

Identification of genomic regions and candidate genes for resistance to pod shatter in Brassica

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Priority traits for NBGIP and outputs

- Drought tolerance
 - Early vigour
 - CID
 - WSC
 - Grain yield
- Blackleg resistance
 - *R* and *QR* genes
- Pod shatter resistance
- Heat tolerance
- Oil content stability
- Mapped 13 biparental populations plus 2 GWAS panels
 - BnASSYT (374 lines)
 - ABnHDS (300 plus lines)
- Accessed ~1,000 lines from overseas
- Made available ~3,000 lines to canola breeding companies + data
- Developed TILLING population (DPI)+ genome resequenced
- Published 20 papers

Globally, pod shattering is a major issue for canola production



❖ Windrowing/Desiccants (Reglone)

❖ Pod sealant

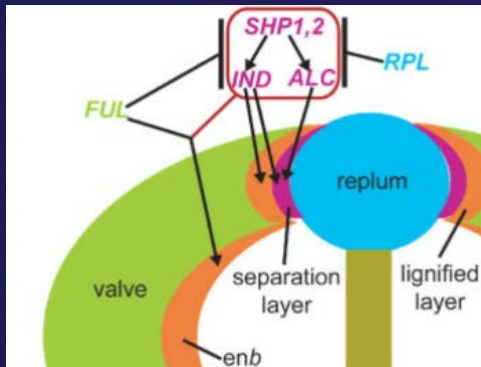
❖ Mechanical harvesting is preferred

❖ Shatter tolerant varieties

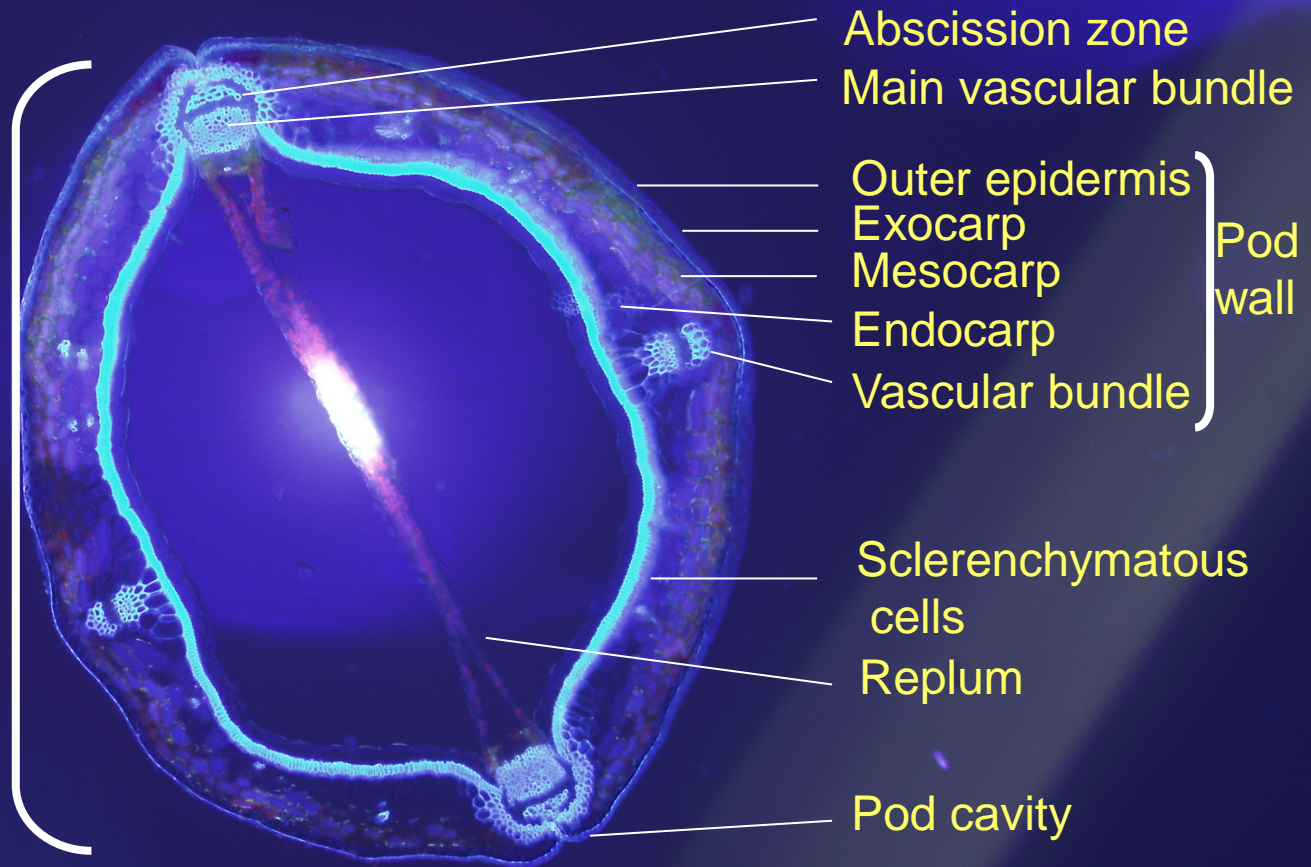


Transverse section of Brassica pod (Raman et al 2014, PLOS ONE)

Valve



Dong and Wang
(2015) Front. Plant
Sci



500 μ m

Pipelines for pod shatter resistance

B. napus

- Three DH populations from BLN2762/Surpass400, R1/R2, and R11/Z11
- Two GWAS panels (180 lines from Australia, 144 lines from China)

B. rapa

- 100 accessions (AGG)
- F_{2:3} population

B. carinata

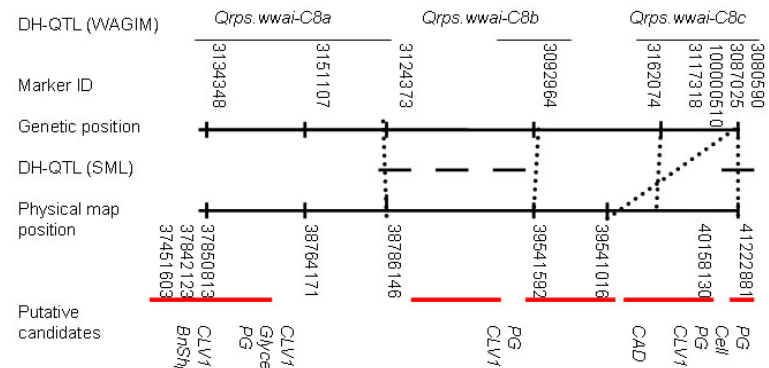
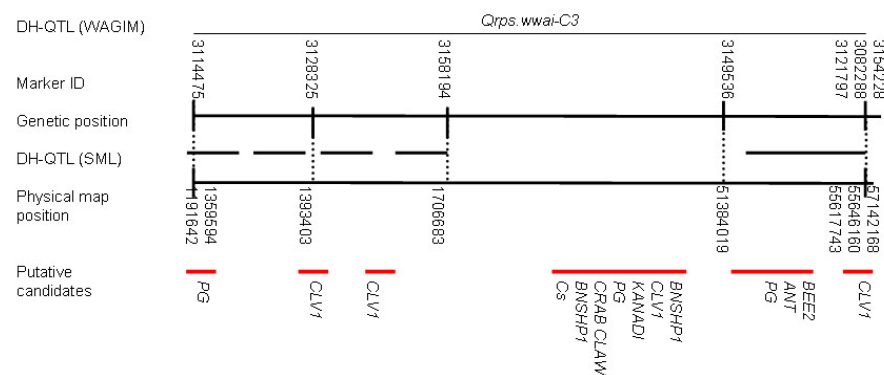
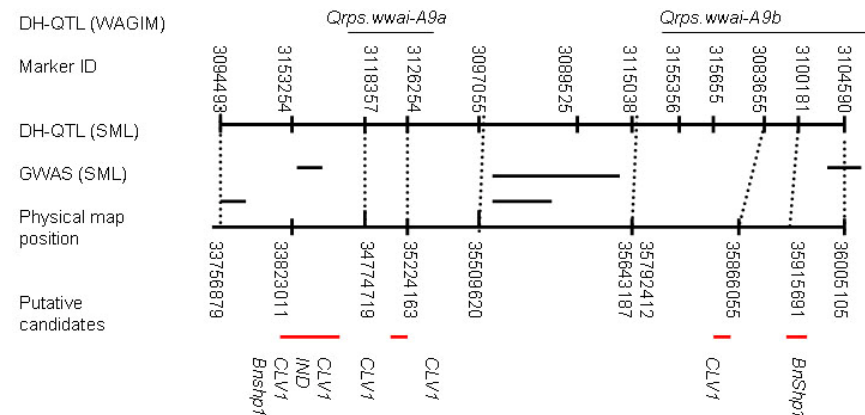
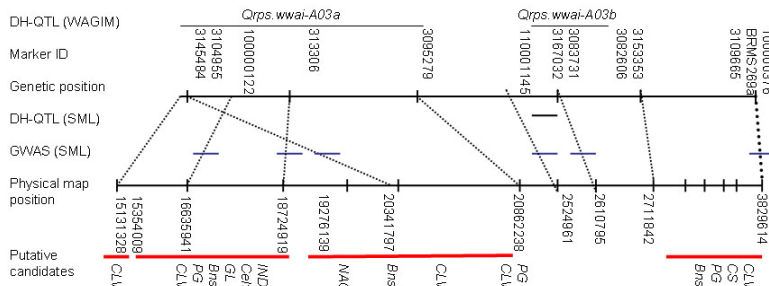
- 83 accessions (AGG)
- F_{2:3} population
- YW DH population (HAU, China)

Pendulum Test

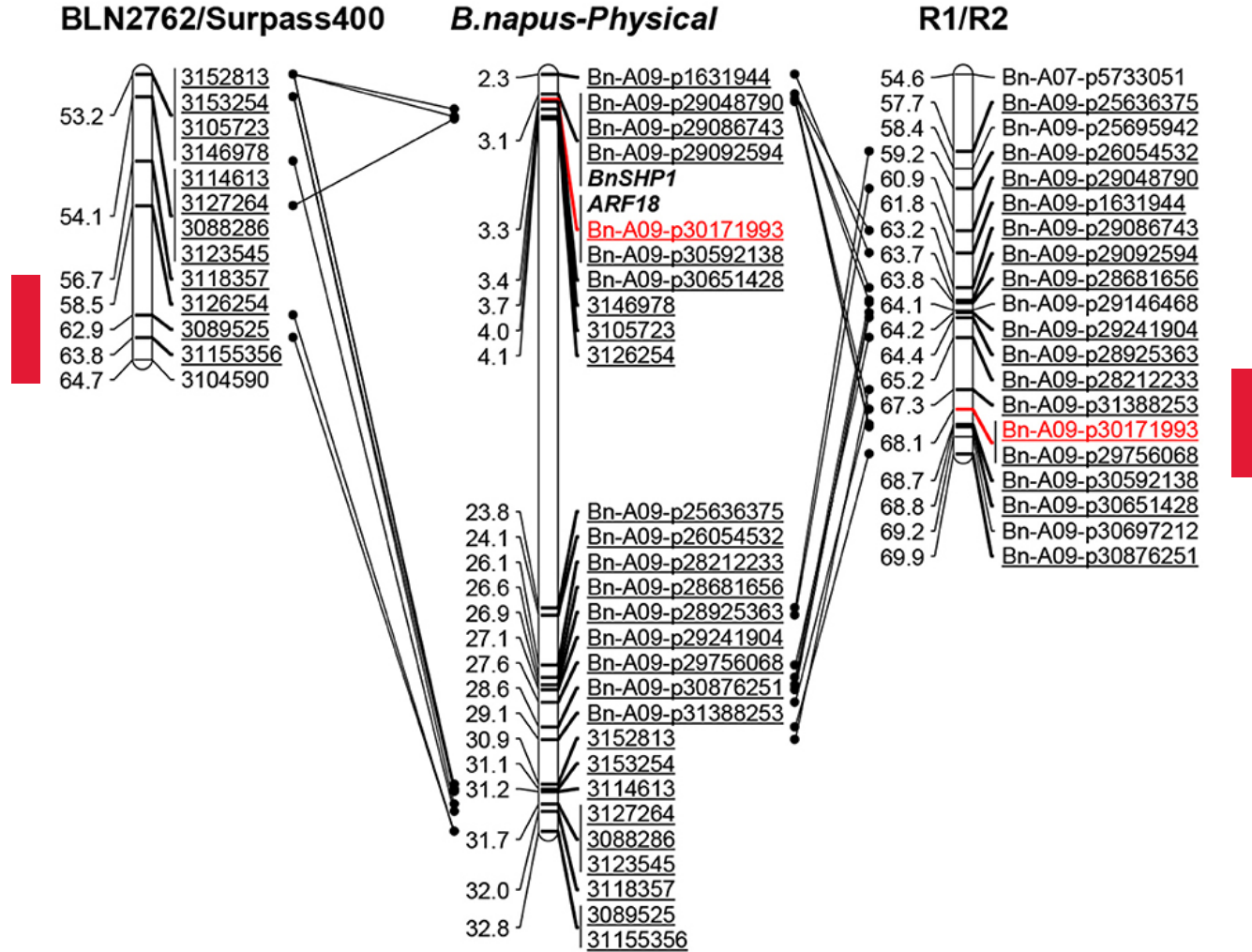
Rupture Energy

Random Impact

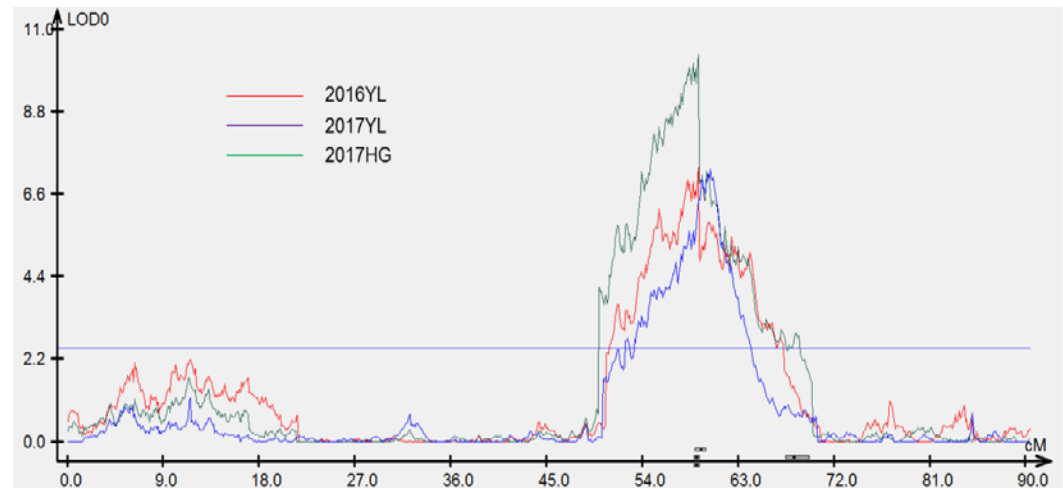
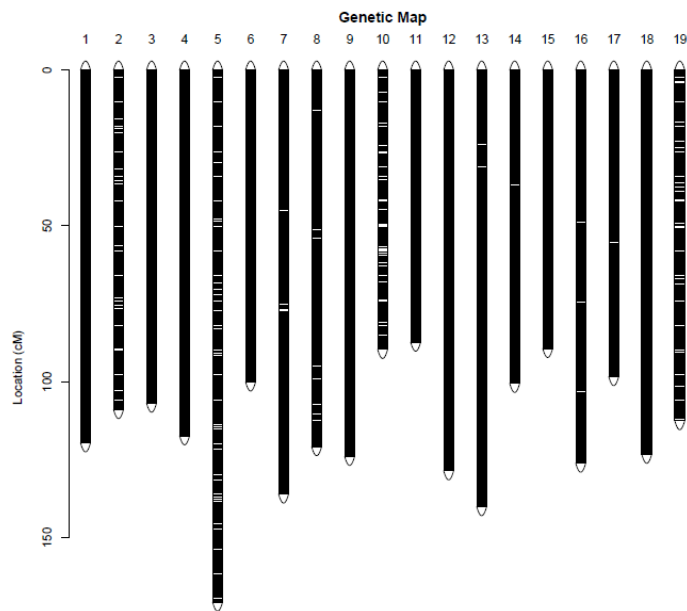
Mapped QTL involved in pod shatter resistance (Raman et al 2014)



Consistent QTL for pod shatter resistance maps on A09 (Raman et al 2014 & Liu et. al. 2016)

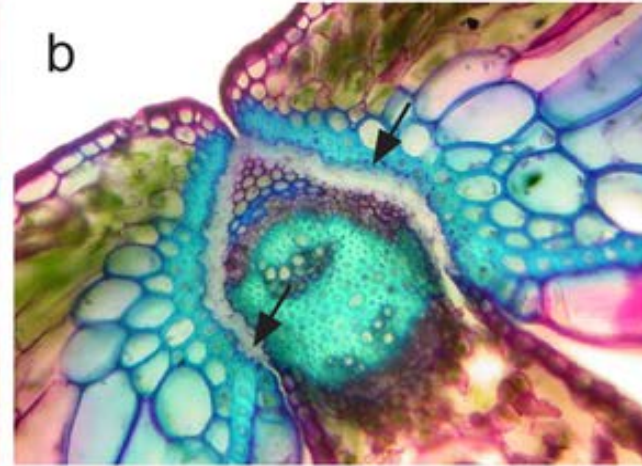
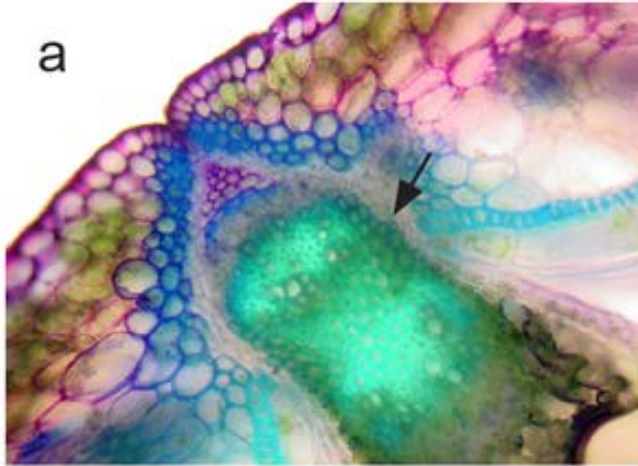


Mapped a stable QTL for pod shatter resistance in the R11/Z11 (Wang et al, in prep)

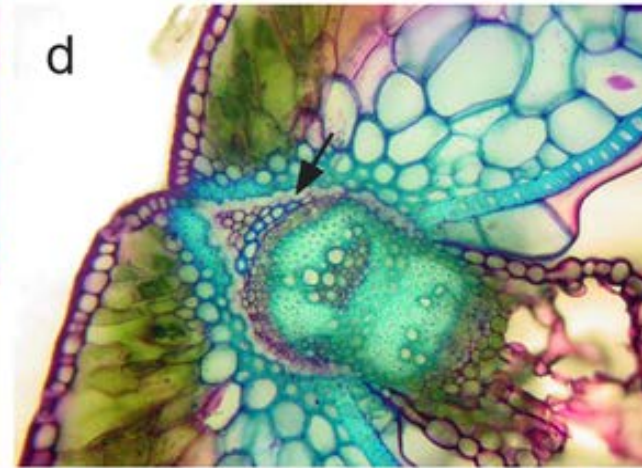
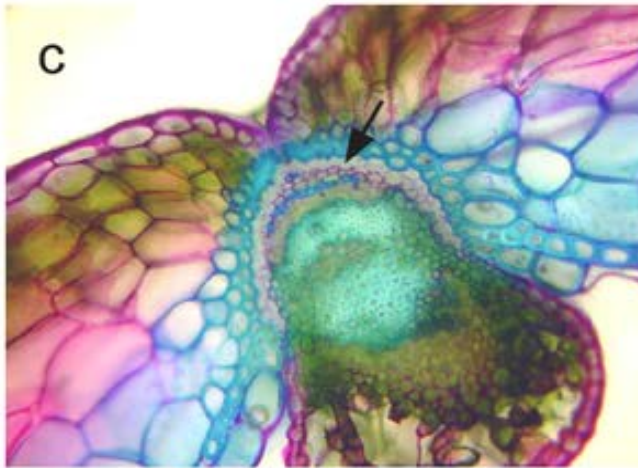


WGR based 16341 markers

Four exemplar haplotypes from the DH population derived from BLN2762/Surpass400



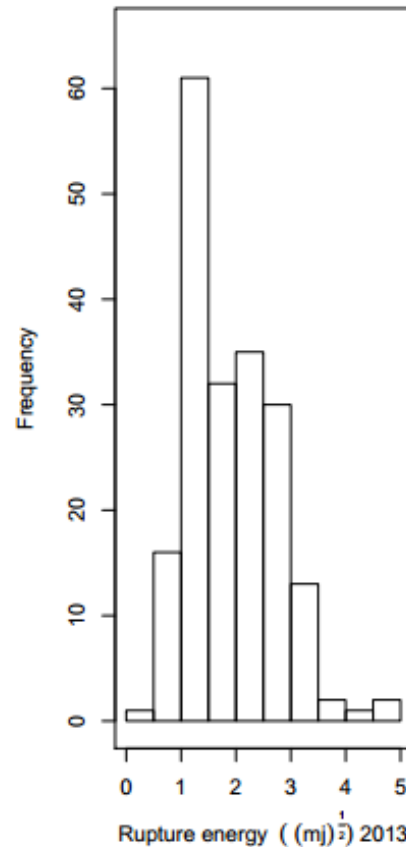
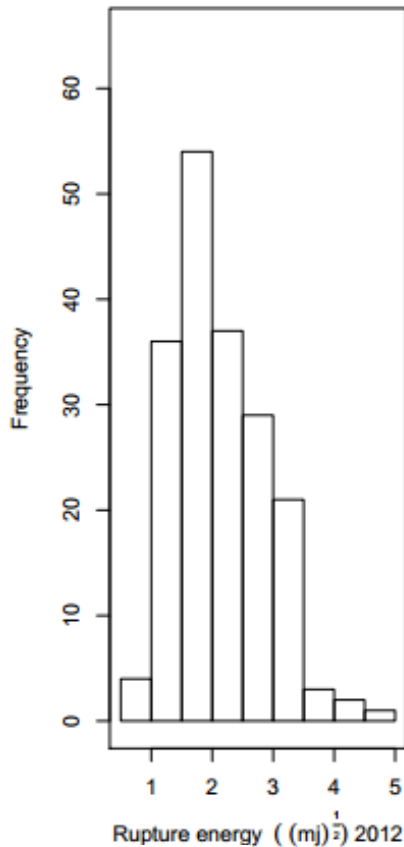
*Shatterproof1-1
Indehiscent 1-1*



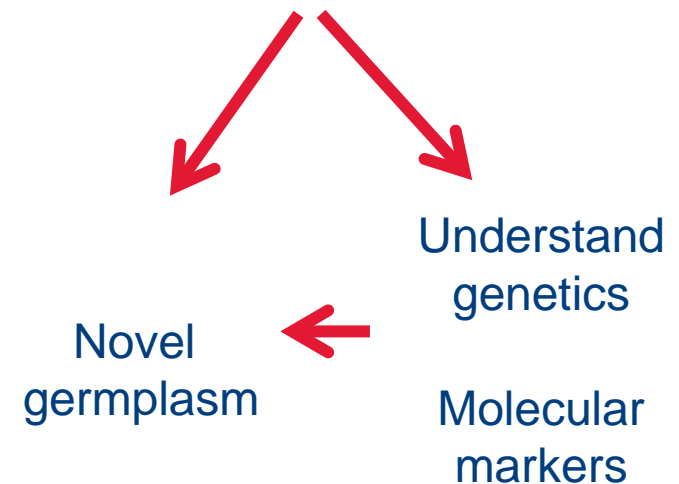
*Shatterproof1-2
Indehiscent 1-2*

Raman H, Raman R, Kilian A, Detering F, Carling J, et al. (2014) Genome-Wide Delineation of Natural Variation for Pod Shatter Resistance in *Brassica napus*. PLOS ONE 9(7): e101673. <https://doi.org/10.1371/journal.pone.0101673>
<http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0101673>

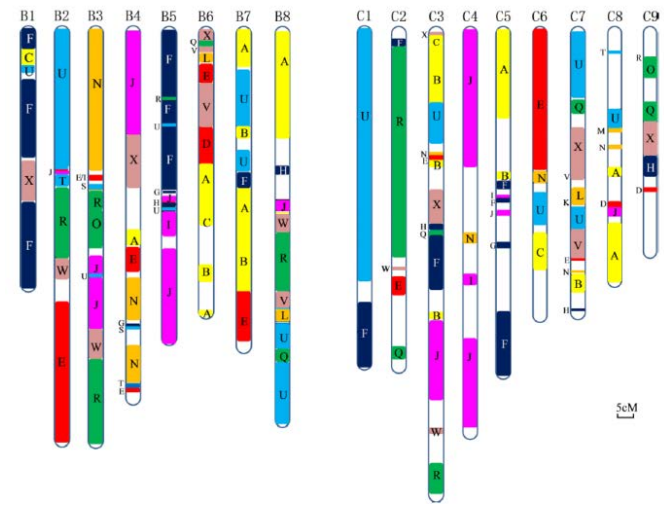
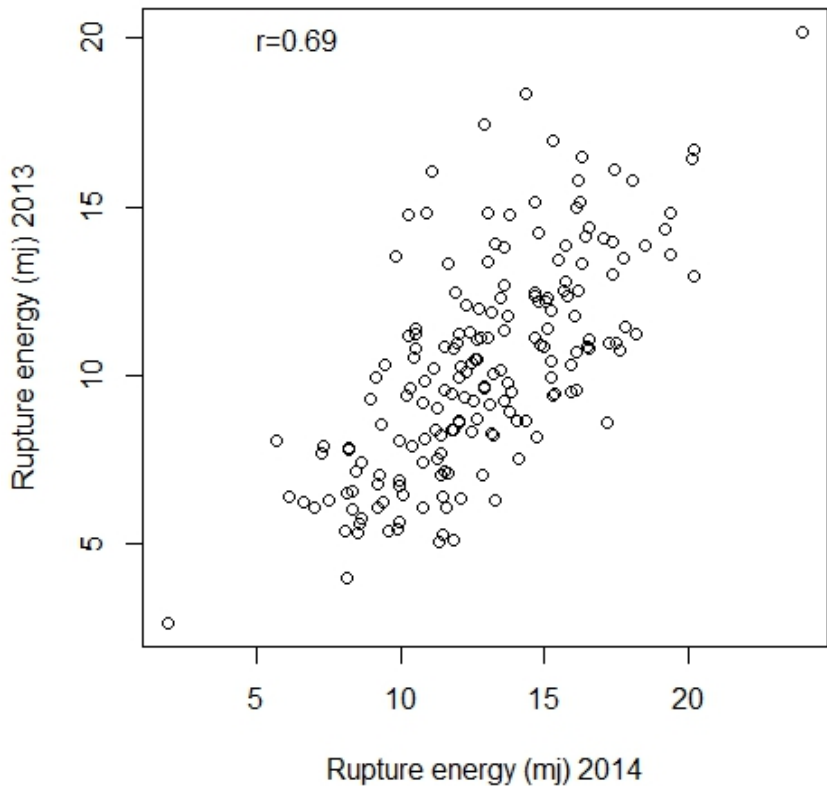
New sources of pod shatter resistance in *Brassicaceae*



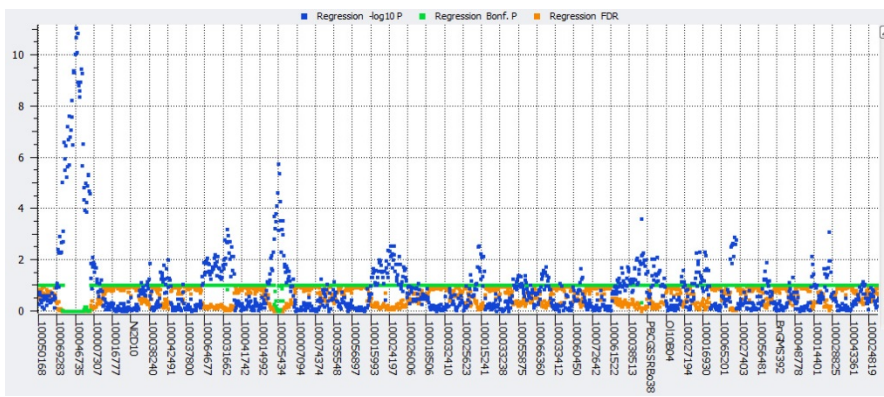
B. napus 2.1 to 4.3mJ
B. rapa 0.41 to 9mJ
B. carinata 2 to 20.8mJ



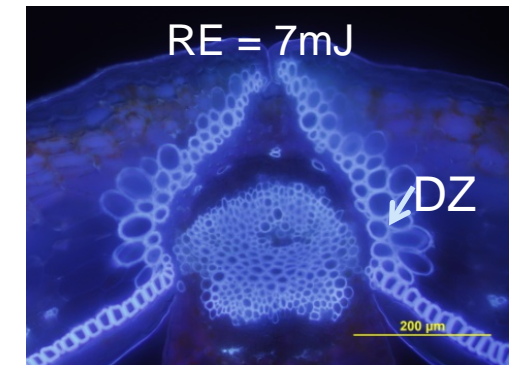
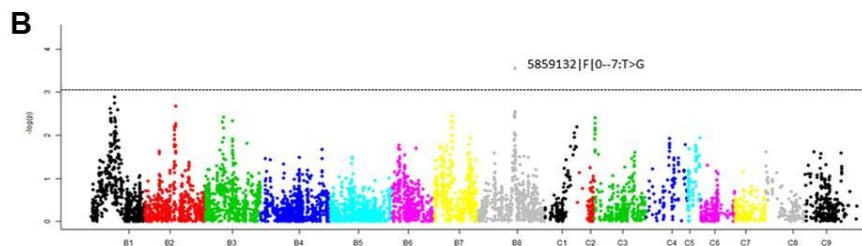
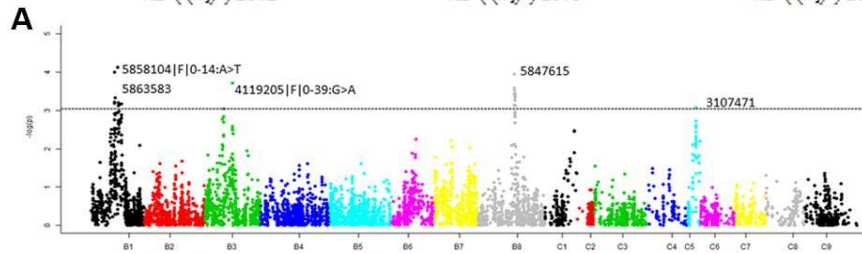
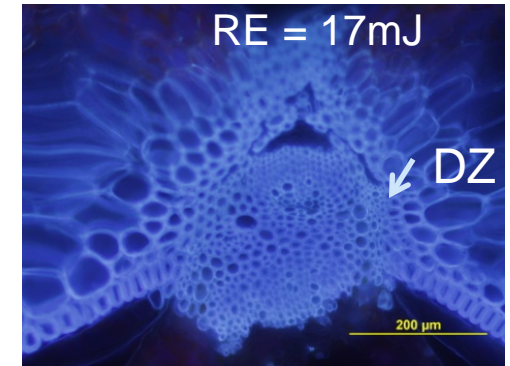
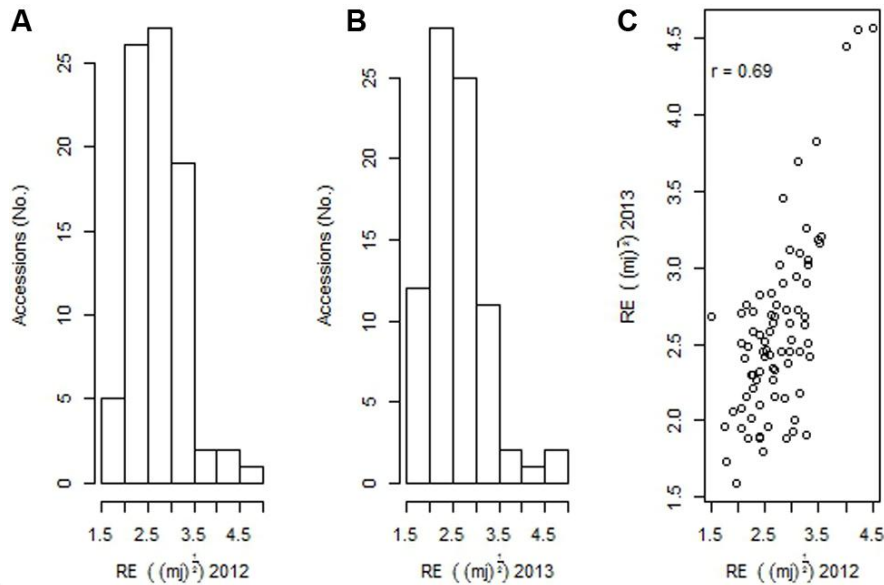
Mapped QTL for pod shatter resistance in *B. carinata* YWDH population (Raman et al, unpubl.)



Theor Appl Genet 127:1593–1605



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

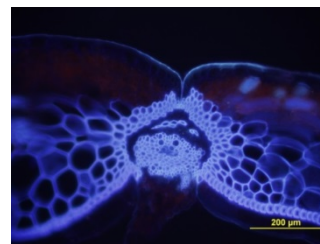


Mapped pod shatter resistance loci in $F_{2:3}$ population of *B. rapa* using WGR (Raman et al, unpublished)

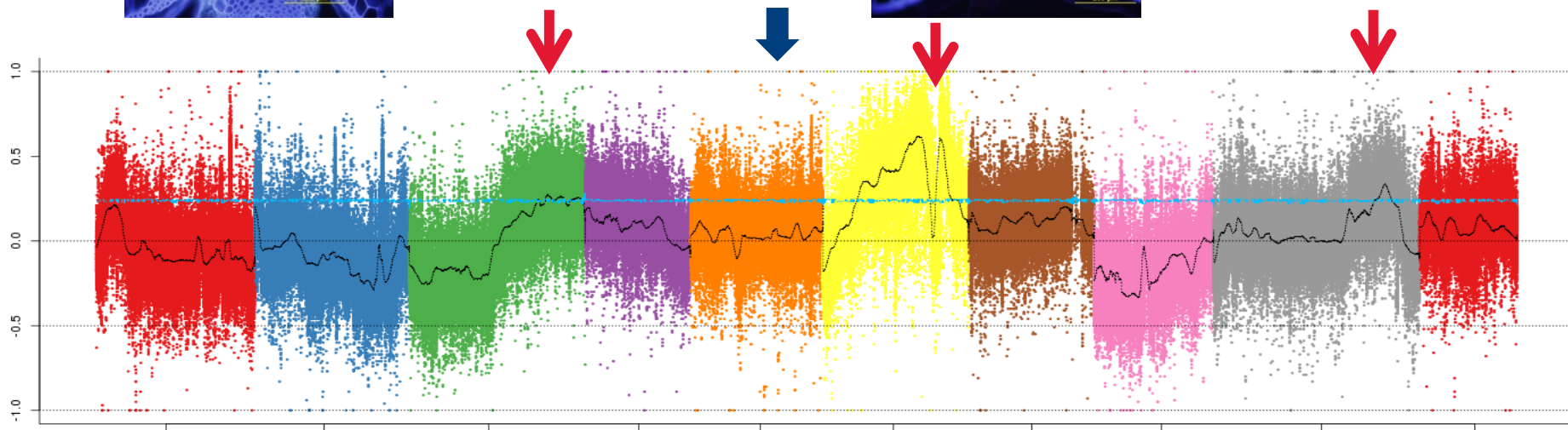


Shatter resistant parent (RE = 8mJ)

X



Shatter prone parent (RE = 2mJ)



Validated genomic regions via QTL mapping

Tracing pod shatter resistance alleles in canola

Pod shatter resistance research on interspecific crosses

B. rapa/
B. carinata

- Combining pod shatter resistance loci from *B. rapa*/*B. carinata* under a GRDC funded project (2017-2020)
- Evaluated germplasm accessed by NSW DPI from HAU, China
- Two promising accessions with pod shatter resistance in 2017 season (**Delayed harvest**)

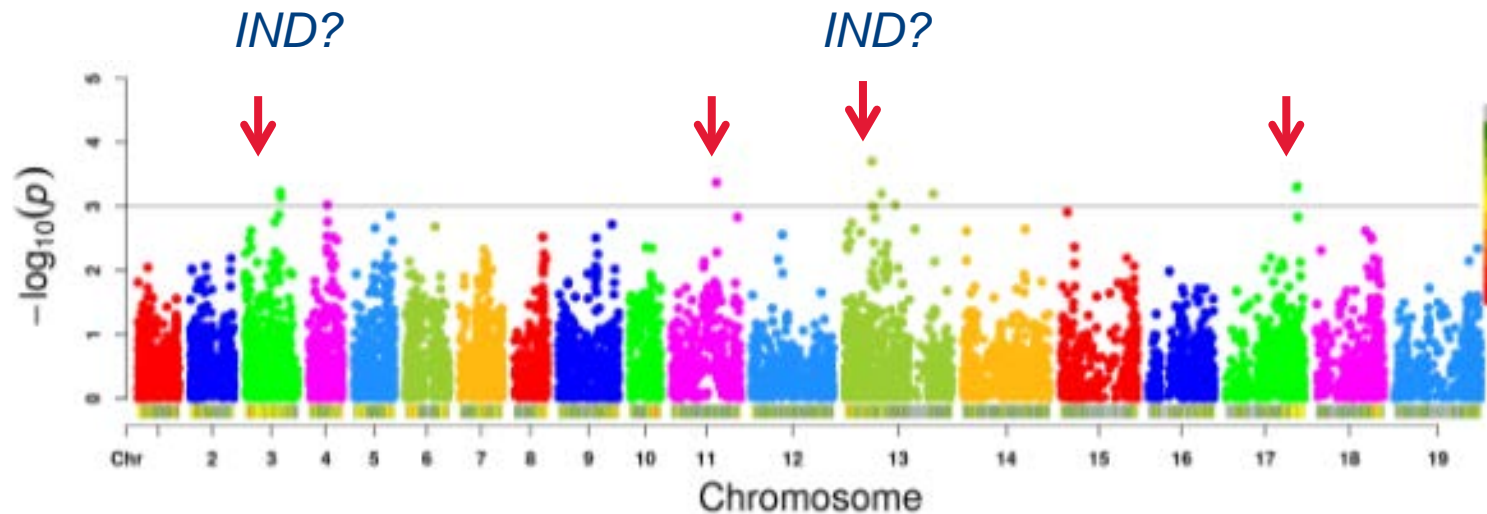
Interspecific
source from
Nuseed

- 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 (2017)

B. napus/*B.*
carinata

- Accessions derived from *B. napus*/*B. carinata* lines 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*

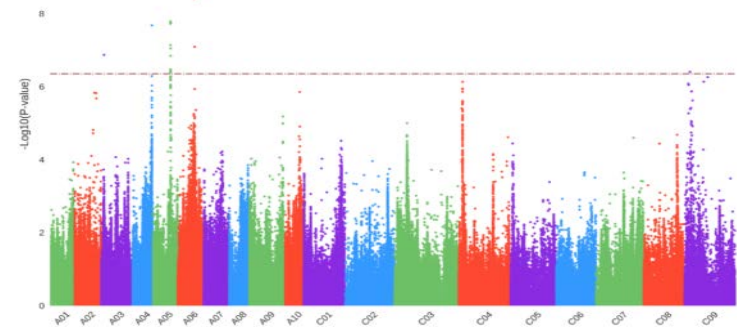
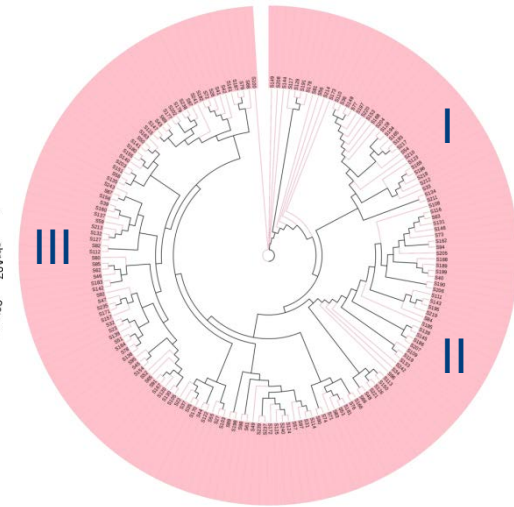
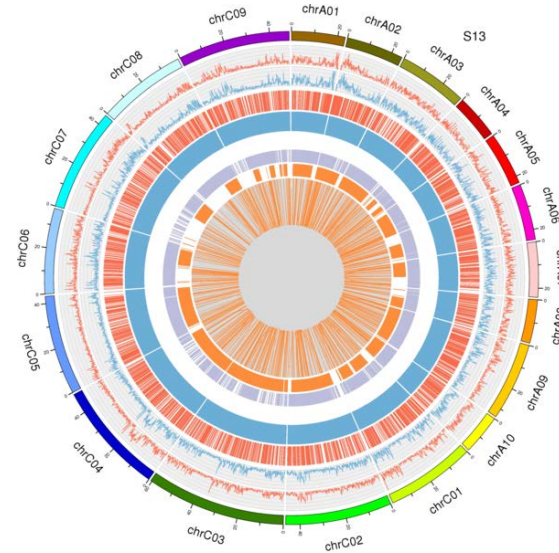
Genetic analysis of *B. napus*/*B. carinata*/*B. napus* lines



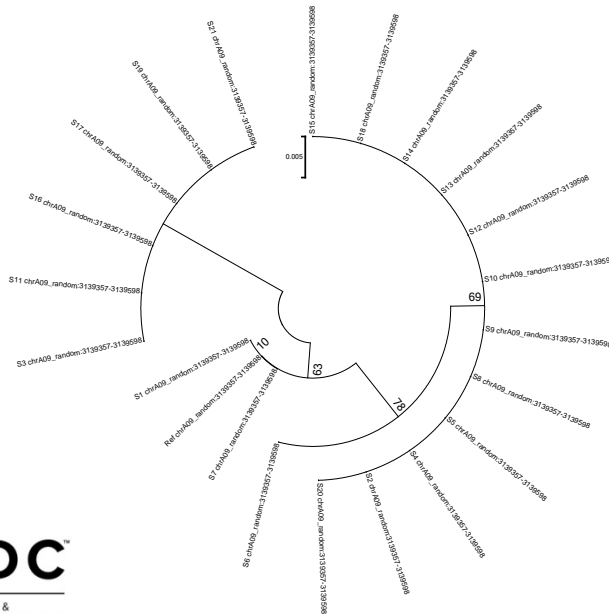
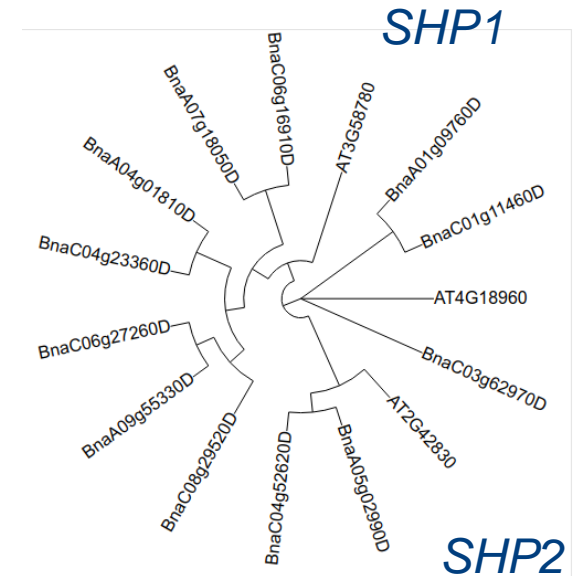
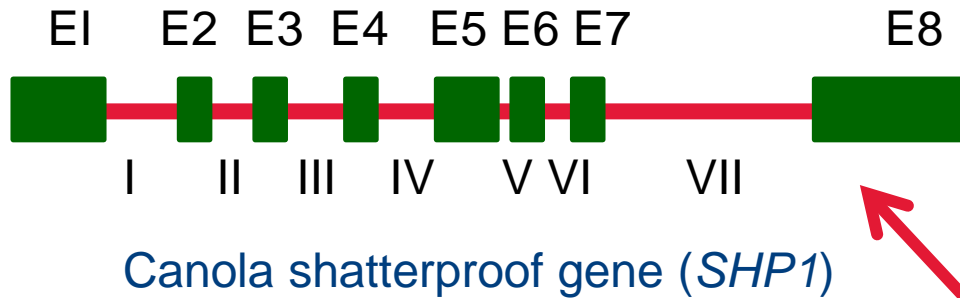
Resequenced parental and GWAS panel of NBGIP (DAN00208)

- 21 parental lines of NBGIP mapping populations (90Gb)
- 5 parental lines of *B. carinata*
- 2 parental lines of *B. rapa*

- 174 line of ABnGDS set
- Population structure, LD, sweep
- Trait genetic analysis for blackleg, grain yield, flowering time, pod shatter, and Mn^{2+}/Al^{3+} tolerance
- Genomic selection (GS)



Allelic variation in candidate genes controlling pod shatter resistance



Acknowledgments

- Jacqui Batley (UQ)
- David Edwards (UQ)
- Simon Diffey
- Andrew Easton (Advanta)
- Greg Buzza (Nuseed)
- Bob Redden (DEDJTR)
- Isobel Parkin (AAFC Canada)
- Fred Fuller (NSW DPI)
- Brett McVittie (NSW DPI)
- Casual Staff (NSW DPI)



Department of
Primary Industries

A scenic landscape featuring a vibrant yellow field in the middle ground, a lush green pasture in the foreground with a flock of sheep, and a line of trees in the background under a cloudy sky. The text "Thank you!" is overlaid in the center, rendered in a brown, textured, 3D-style font with a black outline.

Thank you!