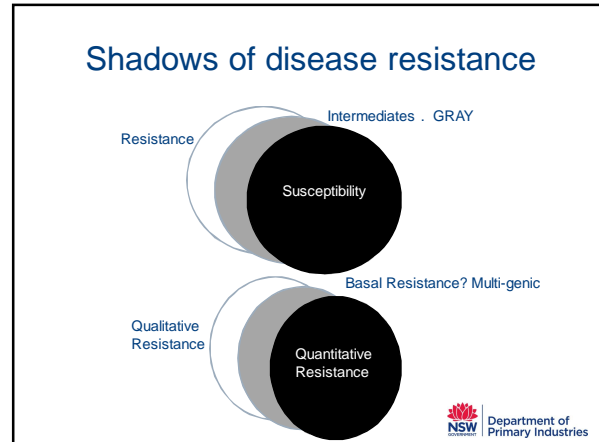


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Shadows of Blackleg Resistance in Canola

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Types of resistance

- Qualitative resistance**
 - Race-specific mediated by an effector, triggered immunity (ETI) mechanism
 - Effectively control blackleg disease at the seedling stage, but may/may not restrict the development of canker formation in mature stems
 - Evidence of gene-interaction
- Quantitative resistance**
 - Race non-specific mediated by pattern, triggered immunity (PTI) mechanism
 - Not effectively control blackleg disease at the seedling stage, but restrict the development of canker formation in mature stems
 - Are they really distinct? Defeated genes?**

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Adult plant resistance

- ≠ always quantitative resistance
- could be due to a single major gene (Qualitative resistance)
 - Not effective at the seedling stage
 - Effective at the adult plant stage

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frontiers in Plant Science | Crop Science and Horticulture

ORIGINAL RESEARCH ARTICLE
Front. Plant Sci., 24 October 2016 | <https://doi.org/10.3389/fpls.2016.01517>

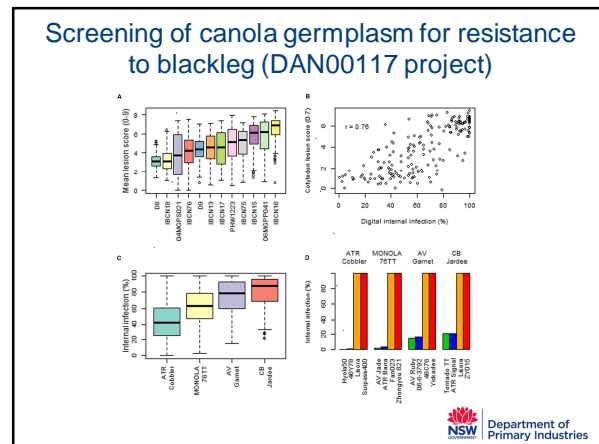
Genome-wide Association Study Identifies New Loci for Resistance to *Leptosphaeria maculans* in Canola

Harsh Raman¹, Rosy Raman¹, Neil Coombes¹, Jie Song¹, Simon Diffey¹, Andrzej Kilian¹, Kurt Lindbeck¹, Denise M. Baroulescu¹, Jacqueline Batley¹, David Edwards¹, Phil A. Salisbury¹ and Steve Marcroft²

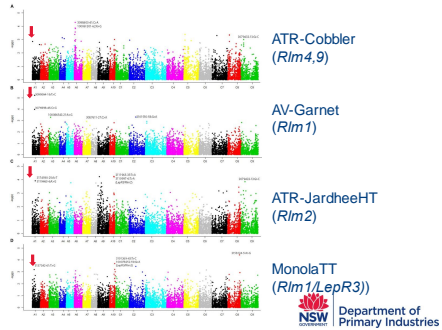
¹Graham Centre for Agricultural Innovation (an alliance between NSW Department of Primary Industries and Charles Sturt University), Wagga Wagga Agricultural Institute, Wagga Wagga, NSW, Australia

1,083 TOTAL VIEWS

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Mapped qualitative and quantitative resistance loci in canola

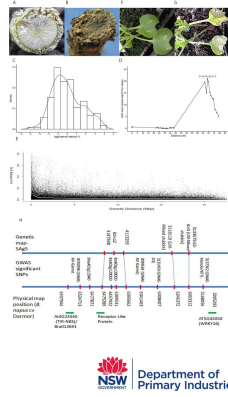


A major locus for adult plant resistance maps on chromosome A01 (Raman et al, 2016)

Marker	Chromosome	Genetic map position	Additive Effect	P value	LOD	R ² (%)
3110119_43-G>T	A01	69.0	-3.31	4.14e-27	26.38	24.57
3145775	A02	36.81	0.70	1.50e-02	1.82	1.42
3154085	A06	0	-0.77	5.51e-03	2.26	1.82
3117277	A07	39.59	-0.78	7.94e-03	2.10	1.69
3084361	C08	27.16	0.75	1.05e-02	1.98	1.61

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Mapped the APR on chromosome A01 and identified putative candidate genes



Larkan et al. BMC Plant Biology (2016) 16:183
DOI 10.1186/s12870-016-0877-2

BMC Plant Biology

RESEARCH ARTICLE

Open Access



Multi-environment QTL studies suggest a role for cysteine-rich protein kinase genes in quantitative resistance to blackleg disease in *Brassica napus*

Nicholas J. Larkan^{1,2}, Harsh Raman¹, Derek J. Lydiate¹, Stephen J. Robinson¹, Fengqun Yu¹, Denise M. Barbulescu⁴, Rosy Raman¹, David J. Luckett³, Wayne Burton^{4,5}, Neil Wratten^{4,5}, Philip A. Salsbury^{6,7}, S. Roger Rimmer^{1*} and M. Hossein Borhan^{1*}

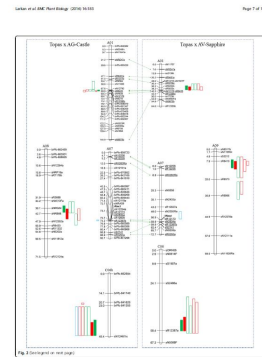
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Survival, internal infection and heritability of Topas/AG-Castle and Topas/AV-Sapphire (Larkan et al 2016)

Population	Location	Year	Replication	Method used for evaluation	Range (%)	h ²
Topas/ AG-Castle	Horsham	2009	3	S	0. 100	0.89
				II	12. 100	0.85
	Wagga Wagga	2009	3	S	0. 100	0.75
				II	12. 100	0.79
Topas/ AV-Sapphire	Wagga Wagga	2010	4	S	0. 100	0.87
				II	4. 100	0.86
	Horsham	2008	3	S	0. 71.1	0.9
				II	8. 100	0.88
Topas/ AV-Sapphire	Wagga Wagga	2009	3	S	0. 100	0.83
				II	4. 100	0.73
	Wagga Wagga	2011	4	S	0. 100	0.87
				II	16. 100	0.84
Topas/ AV-Sapphire	Horsham	2012	4	S	0. 100	0.87
				II	24.2. 100	0.89

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Multi-environment QTL for quantitative resistance to blackleg on A1, A8 (DY and DB pops), (A9 DY) and C6 (DY)



Evaluation of RP004/Ag-Outback population for blackleg resistance

Environment	Source of inoculum	Location	Broad sense heritability (h ² %)
Disease nursery (field)	Natural	Wagga Wagga	79
Disease nursery (field)	Natural	Wagga Wagga	44
Disease nursery (field)	Natural	Green Lake	12
Glasshouse	Mixed stubble for ascospore shower test	Horsham	61
Glasshouse	IBC17 (D4)	Wagga Wagga	97
Glasshouse	IBC176 (D7)	Wagga Wagga	85

- Detected unrepeatable QTL for resistance across different location including on A01
- No effect of R genes was detected under field conditions

Summary

- There are still several gray areas of resistance to blackleg
 - Difficult to tease out
- Efforts are being made to clarify some issue by using
 - ~ Homozygous DH lines from diverse canola germplasm
 - ~ Improved set of SSI (Angela/Steve)
 - ~ High resolution of quantitative resistance loci

Research on blackleg in 2016

- Developed a panel of 300 homozygous diverse set of canola lines
 - Evaluated for blackleg resistance using ascospore shower test (by DEDJTR/Marcroft)
- High resolution mapping of Hyola50 derived resistance
 - Analysed ~ 5000 lines from segregating populations
- Sequence capture of genomic regions associated with R and QR loci to blackleg in canola
- Analysed allelic variants of *LepR3* and *Rlm2* cloned genes in Australian germplasm and verified with phenotyping
- Phenotyped
 - BnASSYST diversity set (2 rep)
 - ~ 384 lines
 - ~ 12 ranges x 64 rows
 - DH pop from Darmor/Yudal (2 rep)
 - ~ 278 DHs, 2 parental lines plus 20 controls
 - ~ 12 ranges x 50 rows

NSWDPI 2016 Blackleg Nursery at Wagga



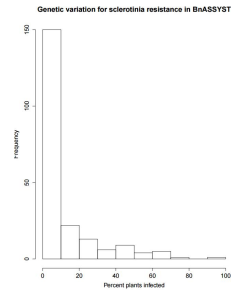
Promising lines for field resistance (survival) to blackleg (BnASSYST set)



Promising lines for field resistance to blackleg (BnASSYST set)



Genetic variation for sclerotinia resistance in BnASSYST lines



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