

Multinational Brassica Genome Project (MBGP) steering committee meeting at PAG 2014

Date: Sunday, January 12, 2014

Time: 10 am

Location: Dover Room, Town & Country Hotel

Chair: Rod Snowdon, JLU Giessen, Germany

1. Introductions

2. Approval of minutes

3. Updates on genetic resources and diversity sets

- *B. napus*

Cornell (Mike Gore lab): 900 accessions, GBS, to be public after publication, also RIL pops POSTER 386

Bancroft (York, UK): Transcriptome sequencing of all viable ASSYST lines [note: confirmed as 389 lines]. Illumina mRNAseq data to be submitted to SRA immediately; SNP scoring matrix will be made public after publication

Snowdon: ERANET-ASSYST Bn diversity collection (curated by JLU Giessen), around 450 inbreds. Seeds publicly available (nominal cost per line for commercial requests) along with different sets of public SNP and phenotype data. List available on brassica.info

Genomic resequencing (12x) on 20 RS and 31 natural Bn (parents of German NAM populations), data will be public in 2015.

Kede Liu (HAU, Wuhan): 150 Chinese accessions, 5x but no reference for alignment

Isobel Parkin (AAFC): 50 spring NAM parents, to be made public

- *B. rapa*

Scott Woody, Wisconsin (Amasino lab) – NSF funded project:

Rapid cycling *B. rapa* line FBsc (B3) sequenced, EMS mutant collection >> resource for genetic education

Also developing of NAM-RIL population

Seeds stock availability via ABRC

B. oleracea

mRNAseq on Warwick *B. oleracea* DFFS? Release plans unknown.

B. juncea collection - Graham King (SCU), currently being fixed

4. Updates on genome sequencing and resequencing activities

B. oleracea: TO1000 paper submission in January 2014 (Isobel Parkin)

Shengyi Liu (OCRI, Wuhan) Nature Communications paper in revision

B. napus: Darmor-Bzh: Boulos is making reference available under an MTA, publication not yet submitted but still hoping to publish as soon as possible.

Isobel: Canadian spring-type, commercial consortium: Release as soon as Darmor reference is published
Chinese reference for Tapidor completed, paper in preparation (Jinling Meng)

B. rapa: R-o-18 de novo generated (Graham King), raw data available via Brassica.info

John McKay sequencing selected mapping parents

Rod Snowdon: Sequencing mapping parents from 4 or 5 WOSR populations

Isobel Parkin sequencing Bju, Bcar, Bnig: Sequencing finished, assembly in progress, anchoring with GBS on mapping pops

Chris Pires (Missouri): BMAP crucifers (<http://www.brassica.info/resource/sequencing/bmap.php>), including e.g. Sinapis

Yong-Pyo. Lim: Raphanus being done in Korea

5. Updates on international research activities

Bancroft/Snowdon/Chevre: ERA-CAPS: Genome evolution in natural and resynthesised B. napus - relating back to trait variation

Eric Schranz: ERA-CAPS - UK, Vienna, Holland: Dormancy project

Nathalie Nesi (INRA): RAPSODYN public-private consortium, Nitrogen use efficiency, funded for 8 years

Cornell: US federal project on broccoli – seed companies, production, storage etc.

Bancroft: BBSRC „Strategic Longer and Larger Award“ project – generating functional genotypes for ASSYST panel and ~200 further Brassica and Brassicaceae accessions, studying genetic basis of co-product accumulation (tocopherols, phytosterols, waxes, functional polysaccharides) and nutrient use efficiency.

Martin Broadley: Root phenotyping in ASSYST panel

Aberystwyth: Martin Dunen

(?which) Brassica lines being used by European phenotyping network

Guusje Bonnema, Rick Amasino: St Louis Lemnatec phenotyping on B. rapa DH core accessions (drought, biomass): Same lines mRNAseq in York

6. Status and future of Brassica SNP array

Cindy Lawley (Illumina): Illumina has made large oligo synthesis to commit to end of 2015 – will send sample numbers

Primary publication of array: Isobel Parkin hoping to draft when she has time – should it be “just” and array paper, or something scientific, e.g. genetic mapping positions etc? (More work, maybe not feasible...): PBJ? [note: use of the array for association genetics, including the mapping of probes onto Bancroft/Trick V4 pseudomolecules, published February 2014: DNA Research 2014; doi: 10.1093/dnares/dsu002]

7. Community data management and annotation

Dave Edwards (UQ): Rice informatics consortium, wheat information system: Tools useful for Brassica community

MAKER seems to be a useful tool but has been difficult to set up by some. King lab (SCU) have it operational, and access to high performance cluster).

Marker (or MAKER?) setup on iPlant: May be able to link in to this?

Expansion of data management: Short read data, SNP database?

Wheat consortium?: Not looking to host/manage data, rather to index to other databases and use a common platform as a search engine

Nathalie Nesi: Genoplante information system for different species. In RAPSODYN project database development. URGI tool available

Rothamstead CropStoreDB: was previously linked to Brassica.info website, now disentangled. Australia has funding to serve and maintain Brassica CropStoreDB for long-term data storage and public availability– needs to ensure continuity of curation. Additional work being carried out in a number of projects to enhance data curation pipeline and interfaces. Adding GIS capability to e.g. trial/phenotype data.

Ian: How is CropStoreDB linked to TGAC (UK) – Graham King should coordinate to make sure no redundancy and plan how new data can be integrated. TGAC will make everything public (only feeding in public data!)

ACTION: Investigate potential for a HORIZON 2020 grant application in 2015 (TGAC, Rothamsted, France, Germany), including co-funding from Australian projects (UQ Brisbane, SCU Lismore)

Chris: Standards for ontologies? Need to agree – link to iPlant etc

John McKay: Info on assembly methods etc. important

Graham King: Raised the question of an agreed system for Brassica gene annotations and naming so that consistent between genomes and resequenced genomes?

At present:

B. rapa (Chiifu-401) = [Bra019255](#)

B. oleracea (TO1000) = Bo1g001010

B. oleracea (O212) = Bol028851 (confusing as 3rd character is an L whereas TO1000 it is 1 to denote chrom number). There is no correspondence between the gene numbers in the two *B. oleracea* systems to date, which is to be expected. However this does place emphasis on needing a very distinct prefix to avoid any confusion)

B. napus (Darmor) = GBSRNA2G000000003001

Is there a plan to incorporate chromosome name as used for Arabidopsis, with an ordered decatonic or higher increment?

E.g. At1gG69120 (chr1) = BolC6012340 (chr C6) = BnaC6012340 (chr C6).

Is there a plan to systematically align to Arabidopsis (At) *functional* annotations, descriptions? How to link gene data between B. ol, B. rapa, B. napus?? Need for community effort!

Wormbase example: One expert who is/has the authority. Question was raised whether the MBGP steering committee has the authority to determine annotations for Brassica: Was agreed that this committee has a community mandate for such authority. *(GK comment – well if MBGP SC doesn't, then there is a vacuum. I would suggest whatever grouping/sub-committee wish to take ownership of this issue, then they seek ratification for their activities via notification to the brassica.info mailing list).*

TAIR example? Manual curation step but a lot can be auto-translated. Tools for identifying ?functional orthologues.

It was noted that the MBGP steering committee previously approved a Brassica gene nomenclature system based on At gene names: see <http://www.brassica.info/info/reference/gene-nomenclature.php> 2008 Plant Methods publication from [Lars Østergaard](#) and [Graham King](#)

What to do when a gene is not in At???

ACTION: Annotation subcommittee (Dave, Graham) to distribute a proposal. Gene model?

Kevin Childs (Maker) says that different annotations/gene identifiers are possible (e.g. rice) but cause problems, especially with genes which aren't in common in all references...

Conclusion: The gene identifier is most important factor, urgent need to achieve a consistent solution!

8. Upcoming meetings

Brassica 2014 – Wuhan, March 31 – April 3, 2014

14th International Rapeseed Congress, Saskatoon, July 5 – 9, 2015

Climate Change Genomics Amsterdam early 2015

9. Miscellaneous

Update on JIC B. rapa TILLING service:

TGAC collaboration (with whom?) to do exome sequencing on 1000 M2 lines

Off the shelf service

Also inherited B. napus population, will be available soon.

BoI TILLING population (broccoli DH line) in development at JIC, available end of 2014
Capsella rubella pop

See <http://revgenuk.jic.ac.uk/> website for details and ordering

Meeting closed 12 noon.

Minutes: Rod Snowdon, Birgit Samans, Sarah Schiessl (JLU Giessen), revisions from Graham King and Ian Bancroft