**International Pea Sequencing Consortium Go-to-Meeting**

**6 March 2012**

**Attending:** Clare Coyne (USDA-ARS, Pullman, USA), Doreen Main (Washington State University, Pullman, USA), Rebecca McGee (USDA-ARS, Pullman, USA), Crystal Chan (Saskatchewan Pulse Growers, Saskatoon, Canada ), Tom Warkentin (University of Saskatchewan, Saskatoon, Canada ), Kirstin Bett (University of Saskatchewan, Saskatoon, Canada), Jaroslav Dolezel (Institute of Experimental Botany, Olomouc, Czech Republic), Judith Burstin (INRA-Dijon, France), Gregoire Aubert (INRA-Dijon, France), Noel Ellis (Aberystwyth University, Aberystwyth, Wales), Julie Hofer (Aberystwyth University, Aberystwyth, Wales), Petr Smýkal (Univerzita Palackeho v Olomouci, Olomouc, Czech Republic), Marie-Laure Pilet-Nayel (INRA-Rennes, France), Alain Baranger (INRA-Rennes, France).

**Minutes**

1. Principles of Cooperation. A discussion led by Noel Ellis.

The consortium should strive to be as open and inclusive as possible.

Members will be accepted at any time as needed/desired.

Applications for funding should build on each other and share as much as reasonable.

The ultimate goal is to sequence pea, but there are many way points with tangible products before the sequencing is complete.

Do we want a more formalized consortium with documentation of our strategies, goals, resources, milestones, assignments, etc. Dorrie will send out documents that other crop groups have put together. This can all be coordinated via a web-based site that the Main Lab has offered to host, it will include a summary of available resources. After discussion, general consensus was reached to utilize a website that will house project information.

2. Obtain a survey sequence for pea genome (Genome Zipper)

This discussion was initiated by Jaroslav. Shot gun sequencing will allow easy access to genes and gene tags, development of SNPs and other markers and determine the synteny with other genomes. It is low cost and provides a lot of information. It requires significant amounts of bioinformatics.

Judith pointed out that this has already has been started by several groups: INRA-Dijon has a unigene set for Cameor and have developed SNP markers from transcripts; INRA-Rennes has developed SNPs from genomic DNA; Univ Saskatchewan has sequenced transcriptome of CDC Bronco and made a Golden Gate Assay, plus another 7,000 SNPs. INRA has made a high resolution genetic map using 10 mapping populations (approx. 1400 RILs) all with one common parent.

Discussion rapidly turned to agenda item 4.

4. Sequence the genome

Jaraslov suggested that a clone-based sequence with a physical map is the most realistic strategy for a genome as large as pea. To have a good physical map, we need 10 – 15x coverage using different enzymes. Dorrie suggested to get that coverage, we would need at least 3 BAC libraries cut with different enzymes. There are currently two pea BAC libraries. ‘Cameor’ has approximately 10x coverage and was cut with *Hind*III and *Eco*RI. The USDA BAC library of a wild accession has approximately 3x coverage (utility very limited).

Should we sequence >1 genotype or just one genotype? Noel suggested >1 as so much of the pea genome is retrotransposons (primarily indel polymorphisms) and that only about 20% of the genome is the same between genotypes. Jaroslav suggested sequencing 1 genotype and using it as a reference and an anchor to compare against. General discussion. Noel summarizes discussion: All are keen to obtain sequencing and physical map with Cameor BAC. Mention of using Illumina for BAC sequencing, 384 tags per channel and 16 channels per run. Estimated 20,000 BAC clones needed for minimum tile (out of the 400,000 BAC clones in Cameor libraries). Jaraslov suggests using sequences of the BACs to anchor to the genetic map and to do it simultaneously. He estimates approximately USD 1.5 million for pea genome physical map. He recommends two labs – UC Davis (Ming-Cheng Luo) or Italy (Michele Morgante). One lab should do all the fingerprinting. Judith also mentioned Genoscope for sequencing and will investigate. Dorrie will contact UC Davis for a price estimate.

Proposed flow of work: sequence the BAC libraries, assemble the contigs, establish minimum tiling path, sequence minimum tiling path contigs and anchor contigs to genetic map.

Do we need another BAC library? Jaroslav said his lab routinely makes them and they can make another one if there is any bottle neck encountered with Cameor or if we need another for cross-referencing. Judith will contact Abdel Bendahmane to find out what he wants done with the Cameor BAC library. If we need another Cameor library with a different restriction enzyme, will need to ensure we have the same genotype. Judith has the original genotype of Cameor and has used it as a parent in mapping populations.

5. Funding.

Dorrie discussed the NSF Plant Genome Grants. Next RFP is March 2013. Noel thought timing was good and that they may be able to secure Euros to match US $. Tom discussed the possibilities that the Saskatchewan Pulse Growers would participate in funding. Noel said it was very important to present the group as a consortium when seeking funding.

Next Meetings

Next ‘go-to-meeting’ will be scheduled to include potential consortium members in New Zealand and Australia and North America, with details sent to all consortium members as they may choose to participate. A third ‘go-to-meeting’ may be scheduled for members in NZ-Australia and Europe. Next meetings in person were proposed to be held as workshops in conjunction with ILCGG in India, Noel Ellis organizing, October 2012 and with the Aschochyta Blight Workshop in Spain, May 2012, Tom Warketin.