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Research Highlights on NBGIP (DAN00208/DAN00117)

Mapped canola populations for blackleg resistance

<table>
<thead>
<tr>
<th>Qualitative</th>
<th>Quantitative</th>
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<tbody>
<tr>
<td>DH populations</td>
<td>DH populations</td>
</tr>
<tr>
<td>Skipton/Ag-Spectrum</td>
<td>Skipton/Ag-Spectrum</td>
</tr>
<tr>
<td>Maxol/Westar</td>
<td>Ag-Castle/Topas</td>
</tr>
<tr>
<td>Columbus/Westar</td>
<td>RP04/Ag-Outback</td>
</tr>
<tr>
<td>BLN2762/Surpass</td>
<td>11-5107 (Hyola50)</td>
</tr>
<tr>
<td>Ag-Castle/Westar</td>
<td>11-5329 (Hyola50)</td>
</tr>
<tr>
<td>RP04/Ag-Outback</td>
<td>ATR-Coblet/BLN3343</td>
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<tr>
<td>11-5107 (Hyola50)</td>
<td>Darmor/Yudal</td>
</tr>
<tr>
<td>11-5329 (Hyola50)</td>
<td>GWAS panels</td>
</tr>
<tr>
<td>ATR-Coblet/BLN3343</td>
<td>BiASBYST (350+ lines)</td>
</tr>
<tr>
<td>Darmor/Yudal</td>
<td>AuHGD5 (100+ lines)</td>
</tr>
</tbody>
</table>

Reference
Raman et al (2013)-TAG
Raman et al (2012)-AJAR
Tollerare et al (2014)-PBJ
Raman et al (2014)-PBJ
Raman et al (2016)-FIPS
Larkan et al (2016)-BMC

Maped resistance loci in Darmor-bzh/Yudal DH population (Raman et al, unpublished)

- Single spore isolates (Wagga)
- Field evaluation (2016, Wagga)- NSW DPI
- Assespro shower test (DELT/Grain Marketing Pathology)
- Resistance scored as Survival and internal infection

Genotyping
- 69K Illumina SNP (INRA)
- 7,066 GBS based DArT markers (NSW DPI)

Markets
- 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%

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

- Bn-A09-p29012402,3133535_34:G>C
- Cation diffusion facilitator
- BnaA09g37250D:
- A T3G58060.1:
- S. hamata
- 3099164_68:A>T

Three pipelines for pod shatter resistance research

- Evaluated 150 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
- 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
- Mapped loci for pod shatter resistance in an F2 population and YWDH population

- 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

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

- Evaluated germplasm accessions from China
- Two promising accessions with pod shatter resistance were identified in 2017
- Combining pod shatter resistance loci from *B. rapa x B. carinata* under a new GRDC funded project (2017-2020)
- Accessions derived from *B. rapa* lines were mainly from UNH45
- Identified one accession that had good pod shatter resistance
- Developed a mapping population from *B. rapa* lines and *B. rapa* (NSW DPI)

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Dissected WUE related traits in canola

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Phen. Genotype</th>
<th>Seed N.W.</th>
<th>N.DVI</th>
<th>Days Differentiational Height</th>
<th>CID</th>
<th>WSC</th>
</tr>
</thead>
<tbody>
<tr>
<td>RP04/Ag-Outback DH 2</td>
<td>Skipton/Ag-Spectrum DH 4</td>
<td>Hyola50 (11-5107) DH 2-3</td>
<td>Hyola50 (11-5329) DH 2-3</td>
<td>Tarcoola-22/Tarcoola-69 DH 2</td>
<td>Charlton/Monty DH 2-3</td>
<td>06-5101 DH 3</td>
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<tr>
<td>Interspecific source from Nuseed</td>
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Gained knowledge on candidate genes involved in vernalisation response in canola

Raman et al 2013, Plant Cell & Environ

Raman et al 2014, PBJ

Raman et al (2016) Plant Cell & Envir

- 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)
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

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