

# The Australian Canola Molecular Marker Program - An Update on mapping loci controlling resistance to blackleg in canola

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# DH populations for mapping R genes

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## I&I NSW (Wagga)

- ❖ Skipton/Ag-Spectrum (191 lines)
- ❖ BLN3347/Carousel-10 (82 lines)
- ❖ BLN1981-5/Surpass400 (139 lines)
- ❖ BLN1990/95-17033 (193 lines)
- ❖ 95-17033/Av-Sapphire (114 lines)
- ❖ Zhongshuang No4/Ag-Spectrum (202 lines)

## VIC DPI (Horsham)

- ❖ Columbus\*3/Westar 10 (318 lines)
- ❖ Maxol\*1/Westar 10 (442 lines)
- ❖ DHC2211/RP012\*S (198 lines)
- ❖ DHC2261/RR005 (372 lines)
- ❖ Ag-Castle\*4/Westar10 (173 lines)
- ❖ RP004/Ag-Outback (183 lines)
- ❖ BLN1400/RN15//RL\*8S/BLN1695\*S (85 lines)

# Screening for blackleg resistance

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**Two DH populations from**

- **Skipton/Ag-Spectrum -188 lines**
- **BLN3347/Carousel-10- 82 lines**

**Phenotyping**

- **Cotyledon stage (Marcroft Grain Pathology labs)**
- **Adult plant resistance (Marcroft Grain Pathology labs)**
- **Field resistance in blackleg nursery (NSW DII Wagga)**
  
- **Resistance was evaluated according to National protocol.**

# Identified appropriate isolates for mapping R gene

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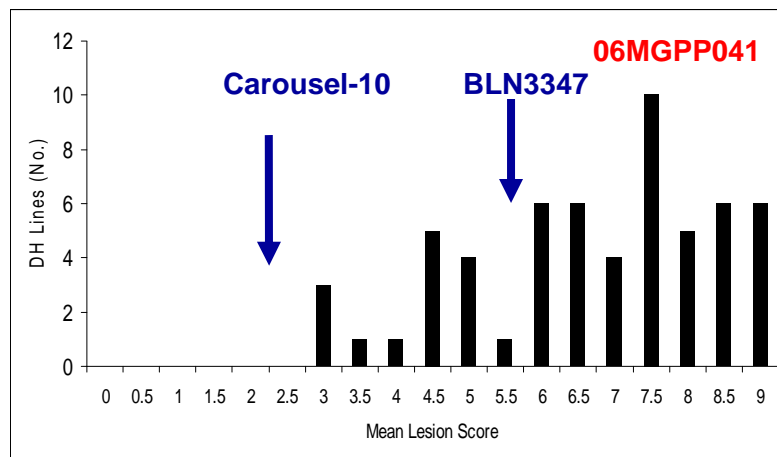
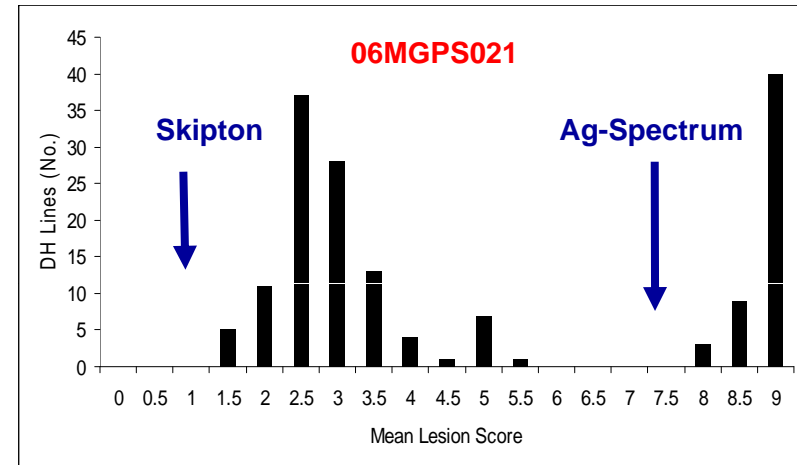
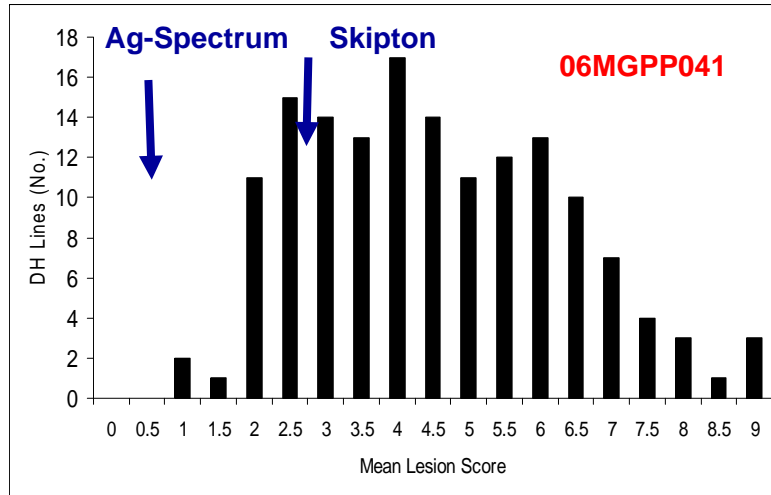
## Eight genotypes of *B. napus*

- ❖ BLN3347
- ❖ Carousel (*Rlm1*, *Rlm2*, poly)
- ❖ Carousel-10 (*Rlm1*, *Rlm2*, poly)
- ❖ Skipton (Poly)
- ❖ Ag-Spectrum (Poly)
- ❖ Beacon (*Rlm3*, *Rlm4*, *Rlm9*)
- ❖ Surpass400 (*LepR3*, *Rlm1*)
- ❖ Q2 (Susceptible, *Rlm3*?)

## 11 isolate of *L. maculans*

- ❖ 04MGPP016
- ❖ 04MGPP031
- ❖ 04MGPP041
- ❖ 04MGPS010
- ❖ 04MGPS014
- ❖ 04MGPS015
- ❖ 04MGPS021
- ❖ 05MGPP028
- ❖ 06MGPP019
- ❖ 06MGPP041

# Phenograms showing segregation for blackleg resistance



# Phenotyping for field resistance at Wagga Wagga

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- **Skipton/Ag-Spectrum population was evaluated for resistance in the blackleg nursery**
  - July 18, 2008
  - 177 DH lines, 2 parents and a susceptible check (Karoo)
  - 2 Replication
- **10 plants/DH line were uprooted and internal infection was assessed**
- **DH lines showed segregation for internal infection**
  - but infection was **NOT** uniform

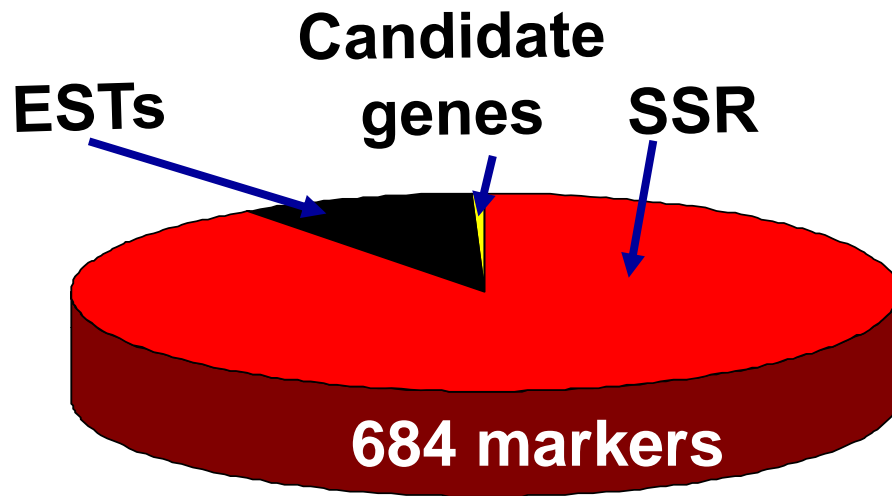
# Publically available SNP markers

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- More than 100 SNP markers have been identified in Brassica species
  - HPLC
  - Dot blot
  - Primer extension
  - InDELS
  - Goldengate assay (ARC)
- At Wagga, I&I procured Rotor gene machine
- Planned for HRM analysis

# Molecular mapping of DH populations

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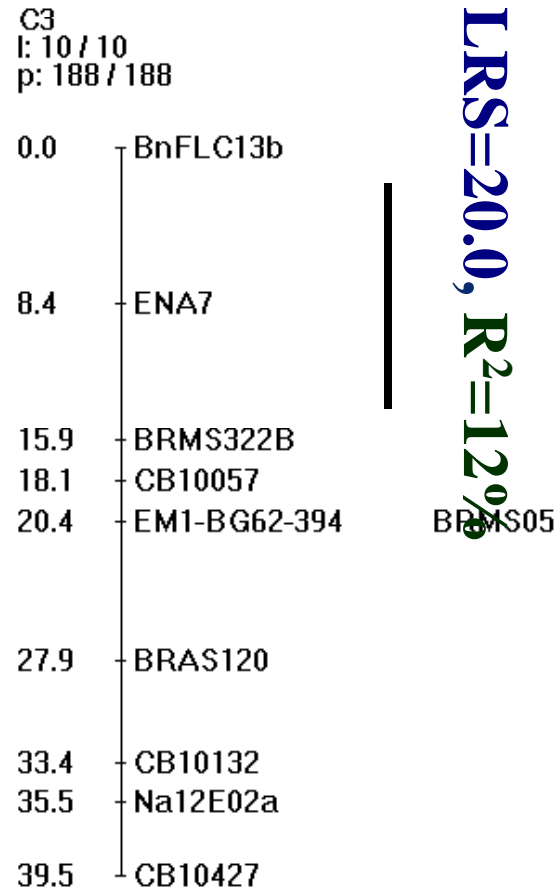
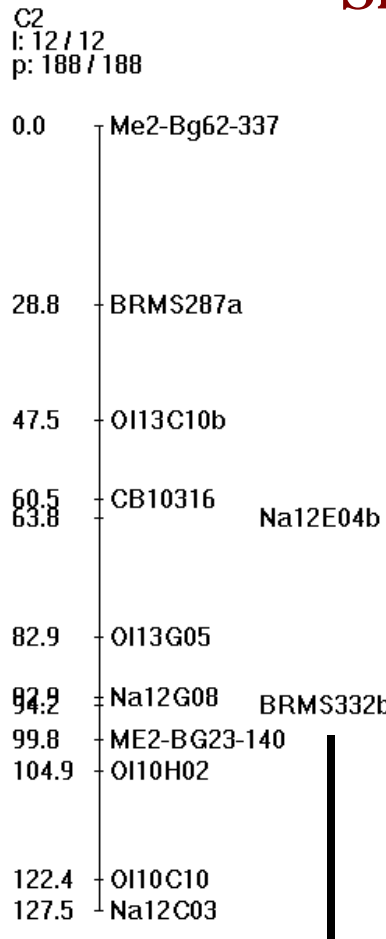


- BLN3347/Carousel-10 ( ~142 SSR markers)
- Skipton/Ag-Spectrum (215 SR/SRAP/EST markers)
- BLN2762/Surpass400 (85 SSR/EST markers)

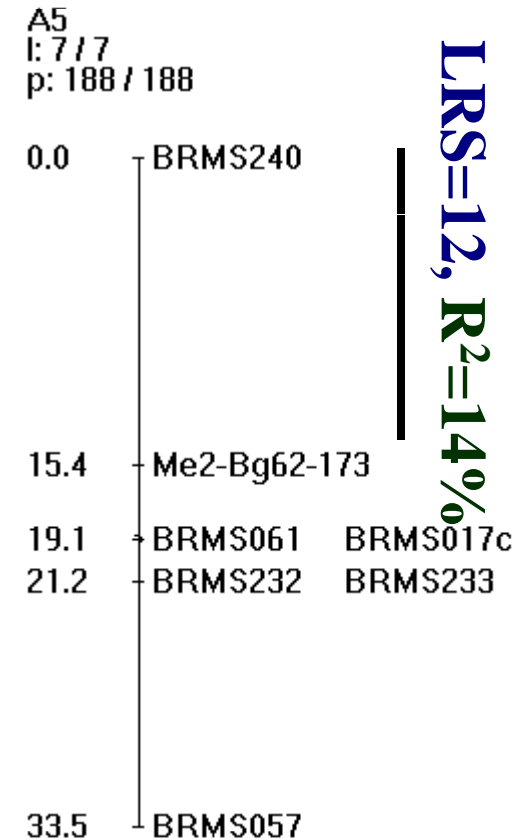


# QTL analysis for field resistance

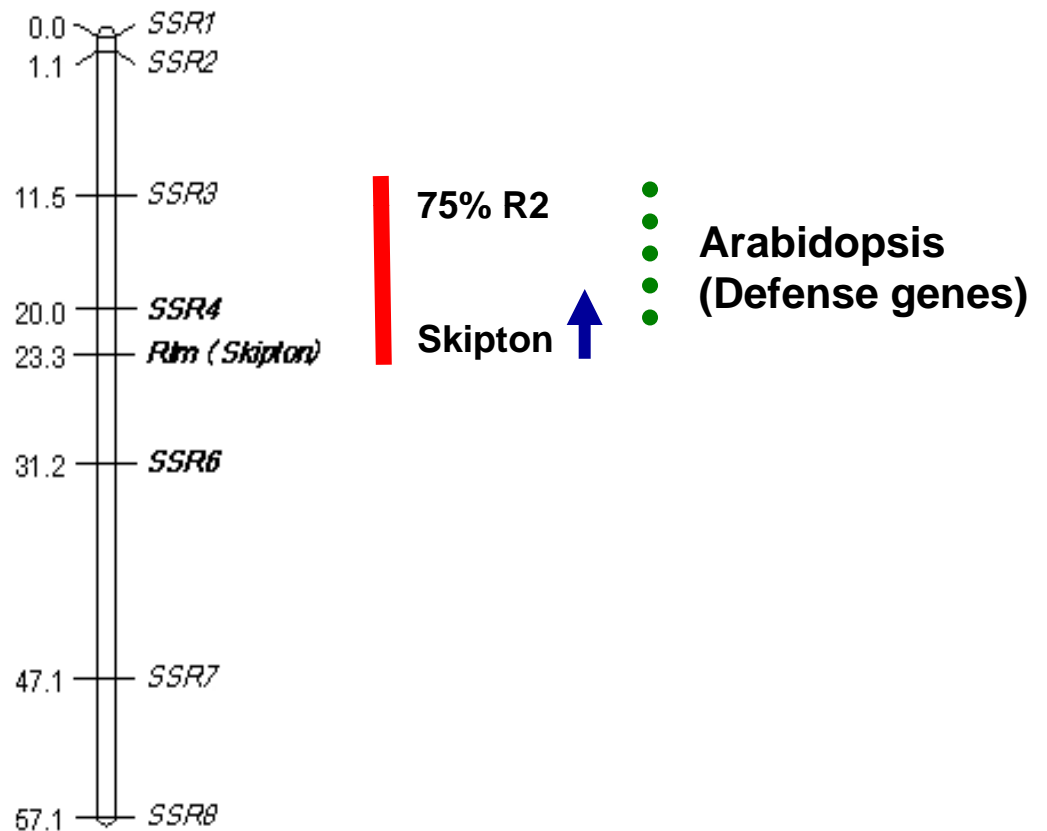
## Skipton alleles



## Ag-Spec allele

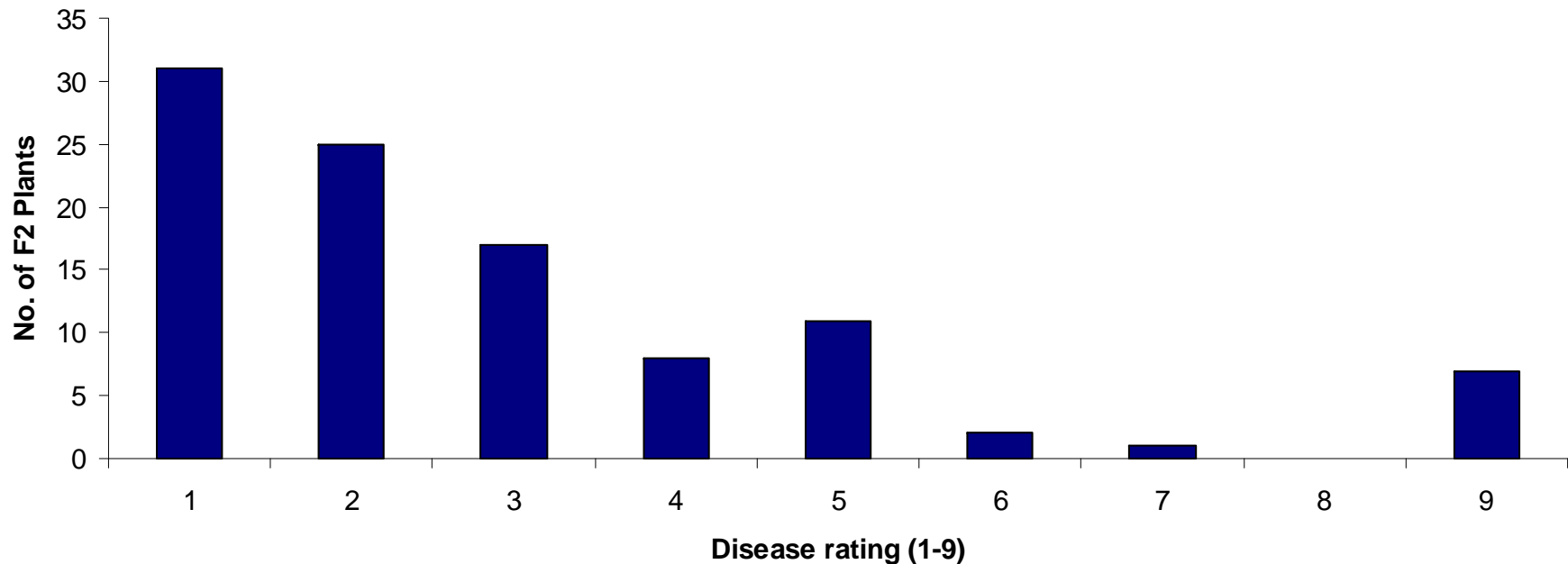


# Mapped a race-specific resistance gene on chromosome A7

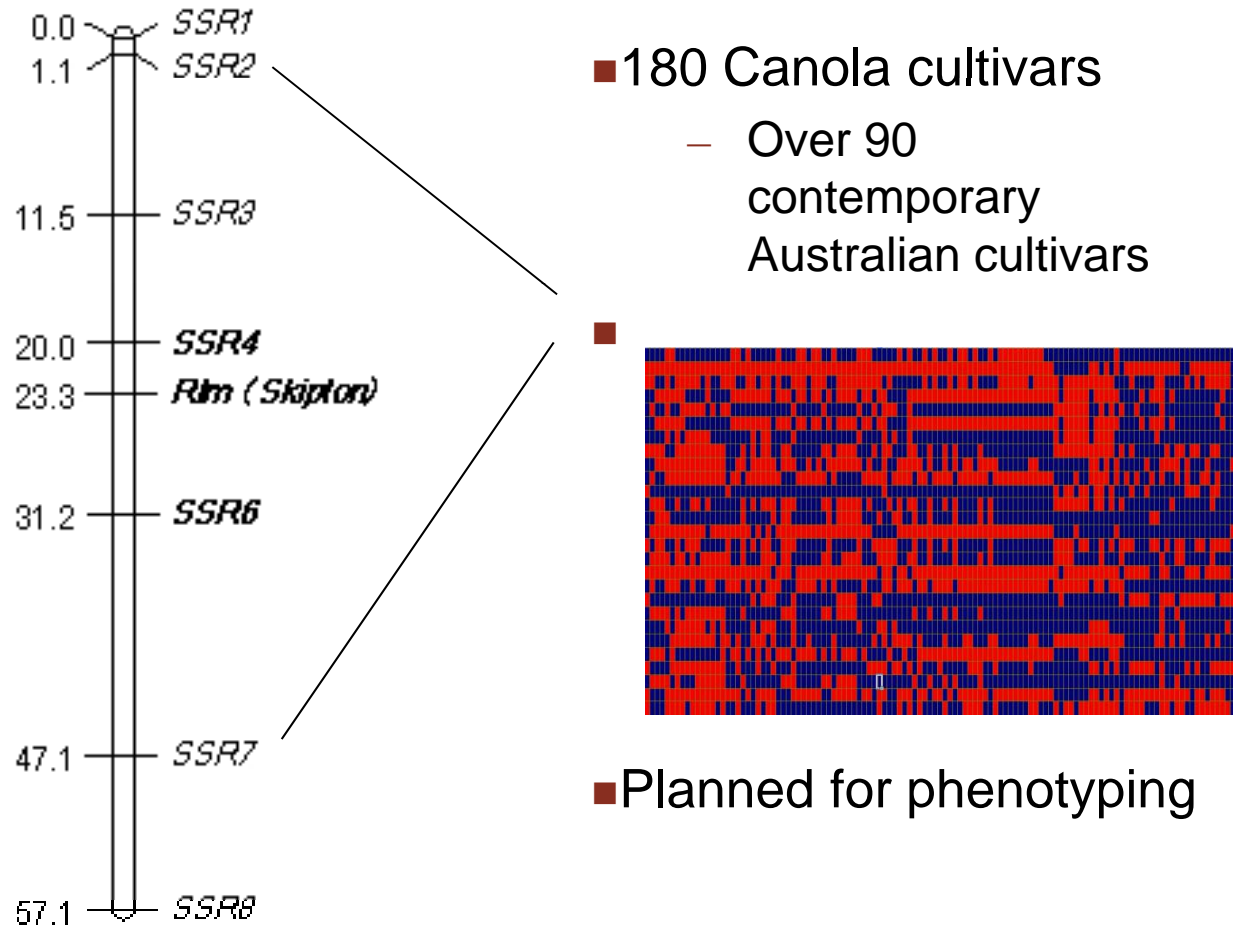


# Rlm(sk) is a dominant R gene

- 102 F2 plants from Skipton/Ag-Spectrum was evaluated with race specific isolate
  - Inoculated at seedling stage
  - 81 R:21S



# Allele diversity at *Rlm(Skipton)* locus



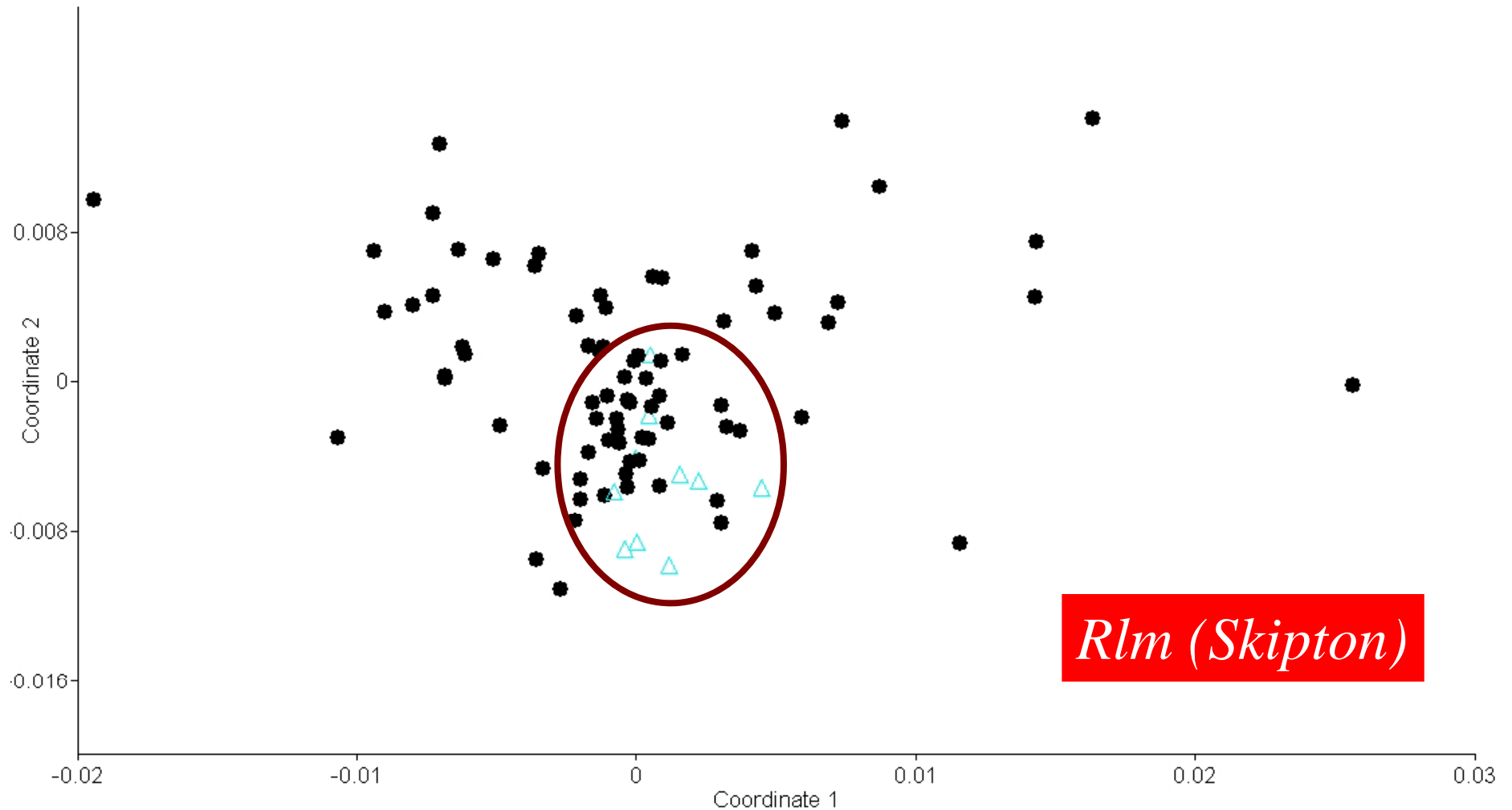
# Validation for blackleg resistance

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- 188 genotypes
- Screened with six markers linked with resistance
- 164bp-allele in cultivars having *Rlm4* gene
  - ATR Barra, AG-Emblem, Av Sapphire, ATR Summit, Dunkeld, Karoo, Major, Maluka, Monty, Oscar, Rainbow, Range, Ripper, Scoop, Shiralee, Skipton, Tarcoola, Tornado, Thunder, Wesroona
  - But not in Hyola61, Hyola76, Tower, Iwao Natane, and WA50097
- SSR Marker is linked with BLR in Skipton and can be used for MAS.

# Relationship among diverse canola genotypes (R may be derived from a single source)

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# First delivery from CMMP

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Closely linked  
markers for  
blackleg  
resistance in  
Skipton



# Mapping of BLR in BLN2762/Surpass400

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- 140 DH lines
- Phenotyping (March-April 2010)
- Framework map ready (Feb 2010)
- Map loci associated with BLR (Oct 2010)



# Conclusions

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- Mapped a major locus for race specific resistance to blackleg on chromosome A7.
- Resistance is dominant
- Identified flanking markers to Rlm (Skipton) gene.
- Tested usefulness of SSR markers in 188 canola cultivars.
- Markers predict BLR sufficient enough for MAS in the Australian Canola Breeding programs

# Acknowledgments

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- Peter Heffernan (I&I NSW)
- Peter Dean (I&I NSW)
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