

Associative Transcriptomics for the OREGIN project

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Rothamsted, 9 May 2018



no.	original.trait.name	no.lines	candidates	trait.from
1	EST_08/11/2015	240	Y	Tom.Wood
2	VIGOUR 08/11/2015	238	N	Tom.Wood
3	LLS 1.6 18/03/2016	239	Y	Tom.Wood
4	LLS 3.5 30/04/2016	238	N	Tom.Wood
5	No. plants with phoma	158	N	Bruce.Fitt
6	% cover	131	Y	Bruce.Fitt
7	Severity score	161	N	Bruce.Fitt
8	LLS incidence (0-10)	92	Y	Tom.Wood
9	LLS severity (0-7)	92	Y	Tom.Wood
10	Phoma	81	Y	Tom.Wood
11	LLS (%)	66	N	Tom.Wood
12	PSC (0-7)	77	N	Tom.Wood
13	Vert D.I.	74	N	Tom.Wood
14	Average of Establishment Score	164	N	Peter.Berry
15	Average of Vigour Score	164	Y	Peter.Berry
16	Average of Estimated plant number (Plants/m2)	164	N	Peter.Berry
17	Average of Pod maturity score (*see key for details)	164	N	Peter.Berry
18	Average of Stem canker score (Phoma)	164	N	Peter.Berry
19	Average of Sclerotinia % plants affected	162	N	Peter.Berry
20	Average of Sclerotinia % of stems affected	162	Y	Peter.Berry
21	RLD (cm root per cm3 soil)	82	N	Peter.Berry
22	RLD >0.5mm thick (cm root per cm3 soil)	82	N	Peter.Berry
23	Diam (mm)	82	N	Peter.Berry
24	SurfArea (cm2 per cm3 soil)	82	N	Peter.Berry
25	Root mass (mg per cm3)	82	N	Peter.Berry
26	Specific root length (m/mg)	82	Y	Peter.Berry
27	Establishment	153	Y	Kate.Storer
28	Early vigour	153	N	Kate.Storer
29	Yield (t ha ⁻¹)	132	Y	John.Hammond
30	EST_08/11/2015	244	Y	Mark.Nightingale
31	VIGOUR_08/11/2015	244	N	Mark.Nightingale
32	LLS_1.6_18/03/2016	243	Y	Mark.Nightingale
33	LLS_3.5_30/04/2016	238	N	Mark.Nightingale
34	LLS_3.4_14/04/2016	242	Y	Mark.Nightingale
35	Emergence	28	N	Tom.Wood
36	phoma.incidence (0-10)	28	N	Tom.Wood
37	phoma.severity (0-5)	28	N	Tom.Wood
38	phoma.area.coverage	28	N	Tom.Wood
39	PhomaLS.UH (0-5)	28	N	Yongju.Huang
40	Miner	28	N	Rachel.Wells
41	Slug	28	N	Rachel.Wells
42	Flea Beetle	28	Y	Rachel.Wells

Y: 15



University of Hertfordshire **UH**

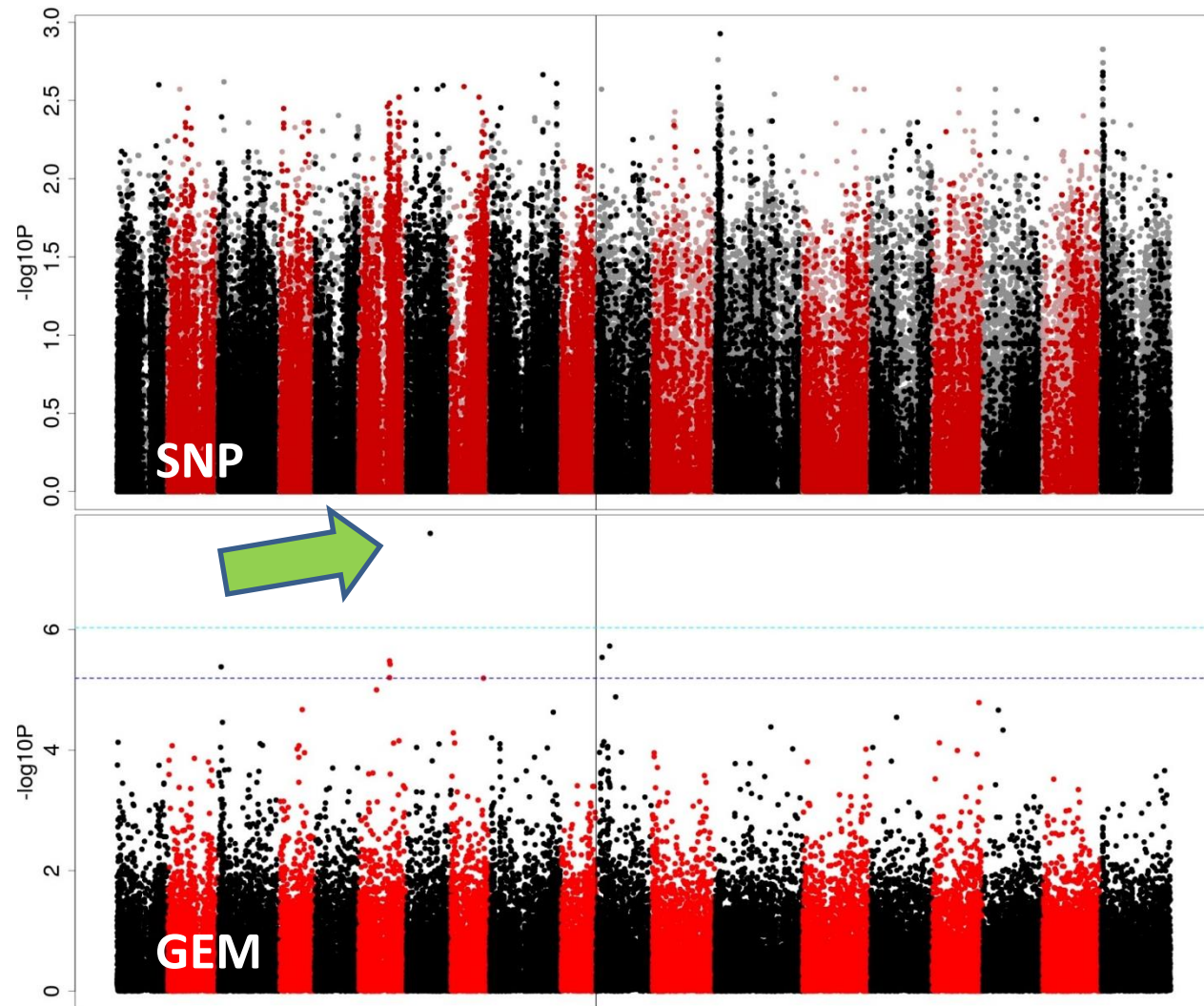


University of Reading



John Innes Centre

Flea beetle

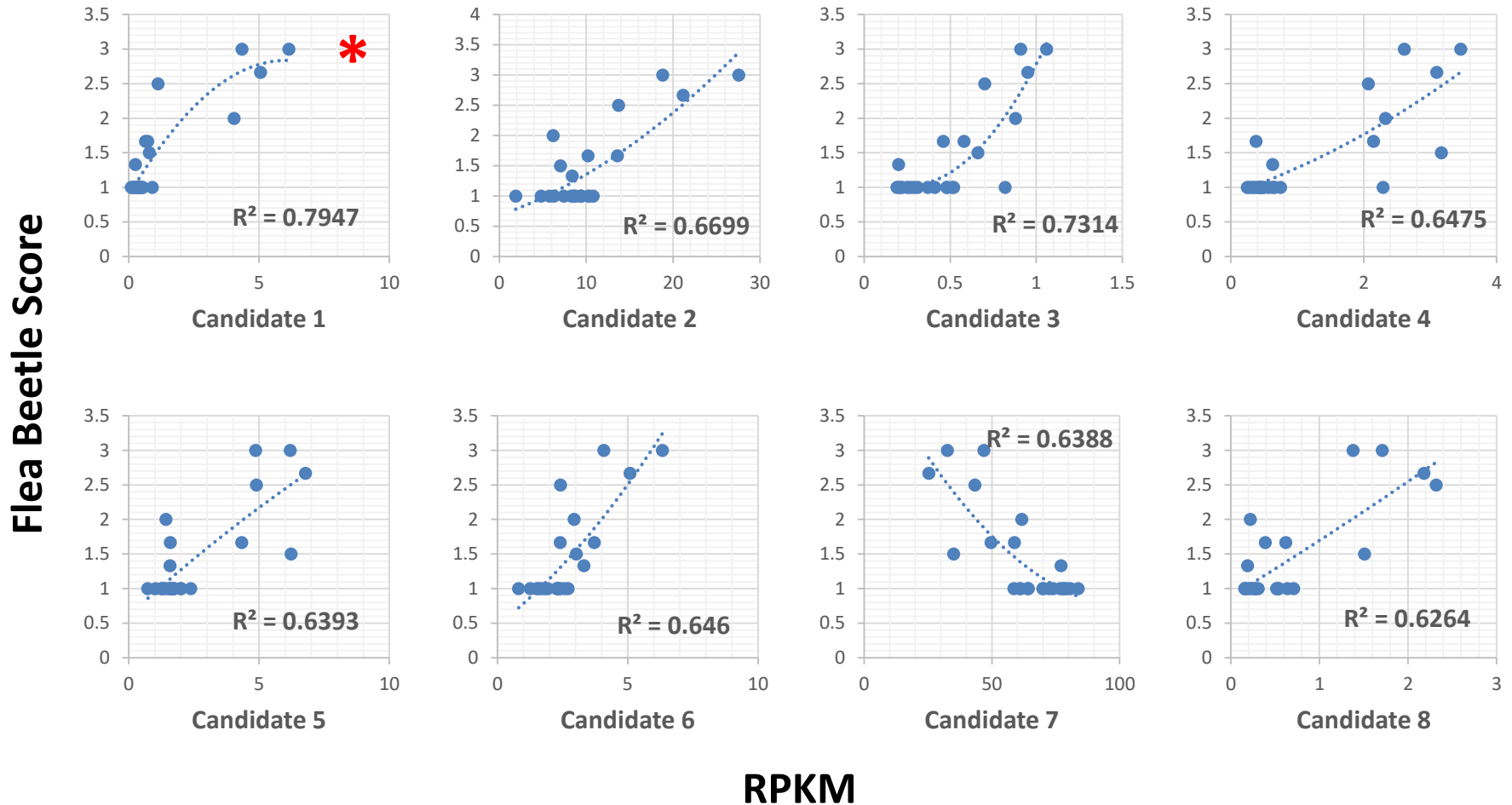


Manhattan plots. SNP, single nucleotide polymorphisms; GEM, gene expression makers.

Flea beetle

- * • impacting pathogen response and cell cycle during geminivirus infection (response to cabbage leaf curl virus (CaLCuV) infection);
- geminiviruses are a large family of single-stranded DNA viruses that are whitefly-transmitted.

Regression plots with polynomial trend lines. R^2 , coefficient of determination.



Community resources:

<http://oregin.info>

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

Yorkknowledgebase.info
York Oilseed Rape Knowledgebase
Bancroft group, University of York

HOME NEWS RESOURCES CONTACT US



- About OREGIN
- Project outline
- Links
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- Functional Genotypes
- Contact OREGIN

Links

The links listed on this page have been arranged in to two categories. OREGIN related links, and links to all Defra Genetic Improvement Networks. The lists are accessible below (or directly from the drop down menu).

OREGIN related links

The table below contains a list of useful links relating to the OREGIN project, including links to the institutes and companies involved in the project.

- Brassica Information Portal - The Brassica Information Portal is a web repository for population and trait scoring information related to the Brassica breeding community.
- York Oilseed Rape Knowledgebase - This site provides access to datasets and information to support oilseed rape pre-breeding.
- Brassica.info This site has been established to collate and exchange information relating to Brassica genomics and genetics worldwide for "The Multinational Brassica Genome Project"

Contact OREGIN
Get in touch with us and find out the latest developments

Links to related information resources

[Brassica.info](#) [CropStore](#) [OREGIN^{new} website](#) [OREGIN^{old} website](#) [Brassica Information Portal](#) [TGAC Brassica Resources](#)

SRA accession codes

SRA project code	Description
PRJEB2588 and PRJEB5294	Leaf mRNAseq from TNDH mapping population
PRJNA309367	RIPR: Brassica napus transcriptome
PRJNA309368	RIPR: Brassicaceae transcriptome
PRJNA295685	Evo-Genapus paper: EXTENSIVE HOMOEOLOGOUS GENOME EXCHANGES IN ALLOPOLYPOID CROPS REVEALED BY MRNASEQ-BASED VISUALIZATION
PRJNA354232	OREGIN top up sequencing



<https://bip.earlham.ac.uk/>

Sign in with ORCID

Brassica Information Portal

The Brassica Information Portal is a web repository for population and trait scoring information related to the Brassica breeding community. It provides information about quantitative trait loci and links curated Brassica phenotype experimental data with genotype information stored in external data sources. Advanced data submission capabilities and APIs enable users to store and publish their own study results in our Portal.

[About us](#) [About BIP](#)

Search for... - or -

Examples: *oleracea* 73.3 p1129

Acknowledgements

THE UNIVERSITY *of York*

Ian Bancroft
Zhesi He
IB group



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