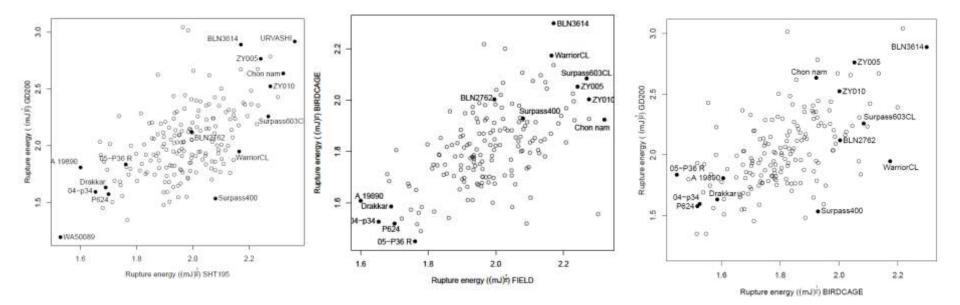




Accessing natural genetic variation for pod shatter resistance in Brassica species

Rosy Raman, Neil Coombes, Yu Qiu, Geoff Burrows, Andrzej Kilian and Harsh Raman Pod shatter in canola is a major issue
Yield losses 8-12%
Volunteer problem in the subsequent rotation
impact on environment

Genetic variation for pod shatter resistance in canola



PLoS ONE 9(7): e101673.



Outline

- Determine the extent of genetic variation for shatter resistance in related Brassica species especially *B. rapa* and *B. carinata*
- Identify loci involved in pod shatter resistance



Accessions evaluated

Species	Accession (no.)	Species	Accession (no.)
A. thaliana	2	B. rapa subsp. chinensis	4
B. barrelieri	1	B. rapa subsp. dichotoma	4
B. carinata	83	B. rapa subsp. nipposinica	4
B. deflexa subsp. leptocarpa	1	B. rapa subsp. oleifera	11
B. juncea	1	B. rapa subsp. perkinensis	3
B. maurorum	1	B. rapa subsp. rapa	1
B. napus	2	B. rapa subsp. trilocularis	1
B. nigra	1	B. ruvo	1
B. nigra var. abyssinica	1	B. tournefortii	1
B. oleracea var. gongylodes	1	E. sativa	1
B. oleracea	7	M. longipetala	1
B. oxyrrhina	1	S. alba	1
B. rapa	61	S. arvensis	2
B. rapa subsp. campestris	1	S. erysimoides	1

Department of Primary Industries

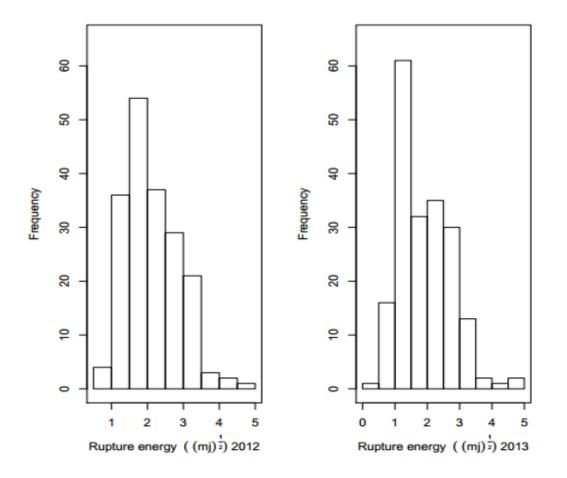
Experimental design

- 200 lines
- 2 Reps
- 2012, 2013
- Phenotyping
 - Pendulum test
 - Anatomical structure of developing pods





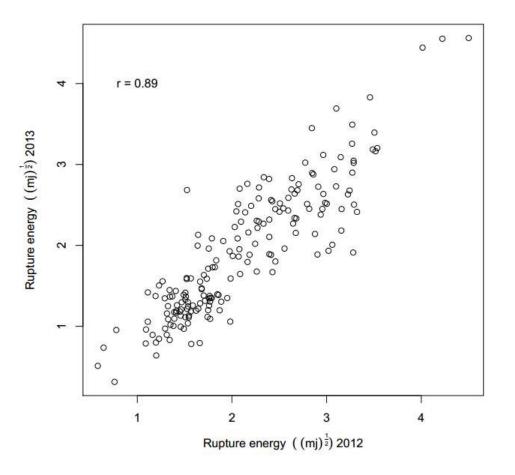
Phenotypic variation for pod shatter resistance in *Brassicacae*



B. napus 2.1 to 4.3mJ *B. rapa* 0.41 to 9mJ *B. carinata* 2 to 20.8mJ

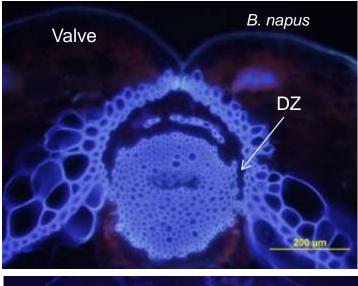


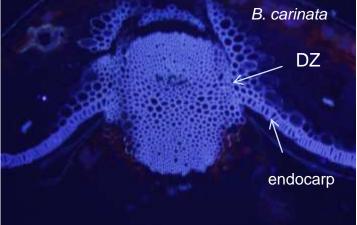
Correlation between rupture energy in 2012 and 2013 trials

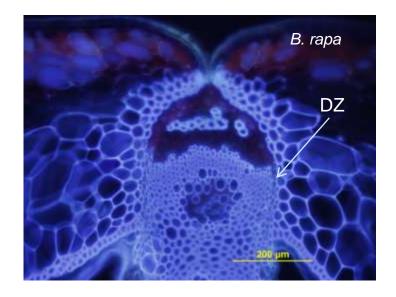




Variation in Pod Anatomy in *B. napus*, *B. rapa* and *B. carinata*

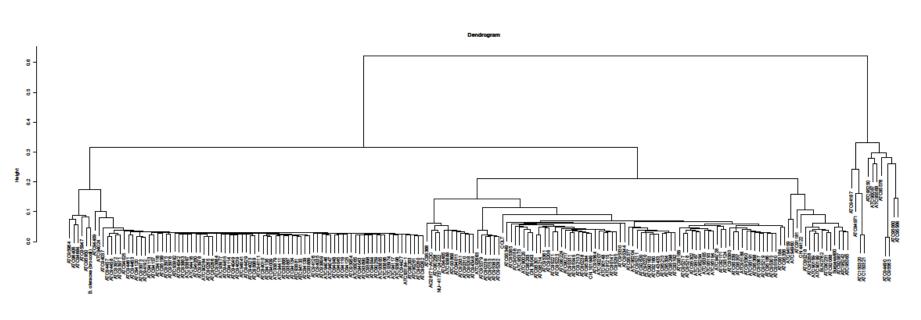








Molecular diversity in Brassica species



dm holust (*, "complete"



Genomic regions associated with Shatter Resistance in *B. rapa*

90 lines

Genotyped with 74,000 SNP and PAM

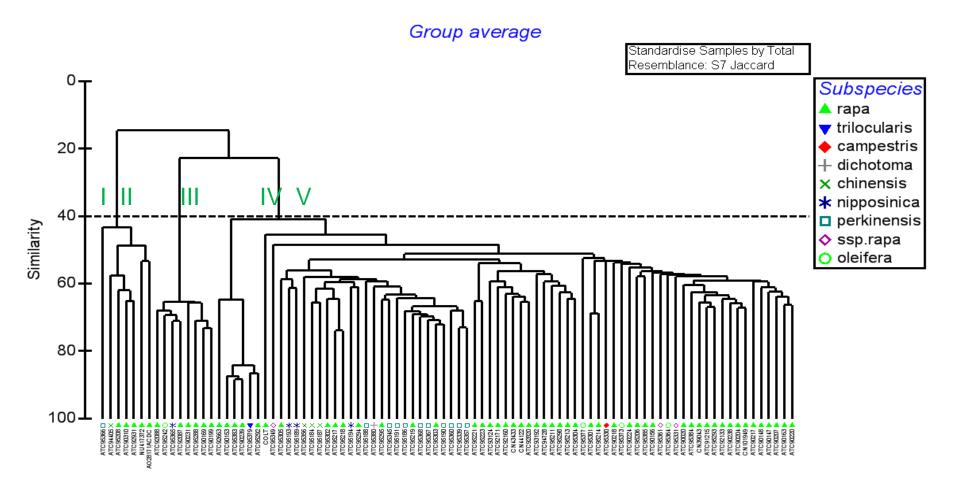
Principal Component Analysis

Identity by descent analysis

GWA Using Mixed Linear Model (Call rate 85%, MAF<0.05) in SVS

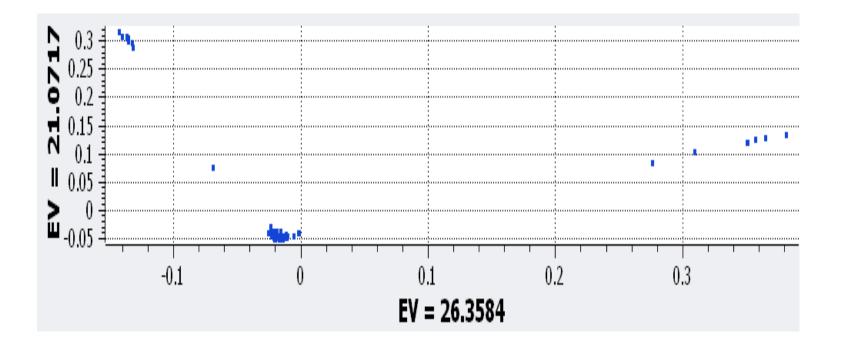


Cluster analysis of *B. rapa* genotypes based on 10420 GBS markers



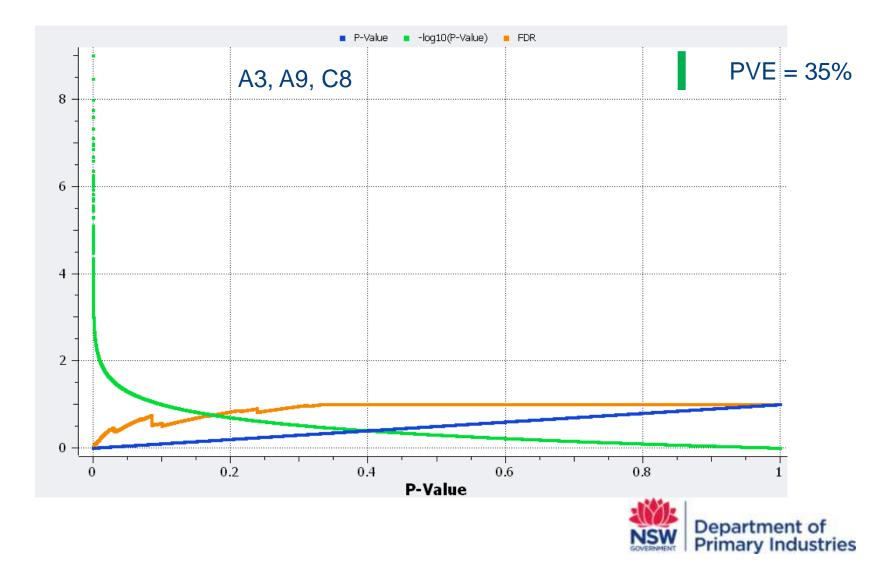


Principal component analysis of *B. rapa* genotypes

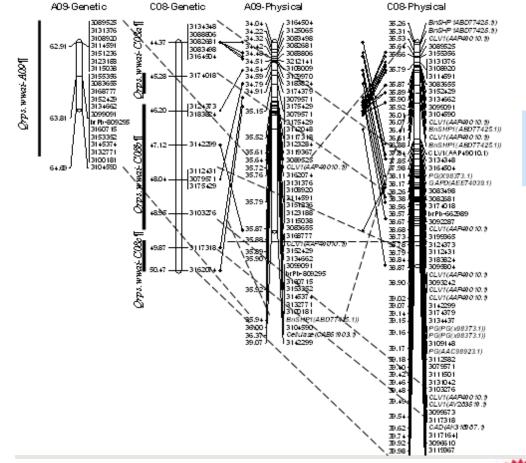




Genome-wide markers associated with shatter resistance in *B. rapa*



Some of QTL identified with GWAS are collocated with QTL in BLN2762/Surpass400



GWAS - Structure Kinship Structure+ Kinship



Genomic regions associated with shatter resistance in *B. carinata*

83 lines

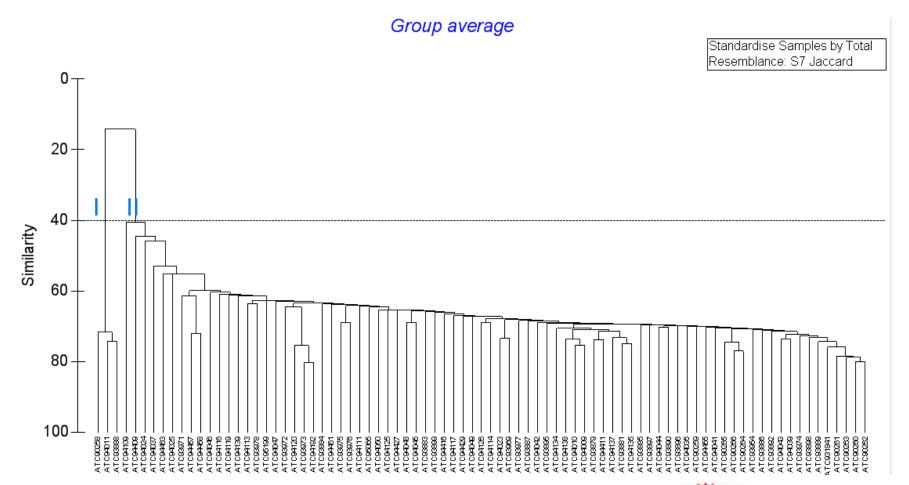
Principal Component Analysis Genotyped with 107,000 SNP and PAM

Identity by descent analysis

GWA Using Mixed Linear Model (Call rate 85%, MAF<0.05)

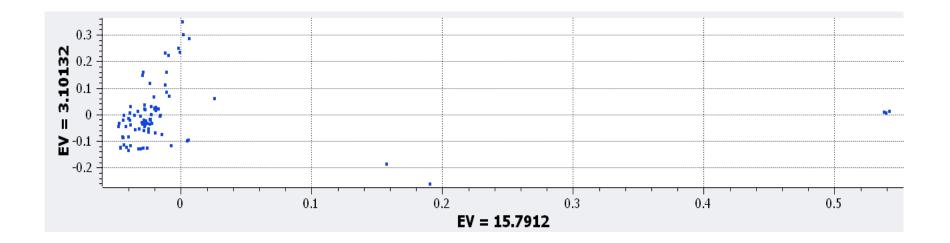


Cluster analysis of *B. carinata* genotypes based on 10420 GBS markers



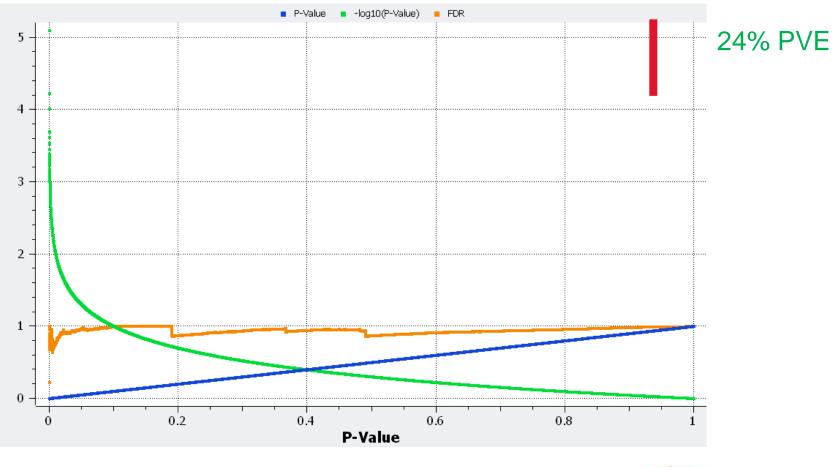


Principal component analysis of *B. carinata* genotypes





Genome-wide markers associated with shatter resistance in *B. carinata*





Summary

- Based on pod strength (high rupture energy) and pod anatomy
 - Identified several accessions of *B. carinata* and five
 - of B. rapa less prone to pod shatter
- Evaluating new-type napus (A^{r/n}A^{r/n}C^{c/n}C^{c/n}) and *B. napus/B. carinata*, *B. napus/B. rapa* introgression lines
 - China (Dr. Jingling Meng)
 - India/Australia (Dr. Phil Salisbury, UM)
 - Nuseed (Dr. Nelson Gororo)
- GWA signals are being validated in the bi-parental populations
- Identifying candidate genes for pod shatter resistance in B. rapa and B. carinata



Acknowledgements

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- Phil Salisbury
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- Andrew Easton



Grains Research & Development Corporation

