


GRDC
Grains Research & Development Corporation


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A review of the implementation of rotation of resistance genes

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Resistance groups concept introduced 5 years ago

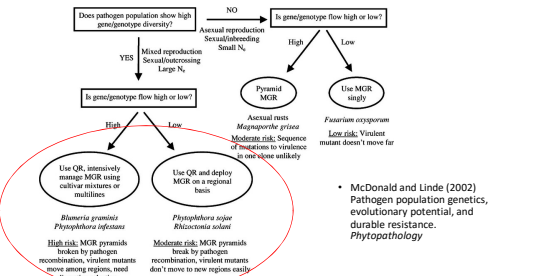


Sylvestris resistance

Non-sylvestris resistance

Suggested rotation of resistance genes can be used to minimise disease

Literature suggested rotation, mixtures or multilines were a good option for high risk pathogens



Does pathogen population show high genogroup diversity?

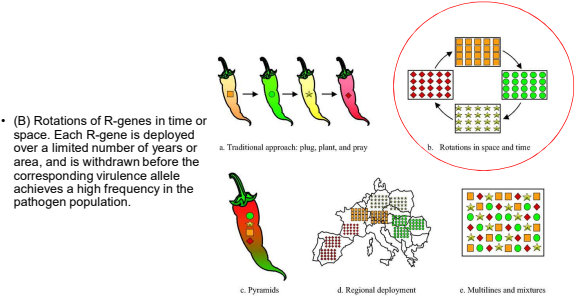
- NO: Annual reproduction, Sexual/intercrossing, Small N_e.
 - High: Pyramidal MGR
 - Low: Use MGR singly
- YES: Mixed reproduction, Sexual/intercrossing, Large N_e.
 - High: Use QR, intensively manage MGR using cultivar mixtures or multilines. (Examples: *Blumeria graminis*, *Phytophthora infestans*)
 - Low: Use QR and deploy MGR on a regional basis. (Examples: *Phytophthora sojae*, *Rhizoctonia solani*)

Additional notes:

- Asexual mass: *Magnaporthe oryzae*
- Moderate risk: Sequence of mutations to virulence in one region unlikely
- Fusarium oxysporum: Low risk; Virulent mutant doesn't move far

• McDonald and Linde (2002) Pathogen population genetics, evolutionary potential, and durable resistance. *Phytopathology*

Proposed as best model by French researchers



(B) Rotations of R-genes in time or space. Each R-gene is deployed over a limited number of years or area, and is withdrawn before the corresponding virulence allele achieves a high frequency in the pathogen population.

- a. Traditional approach: plug, plant, and pray
- b. Rotations in space and time
- c. Pyramids
- d. Regional deployment
- e. Multilines and mixtures

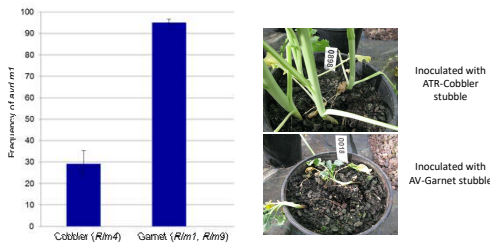
Glasshouse experiments confirm field data



Rlm1 on Rlm1 stubble Rlm1 on Rlm4 stubble

Cultivars exposed to stubble of a different cultivar have less blackleg disease compared to being exposed to their own stubble

Molecular experiments confirm field and glasshouse data



Cultivar	Frequency of virulent isolates (%)
Cobbler (Rlm4) Wagga Wagga	~30
Garnet (Rlm1, Rlm9) Mt Hope	~95

Inoculated with ATR, Cobbler stubble

Inoculated with AV-Garnet stubble

Frequency of virulent isolates varies at different sites and is influenced by the resistance genes present in individual cultivars

Need to know what resistance genes are in commercial cultivars

Resistance groups determined for all commercial cultivars

- Currently differential set = 16 isolates
- Identify major gene resistance (*Rlm1-Rlm9*, *LepR1-4*) using differential isolates
 - Issues with *LepR2* (two different seed sources, both giving different results)
- Information provided to growers

8 resistance groups including:
 Group A – *Rlm1*
 Group B – *Rlm4*
 Group C – *Rlm3*
 Group D – *LepR1*
 Group F – *Rlm6*
 Group G – Juncea (*Rlm5* + *Rlm6*)
 Group H – *Rlm7*
 Group S – *LepR3*
 Many cultivars have multiple groups e.g. ABD

Macrotill et al (2012) Crop and Pasture Science 63: 338-350

Identification of avirulence genes and development of DAIs

- Cloning of avirulence genes allows molecular markers to be made for monitoring populations
 - *AvrLm1*, *AvrLm2*, *AvrLm4-7*, *AvrLm5* (*AvrLmJ1*), *AvrLm6*
- Generate Differential Addition Isolates for characterising “unknown” sources of resistance
 - *Rlm6* in Group F
 - *Rlm1* and *Rlm4* in Group D
 - *Rlm1*, *Rlm4*, *Rlm6* in Group F
- Must have PC2 facilities

Genotypic data using the *LepR3/Rlm2* alleles correlates with phenotypic data

Examples of cultivars in the tree include: Herald A242381, LepR3/AvrLm1, Rlm1, Rlm2, Rlm3, Rlm4, Rlm5, Rlm6, Rlm7, Rlm8, Rlm9, Rlm10, Rlm11, Rlm12, Rlm13, Rlm14, Rlm15, Rlm16, Rlm17, Rlm18, Rlm19, Rlm20, Rlm21, Rlm22, Rlm23, Rlm24, Rlm25, Rlm26, Rlm27, Rlm28, Rlm29, Rlm30, Rlm31, Rlm32, Rlm33, Rlm34, Rlm35, Rlm36, Rlm37, Rlm38, Rlm39, Rlm40, Rlm41, Rlm42, Rlm43, Rlm44, Rlm45, Rlm46, Rlm47, Rlm48, Rlm49, Rlm50, Rlm51, Rlm52, Rlm53, Rlm54, Rlm55, Rlm56, Rlm57, Rlm58, Rlm59, Rlm60, Rlm61, Rlm62, Rlm63, Rlm64, Rlm65, Rlm66, Rlm67, Rlm68, Rlm69, Rlm70, Rlm71, Rlm72, Rlm73, Rlm74, Rlm75, Rlm76, Rlm77, Rlm78, Rlm79, Rlm80, Rlm81, Rlm82, Rlm83, Rlm84, Rlm85, Rlm86, Rlm87, Rlm88, Rlm89, Rlm90, Rlm91, Rlm92, Rlm93, Rlm94, Rlm95, Rlm96, Rlm97, Rlm98, Rlm99, Rlm100.

Hua Yang & Jacqui Batley

Blackleg resistance group monitoring sites

- Representative cultivars from each resistance group are sown at each monitoring site
- Disease assessed at the end of the year
- Isolates collected from sites each year (6000+ representing 2000-2017)

Warnings and regional advice provided to growers

Resistance breakdown warning in 2012

Regional disease severity monitoring provided yearly

Site	Resistance group							
	A	B	C	AD	ABD	ABCF	BF	AS
NSW								
Backum								
Barbara								
Castlemaine								
Cudal								
Gungahy								
Grainfield								
Leachhart								
Mullaley								
Parkes								
Tamworth								
Wagga Wagga								

Molecular analysis of populations supports field data

Frequency of avirulence (%)

avrLm1, avrLm4, avrLm6

Blackleg management guide

**2017 SPRING VARIETY RATINGS
FACT SHEET
BLACKLEG MANAGEMENT GUIDE**

STEP 1: Use Table 1 to determine your farm's blackleg risk

TABLE 1 Regional blackleg factors

Government factors that determine risk of lower blackleg factors	High risk	Low risk	Medium risk	Low risk
Regional waterlogging	10-15	15	15-20	20
Regional waterlogging	10-15	15	15-20	20
Regional waterlogging	10-15	15	15-20	20
Regional waterlogging	10-15	15	15-20	20

STEP 2: Determine each crop's blackleg severity in Spring

Assess the level of disease in your current crop. Sample the crop origins from the end of flowering to senescence (harvesting), that is, randomly choose stems out of the ground cut off the roots with a pair of secateurs and, using the reference photos in Table 2 below, estimate the amount of disease on the stem cross-section. Hold two connecting circles when more than 50% of the cross-section of the cut stem is diseased.

If you have identified that you are in a high-risk situation (Steps 1 and 2), use Steps 3 and 4 to reduce your risk of blackleg by taking actions.

If you are in a low-risk situation and you have not identified your loss due to blackleg infection when managing your crop, continue with your normal management practices.

TABLE 2 Crop blackleg severity

- Released biannually with all management options for minimising disease
- Step by step guide

TABLE 3 2017 Spring Blackleg Ratings and Resistance Groups. See page 3, (Step 4) for information on how to use this table.

Variety	2017 Blackleg Rating	2017 Blackleg Rating	Type	Section A: Resistance group of cultivar	Section B: Resistance group of previous year's cultivar (stubble)										
					A	B	C	AB	AC	ABD	ABF	ABF	ABF	BF	BC
CONVENTIONAL VARIETIES															
Navarro Quatre	10	15	Hybrid	ABD											
SF Scout	5-10	10	White, open pollinated	BC											
Widowmaker	10	15	High stability vL Hybrid	ABD											
Navarro Champion	10	15	Hybrid	ABD											
Big Green	10	15	Open pollinated	A											
STABLE TOLERANT VARIETIES															
Hydra 2017T	10	15	Hybrid	ABD											
Hydra 4441T	10	15	Hybrid	ABD											
Phantom 4452 TT	10-15	15	Hybrid	ABD											
Hydra 5501T	10-15	15	Hybrid	ABD											
Minus 461 TT	10	15	High stability vL, open pollinated	B											
Minus 455 TT	10	15	High stability vL, open pollinated	B											
SF Ignite TT	10	15	Hybrid	BF											
DC 5501T	10	15	Hybrid	BF											
DC 5201T	10	15	Hybrid	BF											
ATR Mariposa	10	15	Open pollinated	A											
ATR GroupA	10	15	Open pollinated	C											
Integra 1 4510	10-15	15	Hybrid	BF											
SF Tundra TT	10-15	15	Hybrid	BF											
Phantom 4510TT	10	15	Hybrid	AB											
ATR Mariposa	10	15	Open pollinated	A											
ATR Mariposa	10	15	Open pollinated	A											

Does rotation of resistance genes work?

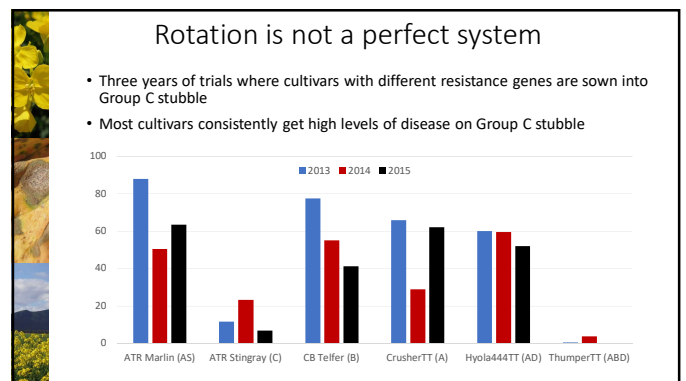
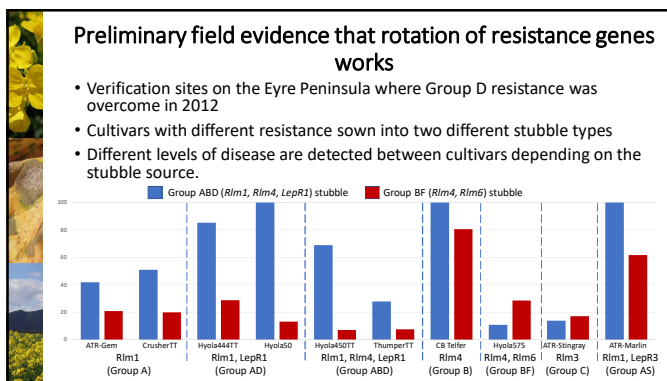
Evidence from the boom and bust on the Eyre peninsula

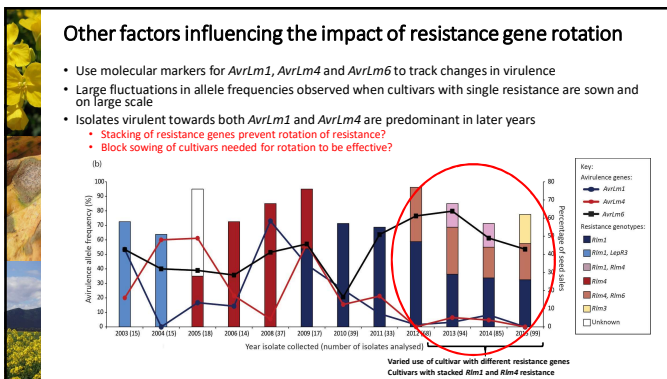
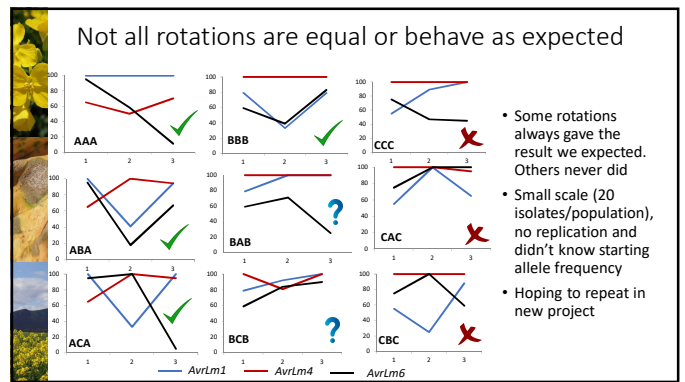
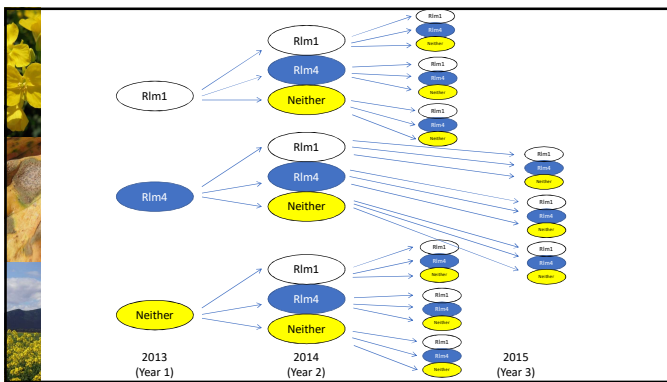
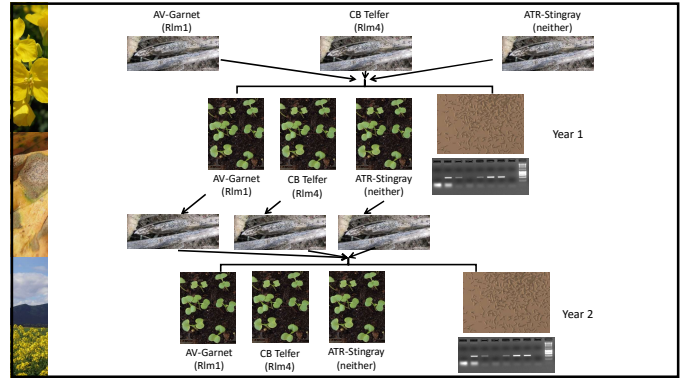
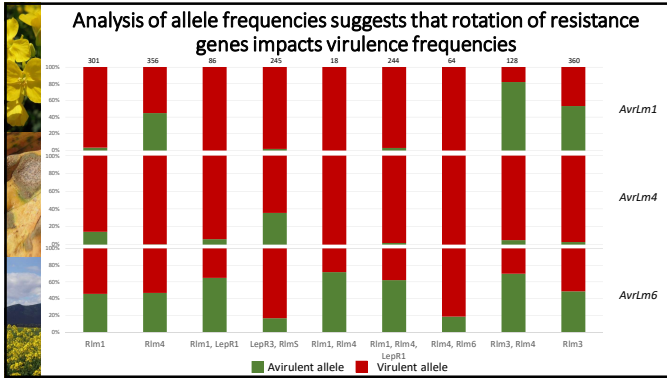
Group S breakdown on the Eyre Peninsula 2003

Group B Group AS

Group D breakdown on the Eyre Peninsula 2012

Group AD Group ABD

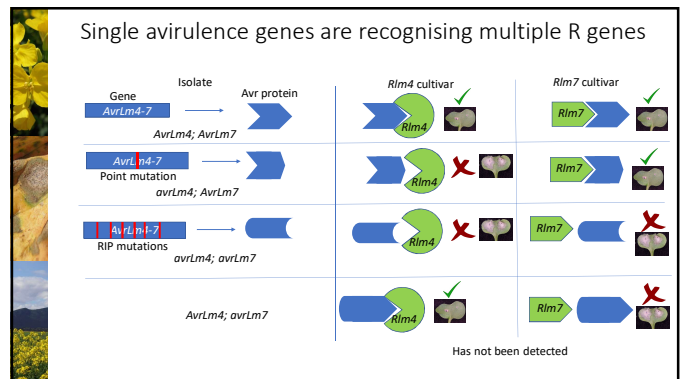
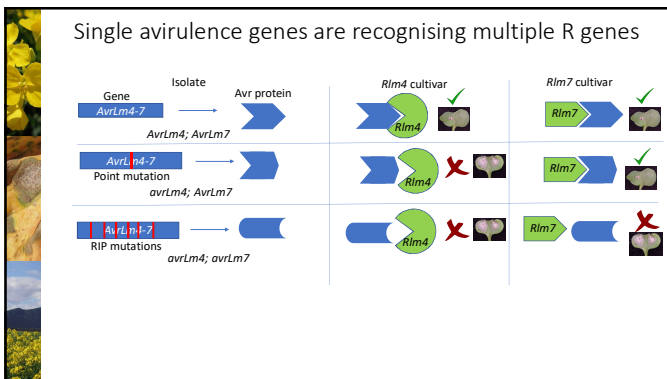
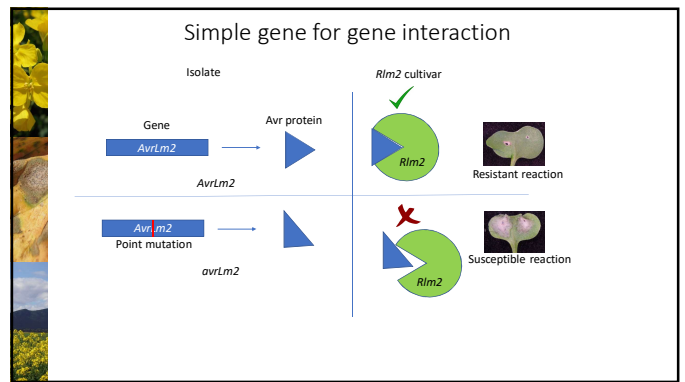
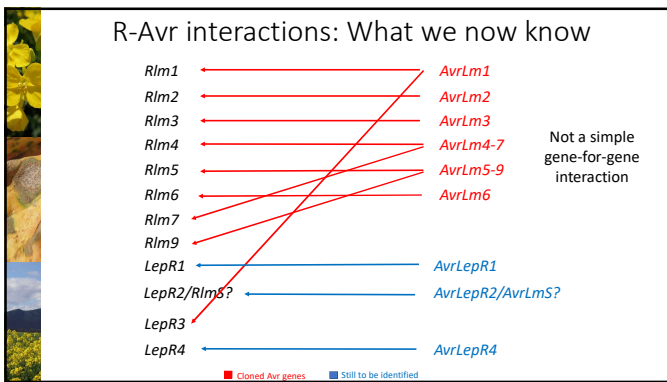
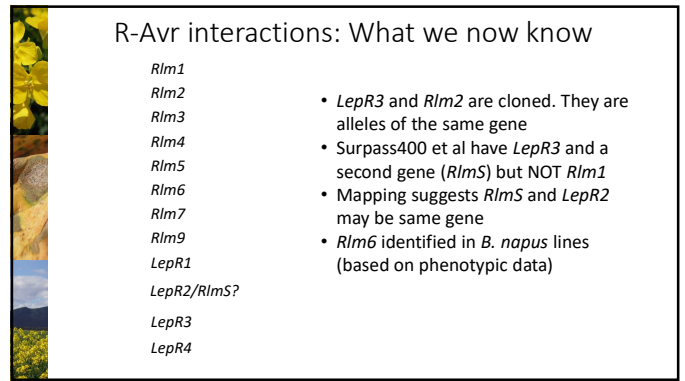
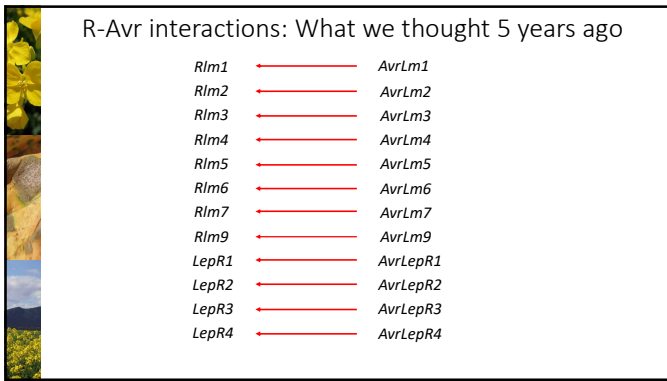


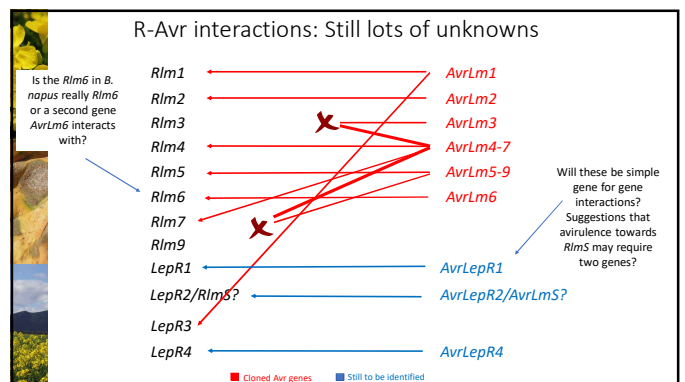
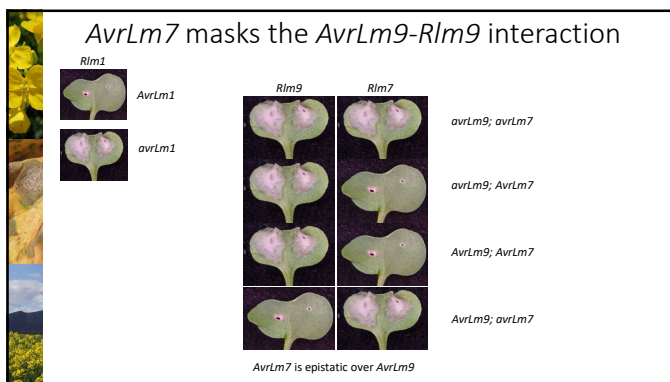
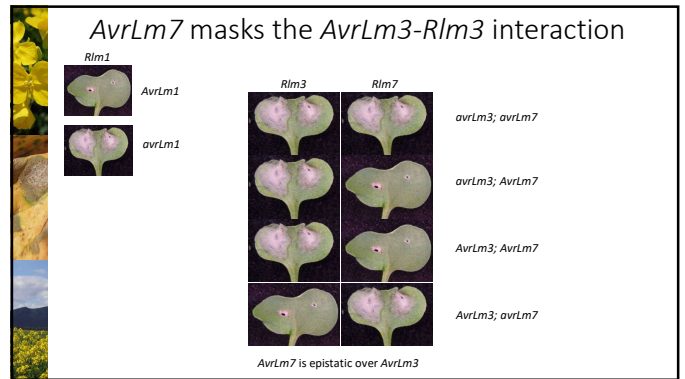
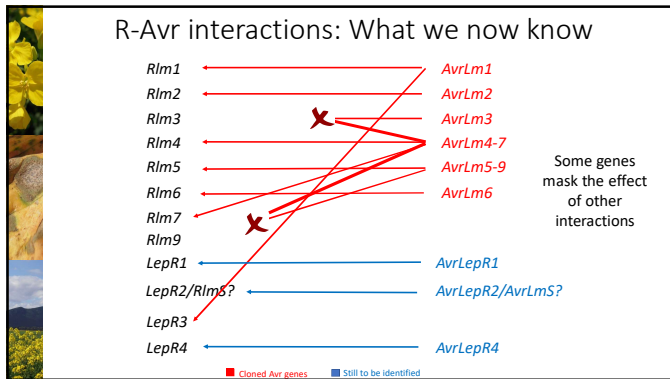


R-Avr interactions: What we thought 5 years ago

Rlm1
Rlm2
Rlm3
Rlm4
Rlm5
Rlm6
Rlm7
Rlm9
LepR1
LepR2
LepR3
LepR4

- Surpass 400, Surpass501TT, Surpass603CL = *Rlm1* and *LepR3* (based on phenotypic data)
- *Rlm5* and *Rlm6* identified in *B. juncea*
- There are other genes reported by French researchers but no one has access to the material





- ### Industry implications
- Rotation of resistance genes influences fungal populations and can minimise disease
 - Unclear what is the best method for rotation (rotate every year or every three years)
 - Are all rotation patterns equal? Probably not
 - Is block sowing needed? Does stacking of resistance genes influence selection?
 - Can defeated resistance genes be reintroduced to the system?
 - Monitoring resistance genes in the field/lab and subsequent warnings for industry have been hugely successful
 - Knowing which cultivars are affected i.e. resistance groups
 - Is the breakdown region specific?
 - **Need to understand both host and pathogen – not a simple system**