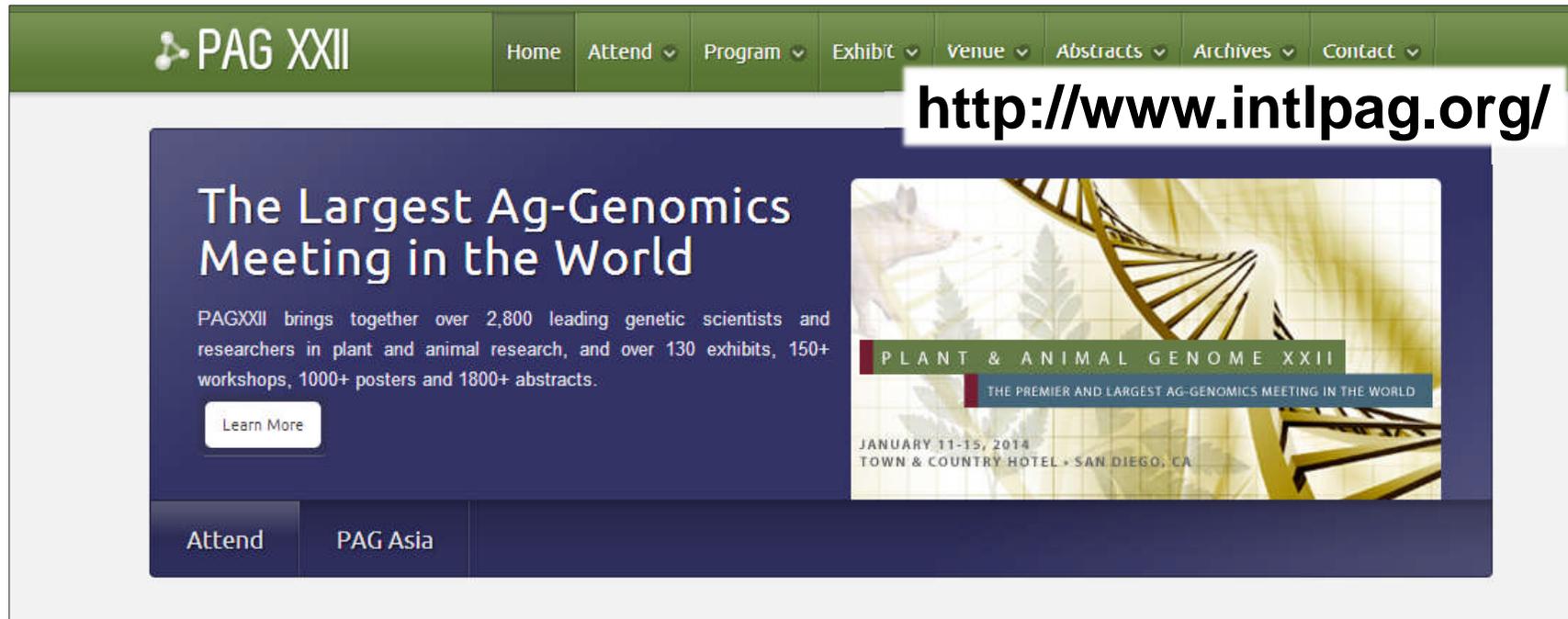


17:55-18:10 Collaboration and communication in *Brassica* genomics

- | | |
|----------------------|--|
| Ian Bancroft | Brassica workshop at Plant and Animal Genome, San Diego |
| Jacqui Batley | Brassica workshop at Plant and Animal Genome, Asia |
| Chris Pires | Brassicaceae Map Alignment Project (BMAP) |
| Rod Snowdon | Multinational Brassica Genome Project (MBGP) |
| Graham King | Brassica.info |

Brassica workshop at Plant and Animal Genome, San Diego



The screenshot shows the homepage of the Plant and Animal Genome XXII conference website. The top navigation bar is green and contains the logo 'PAG XXII' on the left and a menu of links: Home, Attend, Program, Exhibit, Venue, Abstracts, Archives, and Contact. A white box with a black border is overlaid on the top right of the page, containing the URL <http://www.intlpag.org/>. The main content area has a dark blue background. On the left, the text reads 'The Largest Ag-Genomics Meeting in the World' followed by a paragraph describing the conference's scale and a 'Learn More' button. On the right, there is a graphic featuring a DNA double helix, a pig, and a plant leaf. Below the graphic, the text reads 'PLANT & ANIMAL GENOME XXII', 'THE PREMIER AND LARGEST AG-GENOMICS MEETING IN THE WORLD', and 'JANUARY 11-15, 2014 TOWN & COUNTRY HOTEL • SAN DIEGO, CA'. At the bottom of the page, there are two buttons: 'Attend' and 'PAG Asia'.

PAG XXII

Home Attend Program Exhibit Venue Abstracts Archives Contact

<http://www.intlpag.org/>

The Largest Ag-Genomics Meeting in the World

PAGXXII brings together over 2,800 leading genetic scientists and researchers in plant and animal research, and over 130 exhibits, 150+ workshops, 1000+ posters and 1800+ abstracts.

[Learn More](#)

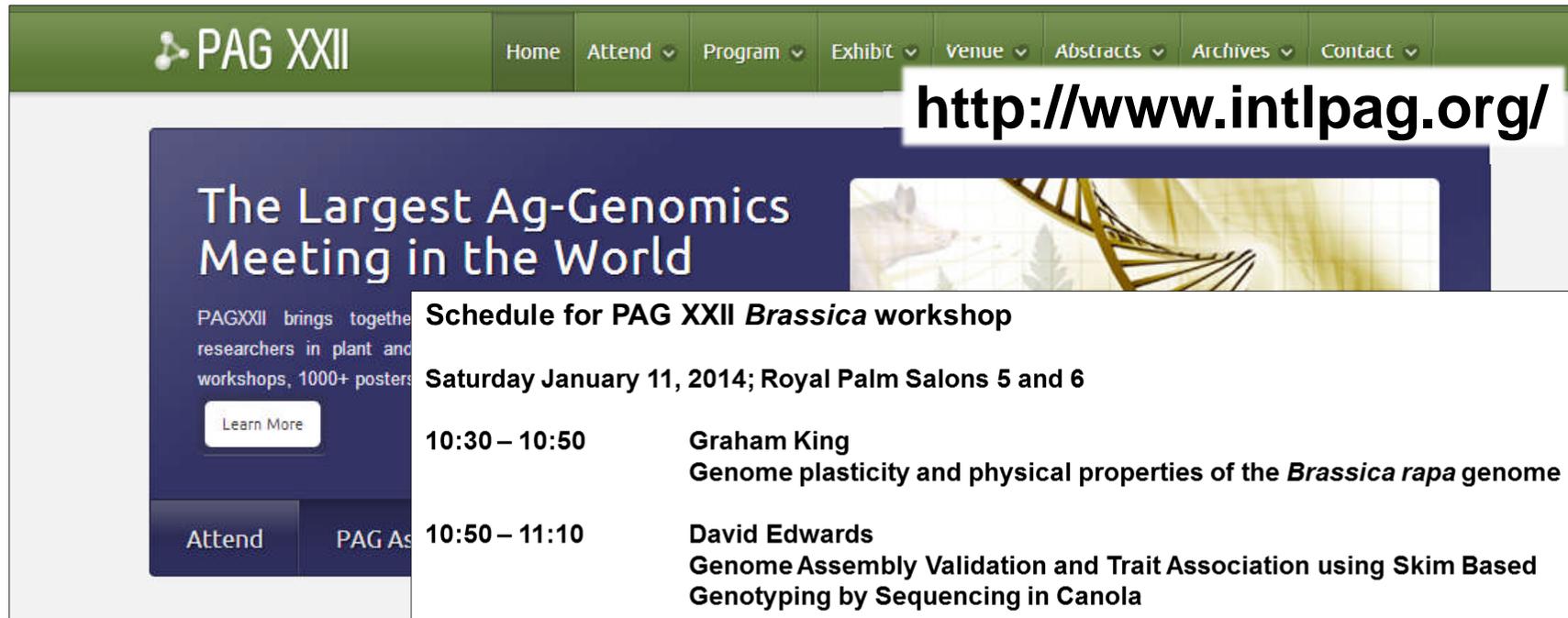
PLANT & ANIMAL GENOME XXII

THE PREMIER AND LARGEST AG-GENOMICS MEETING IN THE WORLD

JANUARY 11-15, 2014
TOWN & COUNTRY HOTEL • SAN DIEGO, CA

Attend PAG Asia

Brassica workshop at Plant and Animal Genome, San Diego



The screenshot shows the PAG XXII website with a navigation menu (Home, Attend, Program, Exhibit, Venue, Abstracts, Archives, Contact) and a main banner for "The Largest Ag-Genomics Meeting in the World". A white box highlights the URL <http://www.intlpag.org/>. Below the banner, a section titled "Schedule for PAG XXII Brassica workshop" lists the following events:

Schedule for PAG XXII Brassica workshop
Saturday January 11, 2014; Royal Palm Salons 5 and 6

10:30 – 10:50	Graham King Genome plasticity and physical properties of the <i>Brassica rapa</i> genome
10:50 – 11:10	David Edwards Genome Assembly Validation and Trait Association using Skim Based Genotyping by Sequencing in Canola
11:10 – 11:30	Margaret Woodhouse <i>Brassica rapa</i> as a model system for studying heritable genome dominance
11:30 – 11:50	Mathieu Blanchette An atlas of over 90,000 conserved noncoding sequences provides insight into crucifer regulatory regions
11:50 – 12:10	Kim Osman Proteomic Analysis of Chromosome Axis-Associated Proteins from Brassica oleracea and Arabidopsis thaliana Provides Insights into Meiotic Recombination
12:10 – 12:30	Rachel Wells Induced genetic variation for rapeseed oil desaturation
12:30	Community announcements <ul style="list-style-type: none">• Update on Brassica.info (Graham King)

Brassica workshop at Plant and Animal Genome, San Diego



The screenshot shows the PAG XXII website with a navigation menu (Home, Attend, Program, Exhibit, Venue, Abstracts, Archives, Contact) and a main banner that reads "The Largest Ag-Genomics Meeting in the World". A white box highlights the URL <http://www.intlpag.org/>. Below the banner, a section titled "Schedule for PAG XXII Brassica workshop" specifies the date and location: "Saturday January 11, 2014; Royal Palm Salons 5 and 6".

PAG-XXIII January 10-14, 2015

Brassica workshop: Saturday January 10, 2015 (provisional)

Potential speakers contact: Chris Pires or Ian Bancroft

Brassica rapa genome
ng Skim Based
e genome dominance

	An atlas of over 90,000 conserved noncoding sequences provides insight into crucifer regulatory regions
11:50 – 12:10	Kim Osman Proteomic Analysis of Chromosome Axis-Associated Proteins from <i>Brassica oleracea</i> and <i>Arabidopsis thaliana</i> Provides Insights into Meiotic Recombination
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PAG ASIA 2014

Home Attend Program Exhibit Abstracts 2013 Archives Contact

We hope you will

Join Us and Attend

PAG ASIA in Singapore.

Plan to Attend Scientific Program Tabletop Exhibits Sponsorship Opportunities

GRAND COPTHORNE WATERFRONT HOTEL
MAY 19-21, 2014
SINGAPORE

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Registration Workshops Plenary Speakers

Proposed 2014 Workshop Topics

Content to include subjects of regional importance, such as:

- ▶ Agrobacterium Mediated Plant Genetic Transformation
- ▶ Brassica & Finding Function in Crop Genomes
- ▶ Buffalo
- ▶ Cattle
- ▶ Fruit
- ▶ Genome Annotation Resources at the EBI
- ▶ Heavy Metals
- ▶ International Rice Informatics Consortium
- ▶ Int'l Wheat Genome Sequencing (IWGSC)
- ▶ Poultry
- ▶ Rice
- ▶ Shrimp Epigenomics
- ▶ Swine
- ▶ Tissue Culture & Double Haploids



PAG ASIA 2014

Home Attend Program Exhibit Abstracts 2013 Archives Contact

We hope you will

Join Us and Attend

PAG ASIA in Singapore.

Plan to Attend Scientific Program Tabletop Exhibits Sponsorship Opportunities

GRAND COPTHORNE WATERFRONT HOTEL
MAY 19-21, 2014
SINGAPORE

Registration Workshops Plenary Speakers

2013

> 360 participants
from 24 countries

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- ▶ Rice
- ▶ Shrimp Epigenomics
- ▶ Swine
- ▶ Tissue Culture & Double Haploids



Brassica

Date: Sunday, March 17, 2013

Time: 1:00 PM-3:00 PM

Room: Grand Ballroom 2

Organizer: *Jacqueline Batley*

Co-Chair: *David Edwards*

- 1:00 PM **W020** Improving Genome Assemblies and Trait Association using Illumina Skim Genotyping by Sequencing
Philipp Emanuel Bayer, University of Queensland; Kenneth Chan, University of Queensland; Michał A. T. Lorenc, University of Queensland; Kaitao Lai, University of Queensland; Sahana Manoli, University of Queensland; Pradeep Ruperao, University of Queensland; Paul Visendi, University of Queensland; Agnieszka Golicz, University of Queensland; Paula Martinez, University of Queensland; Alice C Hayward, University of Queensland; Jessica Dalton-Morgan, University of Queensland; Satomi Hayashi, University of Queensland; Jacqueline Batley, University of Queensland; David Edwards, University of Queensland
- 1:20 PM **W021** Genomic Regulation of Seed Development in Brassica
Graham J King, *Southern Cross Plant Science, Southern Cross University; Justin Bloomfield, Southern Cross Plant Science, Southern Cross University; Terry J Rose, Southern Cross Plant Science, Southern Cross University; Smita Kurup, Plant Biology and Crop Science, Rothamsted Research; Jun Wang, Centre for Molecular Oncology, The Cancer Institute; Clare Hopkins, Department of Pathology, The University of Melbourne; Rod Scott, University of Bath; Andrew Stoute, West In Sugar Cane Breeding Station*
- 1:40 PM **W022** Comparative Analysis of A, B and C Subgenomes of *Brassica* Species Revealed the Structural and Functional Conservation of Morphological and Yield Component Traits
Yong Pyo Lim, *Chungnam National University*
- 1:40 PM **W022** Comparative Analysis of A, B and C Subgenomes of *Brassica* Species Using the Infinium 60K SNP Chip
Annaliese S. Mason, University of Queensland; Alice C Hayward, University of Queensland; Sheng Chen, The University of Western Australia; Wallace A. Cowling, The University of Western Australia; Jacqueline Batley, University of Queensland; Matthew N. Nelson, The University of Western Australia
- 2:00 PM **W023** Exploring Chromosome Interactions in Higher Ploidy Brassica Populations Using the Infinium 60K SNP Chip
Annaliese S. Mason, University of Queensland; Alice C Hayward, University of Queensland; Sheng Chen, The University of Western Australia; Wallace A. Cowling, The University of Western Australia; Jacqueline Batley, University of Queensland; Matthew N. Nelson, The University of Western Australia
- 2:20 PM **W024** Detection and Genotyping of Restriction Fragment Associated Polymorphisms in Allotetraploid *Brassica napus*
Kede Liu, *Huazhong Agricultural University*
- 2:40 PM **W025** Investigating Roles for Nodulation-Like Genes in the Non-Nodulating Brassicaceae
Alice C Hayward, *University of Queensland*
- 3:00 PM **W026** Repeat Polyploidization with a New Nuclear Partner Genome can Result in Very Significant Genomic and Morphological Changes in Brassica Digenomics
Surinder Banga, *Punjab Agricultural University*

PDF file

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1:20 PM **W021** Genomic Re
Graham J K
University of J
Cross Univ.
Cross Univ.
Rothamsted
Cancer Insti
of Melbourn
Sugar Cane

1:40 PM **W022** Comparative

For opportunities to present in the Brassica workshop at PAG Asia 2014 please contact Jacqui Batley (j.batley@uq.edu.au) Dave Edwards (dave.edwards@uq.edu.au)

Brassica Species
1 of Morphological

Brassica Populations

C Hayward,
ity of Western
tern Australia;

Jacqueline Batley, University of Queensland; Matthew N. Nelson, The University of Western Australia

PDF file

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Surinder Banga, Punjab Agricultural University

Brassicales Map Alignment Project (BMAP)

Long-term Goals

The long-term goal is to develop a comparative genomics (and systems biology) research platform that can be used to

- (1) ask fundamental questions in plant biology, and to
- (2) provide essential baseline knowledge for addressing the food and bio-energy needs of our planet for generations.

The Brassicaceae is the obvious clade for this framework:

- Many important food & biofuel crops, and weed species
- Many novel traits and chemistries important to human health and crop improvement
- Relatively small genomes sizes
- Insight into karyotype evolution & chromosome dynamics
- Strong and vibrant *Arabidopsis* and *Brassica* research communities with potential to bridge comparative genomics to comparative systems biology

BMAP Long-term Vision

We think that having high quality “platinum standard” reference genomes is a critical step toward understanding the biology of any important and keystone plant group.

After the initial 20 high quality reference genomes in Brassicales, we want the global community to generate ~150 reference genome sequences (not gene-space assemblies) that can be used as a foundational research base upon which layers and layers of additional data can be added; for example: transcriptomes, proteomes, epigenomes, metabolomes, etc., along with genetic information.

The Top 20 Brassicales – Genomes & Transcriptomes

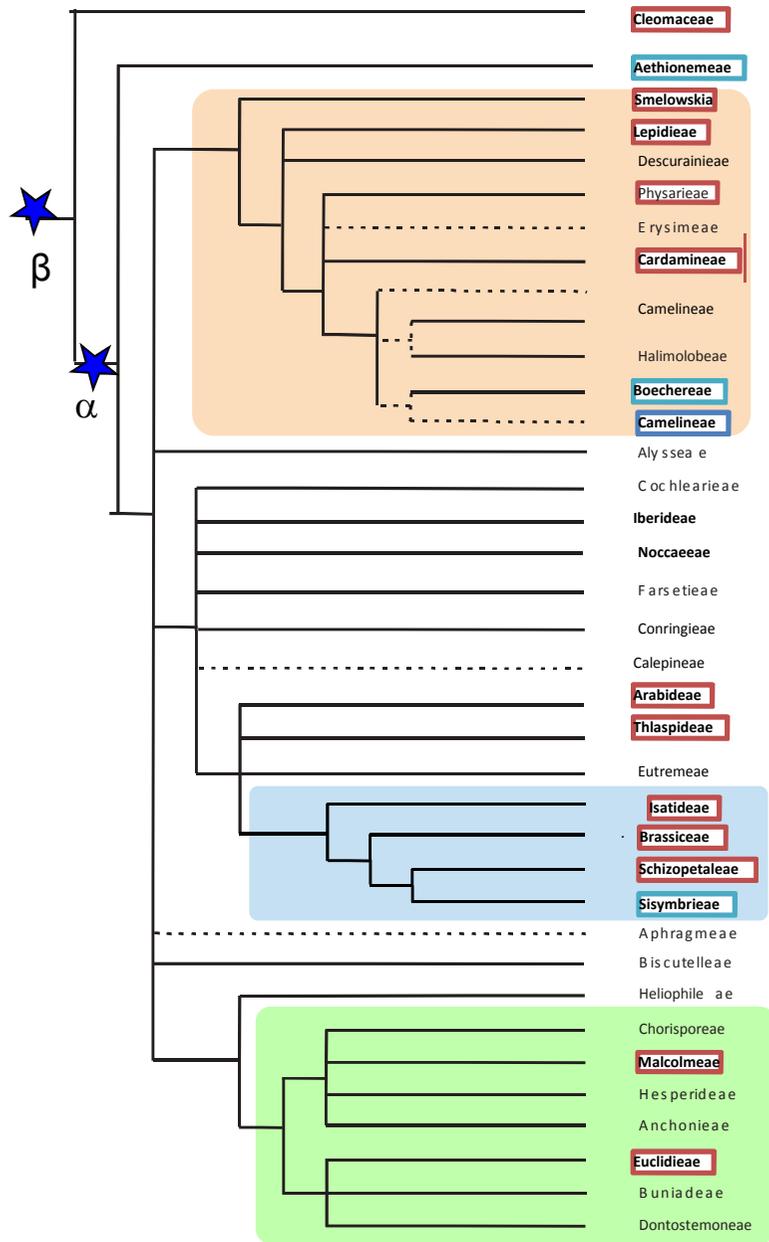
Community Sequencing Program: **Project Proposal**

**Proposer's Name: Rod A. Wing, Tom Mitchell-Olds, J. Chris Pires,
M. Eric Schranz, Detlef Weigel, Stephen Wright**

**Project Title: Empowering functional plant genomics with genomes and
transcriptomes of the Top 20 Brassicales**

Proposal ID: 652

BMAP: TOP20 Brassicales Proposed



Lineage I



Lineage II



Lineage III



Lineage I (3 species):

- *Descurainia sophiodes* (200Mb)
- *Lepidium campestre* (250Mb)
- *Rorippa islandica* (280Mb)

Lineage II (9 species):

- *Myagrum perfoliatum* (325Mb)
- *Caulanthus amplexicaulis* (372Mb)
- *Thlaspi arvense* (560Mb)
- *Crambe hispanica* (580Mb)
- *Cakile maritima* (730Mb)
- *Eruca vesicaria* (740Mb)
- *Sinapis alba* (800? Mb)
- *Stanleya pinnata* (? Mb)
- *Isatis tinctoria* (? Mb)

Lineage III and "Basal" lineages (6 species):

- *Euclidium syriacum* (260Mb)
- *Diptychocarpus strictus* (300Mb)
- *Malcolmia maritima* (310Mb)
- *Alyssum linifolium* (300Mb)
- *Lunaria annua* (490 Mb)
- *Iberis amara* (800 Mb)

Outgroups (2 species):

- *Cleome violacea* (525Mb) Cleomaceae
- *Ochradenus battatus* (400 Mb) Resedaceae

Comparative Genomics in the Brassicaceae



Haudry et al. 2013. *Nature Genetics* 45: 891-900. An atlas of over 90,000 conserved noncoding sequences provides insight into crucifer regulatory regions. Placed At-alpha and At-beta WGD between Aethionem and papaya, and two WGT (Brassica and Leavenworthia)

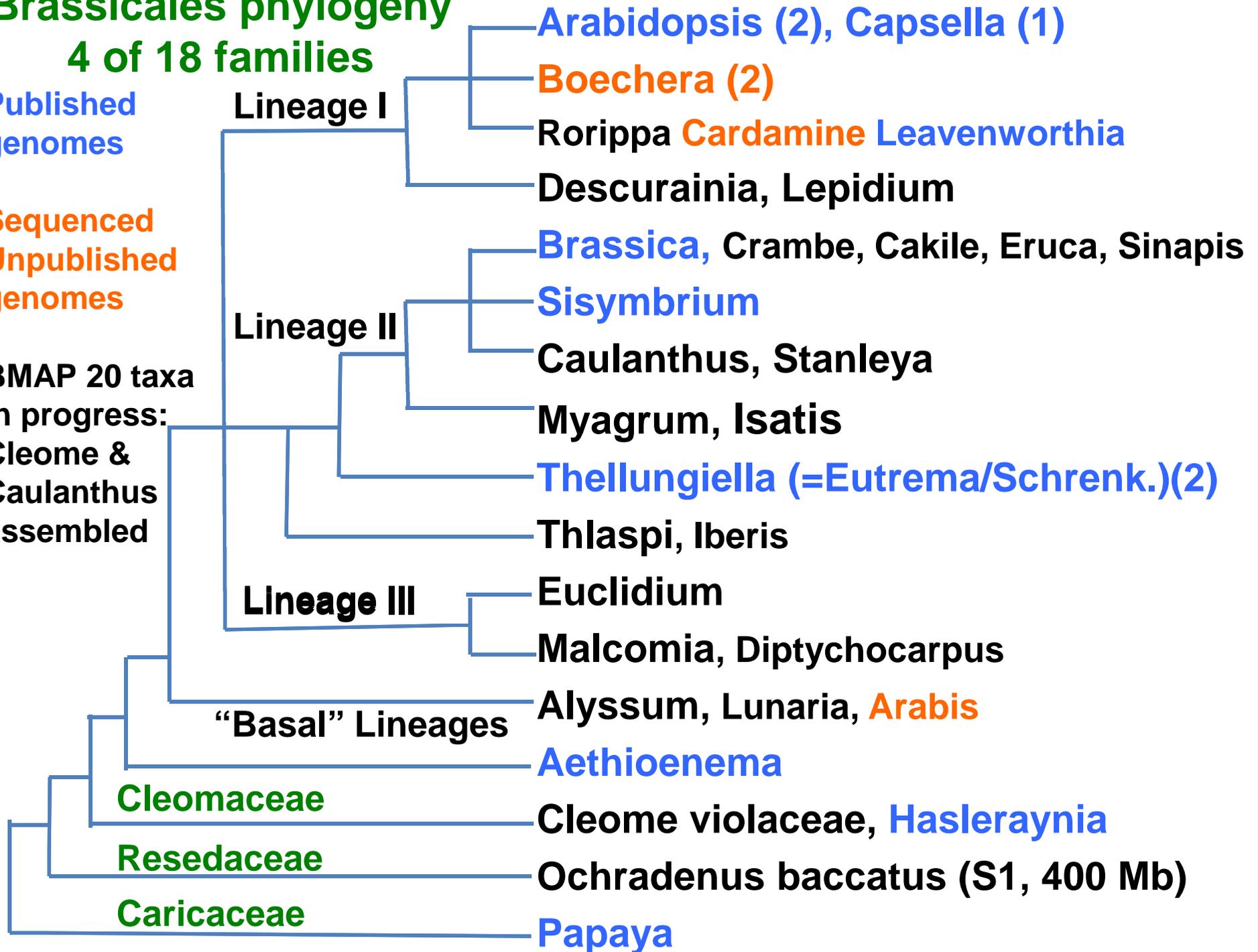
Brassicales phylogeny

4 of 18 families

Published
genomes

Sequenced
Unpublished
genomes

BMAP 20 taxa
In progress:
Cleome &
Caulanthus
assembled



Advantages of creating comparative genomic (and systems biology) research platforms

- 1) All questions can be addressed in a phylogenetic context (e.g. phylogenomics; paleo-genomics; construct ancestral genomes and networks).
- 2) Evolutionary process can be explored at whole genome levels (structure).
 - What are the evolutionary consequences of whole genome duplication?
 - What factors govern genome and chromosome evolution?
- 3) Patterns of conservation and divergence can be elucidated (which will lead to understanding of selective constraints & targets of positive selection).
 - How much noncoding DNA is subject to selective constraints, and what is the functional importance of noncoding regions?
 - What gene/noncoding sequences have been targets of diversifying selection, and what is the biological basis
- 4) Aid in the development of more complex evolutionary models to further our understanding of genome-scale evolutionary processes.
 - What are the genomic consequences of mating system evolution
 - What is the basis of morphological variation; chemical variation, heterosis

BMAP Acknowledgements

- **PIs: Rod Wing, J. Chris Pires, Detlef Weigel, Stephen Wright, M. Eric Schranz and Tom Mitchell-Olds**
- **VEGI team (Tom Bureau, Mathieu Blanchette, Adrian Platts, and others)**
- **Graham King (brassica.info)**
- **DOE JGI – Community Sequencing Program (Jeremy Schmutz, Kerrie Barry, and others)**
- **All who attended prior BMAP meetings & you!**

Multinational Brassica Genome Project (MBGP)

Steering committee established in 2002 with a remit to coordinate and promote collaborative, international Brassica genome research

Current chair: Rod Snowdon (rod.snowdon@uni-giessen.de)

Annual meetings at PAG (San Diego), additional meetings or updates at Crucifer Genetics Workshops

Active involvement of interested scientists from all continents

Overall aim:

Development of genomic resources and tools for the Brassica research community

Initial goals:

- Genetic anchoring of BAC-based physical maps
- Sequencing of the Brassica A genome by an international consortium



Multinational Brassica Genome Project (MBGP)

Major Achievements

2002 – 2007:

- www.brassica.info website
- BAC libraries and physical (BAC) contig maps
- public EST collections
- Collation of public-domain SSR markers
- Development and distribution of public diversity collections for Bra, Bol, Bna
- Collation of genetic maps and mapping populations

2008: Standardisation of nomenclature (e.g. linkage groups, genes)

2010: Affymetrix GeneChip Brassica Exon 1.0 ST Array

2011: Publication of the *Brassica rapa* genome (BrGSP steering committee merged with MBGP in 2010)

2012: Illumina Infinium 50k SNP array

Multinational Brassica Genome Project (MBGP)

Ongoing activities/challenges

- Establishing community standards for consistent annotation and data exchange within/between Brassica genomes
- Integration of genetic and genomic maps: from QTL to genes: New opportunities for consensus mapping and data integration via 50k SNP and/or GBS data?
- Distribution and screening of genetic diversity collections and sharing of corresponding genotype/phenotype data



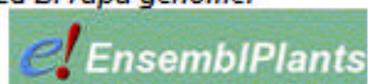
HOME >

Sharing information worldwide for: The Multinational Brassica Genome Project (MBGP)

Welcome

This site collates and exchanges open source information relating to Brassica genomics and genetics, on behalf of the MBGP. The site contains registries of reference datasets and nomenclature standards, and searchable access to relevant databases. This includes a comprehensive compilation of ongoing public domain genome sequencing. In addition, a number of publications are made available exclusively from this site. We also host information for BMAP, the Brassicales Map Alignment Project.

Annotated *B. rapa* genome:



(*B. rapa* genome at EBI Ensembl Plants[†])

BRAD - *B. rapa* Database[†]

(Maintained at IAF-CAAS[†])

Annotated *B. oleracea* genome:



(*B. oleracea* genome at OGI[†])

Additional information and data:



(maintained at Rothamsted Research[†])

Brassica Genome Gateway[†]

(maintained at John Innes Center[†])

latest news

[Minutes of MBGP SC Jan 2014](#)

[3rd International Glucosinolates Conference,](#)

Oct 12-14, Wageningen

(call for abstracts March 2014)

[Brassica.info has moved downunder](#)

next event

[19th Crucifer Genetics Workshop, Wuhan](#)

30th March - 2nd April 2014

[show all event items](#)

site guide

The site is grouped into the following three sections:

RESEARCH - the world of Brassica research and who is involved.

RESOURCES - for research related tools and resources.

INFORMATION - more general information about the MBGP and brassicas in general.

Please use our interactive dropdown menus, the slide menus, or the link tracker to navigate the site.

—see [site-map](#) for overview

[†] indicates external links (we can not be held responsible for the content of external sites)

Google Search

WWW SITE

31,140 Visitors

26 Sep 2010 - 24 Feb 2014



ClustrMaps[®]

Click to see

Maps archived annually, for previous maps click here.

2002 - 2004	HRI Wellesbourne
2004 - 2005	U. Warwick
2005 - 2013	Rothamsted Research
2014 -	Southern Cross University, Australia

- Collates open source information relating to *Brassica* genomics, genetics, and trait biology on behalf of the **Multinational Brassica Genome Project**.
- Contains registries of **reference datasets** and **nomenclature standards**, and searchable access to relevant **databases**.
- **CropStoreDB** will continue to be developed and maintained for *Brassica*, with initial funding from Australian federal RDSI.
- Compilation of ongoing public domain **genome sequencing**.
- A number of **publications** available exclusively from this site.
- Hosts information for BMAP: the **Brassicales Map Alignment Project**.

Please send links, updates, content to graham.king@scu.edu.au



brassica.info

RESEARCH

RESOURCES

INFORMATION



~10,000 visitors per year

Mailing list: >550 members

<http://www.brassica.info/info/mailing.php>