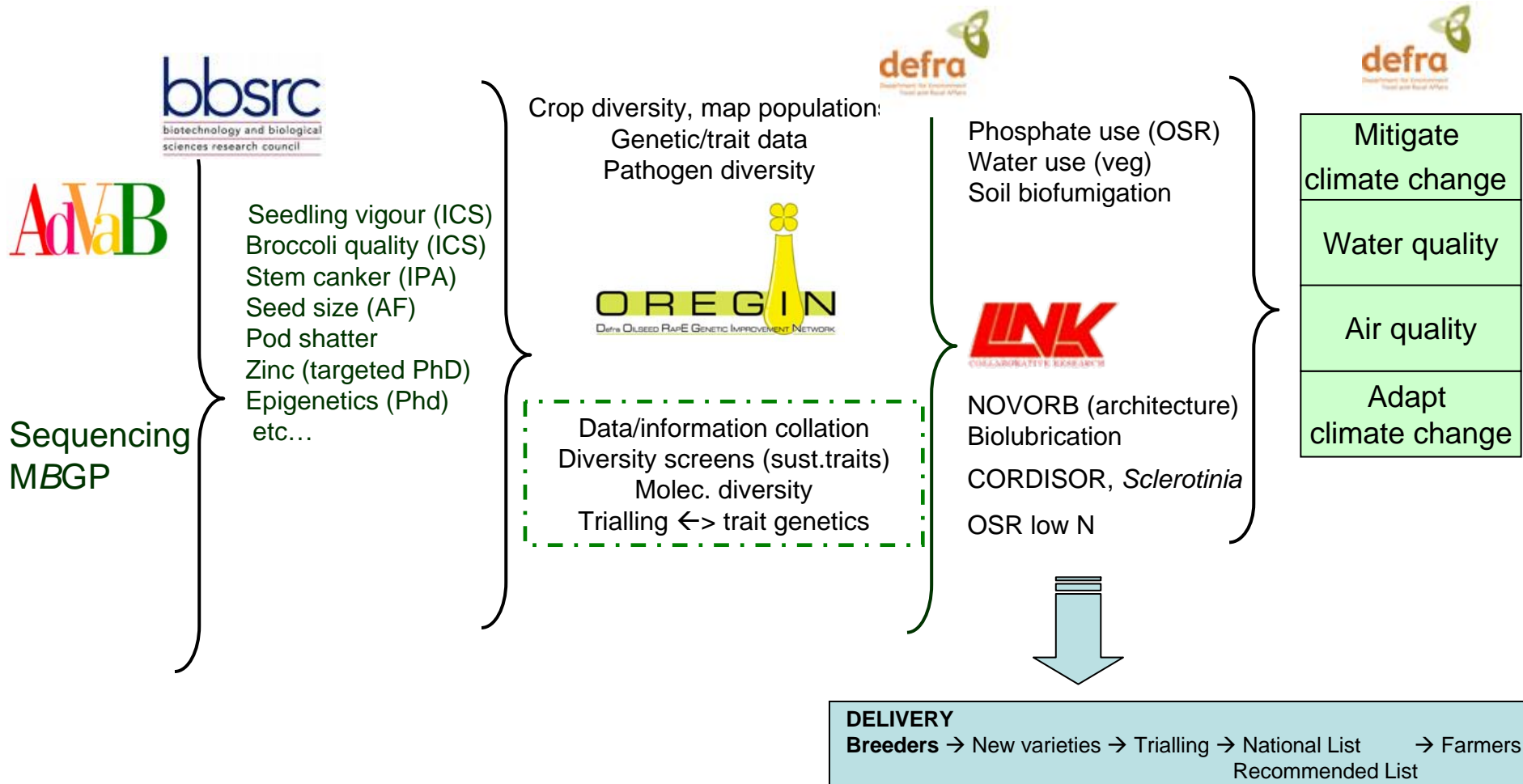


“Joined-up” *Brassica* Crop Science

– filling gaps in the pre-breeding pipeline





Genetic Improvement Networks

Rationale: Sustainable agriculture + market failure in breeding

- Reducing resource inputs – N, water, pesticides
- Reducing pollution
- Addressing Climate change
- Product diversification





<http://www.oregin.info/>

The Defra Oilseed RapE Genetic Improvement Network

Search site:

OREGIN

Part of the Defra Crop Genetic Improvement Networks

Initiated and supported by the Department for Environment, Food and Rural Affairs


Home | Research Activities | Resources | Stakeholders | Admin Login

Welcome To OREGIN

The Defra funded Oilseed Rape Genetic Improvement Network

Use the tabs at the top of this area to navigate around the site:

- Home - What is OREGIN, project outline, news, contact details and information on the other Defra crop genetic improvement networks
- Research activities - An overview of the project and detail of the six workpackages
- Resources - Databases, standard operating procedures, information, relevant links, images and more
- Stakeholders - Who are the OREGIN stakeholders, details of future and past meetings
- Admin login - a password protected area for the OREGIN management team



The OREGIN field experiment, Rothamsted, June, 2004

Site Map (not yet available) | Hosted by Rothamsted Research | Last updated: Tuesday, 16 November, 2004
 Maintained by Neal Evans and Graham King | © Rothamsted Research Limited 2003-2004

Website search technology courtesy of FreeFind

- Engage with Stakeholders
- Conduit for basic science to crop improvement
- Public domain core resources
 - Diversity sets (Plant, Pathogen)
 - TN population
- Information sharing

Phase I (2004-8)



- OREGIN has increasing visibility on national and international stage - perceived as a success
- Clear objectives, delivered within the 4-5 year timescale

Stakeholder Forum and Network has been developing
- farmers, advisors, breeders, processors, end-users

Focused originally on **trait prioritisation**
- ongoing review responds to changing priorities

Responding to increases in crop areas

Increased **awareness** of Nitrogen use, Carbon accounting

Effects of policy shifts on crop selection environment - now a greater connectivity of commercial activity and policy

→ *next*: trialling under low inputs ??



Development of associated LINK Projects

- 1. Components of **Resistance to Diseases** in Winter Oilseed Rape
- 2. Novel Resources for Oilseed Rape Breeding – **Harvest Index**
- 3. Breeding Oilseed Rape with a **Low Requirement for Fertilizer Nitrogen.**
- 4. Reducing the **Carbon Footprint of the Lubricants Industry** by the Substitution of Mineral Oil with Rapeseed Oil.
- 5. Understanding **sclerotinia epidemics** on oilseed rape



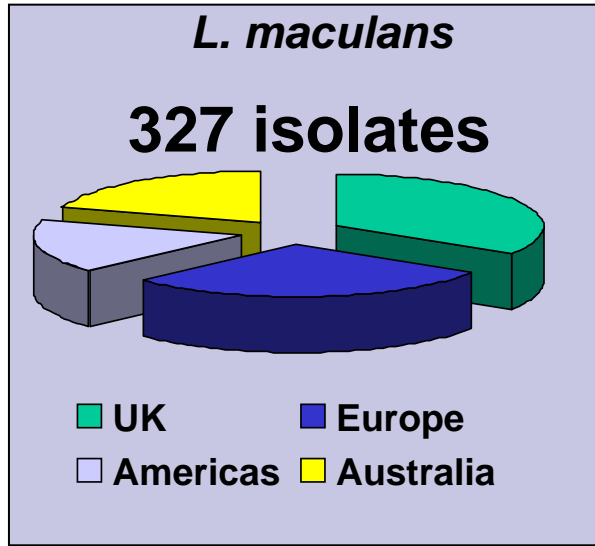
Plant resources becoming available:

***B. napus* Diversity Fixed Foundation Set (188)**

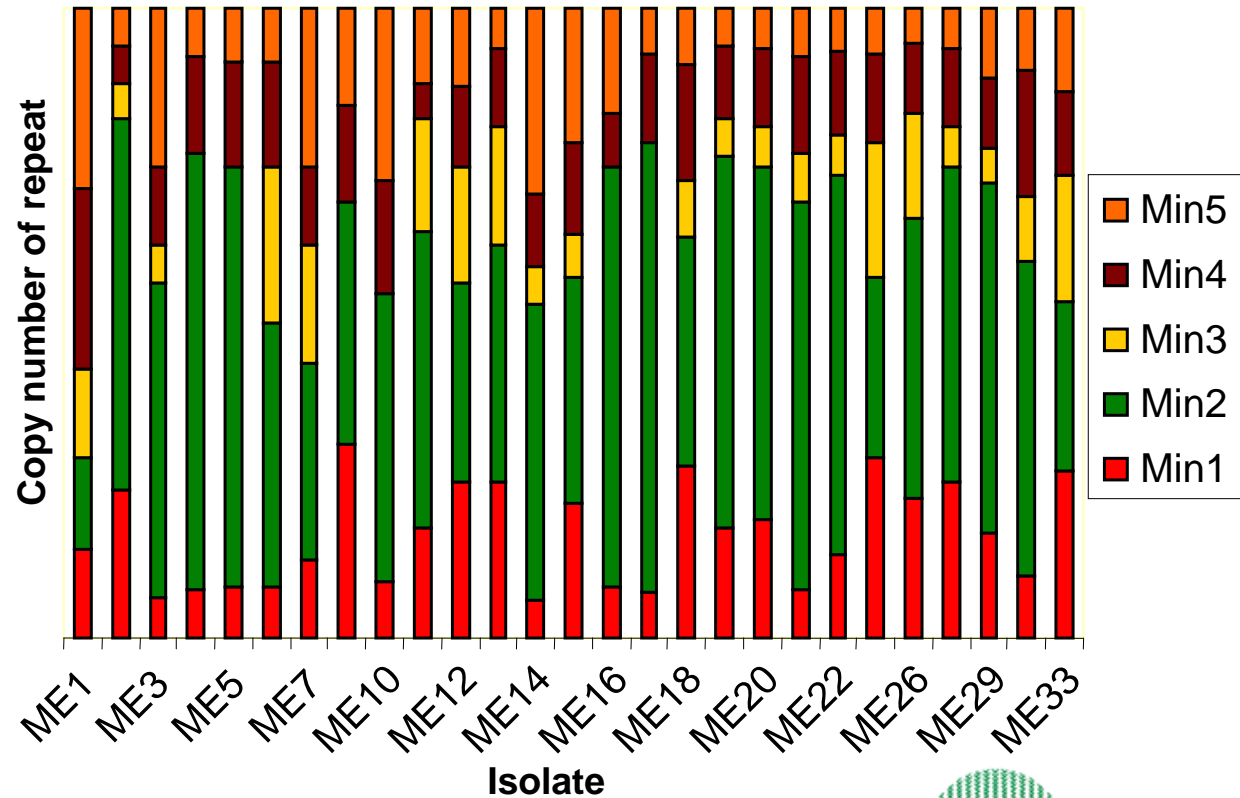


- Public Domain
- Founder plants established
- DNA extracted (+ Genomiphi)
- Seed and DNA available
- Fixing to DH (ongoing)
- Collating molecular and trait data

Investigating global diversity in *L. maculans* populations



DNA fingerprinting of *L. maculans* using minisatellites



With Thierry Rouxel



L. maculans genome sequence released by end 2005

Climate change and oilseed fungal diseases

OREGIN: Paper published on effects of global warming on Phoma stem canker epidemic - Windows Internet Explorer

http://www.oregin.info/index.php?area=home&page=dmchnpap

OREGIN: Paper published on effects of global warm...

Warwick HRI
Part of the Defra Crop Genetic Improvement Networks

OREGIN
defra
Initiated and supported by the Department for Environment, Food and Rural Affairs

Search site: find

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Home | Earth home | Earth news | Earth watch | Comment | Greener living | Earth Pulse | Science

Climate change puts trees and crop
Last Updated: 12:01pm BST 30/09/2007

Popular British trees, garden plants and farm crops will be left devastated as diseases spread around the country due to climate change, new research shows.

Plant experts fear that insect pests, fungi and other diseases that raze the UK will reach epidemic proportions over the next 50 years.

Home | Project Outline | Contacts | Feedback | Other Crop Genetic Improvement Networks

Home | Research Activities | Resources | Stakeholders | Admin Login

OREGIN-Funded Work On Possible Effects Of Climate Change On Phoma Stem Canker Epidemics Published In Royal Society Journal

Interface
FirstCite
J. R. Soc. Interface
doi:10.1098/rsif.2007.1136
Published online

Range and severity of a plant disease increased by global warming

Neal Evans^{1,2}, Andreas Bajer^{1,2}, Mikhail A. Semenov¹, Peter Gladders³ and Bruce D. L. Fitt¹

¹Rothamsted Research, Harpenden, Hertfordshire AL5 2JQ, UK
²Department of Statistics and Decision Support Systems, University of Vienna, Universitätsstrasse 5/9, 1010 Vienna, Austria
³ADAS Research, Ballgate Road, Barnworth, Cambridge CB3 9NN, UK

Climate change affects plants in natural and agricultural ecosystems throughout the world but little work has been done on the effects of climate change on plant disease epidemics. To illustrate such effects, a weather-based disease forecasting model was combined with a climate change model predicting UK temperature and rainfall under high- and low-carbon scenarios for the 2020s and 2050s. Microsite data collected over a 15-year period were used to develop and validate a weather-based model forecasting severity of phoma stem canker epidemics on oilseed rape across the UK. This was combined with climate change scenarios to predict that epidemics will not only increase in severity but also spread northwards by the 2020s. These results provide a stimulus to develop models to predict the effects of climate change on other plant diseases, especially in delicately balanced agricultural or natural ecosystems. Such predictions can be used to guide policy and practice in adapting to effects of climate change on food security and wildlife.

Keywords: climate change; *Leptosphaeria maculans*; phoma stem canker; plant disease epidemiology; weather-based disease forecasts

Printer Friendly Page

L. INTRODUCTION

Climate change is affecting plants in natural and agricultural ecosystems throughout the world (Stem 2007). However, little work has been done to model the effects of predicted twenty-first-century climate change on plant disease epidemics (Barrett et al. 2006). Changing weather (e.g. temperature, rainfall) can induce severe plant disease epidemics (Cookley et al. 1999; Chakraborty 2005), which threaten food security if they affect staple crops (Luo et al. 1995; Chakraborty et al. 2005; Anderson et al. 2006) and can damage landscapes if they affect amenity species (Hansen & Scott 1994; Bengt et al. 2004). Severity of human, animal and plant disease epidemics is greatly affected by climate factors: warmth, humidity and rainfall.

Much discussion on the impact of climate change on plant disease epidemics has used qualitative, rule-based reasoning, which cannot easily accommodate the complex host-pathogen-environment interactions involved (Cookley et al. 1999; Anderson et al. 2006). Modelling approaches have included those matching existing climates in one region with climates predicted for another (Bauer & Scott 1994) or combinations of simulation models for crop growth and disease development (Luo et al. 1995). Before 1999, no work had used predicted climate variables generated by now more sophisticated general circulation models (GCMs); most studies had relied on predictions of local changes in temperature and rainfall (Cookley et al. 1999). Recently, GCMs have been used to predict the increase in range of *Phytophthora*

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WebSTAT
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Light leaf spot forecasting in winter oilseed rape

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Predicted light leaf spot forecast

Updated 2006/07 | Preliminary 2007/08

Risk forecast
Epidemiology
Forecast explained
Historical risk
Recognizing its
Register
Project participants
Offline forecast
Phoma forecast

0.14 15.29 30.44 45.59 60+

Regional forecast for the percentage of crops with >25% affected plants. To advance to the crop specific interactive forecast, please [click here](#). To read a warning on the use of the 2007/08 light leaf spot forecast, please [click here](#).

A paper published in the Royal Society journal Interface on 15 August 2007 highlighted recent research that predicts that the range and severity of the plant disease phoma stem canker is increased by global warming.

A research team led by Rothamsted Research has used a weather-based model developed to

Start | Inboxes - Microsoft Outlook | OREGIN - Windows Inte... | OREGIN: Paper publis... | Microsoft PowerPoint - [...]

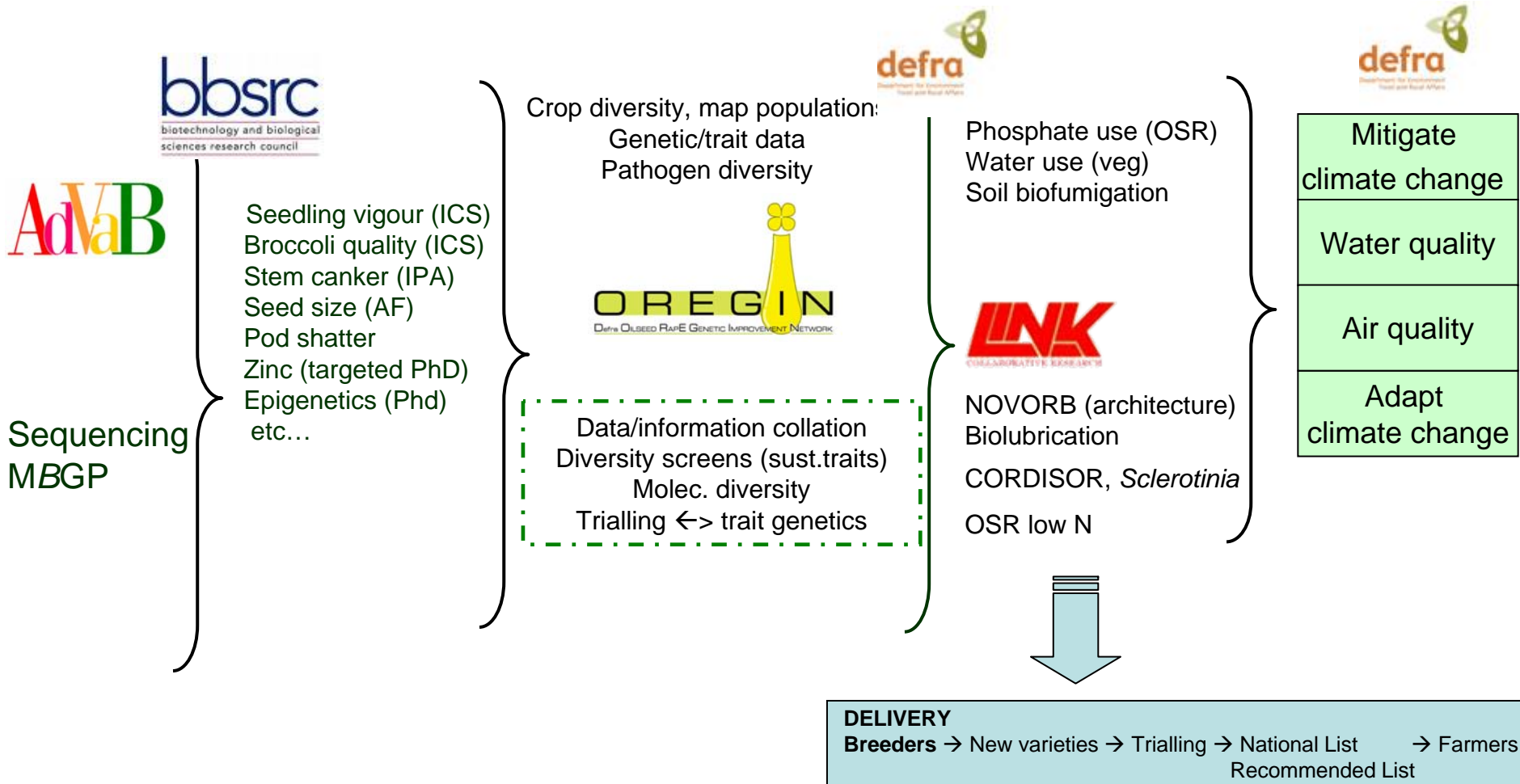
Local intranet | 100% | 10:05

Phase II (2008-13)

- 1. Maintain and develop OREGIN seed and pathogen **genetic resources**, and enable resolution and introgression of useful **variation**
- 2. Quantify and characterise **genetic variation** for key **traits**
- 3. Delivering the **pre-breeding toolkit**: provision of integrated information to maximise utilisation of genetic diversity

“Joined-up” *Brassica* Crop Science

– filling gaps in the pre-breeding pipeline





Adding Value to the UK Brassica Crop Science Community

Graham King
Pierre Carion
Jackie Barker
Clare Hopkins
Stephen Amoah

Lars Ostergaard
Judith Irwin
Penny Sparrow
Cassie Goldsack

Dave Pink
Graham Teakle
+





Adding Value to the UK Brassica Crop Science Community

Objective: 'Gap filling':

Forward genetics

Genetic map integration

Population availability

- reference mapping

- diversity sets

Data management

- incl. QTL collation

Reverse genetics

RNAi pipeline

B. rapa transformation

Induced variation (TILLING)

Functional validation



Dissemination



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genetic maps

[Linkage group assignments](#)

Brassica map collections

A registry of published and other reference versions of *Brassica* genetic linkage maps is being collated here. Below is a non-exhaustive list which will be refined during 2008 in conjunction with the international research community.

Species	Population (registry name)	Original name	Seed available	Data	Reference
<i>B. napus</i>	Bna61-9DH	61-9	-		Parkin et al, 1995; 2005; Lowe et al, 2004
<i>B. napus</i>	Bna72-8DH	72-8	-		Sharpe et al., 1995
<i>B. napus</i>	BnaMSDH	Major x Stellar	-		Osborn et al., 1994
<i>B. napus</i>	BnaDYDH	Danmor x Yudal (DY)	yes		Delourme et al.
<i>B. napus</i>	BnaTNDH	Tapidor x Ningyou7 (TN)	yes		Qiu et al, 2006; Suwabe et al. 2008
<i>B. napus</i>	BnaTVSL	Tapidor x Victor substitution lines	yes		Burns et al., 2003.
<i>B. napus</i>	BnaSGDH	SG	yes		-
<i>B. napus</i>	BnaEVDH	Mansholt's Hamburger Raps x Samouri	-		Ecke et al., 1995
<i>B. napus</i>	BnaMHSR	Express-V8	yes		Snowdon et al.
<i>B. rapa</i>	BraCKDH	Chilfu-401 x Kenshin-402	yes		Choi et al, 2007
<i>B. rapa</i>	BraCKRI	Chilfu-401 x Kenshin-402	?		-
<i>B. rapa</i>	BraJWF3	JWF3	-		Kim et al, 2006
<i>B. rapa</i>	BraAGP2		yes		Suwabe et al., 2003
<i>B. rapa</i>	BraRR1	IMB211 x R500	yes		Iniguez-Luy et al, In prep.
<i>B. rapa</i>	BraRRBC; BraRRF2	R-o-18 x R-o-50	-		Robinson, Jaroslav
<i>B. oleracea</i>	BolAGDH	A12DHd x GDDH33 DH	yes		Bohuon et al., 1996; Sebastien et al., 1999
<i>B. oleracea</i>	BolAGSL	A12DHd x GDDH33 substitution lines	yes		Ramsay et al., 1996; Rae et al., 1999.
<i>B. oleracea</i>	BolINGDH	CA25 x AC498	-		Sebastien et al., 1999
<i>B. oleracea</i>	BolTBDH		yes		Iniguez-Luy et al, In prep.

QTL registry

resources menu

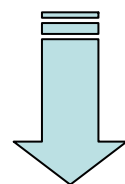
databases

[BrassicaDB](#) [↗](#)[CropStore](#)[Ensembl with Brassica](#)[tracks](#) [↗](#)[physical mapping \(UK\)](#)

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[microsatellite information](#)[exchange](#)[genome](#)[metabolomics](#)[plants](#)[proteomics](#)[sequencing project \(MBrSP\)](#)[status](#)[tools](#)[transcriptomics](#)

Seed
+
DNA



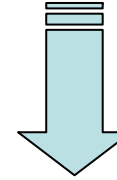
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linkage groups assignments

Summary

<i>B. nigra</i>	<i>B. juncea</i>	<i>B. oleracea</i>	<i>B. napus</i>	<i>B. rapa</i>	NIAB Korea original LG	NIAB Korea chromosome [*]	Suwabe et al. (NVITS) LG
A1 (J1)			A1 (N1)	A1 (R1)	LG10	Chr3	6
A2 (J2)			A2 (N2)	A2 (R2)	LG3	Chr6	8
A3 (J3)			A3 (N3)	A3 (R3)	LG1	Chr2	1
A4 (J4)			A4 (N4)	A4 (R4)	LG4	Chr8	10
A5 (J5)			A5 (N5)	A5 (R5)	LG7	Chr5	3
A6 (J6)			A6 (N6)	A6 (R6)	LG5	Chr4	2
A7 (J7)			A7 (N7)	A7 (R7)	LG6	Chr7	4
A8 (J8)			A8 (N8)	A8 (R8)	LG9	Chr9	7
A9 (J9)			A9 (N9)	A9 (R9)	LG2	Chr1	5
A10 (J10)			A10 (N10)	A10 (R10)	LG8	Chr10	9
		C1 (O1)	C1 (N11)				
		C2 (O2)	C2 (N12)				
		C3 (O3)	C3 (N13)				
		C4 (O4)	C4 (N14)				
		C5 (O5)	C5 (N15)				
		C6 (O6)	C6 (N16)				
		C7 (O7)	C7 (N17)				
		C8 (O8)	C8 (N18)				
		C9 (O9)	C9 (N19)				
B1	B1 (J11)						
B2	B2 (J12)						
B3	B3 (J13)						
B4	B4 (J14)						
B5	B5 (J15)						
B6	B6 (J16)						
B7	B7 (J17)						
B8	B8 (J17)						

Genetics – consensus integrated maps

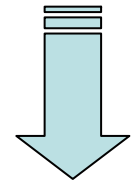
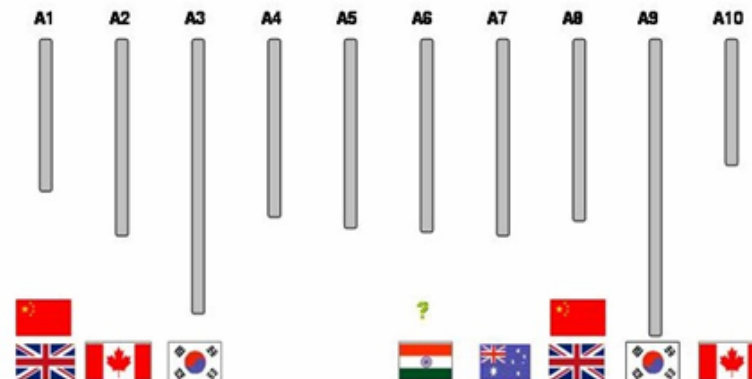


- SSRs added to key maps – ‘glue’
- Genome-ready
- navigate sequence to traits

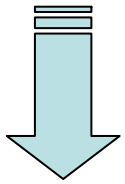
MBrSP: the *Brassica* 'A' genome sequencing project

Overview

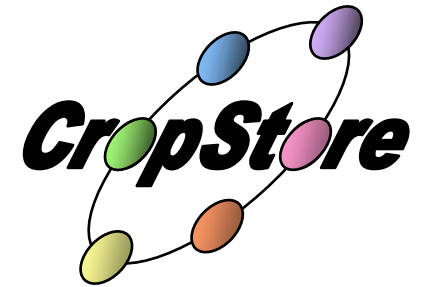
The Steering Committee for the MBGP selected *Brassica rapa* as the first species to be sequenced, as it has the smallest genome (ca. 550 Mb), the lowest frequencies of repetitive sequences and communal BAC libraries and mapping populations are available. Consequently, the *Brassica rapa* Genome Sequencing Project (BrGSP) was launched, based on the Chinese cabbage line Chiifu-401, and associated BAC library resources developed in Korea. The 'A' genome of *B. rapa* is also present in major oil crops of *B. napus* and *B. juncea*.



QTL registry



Data management and dissemination



- Provide **data curation pipeline**
- Develop **nomenclature standards**
- Establish MBGP – **registries** of information
- Disseminate for UK + international community



Focus:

- Populations
- Maps – consensus integrated (MBGP, with Derek Lydiate)
- QTL collation



- Maximise utility of
 - Multinational *Brassica A* genome Sequencing
 - + AC BAC-ends
 - + C genome (USA)



Commentary

Open Access

Standardized gene nomenclature for the Brassica genus

Lars Ostergaard  and Graham J King *Plant Methods* 2008, **4**:10 doi:10.1186/1746-4811-4-10

Published: 20 May 2008

Abstract (provisional)

The genus Brassica (Brassicaceae, Brassiceae) is closely related to the model plant Arabidopsis, and includes several important crop plants. Against the background of ongoing genome sequencing, and in line with efforts to standardize and simplify description of genetic entities, we propose a standard systematic gene nomenclature system for the Brassica genus. This is based upon concatenating abbreviated categories, where these are listed in descending order of significance from left to right (i.e. genus - species - genome - gene name - locus - allele). Indicative examples are provided, and the considerations and recommendations for use are discussed, including outlining the relationship with functionally well-characterized Arabidopsis orthologues. A Brassica Gene Registry has been established under the auspices of the Multinational Brassica Genome Project that will enable management of gene names within the research community, and includes provisional allocation of standard names to genes previously described in the literature or in sequence repositories. The proposed standardization of Brassica gene nomenclature has been distributed to editors of plant and genetics journals and curators of sequence repositories, so that it can be adopted universally.

Plant Methods

Volume 4

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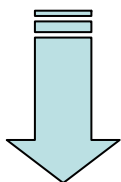
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gene nomenclature

Jan/Feb 2008:

A **standardised nomenclature** is currently being proposed (initiated by Lars Ostergaard, JIC, Norwich and Graham King, Rothamsted Research) for genes described within the *Brassica* genus, that enables distinction to be made between copies associated with the different haploid genomes, as well as at paralogous loci. This convention was discussed at the recent MBGP Steering Committee meeting, and is now open for wider consultation.

This proposed nomenclature system is dependent on support from the community, so your input and comments are of course crucial for the suggestion to be of any general use. We would therefore like to **invite you to give us feed back** on this proposal by e-mailing Lars Ostergaard **before 15th February**. We will then incorporate the comments into a manuscript and submit to a peer-reviewed journal. Subsequently the standardization will be circulated to editors of plant and genetics journals so it can be immediately implemented in the literature.

- a manuscript describing the nomenclature has now been submitted for publication (March 2008)
- [test page of proposed MBGP "Brassica Gene Registry"](#)
- for information - [Gene Class Symbol list for Arabidopsis \(TAIR\)](#)

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brassica crop & end-uses

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nutritional benefits

education & outreach

Carleton College lab [↗](#)

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MBGP meetings

mailing list

news

<GENUS 1 LETTER>[<species 2 letters>]<GENOME 1 LETTER>|<X>.<NAME 3-6 LETTER CODE>.<locus assignment 1 letter>

Test of Proposed MBGP "Brassica Gene Registry"
edited by Lars Ostergaard and Graham King, March 2008

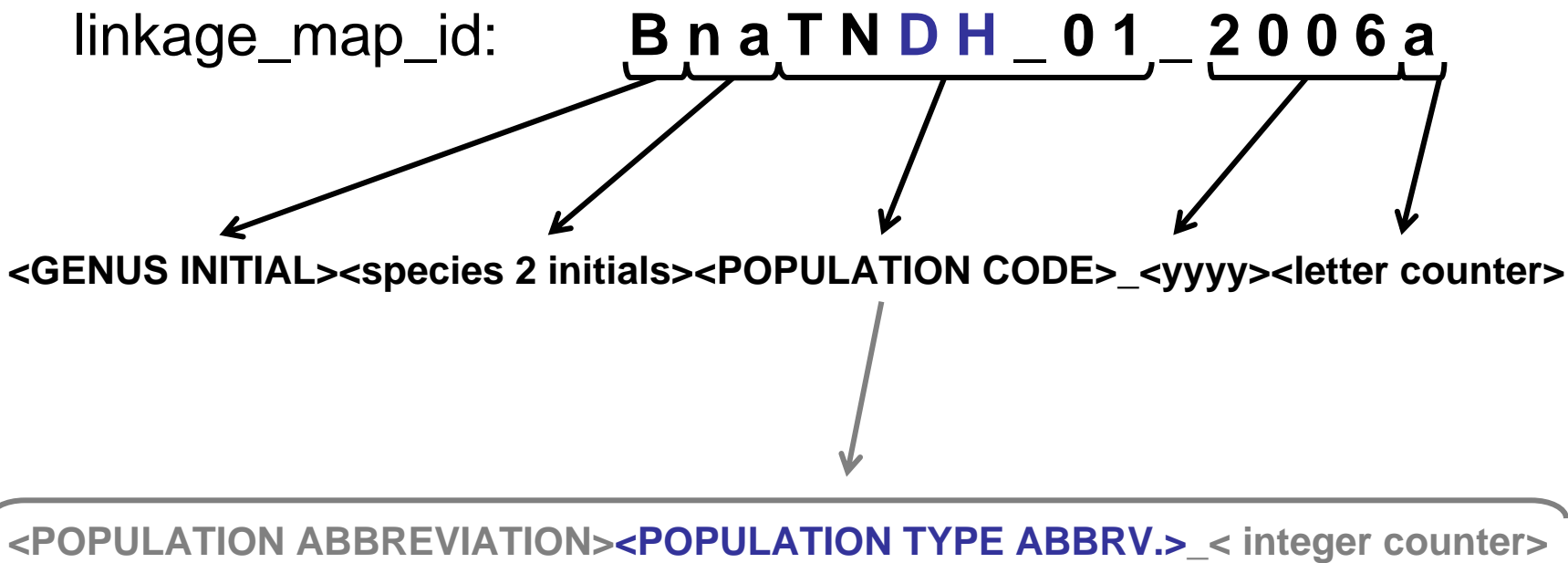
assigned gene name	Genbank accession	species	molecule	Genbank definition	Genbank seq. id	length	Genbank entrydate
<i>BcaX.6PGL.a</i>	AY030298	<i>carinata</i>	mRNA	Brassica carinata putative 6-phosphogluconolactonase (6PGL) mRNA, complete cds.	14009293	1072	08-MAY-2001
<i>BcaX.CIL1.a</i>	EF493830	<i>carinata</i>	mRNA	Brassica carinata CIL1 (CIL1) mRNA, complete cds.	14009294	1009	14-AUG-2007
<i>BcaX.CJAS1.a</i>	AY030296	<i>carinata</i>	mRNA	Brassica carinata defense-related protein (CJAS1) mRNA, complete cds.	14009289	1044	08-MAY-2001
<i>BcaX.CJS1.a</i>	AY030297	<i>carinata</i>	mRNA	Brassica carinata defense-related protein (CJS1) mRNA, complete cds.	14009291	1279	08-MAY-2001
<i>BcaX.LEA1.a</i>	AY804188	<i>carinata</i>	DNA	Brassica carinata LEA1 gene, promoter sequence.	55824388	487	31-DEC-2005
<i>BcaX.PDI1.a</i>	DQ228284	<i>carinata</i>	DNA	Brassica carinata protein disulfide isomerase (PDI1) gene, complete cds.	77999356	4623	26-OCT-2005
<i>BcaX.ZF2.a</i>	DQ858291	<i>carinata</i>	mRNA	Brassica carinata C2H2 zinc finger protein (ZF2) mRNA, complete cds.	114437172	720	01-AUG-2007
<i>BinC.IMS.a</i>	DQ143886	<i>insularis</i>	mRNA	Brassica insularis 2-isopropylmalate synthase 1 (IMS) mRNA, complete cds.	75707982	2044	03-MAY-2006
<i>BjuaX.COL1.a</i>	DQ534066	<i>juncea</i>	mRNA	Brassica juncea constans-like 1 protein (COL1) mRNA, complete cds.	106636022	1033	07-JUN-2006
<i>BjuX.AG.a</i>	DQ060334	<i>juncea</i>	mRNA	Brassica juncea AGAMOUS (AG) mRNA, complete cds.	67043457	759	13-JUN-2005
<i>BjuX.ARD1.a</i>	AY331382	<i>juncea</i>	mRNA	Brassica juncea ARD-like protein (ARD1) mRNA, complete cds.	37791220	899	21-JAN-2005
<i>BjuX.CAT1.a</i>	AF104451	<i>juncea</i>	mRNA	Brassica juncea catalase (CAT1) mRNA, complete cds..	4336751	1778	04-MAR-1999
<i>BjuX.CAT2.a</i>	AF104452	<i>juncea</i>	mRNA	Brassica juncea catalase (CAT2) mRNA, complete cds.	4336753	1778	04-MAR-1999
<i>BjuX.CAT3.a</i>	AF104453	<i>juncea</i>	mRNA	Brassica juncea catalase (CAT3) mRNA, complete cds.	4336755	1769	04-MAR-1999



Nomenclature Conventions



Example



Nomenclature Conventions



entity	BNF form	example
plant_population	[<GENUS INITIAL>{<species 2 initials> <Cytodeme letter>}{<POPULATION ABBREVIATION> <CONSORTIUM>}{<POPULATION TYPE ABBRV.> _set}< integer counter>	BnaTNDH_01
plant_accession	<institute code>_<PERSON INITIALS><yy>{<leading zeroed number> <accession from registry> <plant line name>_a_<integer counter>}	whri_GK0100564
plant_individual	pl_<accession name>_<plant integer counter>	pl_GK0100564_01
trial	<institution code>_<yyyy>_<location code>_<integer counter>	rres_2005_gh28105_01
linkage_map_id	<GENUS INITIAL><species 2 initials><POPULATION CODE>_<yyyy><letter counter>	BnaDYDH_01_2001a
linkage_map_name	<GENUS INITIAL> <species> <POPULATION CODE> <Author citation> <year> [open text]	Brassica napus DYDH Delourme et al. 2001 (A)
linkage_group_id	<GENUS INITIAL><species 2 initials><POPULATION CODE>_<letter counter>_ [<genome assigned letter>]<group number>	BnaDYDH_01_2001a_u11
linkage_group_name	<GENOME LETTER ASSIGNMENT><leading zero number>	A01
mapping_locus	<institute code>_<single letter marker assay type designator>< MARKER ASSAY NAME>{<single letter locus counter> _< 2-digit leading zero number locus counter> _< 3-digit leading zero allele size>}	whri_aE12M59_236
primer	pr[5]3[_<Institution code>_]<primer name>	pr_sN11641F
gene	<GENUS SINGLE INITIAL>[<species 2 initials>]{<Cytodeme letter> X}.{<GENE NAME> <GENE ABBREVIATION>}.<single letter locus accession>	BnaX.CHS-3.a
marker_assay	<institute code>_<single letter marker assay type designator>_< MARKER ASSAY NAME>_a<counter>	whri_aE12M59_a01
gametic_locus_allele	<locus name><allele code>	whri_pW101_a_a

Adding Value to the UK Brassica Crop Science Community

Summary

Objectives

Technical summary

Beneficiaries

UK Brassica sequencing

Forward genetics

Existing linkage maps

Map integration

Reference populations

Diversity sets

QTL collation

Data management

Reverse genetics

Induced variation (TILLING)

MBGP TILLING consortium

RNAi pipeline

B. rapa transformation

Functional validation

Dissemination



funded by BBSRC



A BBSRC Innovations in Crop Science Project

The AdVaB consortium will fill gaps in information and technology to enable research findings relating to *Brassica* genetics and genomics to be translated more rapidly into practical outcomes, particularly through genetic crop improvement. Researchers and plant breeders will be provided with tools and information to enable explicit understanding of crop traits in terms of the function of underlying genes. This will capitalise on the BBSRC-funded UK contribution to the multinational effort to sequence the complete *Brassica* 'A' genome, and previous investment in the related reference plant species *Arabidopsis*.

Brassica crops are major components of UK arable agriculture and horticulture, with opportunity to exploit their vast genetic diversity. Oilseed rape, the primary source of vegetable oil in Northern Europe, is high in polyunsaturates with huge potential to provide new nutritional and renewable non-food products. Brassica vegetables contain beneficial nutrients, with elevated amounts of anti-oxidants, vitamins, anti-carcinogenic compounds, as well as uptake of minerals such as zinc and iron

Project Partners:

Graham King (co-ordinator): Rothamsted Research

Lars Ostergaard, Judith Irwin: John Innes Centre, Norwich

Dave Pink, Graham Teakle: Warwick HRI, University of Warwick



Reference populations

Reference *Brassica* mapping populations will be made available together with the associated key data sets (genetic linkage map, provenance and quality assurance validation). Seed will be provided in the form of quality assured 'starter packs'. DNA from founder lines of species-specific diversity sets will be made available for molecular allelic screening.

Integrated genetic maps

Integrated consensus linkage maps for the *Brassica* A and C genomes with sequence tagged markers and reference 'conserved synteny block' nomenclature will be developed based on existing screening of SSR markers on parent lines. Mapping populations will be scored with polymorphic markers and the data used to generate reference maps based on consensus conserved synteny blocks in common with *Arabidopsis*.

The CropStore database

The CropStore relational database has been developed to address the need for low maintenance, explicit curation and management of integrated datasets for crop plant genetics. [detail](#)

Reverse genetics tools

Exploitation of *Brassica* genome sequence through reverse genetic approaches requires access to TILLING and RNAi capability. *B. rapa* EMS - TILLING and radiation populations will be developed for induced variation. An RNAi pipeline for down regulation of multiple gene copies will be established initially in *B. oleracea* and *B. napus*, and a *B. rapa* transformation system developed for UK researchers.

Collation of QTL data

To underpin ongoing trait-led genetic and genomic projects QTL datasets will be collated and prioritised, and converted to a consensus format for comparative analysis. This will also assist in making direct connections between fundamental research and crop-related traits selected in breeding programmes.

Validation of technologies

Validation of the reverse genetic technologies will focus on specific genes with well characterised phenotypic effects, and will allow comparison of the different approaches in polyploid brassicas.

“Joined-up” *Brassica* Crop Science

– filling gaps in the pre-breeding pipeline

