

# Affymetrix Brassica Exon array

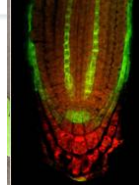
Neil Graham

NASC, University of Nottingham

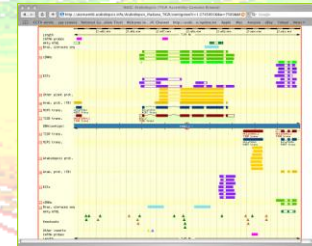
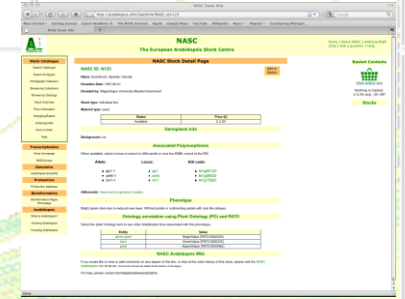


# NASC

## Seed Distribution



## Bioinformatics



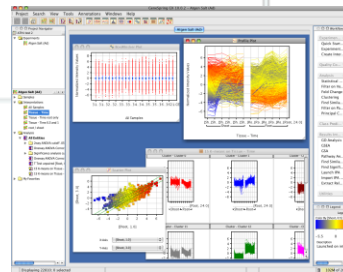
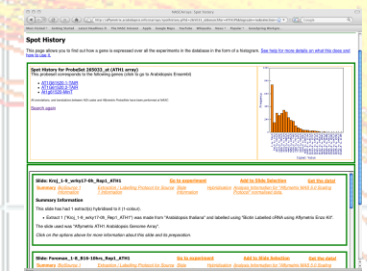
**EAV example using one of our germplasm lines N319**

Phenotype description in free text  
Green dwarf, broader leaves, glabra, yellow seed.  
Free text description

The phenotype description above is the textual description supplied by the donor in his/her own words. By enhancing this description with an ontologized version we can perform more powerful searches for accessions with similar phenotypes in our databases.

| Entity     | Attribute       | Value                 |
|------------|-----------------|-----------------------|
| PT00000000 | (relative_size) | PT00000062 (small)    |
| PT00000000 | (relative_size) | PT00000008 (wide)     |
| PT00000000 | (shape)         | PT00000009 (glabrous) |
| PT00000000 | (color_hue)     | PT00000040 (yellow)   |

EAV description



## Affymetrix Service

# NASC Affymetrix Service

- Process ~1000 arrays per year
- Full service – from total RNA to data
- All Arabidopsis data made public via NASCarrays database and GEO
- Analysis available using NASCarrays tools or Genespring workgroup
- Cost £350 / £450 (+VAT) per sample



# The new Gene Titan system



- New high throughput system
- Plate based arrays
- Process 2 x 96 array plates in 2 days
- Reduced cost
- New Arabidopsis exon array available soon



# The Brassica Exon array

- Initiated as part of a BBSRC funded project on Brassica biofortification (Nottingham, Warwick, Rothamsted Research, SCRI)
- Catalogue array
- 5  $\mu\text{m}$  format
- 2.4 million probes
- Representing 135,201 gene models
- 15 probes per gene, distributed over exons



# Array design (Chris Love)

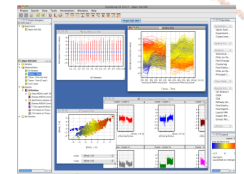
- Based on gene models and transcript data available in late 2009
- JCVI Unigene set (Trick et al) used to develop the Agilent 95k array
- Additional data from *B. rapa* Chiifu KBr BAC sequences, digital transcriptome of *B. napus* Tapidor and Ningyou7 (Trick et al), *B. oleracea* and other ESTs and Arabidopsis genes models not represented
- Data filtered using Affymetrix probe selection pipeline
- Standard Arabidopsis control and reporter sequences
- Probes selected based on 15 probes per gene

# Initial Experiment

- Comparison of root and leaf samples (3 replicates per tissue)
- Same RNA samples hybridised to Agilent 95k oligo array (Warwick)
- Analysed at gene and exon level
- Data made publicly available via NASC

# Brassica array available now from NASC

- Available as part of the standard service (<http://affymetrix.arabidopsis.info/>)
- £350 (+VAT) per sample
- Assistance with experimental design and data analysis
- All data will be made publicly available via NASCarrays / Genespring workgroup (subject to funding)





# Acknowledgements

## **NASC**

- Sean May

## **University of Nottingham**

- Martin Broadley

## **SCRI**

- Phil White

## **Warwick HRI**

- John Hammond
- Helen Bowen

## **Rothamsted Research**

- Graham King
- Chris Love



The University of  
**Nottingham**

*Scottish Crop  
Research Institute*

