

Multinational Brassica Genome Project (MBGP)

Steering committee meeting at IRC 2019 Berlin

Date: Sunday June 16th 2019

Time: 4.30 – 6 pm

Location: Room A05

Minutes (prepared by Annaliese Mason, Jacqui Batley and Graham King)

Present: Jacqui Batley, Rod Snowdon, Yong Pyo Lim, Jenny Lee, Lixi Jiang, Carmell O'Neill, Sebastien Faure, Katarzyna Gacek, Janetta Niemann, Sarah Schiessl-Weidenweber, Jun Zou, Annaliese Mason
(Apology to those having participated and not appearing on the list)

Chair: Current chair Graham King was an apology, Jacqui Batley stepped in as replacement

1. Introduction and welcome

General introduction for participants.

2. Approval of minutes from January 2019

Participants unanimously approved the Minutes of the last MBGP meeting (PAG 2019, San Diego, January 2019)

3. Reports on progress/notable milestones/announcements from members

Jacqui Batley suggested only presenting extra work on top of what was presented at the meeting in January. These are resources available to share, not private data.

Annaliese Mason – passed 55 synthetic *B. napus* lines to Shengyi Liu's group for sequencing (~50x coverage). Planning to do whole genome sequencing at about 20x coverage for 20 - 30 turnip lines (tetraploid and diploid) in the next 6-12 months; any suggestions for including known homozygous varieties/favourite cultivars will be happily accepted and sequence information provided back

Jun Zou –cooperating with Rod Snowdon to re-sequence new-type *B. napus* from the cross *B. rapa* x *B. carinata*: not high coverage but nanopore and short-sequence reads

Jenny Lee – has the Express genome assembled in the second version; all built with long-reads (90x coverage – 50x PacBio and 40x Nanopore); currently waiting on transcriptome data from Rachel Wells for improving the annotation. Current assembly quality is better for two reasons: long read and new genetic maps from NPZ, genetic maps are not built from resynthesised lines

Sarah Schiessl – Agilent exome sequencing on *B. rapa*, *B. oleracea* and *B. napus* to measure mutation rates; aim to cover, but exclude, redundant sequences; set of lines to be sequenced includes spring, winter and resynthesised. Any other interest would drive the cost down for everyone else. Current plan is to send first samples next summer – please contact Sarah directly if you may want to run some samples using this technique. Probes to be designed from the pan genome.

Janetta Niemann - Interested in collaborating on wild species hybridized with *Brassica*; looking for resistance gene phenotype collaborations

Katarzyna Gacek – in collaboration with Jacqui Batley has sequenced two mapping populations, yellow seeded by black seeded oilseed rape; looking at fibre, protein content, glucosinolates; quality traits related to rapeseed meal quality for animal nutrition.

Sebastien Faure – Now Innolea (previously Biogemma), planning to sequence another variety using Nanopore as per previous method mentioned at PAG – data should be available by end of year

Lixi Jiang – resequenced more than 1000 germplasm accessions last year, sequencing depth too low so selected >20 accessions for deep resequencing; also newly assembled three cultivars: Darmor from IPK, Westar and Zhongshuang1. Not having an easy time with the assembly but should be done in a month or so. Aim to have a reference from a spring or semi-winter to map data to instead of Darmor. Sending a student to Dave Edwards on a CSC scholarship this year to look at structural variation analysis. Established a core collection for GWAS which represents 99.7% of SNPs and 98% of indels; examples for agronomic traits (paper under review).

Rod Snowdon noted that it is hard to download the data from the SRA, and asked is it possible to get data on hard-drives?

Lixi Jiang: people can ask and they will arrange

Carmell O'Neill - part of the BRAVO project (with Rachel Wells) – a lot of transcriptome data being generated – spring, semi-winter and winter oilseed rape; developmental time series. Asked whether someone (Isobel?) has a genome browser or money for one?

Yong Pyo Lim – working on *B. rapa*; recently sequenced a core collection of lines for GWAS, as well as some mapping populations, 232 homozygous lines sequenced – 3 to 70x level; for 40 lines used Illumina Novaseq 1000, also radish (several inbred lines; focusing on agronomic traits) and *B. juncea*, *B. nigra* (collaborative project with Isobel Parkin; homozygous lines provided); aiming to reconstruct the breeding history of Chinese cabbage. Development of SNPs from panel for GWAS, trait mapping like clubroot resistance, 42 morphological traits. Papers under review/submission. Some material will be available after publication (dependent on seed company). Horizon2020 project with Fernando Branco on cabbage etc.; organic agriculture project – blackrot resistance; 400 germplasm lines in lab (European core collection ~1000 lines)

Rod Snowdon – planning to start a big project on structural variants with nanopore data; planning to sequence 100 – 200 accessions (not at high coverage) to pick up small deletions and copy number variants; hoping to get a project funded next year to sequence twice as many lines. Perhaps there could be discussion about which lines should be selected for sequencing, which lines are most interesting to people? Ideally the lines will be in the ERA-Net diversity set because we know that these lines are homozygous.

Rod asked Lixi Jiang where he got the accessions he sequenced and how did he know about homozygosity etc.? Lixi Jiang: Lines said to be homozygous when supplied from IPK Gatersleben. Accessions list cleared with germplasm curator; other lines selfed since 2008 personally. Rod noted that they have seen variation in lines acquired from different sources, and also chromosome copy number variation within one generation.

Jacqui Batley: just got funding to look at sources of blackleg resistance from wild Brassicaceae etc.; will be looking at sequencing introgression lines in future, but project just starting. Will update more about the sequencing at the next meeting

4. **Updating reference genomes for Ensembl Plants (notes from Graham King):**

B. rapa – three genomes now checked through Ian Bancroft/Zhesi He genome-ordered graphical genotype ‘GOGG’ pipeline: to check integrity of gene order.

- Chiifu-401 v 3
- Z1
- R-o-18

Final adjustments now being made in scaffold order/orientation prior to Pan-genome alignment in Edwards lab and assignment of common gene names to agreed nomenclature standard.

Similar process started for *B. oleracea*

GK visited Bruno Contreras and Guy Naamati at EBI-Hinxton in May. Outlined detail of plans for submitting revised *Brassicagenomes* to Ensembl Plants. They are keen to work with us and also outlined plans for a) revised ‘new’ Ensembl that will be more interactive and able to be distributed for annotation etc; b) work they are planning on managing/representing pan-genomes and polyploid gene relationships, including updates to how Compara pipeline works with paralogues. They think Brassica provides a good model for these developments.

5. **Update on Brassica Information System from GK**

GK starting to approach questionnaire respondees to build inventory of available datasets (a couple of months behind schedule)

Work on deploying Brassica Information Portal (ex Earlham Institute) at SCU –ongoing but getting there.

6. **Scope for multinational collaborative projects**

Opportunities for co-funding and international funding were discussed (updates from January).

Yong Pyo Lim – possibility for exchange programs etc. with Korea – 150 000 dollars per year for four years: any interest? YP Lim can’t be PI but can recommend other researchers for collaborations. Co-submission of grants – acceptance by foreign country grant round leads to acceptance from the Korean side. Proposals currently mostly with US, Japan – other countries would be seen favourably. Currently head of the “golden seed” project – connection to many small seed companies working in cabbage, Chinese cabbage, any kind of *Brassica*.

Lixi Jiang – Ministry of Science and Technology, NSFC (natural science foundation of China) department of foreign cooperation – key is relatively large money

Jacqui Batley – Australia/Canada funding for blackleg research: developing a set of standardised blackleg isolates and hosts (*B. napus* plants); understand diversity and make a set of standards, link back to sequences. Hoping to link out to other countries in the future. All isolates, seeds and sequence will be available

7. **Any other items/meeting announcements**

Brassica 2020: This meeting will now be in Saskatoon, probably September 2020. IP to organise. RS said that he is happy to host in 2022 in Giessen

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