

UK CropNet Databases (click database name for more info.)		
Database	Species	Database Access
Arabidopsis Genome Resource	<i>Arabidopsis thaliana</i>	AceBrowser WebAce
BarleyDB	Barley	AceBrowser WebAce
BrassicaDB	<i>Brassica spp.</i>	AceBrowser WebAce
CropSeqDB	UK crop plant species	AceBrowser WebAce
FoggDB	Forage Grasses	AceBrowser WebAce
MilletGenes	Millet and tef	AceBrowser WebAce

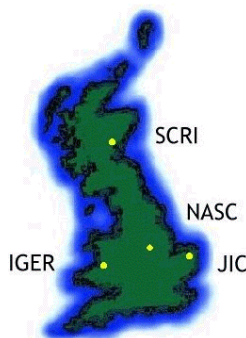
Databases mirrored from Cornell University		
Database	Species/Description	Database Access
AlfaGenes	Alfalfa	AceBrowser WebAce
BeanGenes	<i>Phaseolus, Vigna</i>	AceBrowser WebAce
CassavaDB	<i>Manihot</i>	AceBrowser WebAce
ChlamyDB	<i>Chlamydomonas</i>	AceBrowser WebAce
CompositDB	<i>Compositae</i> - currently contains Lettuce and Sunflower data	AceBrowser WebAce
CoolGenes	Cool season food legumes	AceBrowser WebAce
CottonDB	<i>Gossypium hirsutum</i>	AceBrowser WebAce
DictyDB	<i>Dictyostelium</i>	AceBrowser WebAce

Stock Centre
[Roslin Institute](#)
 Animal databases at the Roslin Institute
[SCRI](#)
 Scottish Crop Research Institute
[John Innes Centre](#)
 Research centre for Plant Science. Also home to BrassicaDB, MilletGenes and ComapDB
[IGER](#)
 Institute of Grassland and Environmental Research
[MaizeDB](#)
 Access the MaizeDB database
[FTP site](#)
 Download our databases from the CropNet FTP site

Where to find us

The six projects that comprise UK CropNet are located at four different institutions around the UK. These are based at

- [Institute of Grassland and Environmental Research \(IGER\)](#) in Aberystwyth
- [John Innes Centre \(JIC\)](#) in Norwich
- [Nottingham Arabidopsis Stock Centre \(NASC\)](#) at the University of Nottingham
- [Scottish Crop Research Institute \(SCRI\)](#) in Dundee



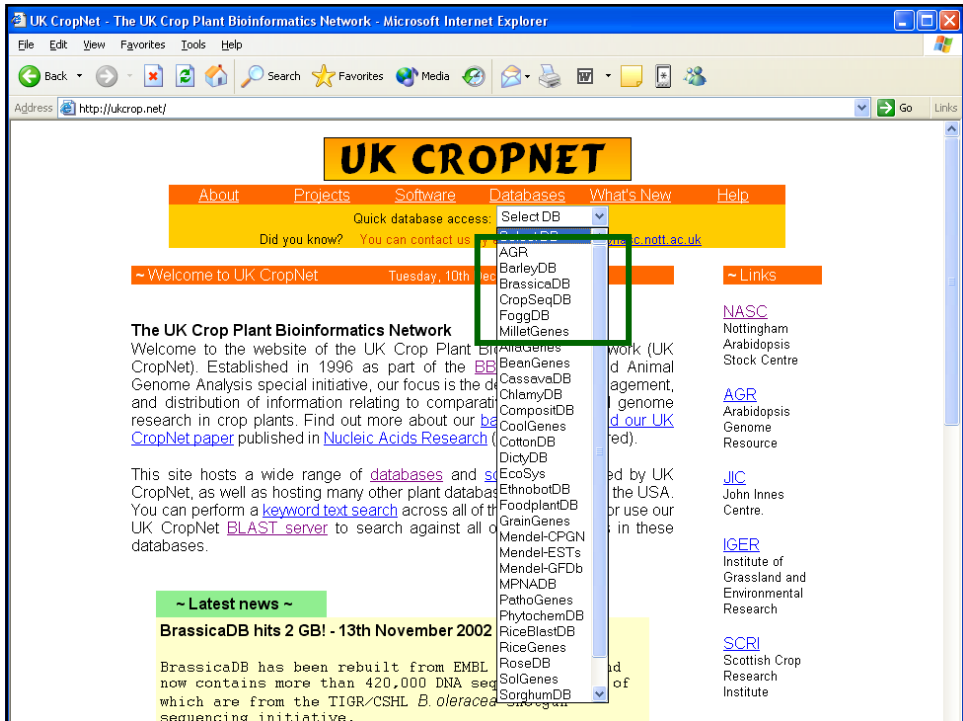
[Contact us](#)

Please email us if you have any questions.

Since 1999, we have been running an ongoing series of [training events](#) at each of the four member institutions, where we provide hands-on tuition in our databases and software. We would also be more than happy to try to arrange training sessions and/or present talks at your institution. [Contact us](#) for more details.

Accessing data

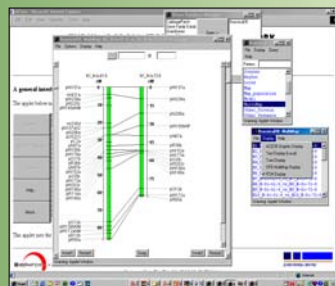
All UK CropNet databases are freely available for anyone to download from our [FTP site](#) (though you will also need to download the necessary [ACEDB software](#)). Although the ACEDB software was principally designed for UNIX



All these databases can then be:
 Searched by text (e.g. by gene)
 Viewed for structure and properties.

.. Placed in genomic context

.. And in genetic / physical context



Investigating Gene Function (£28M including animals)

- Arabidopsis
- Brassica
- Cereals

- Plant fungal pathogens
- Physcomitrella

The screenshot shows a web browser window with the URL <http://www.moss.leeds.ac.uk/startpage.html>. The page title is "Welcome to PEP: The Physcomitrella EST Programme". Below the title, there is a navigation bar with links for "Search ESTs", "Products & Services", and "Training Workshops". The main content area includes a "NEW!" announcement about BAC libraries, a "Latest News" section with a link to "Homology between PEP sequences and Arabidopsis", and a "What is PEP?" section. At the bottom, there is a list of five services offered by the program and a footer indicating the page is maintained by [Boris Lohme](#).

Welcome to PEP: The Physcomitrella EST Programme

We specialize in identifying functions of plant genes by using our PEP Programme.

NEW!
BAC libraries now available...see [Products and services](#)

[Search ESTs](#) [Products & Services](#) [Training Workshops](#)

Latest News

The PEP and Okazaki collections now contain 60 000 Physcomitrella ESTs. Redundancy reduced contigs from these are now searchable from our blast server [Homology between PEP sequences and Arabidopsis](#). All Arabidopsis sequences with homology in Physcomitrella can be viewed via the [AGAP Website](#).

What is PEP?

PEP is a UK based BBSRC funded programme to sequence 30,000 ESTs from the moss Physcomitrella patens. It builds on a research collaboration between the University of Leeds, UK and the University of Washington, St Louis, USA. These ESTs are deposited immediately into the Bank.

Physcomitrella patens has been researched continuously at Leeds since Professor David Cove, an international expert in the field of Bryology brought the organism with him from Cambridge in 1977 and established it as a model organism for the study of Plant development.

Physcomitrella patens is unique among plants in possessing an efficient "gene targeting" mechanism (Eckstein S, Zyl J, 1997 11 1195) (Shopp et al 1998 PNAS 95 4265). We aim to exploit this ability to integrate transforming DNA by homologous recombination at high frequency. This enables a "gene targeting" approach to determining gene function.

[Search ESTs](#) [Products & Services](#) [Training Workshops](#)

What we can offer you?

1. We sequence 30,000 ESTs from Physcomitrella patens and submit to the bank and "blast" our own BLASTable databases.
2. You search for most homologues of your genes of interest in our [BLAST screen database](#).
3. You isolate homologues from cDNA/Genomic libraries or by PCR.
4. You conduct transformation studies.
5. We [transform](#) moss with your vectors and create at least 10 antibiotic-resistant transgenics and return them to you.


Alternatively you may join one of our [function workshops](#) to learn how to do it yourself. The workshops are free for BBSRC funded researchers.

[Search ESTs](#) [Products & Services](#) [Training Workshops](#)


This page is maintained by [Boris Lohme](#)

BBSRC Brassica Genome Project - Welcome to the Brassica Genome Project web site - Microsoft Internet Explorer

Address: http://brassica.bbsrc.ac.uk/ICF/



Brassica Genome Project



2 2 : 5 0 Thursday 1 0 th December Database rebuilt 14th November 2002 ...

Brassica ICF project

Who does what

Access the database

Keyword Search

Nominate a probe

Selected GST probes

Order BAC clones

Steering committee

Other Resources


Contact us


Welcome to the website of the Brassica Genome Project, funded by the BBSRC's [ICF programme](#). Our objectives are to:

- create physical maps of the Brassica 'A' and 'C' genomes by fingerprinting BAC libraries
- integrate these with the Arabidopsis genome sequence by hybridization with selected gene anchor probes
- be responsive to the Brassica and Arabidopsis user communities, publishing data in real time, soliciting nominations for the anchor probes and supplying BAC clones on request

Project Progress on 14/11/2002

	0%	100%
Probes designed	100%	100%
Probes generated	98%	100%
Hybridisations	52%	100%
A genome fingerprinting [stats]	100%	100%
C genome fingerprinting	17%	100%

These activities are overseen by a [Steering Committee](#) whose remit is to monitor progress, ensure quality of service and to aid in the prioritisation of requests, resolving conflict where necessary. Through this website you can browse the database, nominate specific sequences for anchor probes and request BAC clones. Where you see this symbol  additional help is available, to view this place your mouse over the symbol, the relevant help will then be displayed. If you have any comments or questions regarding this web site please [contact us](#).

Powered by  [\[Access Stats\]](#)

Page Applit by Alberto Venturoli

JOHN INNES CENTRE

BBSRC Brassica Genome Project - Methodology - Microsoft Internet Explorer

Address: http://brassica.bbsrc.ac.uk/ICF/project.htm



Brassica Genome Project



2 2 : 4 7 Thursday 1 0 th December A Genome I

Brassica ICF project

Who does what

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Introduction

There are four [partners](#) in the project. BAC libraries for the *R. advarsiva* C genome (IbA & IbB) and *R. rapa* A genome (IbA) and HRI. These are being individually fingerprinted, the combined IbA and IbB libraries at HRI and the IbA library at JIC, and assembled into contigs using the [Image](#) and [FPC](#) programs developed at the Sanger Centre. High-density gridded filters of the entire IbA and IbB libraries (comprising more than 30,000 clones each) are provided to all four partners for colony hybridizations. Each partner will be supplied with a set of Arabidopsis GST (Gene Sequence Tag) probes defined and sequence-authenticated by JIC. We have estimated that we need about 1300 GST probes, or one every 100 kb, in order to anchor within the Arabidopsis genome sequence each of the thousand Brassica map-contigs we might expect to generate.

Designing the probes

Probe selection is a non-trivial task and requires computational effort. Gene models are sampled at intervals along the pseudo-chromosome sequence and each exon longer than 250 bp tested in silico against the entire Arabidopsis genome for uniqueness. Where possible, preference is given to gene candidates with putative or proven functions of interest to the community. In addition, provision is made for [nominations](#) of specific gene sequences. These are tested for feasibility in exactly the same way as the framework anchor probes and the results posted [here](#). Detailed information on the current anchor probe set is given [here](#). PCR primers are then designed and probes amplified from the originating Arabidopsis BACs as a final QC check. As a complement to the GST anchor probe set, we are using genetically mapped Brassica RFLP probes to provide an internal framework for the contig building.

Publishing the data

The [current database](#) is rebuilt every two months using the latest hybridization data. This in turn is used to update the two FPC databases so that relevant marker data is available to each fingerprinting project. The new FPC data are then imported back into the project db so that it contains the newly built and rebuilt contigs. The standard FPC rebuilds will be incremental but, periodically, we will rebuild the contigs *ab initio*. Thus, although the hybridization data is essentially cumulative, the physical contig data is expected to radically change during the course of the project. A [query form](#) is provided to enable the user to easily interrogate the database, obtaining the hybridization results for each probe and linking to any contigs that it might anchor. In addition, the user may directly browse or query the [database](#).



Arabidopsis: GARNet

- Transcriptomics
- Proteomics
- Metabolomics
- Knockouts / sequence tags
- Bioinformatics (warehousing)
- Co-ordinated by Ottoline Leyser (York)

http://www.bio.cam.ac.uk/proteomics/IGF/projects.html

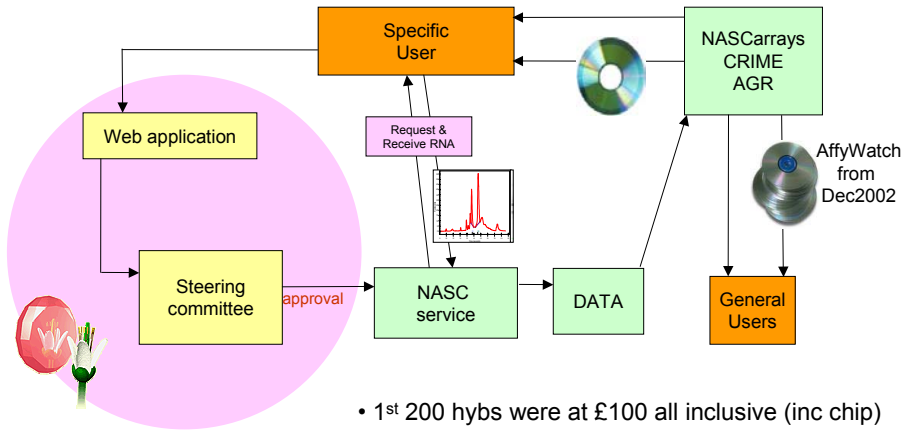
BBSRC IGF Initiative Funded Projects in Progress

Proteomics service

Arabidopsis

Group Leader/Co-writer	Code	Institute	Project Title	Status
Dr. F. Theissen	AR001	IACR-Rothamsted	Proteomics of the vacuole	in progress
Dr. P. Jarvis	AR002	University of Leicester	Identification of substrates of Tic75-IV	in progress
Dr. J. Coleman/Dr. R. Haslam	AR003	IACR-Rothamsted	Characterisation of Arabidopsis Apoptosis Proteins	in progress
Prof. C. Leaver/ Dr. L. Sweetlove	AR004	University of Oxford	Identification of protein involved in programmed cell death	completed
Prof. C. Leaver/ Dr. L. Sweetlove	AR005	University of Oxford	Characterisation of Mitochondrial protein complexes	completed
Prof. A. Smith/R. Ingle	AR006	University of Oxford	Identification of nuclear responsive proteins in the hyperaccumulator <i>Alysicornis latibaccum</i>	completed
Dr. S. Gibson	AR007	Rice University, Houston, TX, USA	Identifying sugar regulated genes from wild-type and sugar insensitive (si) <i>Arabidopsis</i>	pending
Dr. M. Grant	AR008	Imperial College at Wye	Comparative analysis of the defence proteome of <i>Arabidopsis thaliana</i>	in progress
Dr. L. Hunt	AR009	University of Sheffield	The response of <i>Arabidopsis</i> guard cells to ABA	in progress
Dr. Jorge Casal	AR010	University of Buenos Aires, Argentina	Modulation of leaf proteomics by phytohormones and crytotoxins	in progress
Dr. P. Dupree/Dr. O. Fein	AR011	University of Cambridge/ MPI, Geln, Germany	Comprehensive investigation of heterosis effects in <i>A. thaliana</i> crosses by combined transcriptomics, proteomics, metabolomics, and phenotype analysis	in progress
Dr. P. Quick	AR012	University of Sheffield	The response of a tolerant plant to water stress and protein as compared to <i>Arabidopsis</i>	in progress
Prof. D. Twill	AR013	University of Leicester	Proteomic analysis of membrane-linked proteins in <i>Arabidopsis</i> pollen	in progress
Dr. E. Harrison	AR014	HDL, Wellesbourne	The role of nuclear proteins in the regulation of leaf senescence	pending
Dr. W. Willatts	AR015	University of Leeds	Identification of proteins associated with the pectic matrix of plant cell walls	in progress
Dr. P. Dupree	AR016	University of Cambridge	Protein composition of lipid rafts in <i>Arabidopsis</i>	in progress
Dr. F. Aniento	AR017	University of Valencia, Spain	Identification of a toxin-binding protein from <i>Arabidopsis thaliana</i>	in progress

Affy service

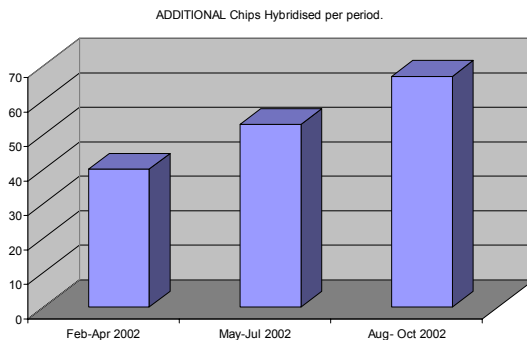


- 1st 200 hybs were at £100 all inclusive (inc chip)
- Currently, we charge £250 all inclusive (inc. chip)
= ~ 50% subsidy



Affy service

~250 Arabidopsis chips hybridised so far



Customers so far have mainly been from UK, NL, Poland, South Africa and the US.

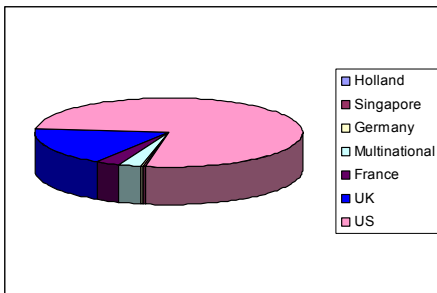
- * Baseline Development/ tissue types
- * Baseline ecotypes
- tissue_organ_specificity
- Cross species
- * Effect of gene insert knock out
- * Other mutant/Wildtype comparisons
- transgenics
- * effect of gene overexpression
- DNA methylation
- Hyponastic growth
- Lignification
- Male sterility
- Meristem activity
- Mineral nutrition
- Mycorrhizasa symbiosis
- Nitric Oxide treatment
- Ozone treatment
- Phosphate
- Photoreceptor interactions
- Photosynthesis
- phytoremediation
- Pollen
- Potassium deficiency
- Programmed Cell Death
- Protoporphyrin IX
- Salt treatment
- Signal transduction
- Temperature sensitivity
- time course
- Carbon dioxide treatment
- Cold treatment
- * Cell Treatments
- * other complex treatment

* Denotes multiple experiments of this type

Co-operative experience

- CATMA – cross Europe collaboration leading to CAGE and AGRIKOLA.
- PLANET – linked databases.
- Stockcentre – donations from several countries and distribution to all.

Functional genomics seed tools: donors



International statistics for openly distributed genetic resources.



Canada	Malaysia	Brazil	Hong Kong
Hungary	India	N. Korea	South Africa
Taiwan	Argentina	S. Korea	New Zealand
Norway	Portugal	Czech Republic	Singapore
Australia	Finland	Israel	Poland
Austria	China	Denmark	USA
Italy	Belgium	Japan	The Netherlands
Sweden	Switzerland	Spain	France
Germany	UK		

Seed tools: recipients (since May 2002)

