

NSW Department of Primary Industries | GRDC

Research Highlights on NBGIP (DAN00208/DAN00117)

Harsh Raman
Wagga Wagga Agricultural Institute

Mapped canola populations for blackleg resistance

Qualitative	Quantitative	Reference
10 DH populations	DH populations	
Skipton/Ag-Spectrum Maxol/Westar Columbus/Westar BLN2762/Surpass Ag-Castle/Westar RP04/Ag-Outback 11-5107 (Hyola50) 11-5329 (Hyola50) ATR-Cobbler/BLN3343 Darmor/Yudal	Skipton/Ag-Spectrum Ag-Castle/Topas RP04/Ag-Outback 11-5107 (Hyola50) 11-5329 (Hyola50) Darmor/Yudal GWAS panels BnASSYST (350+lines) AuHGDS (300+ lines)	Resistance loci mapped and data made available Reference Raman et al (2013)-TAG Raman et al (2012)-AJAR Tollerare et al (2014)-PBJ Raman et al (2016)-FIPS Larkan et al (2016)-BMC

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Mapped resistance loci in Darmor-bzh/Yudal DH population (Raman et al, unpublished)

Phenotyping

- Single spore isolates (Wagga)
- Field evaluation (2015, Wagga)- NSW DPI
- Field evaluation (2016, Wagga)-NSW DPI
- Ascospore shower test (DEDJTR/Marcroft Grains Pathology)
- Resistance scored as Survival and internal infection

Genotyping

- 60K Illumina SNP (INRA)
- 7,806 GBS based DaT markers (NSW DPI)

Markers

- Mapped *Rlm9* for qualitative resistance on A07 chromosome
- Mapped QR on several chromosomes on A and C subgenomes
- Consistent QTL were identified on A02, A07, A09, A10, and C09
- Genetic analyses across continents suggest that 'Global' QTL for QR exist

Genotypic variance explained by QTL: 2-16.5%

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Mapped manganese tolerance locus in Darmor/Yudal (Raman et al 2017, FIPS)

Genetic map showing the location of the manganese tolerance locus on chromosome A07. The map includes markers such as BnA09-g20012402.3133535_34-G-C and BnA09-g20012402.3133535_34-G-C. The phenotypic images show the growth of plants under different manganese conditions.

Cation diffusion facilitator
BnaA09g37250D: *B. napus*
AT3G58060.1: *A. thaliana*
AAO38707.1: *S. hamata*

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Three pipelines for pod shatter resistance research

B. napus

- Evaluated 180 accessions of *B. napus* for pod shatter resistance
- Identified shatter resistance sources, developed populations and mapped loci in canola
- Raman et al (2014) PLOS one
- Liu et al (2016) FIPS

B. rapa

- Evaluated 100 accessions of *B. rapa* for pod shatter resistance (AGG)
- Identified donor sources and developed populations segregating for pod shatter resistance
- Mapped loci for pod shatter resistance in an F2:3 population

B. carinata

- Evaluated 83 accessions of *B. carinata* for pod shatter resistance (AGG)
- Identified donor sources and developed two populations segregating for pod shatter resistance
- Mapped loci for pod shatter resistance in an F2 population and YWDH population

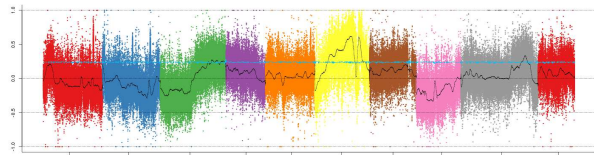
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Mapped pod shatter resistance loci in *B. carinata* (Raman et al 2017, Front. Plant Sci.)

Genetic maps (A, B, C) showing the location of pod shatter resistance loci on chromosomes A, B, and C. The phenotypic images show the pod shatter resistance in *B. carinata* under different conditions.

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Mapped pod shatter resistance loci in F2:3 population of *B. rapa* using Reseq (unpublished)



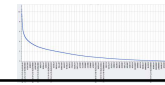
Validating genomic regions via whole genome mapping

Tracing pod shatter resistance alleles in canola



Pod shatter resistance research on interspecific crosses

- B. rapa* x *B. carinata***
 - Evaluated germplasm accessed by NSW DPI from HAU, China
 - Two promising accessions with pod shatter resistance were identified in 2017 season
 - Combining pod shatter resistance loci from *B. rapa* x *B. carinata* under a new GRDC funded project (2017-2020)
- B. napus* x *B. carinata***
 - Accessions derived from *B. napus*/*B. carinata* lines were mainly accessed from UM045
 - Identified one accession that had good pod shatter resistance
 - Developed a mapping population from *B. napus*/*B. carinata* line x *B. napus* (NSW DPI)
- Interspecific source from Nuseed**
 - Evaluated interspecific lines accessed from Nuseed over 3-4 generations
 - Developed an F2 population segregating for pod shatter resistance
 - Mapped loci for pod shatter resistance in an F2 population



Dissected WUE related traits in canola

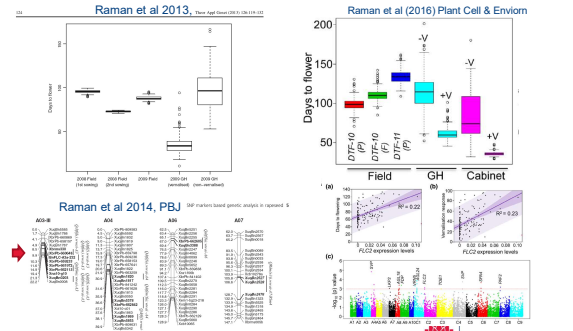
Cross	Population	Phen. Environ.	QTL Identified							
			Yield	Biomass	NDVI	Days to flower	Height	CID	WSC	
RPD4/Ag-Outback	DH	2								
Skipiton/Ag-Spectrum	DH	4								
Hyola50 (11-S107)	DH	2-3								
Hyola50 (11-S329)	DH	2-3								
Tarcoola-22/Tarcoola-69	DH	2								
Charlton/Monty	DH	2								
06-S101	DH	3								
BnASSYST	Diversity panel	4								
Aus Homozygous GDS	Diversity panel	2								
AUGDS (DAN108/DAN117)	Diversity panel (144 lines)	6-7								

Not evaluated

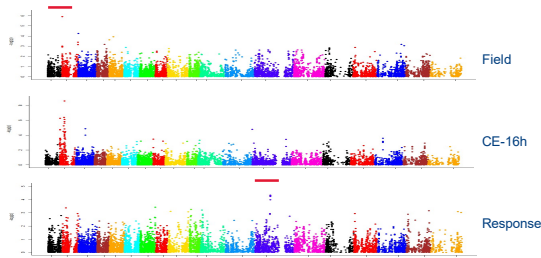
Phenotyped and Genotyped



Gained knowledge on candidate genes involved in vernalisation response in canola

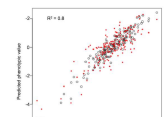
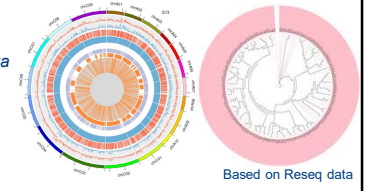


Gained knowledge on candidate genes involved in photoperiod response in canola



Resequenced parental and GWAS panel of NBGIP (DAN00117/00208)

- 21 parental lines of NBGIP mapping populations (1Gb)
- 5 parental lines of *B. carinata*
- 2 parental lines of *B. rapa*
- 174 line of AuHGDS set
- Population structure
- Trait genetic analyses for blackleg, grain yield, flowering time, pod shatter, and Mn2+/Al3+ tolerance
- Genomic selection (GS)



Proof of concept for GS (Raman et al 2016, Plant Cell and Envir.)



Research Priorities

- Depends on the needs of canola breeding companies & investment from GRDC and public sector
- NSW DPI is well-placed to support canola industry
 - Developed phenotypic tools to measure traits more precisely
 - Gained knowledge of canola traits and underlying genetics
 - Promising germplasm with traits of interest such as pod shatter resistance, blackleg resistance, WUE, stable grain yield, & heat tolerance
 - Improved interaction with breeding companies



Acknowledgments

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DAN00117/DAN00208

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