

Genetic analysis of stripe rust resistance in a common wheat landrace Aus28166

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Introduction

- Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici* (Pst), is one of the major threats to global wheat production and it was estimated to cause losses of A\$127 m annually in Australia (Murray and Brennan, 2009).
- Breeding for resistance is the most preferred method to control stripe rust of wheat due to its eco-friendly nature.
- A common wheat landrace Aus28166 exhibited resistance against all currently predominating Australian Pst pathotypes and was chosen for detailed genetic analysis.

Objectives:

- To study inheritance of stripe rust resistance in Aus28166
- To determine chromosomal location(s) of the resistance gene(s) involved

Materials and methods

- Aus28166 was crossed with a stripe rust susceptible genotype Avocet S (AvS) and a recombinant inbred line (RIL) population (F5:6) was generated.
- RIL population and parents were tested in the greenhouse for seedling stripe rust response using the Pst pathotypes 134E16A+Yr17+Yr27+ according to [Bariana and McIntosh \(1993\)](#).
- Single gene segregating populations (SGSP) were developed from F3 families that showed monogenic segregation.
- DNA was extracted using the CTAB method ([Bansal, et al, 2009](#)) and sent for bulk segregant analysis with 90K SNP array.

Results

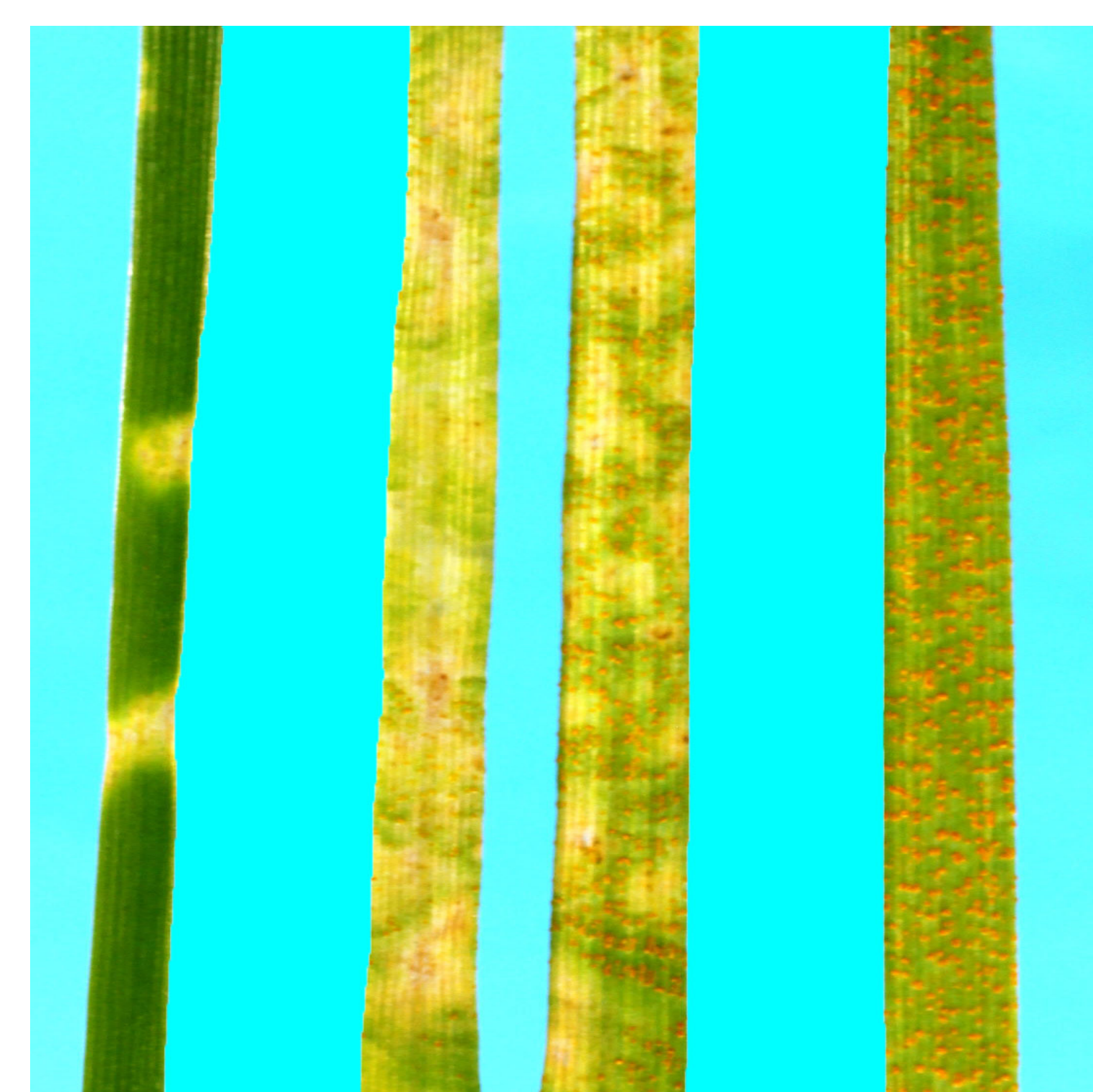
- Aus28166 displayed a resistant infection type (IT) ;c to ;1·C, whereas the susceptible genotype AvS showed IT 3+ (Fig. 1) at the seedling stage.
- Phenotyping of Aus28166/AvS RIL population using the Pst pathotype 134E16A+Yr17+Yr27+ at the seedling stage showed di-genic segregation for stripe rust resistance (Table 1).

Table 1 Distribution of Aus28166/AvS RIL population when tested with Pst pathotype 134 E16A+Yr17+Yr27+ at the two-leaf stage in the greenhouse

Stripe rust response Class	Number of lines		χ^2
	Observed	Expected	3:1
Homozygous resistant	82	78	0.205
Homozygous susceptible	22	26	0.615
Total	104	104	0.82

Table value of $\chi^2_{0.05}$ and 1 d.f. = 3.841

- The two all stage resistance (ASR) genes for stripe rust resistance were temporarily named as 'YrAW8' and 'YrAW9' based on their typical IT11+c and 23c, respectively (Fig. 2).
- Bulk segregant analysis (BSA) using the iSelect 90K Infinium SNP array suggested the locations of YrAW8 and YrAW9 in chromosomes 5B and 3B, respectively.
- SGSPs for YrAW8 and YrAW9 are being advanced to F6 generation to facilitate detailed mapping.
- YrAW8 and YrAW9 are being transferred into two Australian wheat cultivars and backcross-derivatives will be provided to breeding companies.
- Backcross-derivatives will also be useful for validation of YrAW8 and YrAW9 linked markers



Aus28166 YrAW8 YrAW9 Avocet S

Figure 1 Infection types of the resistant parent, resistant RILs carrying YrAW8 and YrAW9 and the susceptible parent when tested against Pst pathotype 134 E16A+Yr17+Yr27+ at the seedling stage

Conclusions

- Aus28166 carries ASR genes YrAW8 and YrAW9.
- YrAW8 and YrAW9 are effective against all Australian Pst pathotypes tested.
- YrAW8 and YrAW9 were located on chromosomes 5B and 3B, respectively
- Detailed mapping of genomic regions carrying YrAW8 and YrAW9 is in progress

References

- Bansal UK, Hayden MJ, Gill MB, Bariana HS (2009) Euphytica 171: 121-127.
Bariana HS, McIntosh RA (1993) Genome 36: 476-482
Murray DM, Brennan JP (2009) Australasian Plant Pathology 8: 558-570

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