1L* (leaf), and *Got-3* (= aspartate aminotransferase) were determined. There were significant deviation from Mendelian expectations in two of the 24 segregation ratios analyzed. There was evidence of weak linkage of *Pgm-2* to *Aps-1* (r = 0.39), *Adh-1* to *Pgm-1* (r = 0.45), and *Lap-1* to *Aps-3L* (r = 0.44).

Gotoh and Ikehashi (1992)
F_2 segregation analysis of a cross between two cauliflower [= var. *botrytis*] inbred lines HP50 and HP51 indicated monogenic segregation for *Got-3* (= aspartate aminotransferase) and duplicated loci *Pgm-2* and *Pgm-3*.

AAT (Aspartate aminotransferase, EC 2.6.1.1)/*Brassica rapa*

Truco and Arús (1987)
The genetic basis for six isozyme loci *Adh-2*, *Got-3* (= aspartate aminotransferase), *Lap-1*, *Pgi-2* (= glucose-6-phosphate isomerase), *Pgm-1*, and *Pgm-2* was reported for *B. rapa*.

McGrath and Quiros (1991)
Mendelian inheritance was established for the four loci *Got-1* (= aspartate aminotransferase), *Mdh-1*, *Pgi-2* (= glucose-6-phosphate isomerase), and *Pgm-3*.

Simonsen and Heneen (1995)
The inheritance of seven loci was determined in crosses between *B. rapa* yellow sarson [= subsp. *trilocularis*] lines K-151 and Swedish lines Sv 85-38301 and GJ 2891 [= subsp. *oleifera*], and one Chinese landrace, no. 21. F_2 segregation data supported single loci for diaphorase *Dia-2A* (= dihydrolipoamide dehydrogenase), *Est-2A*, *Fbp-3A*, *Got-1A* (= aspartate aminotransferase), *Icd-1A* (= isocitrate dehydrogenase), *Mdh-2A*, and *Pgm-1A*.

ACO (Aconitase, see ACOH)

ACOH (Aconitase hydratase, EC 4.2.1.3)/*Brassica nigra*

Chèvre *et al.* (1995)
The genetic analysis of seven isozyme systems in *B. rapa*, *B. nigra*, and *B. oleracea* (genomes A, B, and C, respectively) was described. The isozyme loci included four loci for aconitase hydratase (*Aco-1*, *Aco-2*, *Aco-3*, and *Aco-4*), one locus for acid phosphatase in leaf tissue (*Aps-1L*), two loci for leucine aminopeptidase (*Lap-1* and *Lap-2*), duplicate loci for plastidic *(6Pgd-1* and *6Pgd-1'*) and cytosolic *(6Pgd-2* and *6Pgd-2'*) phosphogluconate dehydrogenase, two loci for plastidic (*Pgi-1*) and cytosolic (*Pgi-2*) glucose-6-phosphate isomerase, two loci for phosphoglucomutase (*Pgm-1* and *Pgm-2*), and duplicated loci for plastidic (*Tpi-1* and *Tpi-1'*) and cytosolic (*Tpi-2* and *Tpi-2'*) triose-phosphate isomerase.

ACOH (Aconitase hydratase, EC 4.2.1.3)/*Brassica oleracea*

Arús (1989)
The genetic basis for three loci for aconitase hydratase (*Aco-1*, *Aco-3*, and *Aco-4*), one locus for malate dehydrogenase (*Mdh-1*), one locus for phosphogluconate dehydrogenase (*6Pgd-1*), and a third locus for phosphoglucomutase (*Pgm-3*) was provided for *Brassica oleracea.* Two isozyme linkage groups were identified (*Pgm-3, Pgi-2, 6Pgd-1*) and (*Aco-4, Mdh-1, Aco-1, Lap-1*).

Chèvre *et al.* (1995)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/ *Brassica nigra*.

ACOH (Aconitase hydratase, EC 4.2.1.3)/*Brassica rapa*

Chèvre *et al.* (1995)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/ *Brassica nigra*.

ACOH (Aconitase hydratase, EC 4.2.1.3)/*Raphanus sativus*

Ellstrand and Devlin (1989)
The inheritance patterns of 12 isozyme loci [*Aco* (= aconitase hydratase), *Acp*, *Est*, *Idh*, *Lap*, *Pgd* (= phosphogluconate dehydrogenase), *Pgi* (= glucose-6-phosphate isomerase), *Pgm-1*, *Pgm-2*, *Pgm-3*, *Prx* (= peroxidase), and *Tpi*] in plants from wild populations from California, U.S.A., were consistent with Mendelian inheritance and codominant alleles. Two linkage groups were detected, one involving the loci *Pgm-2*, *Aco*, *Acp*, and *Lap*, the other involving the loci *Est* and *Prx*.

ACP (Acid phosphatase, EC 3.1.3.2)/*Brassica nigra*

Chèvre *et al.* (1995)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Brassica nigra*.

ACP (Acid phosphatase, EC 3.1.3.2)/*Brassica oleracea*

Arús and Orton (1983)
See Isozymes and molecular traits/Isozymes/AAT (Aspartate aminotransferase, EC 2.6.1.1)/*Brassica oleracea*.

Chèvre *et al.* (1995)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Brassica nigra*.

ACP (Acid phosphatase, EC 3.1.3.2)/*Brassica rapa*

Chèvre *et al.* (1995)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Brassica nigra*.

ACP (Acid phosphatase, EC 3.1.3.2)/*Raphanus sativus*

Ellstrand and Devlin (1989)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Raphanus sativus*.

ADH (Alcohol dehydrogenase, EC 1.1.1.1)/*Brassica oleracea*

Arús and Orton (1983)
See Isozymes and molecular traits/Isozymes/AAT (Aspartate aminotransferase, EC 2.6.1.1)/*Brassica oleracea*.

ADH (Alcohol dehydrogenase, EC 1.1.1.1)/*Brassica rapa*

Truco and Arús (1987)
See Isozymes and molecular traits/Isozymes/AAT (Aspartate aminotransferase, EC 2.6.1.1)/ *Brassica rapa*.

APS (Acid phosphatase, see ACP)

DDH (Dihydrolipoamide dehydrogenase, EC 1.8.1.4)/ *Brassica rapa*

Simonsen and Heneen (1995)
See Isozymes and molecular traits/Isozymes/AAT (Aspartate aminotransferase, EC 2.6.1.1)/ *Brassica rapa*.

DIA (Diaphorase, see DDH)

EST (Esterase, EC 3.1.1.-)/*Brassica rapa*

Simonsen and Heneen (1995)
See Isozymes and molecular traits/Isozymes/AAT (Aspartate aminotransferase, EC 2.6.1.1)/ *Brassica rapa*.

EST (Esterase, EC 3.1.1.-)/*Raphanus sativus*

Ellstrand and Devlin (1989)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Raphanus sativus*.

FBP (Fructose-bisphosphatase, EC 3.1.3.11)/*Brassica rapa*

Simonsen and Heneen (1995)
See Isozymes and molecular traits/Isozymes/AAT (Aspartate aminotransferase, EC 2.6.1.1)/ *Brassica rapa*.

FBP (Fructose-bisphosphatase, EC 3.1.3.11)/*Sinapis arvensis*

Warwick and Anderson (1997)
Inheritance studies conducted on select plants grown from seed from wild Canadian accessions confirmed Mendelian inheritance at seven isozyme loci (*Fbp-2*, *Gpi-2*, *Idh-2*, *Pgm-2*, *Pgm-2'*, *Tpi-1*, and *Tpi-1'*).

ß-GAL (ß-Galactosidase, EC 3.2.1.23)/*Brassica rapa*

Singh and Knox (1985)
ß-Galactosidase deficiency in rapeseed [= subsp. *oleifera*] cv. T15 was found to be under the control of a single recessive gene *gal*.

GDH (Glutamate dehydrogenase, see GTDH)

GOT (Glutamate-oxaloacetate transaminase, see AAT)

GPI (Glucose-6-phosphate isomerase, EC 5.3.1.9)/*Brassica napus*

Chen *et al.* (1989)
The inheritance of glucose-phosphate isomerase (GPI) isozymes was examined in a cross between Swedish breeding line Sv 02372 and a synthetic *B. napus* genotype, line No. 7076. It was determined that genotype Sv 02371 carried an allele on the C genome and a null allele on the A genome, whereas line No. 7076 had duplicate loci, *i.e.* an allele on both genomes.

GPI (Glucose-6-phosphate isomerase, EC 5.3.1.9)/*Brassica nigra*

Chèvre *et al.* (1995)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Brassica nigra*.

GPI (Glucose-6-phosphate isomerase, EC 5.3.1.9)/*Brassica oleracea*

Arús and Orton (1983)
See Isozymes and molecular traits/Isozymes/AAT (Aspartate aminotransferase, EC 2.6.1.1)/*Brassica oleracea*.

Chèvre *et al.* (1995)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Brassica nigra*.

GPI (Glucose-6-phosphate isomerase, EC 5.3.1.9)/*Brassica rapa*

Truco and Arús (1987)
See Isozymes and molecular traits/Isozymes/AAT (Aspartate aminotransferase, EC 2.6.1.1)/*Brassica rapa*.

Chen *et al.* (1990)
Turnip rape line [= subsp. *oleifera*] Sv85-38301 was crossed to yellow sarson [= subsp. *trilocularis*] lines K-151, K-88, and RS-24. Monogenic inheritance with either codominant alleles or dominant-recessive alleles when a null allele was involved was observed from F_2 progeny for the six loci *Gpi-2A*, *Lap-2A*, *6Pgd-2Ac* (= phosphogluconate dehydrogenase), *Pgm-3A*, *Sdh-1A* (= shikimate dehydrogenase), and *Sdh-2A*. Complete linkage was observed between *Lap-2A* and *6Pgd-2Ac*.

McGrath and Quiros (1991)
See Isozymes and molecular traits/Isozymes/AAT (Aspartate aminotransferase, EC 2.6.1.1)/ *Brassica rapa*.

Chèvre *et al.* (1995)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/ *Brassica nigra*.

GPI (Glucose-6-phosphate isomerase, EC 5.3.1.9)/*Raphanus sativus*

Ellstrand and Devlin (1989)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/ *Raphanus sativus*.

GPI (Glucose-6-phosphate isomerase, EC 5.3.1.9)/*Sinapis arvensis*

Warwick and Anderson (1997)
See Isozymes and molecular traits/Isozymes/FBP (Fructose-bisphosphatase, EC 3.1.3.11)/ *Sinapis alba*.

GTDH (Glutamate dehydrogenase, EC 1.4.1.2)/*Capsella bursa-pastoris*

Hurka and Düring (1994)
The genetic basis of isozymes of L-glutamate dehydrogenase was studied in *C. grandiflora* (diploid), *C. rubella* (diploid), and *C. bursa-pastoris* (tetraploid). Progeny analyses and crossing experiments revealed two genetic loci within the diploid species. Locus *Gdh-1* had a single allele. Locus *Gdh-2* was polymorphic and segregated for three alleles determining allozymes in accordance with Mendelian inheritance. In the tetraploid species, both loci were apparently duplicated so that four instead of two genes determined the polypeptide structure of plastidic GDH. These loci shared the same alleles with the diploid species and no additional allozymes were detected.

GTDH (Glutamate dehydrogenase, EC 1.4.1.2)/*Capsella grandiflora*

Hurka and Düring (1994)
See Isozymes and molecular traits/Isozymes/GTDH (Glutamate dehydrogenase, EC 1.4.1.2)/ *Capsella bursa-pastoris*.

GTDH (Glutamate dehydrogenase, EC 1.4.1.2)/*Capsella rubella*

Hurka and Düring (1994)
See Isozymes and molecular traits/Isozymes/GTDH (Glutamate dehydrogenase, EC 1.4.1.2)/*Capsella bursa-pastoris*.

ICD (Iso-citric acid dehydrogenase, see IDH)

ICL (Isocitrate lyase, EC 4.1.3.1)/*Brassica oleracea*

Kianian and Quiros (1992b)
See Yield and quality traits/Seed glucosinolates/*Brassica oleracea*.

IDH (Isocitrate dehydrogenase, EC 1.1.1.42)/*Brassica rapa*

Simonsen and Heneen (1995)
See Isozymes and molecular traits/Isozymes/AAT (Aspartate aminotransferase, EC 2.6.1.1)/*Brassica rapa*.

IDH (Isocitrate dehydrogenase, EC 1.1.1.42)/*Raphanus sativus*

Ellstrand and Devlin (1989)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Raphanus sativus*.

IDH (Isocitrate dehydrogenase, EC 1.1.1.42)/*Sinapis arvensis*

Warwick and Anderson (1997)
See Isozymes and molecular traits/Isozymes/FBP (Fructose-bisphosphatase, EC 3.1.3.11)/*Sinapis alba*.

LAP (Leucine aminopeptidase, EC 3.4.11.1)/*Brassica nigra*

Chèvre *et al.* (1995)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Brassica nigra*.

LAP (Leucine aminopeptidase, EC 3.4.11.1)/*Brassica oleracea*

Arús and Orton (1983)
See Isozymes and molecular traits/Isozymes/AAT (Aspartate aminotransferase, EC 2.6.1.1)/ *Brassica oleracea*.

Chèvre *et al.* (1995)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Brassica nigra*.

LAP (Leucine aminopeptidase, EC 3.4.11.1)/*Brassica rapa*

Truco and Arús (1987)
See Isozymes and molecular traits/Isozymes/AAT (Aspartate aminotransferase, EC 2.6.1.1)/ *Brassica rapa*.

Chen *et al.* (1990)
See Isozymes and molecular traits/Isozymes/GPI (Glucose-6-phosphate isomerase, EC 5.3.1.9)/ *Brassica rapa*.

Chèvre *et al.* (1995)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Brassica nigra*.

LAP (Leucine aminopeptidase, EC 3.4.11.1)/*Raphanus sativus*

Ellstrand and Devlin (1989)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Raphanus sativus*.

MDH (Malate dehydrogenase, EC 1.1.1.37)/*Brassica oleracea*

Arús (1989)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Brassica oleracea*.

MDH (Malate dehydrogenase, EC 1.1.1.37)/*Brassica rapa*

McGrath and Quiros (1991)
See Isozymes and molecular traits/Isozymes/AAT (Aspartate aminotransferase, EC 2.6.1.1)/ *Brassica rapa*.

Simonsen and Heneen (1995)
See Isozymes and molecular traits/Isozymes/AAT (Aspartate aminotransferase, EC 2.6.1.1)/ *Brassica rapa*.

MS (Malate synthase, EC 4.1.3.2)/*Brassica oleracea*

Kianian and Quiros (1992b)
See Yield and quality traits/Seed glucosinolates/*Brassica oleracea*.

NADH (Nitrate reductase, EC 1.6.6.1)/*Brassica napus*

Wang and Qiu (1990)
See Yield and quality traits/Yield/Protein/*Brassica napus*.

PER (Peroxidase, EC 1.11.1.7)/*Raphanus sativus*

Ellstrand and Devlin (1989)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Raphanus sativus*.

PGD (Phosphogluconate dehydrogenase, see PGDH)

6PGD (6-Phosphogluconate dehydrogenase, see PGDH)

PGDH (Phosphogluconate dehydrogenase, EC 1.1.1.44)/*Brassica nigra*

Chèvre *et al.* (1995)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Brassica nigra*.

PGDH (Phosphogluconate dehydrogenase, EC 1.1.1.44)/*Brassica oleracea*

Quiros *et al.* (1987)
The presence of duplicated loci was reported for both plastidic *(6Pgd-1* and *6Pgd-1'*) and cytosolic *(6Pgd-2* and *6Pgd-2'*) phosphogluconate dehydrogenase, in *B. oleracea* and *B. rapa.* The presence of duplicated loci was reported for both plastidic (*Tpi-1* and *Tpi-1'*) and cytosolic (*Tpi-2* and *Tpi-2'*) triose-phosphate isomerase in *B. rapa.*

Arús (1989)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Brassica oleracea*.

Chèvre *et al.* (1995)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Brassica nigra*.

PGDH (Phosphogluconate dehydrogenase, EC 1.1.1.44)/*Brassica rapa*

Quiros *et al.* (1987)
See Isozymes and molecular traits/Isozymes/PGDH (Phosphogluconate dehydrogenase, EC 1.1.1.44)/*Brassica oleracea*.

Chen *et al.* (1990)
See Isozymes and molecular traits/Isozymes/GPI (Glucose-6-phosphate isomerase, EC 5.3.1.9)/*Brassica rapa*.

Chèvre *et al.* (1995)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Brassica nigra*.

PGDH (Phosphogluconate dehydrogenase, EC 1.1.1.44)/*Raphanus sativus*

Ellstrand and Devlin (1989)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Raphanus sativus*.

PGI (Phosphoglucoisomerase, see GPI)

PGM (Phosphoglucomutase, EC 5.4.2.2)/*Brassica nigra*

Chèvre *et al.* (1995)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Brassica nigra*.

PGM (Phosphoglucomutase, EC 5.4.2.2)/*Brassica oleracea*

Arús and Orton (1983)
See Isozymes and molecular traits/Isozymes/AAT (Aspartate aminotransferase, EC 2.6.1.1)/*Brassica oleracea*.

Arús (1989)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Brassica oleracea*.

Gotoh and Ikehashi (1992)
See Isozymes and molecular traits/Isozymes/AAT (Aspartate aminotransferase, EC 2.6.1.1)/ *Brassica oleracea*.

Chèvre *et al.* (1995)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Brassica nigra*.

PGM (Phosphoglucomutase, EC 5.4.2.2)/*Brassica rapa*

Truco and Arús (1987)
See Isozymes and molecular traits/Isozymes/AAT (Aspartate aminotransferase, EC 2.6.1.1)/ *Brassica rapa*.

Chen *et al.* (1990)
See Isozymes and molecular traits/Isozymes/GPI (Glucose-6-phosphate isomerase, EC 5.3.1.9)/ *Brassica rapa*.

McGrath and Quiros (1991)
See Isozymes and molecular traits/Isozymes/AAT (Aspartate aminotransferase, EC 2.6.1.1)/ *Brassica rapa*.

Chèvre *et al.* (1995)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Brassica nigra*.

Simonsen and Heneen (1995)
See Isozymes and molecular traits/Isozymes/AAT (Aspartate aminotransferase, EC 2.6.1.1)/ *Brassica rapa*.

PGM (Phosphoglucomutase, EC 5.4.2.2)/*Raphanus sativus*

Ellstrand and Devlin (1989)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Raphanus sativus*.

PGM (Phosphoglucomutase, EC 5.4.2.2)/*Sinapis arvensis*

Warwick and Anderson (1997)
See Isozymes and molecular traits/Isozymes/FBP (Fructose-bisphosphatase, EC 3.1.3.11)/*Sinapis alba*.

PRX (Peroxidase, see PER)

SDH (Shikimate dehydrogenase, see SKDH)

SKD (Shikimate dehydrogenase, see SKDH)

SKDH (Shikimate dehydrogenase, EC 1.1.1.25)/*Brassica rapa*

Chen *et al.* (1990)
See Isozymes and molecular traits/Isozymes/GPI (Glucose-6-phosphate isomerase, EC 5.3.1.9)/*Brassica rapa*.

TPI (Triose-phosphate isomerase, EC 5.3.1.1)/*Brassica nigra*

Chèvre *et al.* (1995)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Brassica nigra*.

TPI (Triose-phosphate isomerase, EC 5.3.1.1)/*Brassica oleracea*

Quiros *et al.* (1987)
See Isozymes and molecular traits/Isozymes/PGDH (Phosphogluconate dehydrogenase, EC 1.1.1.44)/*Brassica oleracea*.

Chèvre *et al.* (1995)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Brassica nigra*.

TPI (Triose-phosphate isomerase, EC 5.3.1.1)/*Brassica rapa*

Quiros *et al.* (1987)
See Isozymes and molecular traits/Isozymes/PGDH (Phosphogluconate dehydrogenase, EC 1.1.1.44)/*Brassica oleracea*.plastidic (*Tpi-1* and *Tpi-1'*) and cytosolic (*Tpi-2* and *Tpi-2'*) triose-phosphate isomerase in *B. rapa.*

Chèvre *et al.* (1995)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Brassica nigra*.

TPI (Triose-phosphate isomerase, EC 5.3.1.1)/*Raphanus sativus*

Ellstrand and Devlin (1989)
See Isozymes and molecular traits/Isozymes/ACOH (Aconitase hydratase, EC 4.2.1.3)/*Raphanus sativus*.

TPI (Triose-phosphate isomerase, EC 5.3.1.1)/*Sinapis arvensis*

Warwick and Anderson (1997)
See Isozymes and molecular traits/Isozymes/FBP (Fructose-bisphosphatase, EC 3.1.3.11)/*Sinapis alba*.

Molecular traits

Mitochondrial genome/*Brassica napus*

Sakai *et al.* (1992)
The stability of mitochondrial genomes in male sterile cybrids between *B. napus* and *Raphanus sativus* was investigated. In two cybrids, no. 12-9 and no. 18-3, the hybridization patterns for the mitochondrial genome varied in BC generations.

Mitochondrial genome/*Raphanus sativus*

Sakai *et al.* (1992)
See Isozymes and molecular traits/Molecular traits/Mitochondrial genome/*Brassica napus*.

Mitochondrial plasmid/*Brassica napus*

Erickson *et al.* (1989)
Experiments demonstrated that a cytoplasmic genetic element (11.3 kb mitochondrial plasmid) could be inherited non-maternally.

Ribosomal DNA/*Brassica nigra*

Waters and Schaal (1996)
The effects of heat shock on inheritance of genomic components were investigated. Plants were submitted to heat stress and the copy number of two nuclear-encoded single-copy genes, rRNA-encoding DNA (rDNA), and a chloroplast DNA gene, was determined and compared to a nonstressed control group. Copy number was examined in the selfed progeny of control and heat-treated individuals. There was no effect of heat shock on copy number of the single-copy nuclear genes or on chloroplast DNA. Heat shock, however, caused a statistically significant reduction in rDNA copies inherited by the F_1 generation.

Ribosomal RNA/*Brassica oleracea*

Kianian and Quiros (1992b)
See Yield and quality traits/Seed glucosinolates/*Brassica oleracea*.

RAPD markers/*Brassica juncea*

Frello *et al.* (1995)
The inheritance of 20 oilseed rape-specific RAPD markers and a herbicide resistant transgene was examined in 54 BC_1 progeny from the cross *B. juncea* x (*B. juncea* x *B. napus*). The plants contained 0 to 20 oilseed rape [= subsp. *oleifera*] markers and the frequency of inheritance of individual markers ranged from 19 to 93%. The transgene was inherited by 52% of the plants analyzed (27 plants).

RAPD markers/*Brassica napus*

Frello *et al.* (1995)
See Isozymes and molecular traits/Molecular traits/RAPD markers/*Brassica juncea*.

Mikkelsen *et al.* (1996)
The inheritance of 33 RAPD markers from oilseed rape [= *Brassica napus* subsp. *oleifera*] was studied in the BC progeny of interspecific crosses between oilseed rape cv. Drakkar and turnip rape [= *Brassica rapa* subsp. *oleifera*] cv. Indus. Markers were transferred with a frequency ranging from 26 to 91%. The majority of markers were transferred with a 50% frequency.

RAPD markers/*Brassica rapa*

Cho *et al.* (1994)
The inheritance of RAPD markers was studied in the progeny of a cross between Chinese cabbage [= subsp. *pekinensis*] cvs. Chungbang and Hiraska. Polymorphic bands were dominant in the F_1 plants and inherited from one of the parents. Polymorphic bands segregated as alleles in the F_2 population.

Mikkelsen *et al.* (1996)
See Isozymes and molecular traits/Molecular traits/RAPD markers/*Brassica napus*.

RFLP markers/*Brassica napus*

Ferreira *et al.* (1994)
An F_1-derived doubled haploid (DH) population obtained from a cross between annual canola [= subsp. *oleifera*] cv. Stellar and biennial rapeseed cv. Major was used to construct a linkage map of 132 restriction fragment length polymorphism loci. The marker loci were arranged into 22 linkage groups and six pairs of linked loci covering 1016 cM. The DH map was compared to a partial map constructed with a common set of markers for an F_2 population derived from the same F_1 plant, and the overall maps were not significantly different. Deviation from Mendelian segregation ratios ($P < 0.05$) was

observed for 30% of the marker loci in the DH population and for 24% in the F_2 population. Deviation towards each parent occurred at equal frequencies in both populations and marker loci that showed deviation clustered in specific linkage groups.

Tanhuanpää *et al.* (1994)
The segregation of RFLP and RAPD markers was examined in F_2 and doubled haploid progenies of a cross between Swedish oilseed rape [= subsp. *oleifera*] cv. Topas and line R4, a low linolenic acid line. Six of eight RFLPs were codominant, and two were dominant with null alleles. There was an excess of Topas alleles for five RAPD loci in the doubled haploid progeny. In the F_2 population, one RAPD marker revealed a distorted segregation in favour of R4 alleles.

Parkin *et al.* (1995)
The majority of 162 RFLP markers in doubled haploid lines derived from a F_1 plant (N61-9) from a cross between a *B. napus* synthetic line (SYN1) and a doubled haploid *B. napus* line (N-o-9) exhibited disomic inheritance, *i.e.* the presence of one of two parental alleles. Some loci on linkage groups N2 and N12 exhibited tetrasomic inheritance, *i.e.* the presence of two of four parental alleles.

RFLP markers/*Brassica rapa*

McGrath and Quiros (1991)
A total of 49 RFLP loci (EcoRI-based) were identified using three genomic and 28 cDNA clones as probes in a turnip x mock pak-choi F_2 population. all loci showed co-dominant segregation, with 13 of the loci exhibiting dominant/null alleles.

Song *et al.* (1995)
See Morphological traits/Leaf/Lobe number/*Brassica rapa*.

VNTR markers/*Brassica rapa*

Rogstad (1994)
The inheritance of variable number tandem repeat (VNTR) genetic markers from two turnip [= subsp. *rapifera*] parents to 20 F_1 offspring was examined using nine PCR synthetic tandem repeat (STR) probes. A total of 79 parental fragments were found and, of these, 65% (51) appeared to be heterozygous in one or both parents, with 52% (41) appearing to be heterozygous in one of the parents exclusively. In general, markers were transmitted in a Mendelian fashion. For the fragments that were heterozygous in one of the parents only, seven alleles exhibited complete linkage in three groups, 12 alleles were incompletely linked in six groups, and four allelic groups involving 11 alleles were identified.

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