



Summary of IWGSC meetings

Victor Harbour, Australia

August 2006

The IWGSC held two official, open, business meetings immediately before and during the ITMI conference in Victor Harbour, Australia, in August 2006. As had been announced, the first meeting was held on 27 August 2006. After the first meeting, it was determined by the consortium co-chairs that a second meeting was needed to refine and delineate a strategic roadmap for the development of a physical map for hexaploid wheat that could be agreed upon by the community. The second meeting was held on 30 August 2006. Both meetings were well attended with approximately 40 persons at each meeting. The principal outcome of the two meetings was an agreed upon roadmap of activities for the next four years designed to obtain a completed physical map of *Ae. tauschii* and of the D-genome of hexaploid wheat while running pilot projects to determine the best strategy for the second phase of the A and D genomes map.

Meeting I: Sunday, 27 August 2006

The meeting included the following:

- Reports on the ongoing projects and funding successes for the consortium (sponsors include the INRA, Kansas Wheat Commission, Kansas State University, Limagrain/Biogemma, and the Nebraska Wheat Board (K. Eversole))
- Reports on several funded projects, including
 - USDA – 3AS (B. Gill)
 - Genoplante/Genoscope large sequencing projects on 3B (C. Feuillet)
 - NSF Comparative Project on wheat, brachypodium, and rice (O. Anderson)
- Reminder that annotation guidelines have been established and annotation pipelines are being developed. C. Feuillet described the TRIANNOT project at the INRA Clermont that aims to create a publicly available, user friendly annotation pipeline. C. Feuillet also announced that she proposes to organise a working meeting of the bioinformaticians at PAG to discuss the development of annotation pipelines for wheat. Barley researchers want to be integrated as well with the ITMI/IWGSC effort to create a pipeline. **Action: C. Feuillet to discuss with Robin Buell if it is possible to have a workshop or meeting and to check with D. Matthews if a slot for a bioinformatics session is available.**
- Proposal by C. Feuillet for renaming the markers on the genetic maps of wheat for anchoring the physical maps by adding, after the marker name, the chromosomal location. For example, BARC75-3B. **Action: C. Feuillet to**

contact D. Matthews to determine best approach for moving forward on a nomenclature protocol.

After the reports, the focus of the meeting was on the development of a strategic concept on building the physical map to allow, in the first phase, sequencing of agronomically significant target regions. Topics and conclusions included the following:

- Several approaches for obtaining a physical map: chromosome by chromosome, whole genome, or a hybrid approach as proposed by B. Gill. There was general support for the idea of developing small consortia for each chromosome groups as a mechanism for coordinating the chromosome by chromosome based effort in hexaploid wheat. There was a consensus that we need to gain a commitment to engage J. Dvorak's group to complete the *Ae. tauschii* map (currently 7,000 contigs and 6x coverage) as a framework upon which to build a physical map of the D genome of hexaploid wheat.
- Chromosome sorting and BAC library construction are not rate limiting steps due to the special investment of the Czech republic (J. Dolezel has doubled lab capacity and can produce 5 chromosome specific BAC libraries per year using a chromosome arm approach). He emphasized the need for sufficient material of good quality (e.g., high germination rate) to ensure efficiency. There was a brief question about whether we need to integrate the production of the seeds in each project to ensure sufficient stocks.
- There was agreement that the major issue is anchoring and there was a consensus that this will require the combination of several approaches, including
 - Establishment of EST-based shared markers (COS markers). It was reported that J. Snape has a BBSRC project on COS markers between rice/brachypodium/wheat. At this time, his project is small scale, so it would need to be scaled up for the international efforts in wheat and barley. There was a suggestion that J. Snape take the lead on this and apply for a larger project endorsed by the consortium.
 - Radiation hybrids as a tool to anchor the maps (S. Kianian)
 - Development of more deletion lines (Gill/Endo)
 - Large scale BAC end sequencing from whole genome and individual BAC libraries.

P. Langridge suggested that we figure out a way to allow individual groups or countries to focus on a chromosome group. There was a brief discussion about the NSF call for plant genome proposals. S. Kianian indicated that he wanted to pursue a RH map proposal on the D-genome of hexaploid wheat and of *Ae. tauschii*. There was general agreement that the IWGSC should support his efforts. There was support as well for finishing the physical map of the *Ae. tauschii* genome, finishing and fingerprinting the libraries of the D-genome of hexaploid wheat, and adding more deletion lines for all 21 chromosomes of hexaploid wheat.

Meeting II, Wednesday, 30-August 2006

There was a second meeting of the IWGSC to refine the strategy for developing a physical map and to make a decision on the approach in view of the NSF applications that are due in October and the meetings of K. Eversole and C. Feuillet with the ARC,

GRDC, CSIRO, and the chief scientist of Australia. As is the case for all IWGSC meetings, the meeting was open to everyone attending the conference and was well attended. There were lively discussions about the whole genome hybrid approach and the decision by the community was to not endorse this approach at this time as no data has been produced to prove that it is feasible to assemble 2 million fingerprints and homoeologous regions in any organism (i.e., no pilot projects have been designed to test that aspect to date). The general strategy agreed upon is to complete ongoing and planned pilot projects so that we will know whether we can use a whole genome or chromosome by chromosome approach to create a sequence ready physical map of the hexaploid wheat genome. In particular, there was agreement that before making a decision, B. Gill's project on 3AS would need to be completed as well as a comparative project on group 3.

The major outcome of this meeting was the development of a strategic roadmap for projects over the next 4 years (Phase I) that was agreed upon by all members of the consortium and others present at the meeting. The goal is to have a completed physical map of *Ae. tauschii* and a sequence ready physical map of the D-genome within the next four years following a coordinated approach at the international level with different countries selecting different chromosomes (see below). The *tauschii* map will assist in anchoring the hexaploid D-genome map providing extensive genetic polymorphism that is lacking in hexaploid wheat for this genome. At the same time, projects to develop physical maps of homoeologous chromosome groups will be undertaken for group 3 to complete the ongoing projects on 3B and 3AS (anchoring of 3D and 3AL remains to be done) and develop a pilot project to determine whether homoeologous BACs can be assembled when fingerprinted as a whole (see below). Group 7 that contains a number of high priority traits for Australia will be tackled possibly by a national initiative. These projects will take advantage of the resources (physical maps, genome and BES sequences) that are or will be developed within the next year for the rice and brachypodium model genomes and will also be performed in coordination with the construction of a physical map of barley (for which an international genome sequencing consortium has been launched at the ITMI meeting).

In the frame of this roadmap, there was agreement that several IWGSC applications to the October NSF call should be developed in coordination between the different PIs and seen by the CC for endorsement by the consortium. It was stressed that the projects need to refer to each other specifically and that each are independent enough that it can be completed if funding for the other projects is not approved during this call. These projects included the following:

- Complete physical map of *Ae. tauschii* so that it can be used as a framework for anchoring the D-genome.
- Project on the D-Genome of hexaploid wheat that would
 - Complete the remaining chromosome libraries, fingerprint all D-genome libraries and anchor the 1D, 4D and 6D chromosomes to the genetic map using the BAC library containing the three chromosomes of CS
 - Test for a whole genome approach on chromosomes 3A, 3B, & 3D (mix BACs)
 - Develop additional deletion lines for the whole genome

- Include international participation on different chromosomes by announcing that individuals can indicate their commitment to participate.
- Develop a RH map of the D-genomes of hexaploid wheat and of *Ae. tauschii*.
- Project for BES.

There was general agreement that the international community would be engaged on anchoring of the D-genome and that we would try to gain individual country or regional sponsorship of one or more chromosomes to ensure completion. At the same time, we could develop targeted approaches on the A and B genomes.

It was noted that at the ISPMB meeting scientists from India had expressed interest in working on chromosome 1BS.

K. Eversole indicated that she would distribute the minutes and the write-up of the strategic roadmap to the co-chairs and then to the entire coordinating committee of the consortium.