Resistance Groups

GRDC
Grains Research & Development Corporation

Resistance groups now based only on "Seedling" major R genes

- Cultivars will not change Resistance groups over time.
- All cultivars will receive a resistance group, regardless of the Blackleg Rating.
- Most cultivars will end up in multiple groups as they have multiple resistance.

Old system -cultivars assigned a group based on seedling resistance and "adult" stem canker resistance. If they were susceptible to an individual blackleg population in the tub screen they also received that group.
eg cultivarX had Rlm 1 seedling resistance and was susceptible to Group D Hyola50 stubble.
CultivarX Group AD.

Cultivar	Seedling resistance group
08H5050	A, B, F
10H4061	No seedling resistance detected
ARCHER	No seedling resistance detected
ATRBONITO	Unknown
ATRGEM	A
ATRSTINGRAY	C
ATRWAHOO	A
AVGARNET	A
AVZIRCON	Unknown
BAYERAN11R5195	E
BAYERAN11R5197	A, D
BAYERAN11R5201	A, B
BAYERAN12R5264	A, B
BAYERAN12R5276	A, B, F
BRAZZIL	B, C
CARBINE	A
CB1301TT	B, C
CB1302TT	A, B
CB1303TT	B, C

Resistance group categories

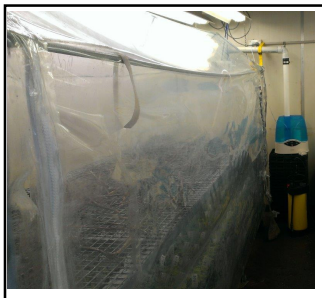
R gene	Corresponding R group	Comments
Rlm1	A	
Rlm4	B	
Rlm3	C	
LepR1	D	Evidence suggests this is conferred by LepR1 - eg Hyola 50
RlmE	E	Differential pattern the same as ThumperTT
RlmF	F	Differential pattern the same as Mustang based resistance. Found in combination with Rlm4
RlmJ	G	Juncea based resistance. Probably Rlm5 and Rlm6
LepR3	S	Original sylvestris resistance. Previously RlmS

Chart for advisors / growers

Cultivar contains the following Major Resistance genes	Stubble of cultivars grown over the previous 3 years															
	A	B	C	D	E	F	S	G	AB	AD	AS	ABD	ABF	ABS	BC	BF
A																
B																
C																
D																
E																
F																
S																
G																
AB																
AD																
AS																
ABD																
ABF																
ABS																
BC																
BF																

What we will release to industry

Cultivar	Resistance genes	CULTIVAR GROWN OVER PAST 3 YEARS													
		A	B	C	D	E	G	AB	AD	AS	ABD	ABF	ABS	BC	BF
ARCHER	Adult resistance only														
ATRBONITO	Unknown resistance														
ATRGEM	A														
ATRSTINGRAY	C														
ATRWAHOO	A														
AVGARNET	A														
AVZIRCON	Unknown resistance														
BRAZZIL	B, C														
CARBINE	A														
CBAGAMAX	C														
CBATOMICHT	A, B														
CBCOMBOHTRR	B, C														
CBEDIMAXCL	C														
CBFUSIONHTRR	A, B														
CBSCADDAN	A, B														
CBTELFER	B														
CRUSHERTT	A														
GTCOBRA	A														



Interactions tested against 6 stubble.

Predicted interactions 84% correct

Cultivar	Blackleg rating	Resistance genes	PREDICTED CULTIVAR GROWN OVER PAST 3 YEARS (information that farmers will have)					
			AS	B	C	ABD	E	BF
HYOLA404RR	R	A, B, D						
HYOLA474CL	R	B, F						
HYOLA50	R	A, D						
HYOLA500RR	R	A, B, D						
HYOLA575CL	R	B, F						
HYOLA656TT	R	A, B, D						
NUSEEDGT50	R	A, B, F						
THUMPERTT	R	E						
XCEEDOASISCL	R	G						
HYOLA400RR	R	A, B, D						
GTCOBRA	R-MR	A						
HYOLA444TT	R-MR	A, B, D						
HYOLA450TT	R-MR	A, B, D						
HYOLA555TT	R-MR	D						
H50RR	R-MR	A						
Nuseed Diamond	R-MR	A, B, F						
NUSEEDGT41	R-MR	A, B, F						
ATRSTINGRAY	MR	C						
ATRWAHOO	MR	A						
AVGARNET	MR	A						
BRAZZIL	MR	B, C						
HYOLA971CL	MR	A						
H30RR	MR	A, B						
PIONEER43Y85CL	MR	A						
VICTORYV5002RR	MR	A, B						
ATRGEM	MR	A						

Why we get it wrong

- If predicted score was high but it was actually low, this is likely to be the effect of adult plant resistance, this occurred in 13 out of the 25 cases where the prediction was wrong.

Cultivar	Blackleg rating	Resistance genes	Green and red are interactions predicted correctly, yellow are incorrect predictions					
			AS	B	C	ABD	E	BF
HYOLA971CL	MR	A	36	45	55	21	20	26

Why we get it wrong

- The pathogen population evolution caused by stacks (as described by Angela) may also result in the tub screen causing multiple virulence's across groups.

Why we get it wrong

- Group E and F are still unknown but they definitely have more than 1 resistance gene. So they will share the same resistance genes with other groups e.g. Group D and E may both have LepR1 etc.
- We are continuously identifying new isolates to be able to accurately determine each resistance gene for all cultivars.

Issues

Present situation

- In 2013 we could predict 84% of interactions.
- A percentage of the ones we predicted wrong actually had less disease (adult resistance)

Future issues

- Evolving pathogen populations that will be able to attack multiple resistance groups, due to stacking of resistance genes.
- Populations that can attack all resistance groups?
- Can we help breeders to avoid stacks in future cultivars?
- Can we assure that new R genes are used as single resistance genes and not placed into a stack??

Blackleg ratings

- Starting 2014 all sites will be designed in the NVT data base.
- Winters only screen in NSW and Vic.
- In March each year all NVT entries that were screened in the previous year will be assigned a blackleg rating.
- Most cultivars will have a rating 12 months prior to commercialisation.

Screening NVT lines for R genes and tub screen

- In 2013 there were 136 NVT entries and 7 new cultivars. Therefore a lot of lines are screened that are never commercialised.
- Starting 2014 we will only screen retentions and imminent release lines.
  - NVT lines in system 2 year prior to commercialisation, we will only screen if they are retained into the 2nd year.

Blackleg Ratings

- Ratings and R groups kept on the cloud so that they can be updated every time a cultivar is commercialised.
- However no lines will be released until the review committee ratifies the analysis.