

**MINUTES: Multinational Brassica Genome Project (MBGP)
Steering committee meeting at PAG XXIII, San Diego**

Date: Sunday, January 10, 2016

Time: 1:30 pm until 3 pm

Location: Dover Room, Town & Country Hotel

Chair: Boulos Chalhouh, INRA, France

Participants:

Boulos Chalhouh (INRA, France), Rod Snowdon (JLU, Germany), Jacqui Batley (UWA, Australia), , Mark Beilstein (U of Arizona, USA), Andrew Nelson (U of Arizona, USA), Jorge Duarte (Biogemma, France), Clotilde Claudel (Biogemma, France), Lixi Jiang (Zhejiang University, China), Honggang Zheng (Cargill Specialty Seeds & Oils), Feng Cheng (Institute of Vegetables and Flowers, Chinese Academy of Agricultural Sciences, China), Jinghua Yang (Zhejiang University, China), Steve Robinson (AAFC, Canada), Geoffrey Wagner (Bayer Crop Science, Belgium), Jim Beynon (Warwick University, UK), Juan Montenegro (University of Queensland, Australia), Michael Alaux (INRA France), Ian Bancroft (University of York, UK), Yong Pyo Lim (CNU, South Korea), Suhyoung Park (National Institute of Horticulture and Herbal Science, South Korea), Isobel Parkin (AAFC, Canada), Mathieu Rousseau-Gueutin, INRA, Rennes, France), Nathalie Nesi (INRA, Rennes, France), Philipp Bayer (UQ, Australia), Birgit Samans (JLU, Germany)

Apologies: Dave Edwards (UWA, Australia), Eric Schranz (Wageningen, Netherlands), Graham King (Southern Cross University, Australia), Andrew Paterson (USA), Andy Sharp ((AAFC, Canada)

Agenda

1. Introductions

List of participant compiled by Rod Snowdon

2. Approval of minutes from PAG 2015 meeting

Minutes were unanimously approved and are available on www.brassica.info.

3. Updates on genome sequencing and resequencing initiatives

(ex: the remaining U triangle species, Transcriptome and other 'omics' projects)

3-A- De novo genome sequencing and assemblies

The Brassica U triangle species

B. juncea

Jinghua Yang: *B. juncea* (a Chinese vegetable variety) has been sequenced and assembled. The genome will be released this year.

Isobel Parkin: Sequencing and assembly of genome of another *B. juncea* variety (Canadian oilseed type) was also completed.

Jinghua Yang and Isobel Parkin will contact each other to coordinate publications and release

B. nigra* and *B. carinata

Isobel Parkin: *De novo* genome sequencing and assemblies were also completed by Isobel Parkin's group. It is hoped that time permitting all of the current assemblies will be released in 2016.

***B. napus de novo* assemblies (other than Darmor-bzh)**

Boulos Chalhoub: In addition to the published reference genome of Darmor-Bzh (Chalhoub et al. 2014), the *de novo* assembly of a Chinese type of *B. napus* (Zonghf 11) is publicly available in databases.

Isobel Parkin: The Canadian type sequenced by Isobel Parkin group will be released this year upon its publication (in collaboration with Dr John McKay, Colorado State University).

Philipp Bayer: *De novo* assembly of cultivar Tapidor of *B. napus* will be also available in 2016 (group of Dave Edwards, University of Western Australia).

Boulos Chalhoub: Scientists of MBGP have heard at PAG about progress in accurate *de novo* sequencing and assembly, with various technologies. Among these, there were a great breakthrough presented by NRGene company, especially in wheat. This would be followed and promoted by MBGP so that we continue promoting generation of accurate Brassica sequence data

3-B- Sequencing of other Brassicacea species

Chris Pires: update about the BMAP-JGI project of sequencing of 19 Brassicaceae genomes, including *Sinapis alba*. The project follows the JGI standards and is integrating PACBIO data for triplicated genomes. There would be an announcement at PAG 2017.

3-C- Resequencing

Numerous *B. napus* cultivars are being resequenced:

Rod Snowdon: German NAM consortium released sequences of 51 *B. napus* lines (NAM founder lines) in September 2015.

Isobel Parkin: her group has also re-sequenced 51 *B. napus* lines (spring type founder of NAM population), likely will be released in early 2017.

Yong Pyo Lim: He collected 74 species for selection and resequencing.

3-D- Transcriptome (RNA) sequencing

Ian Bancroft: His group has completed mRNA-Sequencing (from leaves) on a set of 387 *B. napus* accessions, and around 200 further accessions of *B. rapa*, *B. oleracea* and other Brassicaceae. Leaf mRNAseq data have also been obtained from a diversity panel of 205 *B. juncea* and the *B. juncea* VHDH mapping population (121 lines).

4. Updates on international research cooperation's

Lixi Jiang: A joint collaborative project between Zhejiang University (Professor Lixi Jiang), China and University of Kiel in Germany (Professor Christian Jung) are collaborating on *B. napus* research including TILLING. Lixi Jiang is also collaborating with University of Göttingen, Germany (Prof. Heiko Becker) on heterosis and polyploidy in synthetic *B. napus*, DNA and transcription levels.

Ian Bancroft: His group had developed a nice tool for visualizing alien introgression based on RNA sequencing. He is seeking collaborators to share lines to characterize and visualize introgressions, including homoeologous exchanges. Alien introgressions could be between Brassica species or from related species, like Rfo/CMS system.

5. Update on *brassica.info* website

A message from Graham King who was not able to attend the MBGP meeting:

"Peoples are encouraged to share information via the brassica.info website. Examples, announcement for conferences and workshop, minutes from MBGP meetings, gene naming and nomenclatures, etc...."

6. Community data resources, management and annotation

A message from Mike Freeling who was not able to attend the meeting:

"Those of us Brassica researchers generating read data via, for example, RNAseq experiments where the Fastq goes, eventually, to the SRA: please use at least one very, very specific cellular or timing source for the RNA or chromatin. When our cellular/timing data are all mixed up together, their power diminishes."

Community Brassica platforms for international collaborations.

Brassica Bioinformatics Platform project proposal (Giessen University, Germany):

Rod Snowdon: **Brassica Bioinformatics Platform project proposal (Giessen University, Germany)**. Rod Snowdon group has submitted a proposal in a German National funding Call (under review) for a consortium between 3 German groups to establish a “*Brassica napus* Resource Center” (BnRC) for management and distribution of community plant populations and data.

The *BnRC* platform is intended as a repository and distribution focus for large, public plant populations and associated genomics data. The initial basis will be on genome sequences, 60k SNP data and QTL from the German *B. napus* NAM populations (n~2500) along with the public ERANET-ASSYST diversity population (n~400) and DH populations from University of Giessen (n~800). An interactive database will be built on a genome browser template, designed to enable and encourage feedback and continual growth with additional data. Genomics, GWAS, QTL, transcriptome or metabolic data, populations and data from other groups will also be integrated where possible. The overriding aim is to link from genome sequences to association with traits, across populations and between different Brassica species/genomes.

All data accumulated will be publically available and interlinked to external data; the aim is to provide a platform for data sharing, and implement common data annotations and exchange standards that enable integration and comparisons of related, publicly available datasets. It is expected that the ability to incorporate multiple datasets in meta-analyses will give users considerable added value from new analyses of their own data.

Other groups interesting in cooperating, or contributing major public datasets, are encouraged to contact Rod Snowdon for more information.

Nathalie NESI: Her group has developed a Brassica information system where all the *Brassica napus* genomic data of the French Rapsodyn project are being deposited (**INRA-Rennes, France**). In France Nathalie Nesi would not be able to integrate data from other populations. This is done with URGI of INRA-Versailles that has developed a user-friendly system for many other crops, such as the one internationally used by the wheat community. This system is particularly well suited for genomic data but also for phenotypic data and metadata. She is questioning about the interest to put all the data in the same depository? There are existing solutions to connect the indexed databases (see below details given by Michael Alaux).

Michael Alaux: He gave more details about the systems that have being developed at URGI (INRA-France). URGI is developing a quick search system that search indexed data in distributed databases. This tool relies on the SolR technology and is developed in the frame of the EU transPLANT project and the International WheatIS project. He suggested using for free the SolR tool for the MBGP community. To help the installation in individual labs a small package with the SolR tool and README is available. There are no specific requirements. It is an open model.

EBI and IPK are integrated with the transplant system. Everyone could follow this simple model.
To better understand, we can look on the below links:

Example of the search for transPLANT:

<http://www.transplantdb.eu/search/transPLANT/rubisco>

For the WheatIS:

<https://urgi.versailles.inra.fr/wheatis/>

Download the SolR package:

<http://wheat-urgi.versailles.inra.fr/Projects/Wheat-Information-System/SolR-tool-package>

Data model to follow to index the data (set up in the frame of the transPLANT project) is appended to these minutes.

All: There is a consensus on the interest for a community Brassica Informatics Platform for international collaborations. Birgit Samans from Rod Snowdon's group will lead the German project and plans to visit groups interested in contributing in order to coordinate and harmonize efforts. If funding is not awarded in the present call the proposal will be submitted elsewhere in modified form, potentially via an EU-wide project with other interested partners.

7. Update on gene model (and other entities) *nomenclature*

Progress since MBGP recommendations (Wuhan April 2014 and later meetings), Please see at: http://brassica.info/info/genome_annotation.php)?

Only the *B. napus*- Darmor-Bzh project appears to have fully adopted the gene style.

The community agreed that all new Brassica genome annotation may follow recommendations http://brassica.info/info/genome_annotation.php

-Chris Pires raises the question the reviewing standardization in relation to the Pan-genome initiatives

-Based on suggestion of Ian Bancroft, it has been agreed the interest of renewing the working group, to update but mainly to make recommendations usable in any new coming annotations

8. Upcoming meetings and conferences

Brassica 2016 conference (3-6 October 2016, Melbourne, Organized by Prof Jacqueline Batley, UWA).

A MBGP meeting will be organized during the conference.

9. Miscellaneous

No further items.

The Chair thanked all participants for their input and support closed meeting at 3:00 pm.

Next MBGP meeting October 2016 during the Brassica conference (3-6 October 2016, Melbourne, Organized by Prof Jacqueline Batley, UWA).