Development & Analysis of Comparative Genomics Platforms from Closely Related Species: *Oryza* & *Brassicaceae* as Case Studies

Rod A. Wing, Arizona Genomics Institute, University of Arizona
From OMAP to BMAP: What I Did on My Sabbatical in Germany
Brassicaceae Comparative Genomics

Exemplars (Red Boxes)
- JGI01 Boechera stricta (0.24pg / 1C) & other spp.
- JGI02 Brassica rapa (B3) (0.6pg / 1C)
- JGI03 Myagrum perfoliatum (0.31pg / 1C)
- JGI04 Caulanthus amplexicaulis (0.38pg / 1C)
- JGI05 Arabis alpina (0.4pg / 1C)
- JGI06 Thlaspi arvense (0.54pg / 1C)
- JGI07 Cardamine hirsuta (0.23pg / 1C)
- JGI08 Iberis amara (0.56pg / 1C)
- JGI09 Euclidium syriacum (0.26pg / 1C)
- JGI10 Cleome violacea (?. Estimated 0.3 - 0.4pg)

In progress (Blue Boxes)
- CAN01 Leavenworthia alabamica
- CAN02 Sisymbrium irio
- CAN03 Aethionema arabicum

Brassicaceae Map Alignment Project (BMAP)
(J.C. Pires, D. Weigel, R. Wing – Coordinators)

- **Objective**
  - Establish an international collaborative network that will formulate a roadmap for the generation of a comparative genomics platform for the Brassicaceae family

- **Specific arguments include**
  - Many important food & biofuel crops, and weed species
  - Many novel traits and chemistries important to human health and crop improvement
  - Relatively small genomes sizes
  - Rich knowledge of karyotype evolution & chromosome dynamics
  - Potential to bridge comparative genomics to comparative systems biology, making use of the rich knowledge from *Arabidopsis*
  - A strong and vibrant *Arabidopsis thaliana* research community
Brassicaceae Map Alignment Project (BMAP)

- **Mechanism/Time Frame**
- **Hold four international meetings (Phylogeneticists, Biologists)**
  - Plant & Animal Genome Meeting, San Diego, January 2010
  - Max Plant Institute, Tubingen, Deutschland, March 2010
  - Arabidopsis 2010 Meeting, Yokohama, Japan, June 2010
  - Huazhong Agricultural University, Wuhan, China, June 2010
- **Objectives**
  - Identification of a set of grand challenge questions that need to be addressed in the Brassicaceae.
  - Establish a prioritized list of species to be sequenced. Emphasis will be placed on the generation of high-quality reference genome sequences for key species that can subsequently be used as resequencing templates for more closely related species/populations.
  - Discussion of a public repository for genetic stocks, DNA/RNA.
  - Discussion of plans to develop a white paper for use by the international community obtain funding to support this project (October 2010).
Criteria for Choosing Genomes to be Sequenced – San Diego

• A. Phylogenetic position
• B. Small genome size
• C. Ability to self and make crosses; easy to grow and use as a “model” (NAM/MAGIC lines)
• D. Homozygous genotypes (Selfed by single seed descent, doubled haploids, etc)
• E. Important agronomic/biological features (novel chemistry, ecology, life history, etc.)
• F. Used by a large research community (i.e., Arabidopsis, Brassica, Cardamine, Lepidium, etc.)
Grand Challenge Questions/Themes from BMAP I – San Diego

• A. Whole genome duplications (ancient, “meso”, and recent polyploidy). Distinct from animals.
• B. Genome and chromosome evolution – selection/mutation/CNS/transposons/breakpoints
• C. Morphological variation (evolutionary development studies); crop plant domestication
• D. Chemical variation (glucosinolates, etc); plant/animal interactions; crop plant domestication
• E. Hybrid vigor/heterosis; gene expression/proteome/metabolome/trait evolution
• F. Comparative systems biology of Brassicaceae; rhizosphere/metagenomics; synthetic biology
Grand Challenge Questions/Themes from BMAP II – Tübingen

- A. Sequencing of three alloplloid Brassicacea taxa (lineage I) of different phylogenetic age. Is hybridization/alloploidy a trigger for adaptive radiations?
- B. Comparisons of annual vs. perennial at the whole genome level
- C. Australian crucifers experienced a whole genome duplication and extensive genome reshuffling (diploidization). These species have an interesting repertoire of repetitive elements, heterochromatic arrays, and remarkable phylogeographic history.
- D. Differences in mating systems and ploidy
- E. Uncover the basis of physiological adaptations (edaphic, stress) of “extremophile” species/”extreme” traits of heavy metal hypertolerance and Hyperaccumulation.
BMAP – Yokohama and Wuhan (June 2010)

- Arabidopsis 2010 Meeting Workshop, Japan
  - Enthusiastic
  - Too ambitious

- Wuhan, Huazhong Agricultural University
  - Emphasis on crop genome sequencing and quality
  - Need for translational tools to empower breeders to develop next generation *Brassica* cultivars
  - Cloud Computing
Brassicaceae Map Alignment Project (BMAP)

Summary
These pages have been set up to hold information (including notes from meetings, a list of target species etc.) for the Brassicaceae Map Alignment Project (BMAP). BMAP is analogous to a similar initiative that has been established for Oryza (OMAP).

Relevant information is currently being collated and will be made available as soon as possible.

Aims

Meetings
- San Diego, Jan 2010
- Tubingen, March 2010
- Yokohama, June 2010
- Saskatoon, Sept 2010

List and status of target species to be sequenced
- Draft list of 150 species, April 2010

Coordinator and contacts
- Rod Wing, University of Arizona, Arizona Genomics Institute
- Chris Fries, University of Missouri
- Detlef Weigel, Max Planck Institute, Tubingen

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BMAP Future Plans

• Complete white paper draft and post for comments >>> Submit for Publication
• Continue to identify additional partners
• Hold next BMAP Workshop at PAG, San Diego
• Hold BMAP Workshops at annual Brassica/Crucifer Meetings – Prague, CZ
Now we have a genome sequence –
What do we do with it?
What’s next?
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