

# Obtaining genetic resistance to *Fusarium* crown rot in bread wheat

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## ABSTRACT

Crown rot is a major soilborne disease problem in the wheat and barley industries of many countries, including Australia. This work was designed to shed light on the genetics of crown rot resistance to assist in crown rot resistance breeding.

Results from a series of nine parent half-diallel experiments indicated that both general and specific combining ability were significant, and that breeding based on the parental phenotype will not always be the optimal approach.

To better understand the resistance genes, experimentation was conducted using the 'generation means' quantitative genetics design, which provides much more detail about each cross combination.

Twenty-nine cross combinations were tested with glasshouse methods. The majority of the combinations with better crown rot resistance also had a more complex genetic model of resistance. This does not mean improved resistance is unobtainable, as detailed knowledge of the genetics of each cross enables the optimal combinations to be pursued, with the highest heritability, lowest number of genes, combined with the highest resistance. From this shortlist, those which already contain agronomic advantages can be favoured, as they will increase the speed of release of improved crown rot resistance lines.

The genetics of crown rot resistance have proven to be complex, and highly dependant on which resistant parent is used, as well as being influenced by gene interactions. The knowledge obtained through this work has enabled a selection of populations to be targeted for their superior ability to transfer high levels of resistance to progeny, coupled with some potential for combined agronomic traits, increasing their usefulness to breeders.

## INTRODUCTION

Crown rot, caused predominantly by *Fusarium pseudograminearum* (teleomorph *Gibberella coronicola*), is a major soilborne disease problem in the wheat and barley industries. The disease is widespread and causes losses in yield and quality in Queensland, New South Wales, Victoria, and South Australia. Brennan and Murray (1998) estimated that the disease was causing losses of up to \$56M in bread wheat

throughout Australia. In Queensland, losses have been estimated at up to 50% in some areas and losses of 20 to 30% occur regularly, while the disease can inflict yield loss of up to 89% (Klein *et al.* 1991).

Breeding for resistance to crown rot has been difficult, partly due to variability associated with phenotyping, but also due to an incomplete understanding of the nature of the resistance genetics.

A combining ability study on seedling resistance to crown rot found that both general combining ability and specific combining ability were highly significant (Herde *et al.* 2008), indicating that the parental phenotype will be passed to the offspring, however in many cases interactions will occur producing unexpected progeny results.

The 'generation means' quantitative genetics design was used to provide more detail about the resistance genes in each cross combination.

## MATERIALS AND METHODS

To better understand the resistance genes, experimentation has been conducted using the 'generation means analysis' quantitative genetics design, which provides much more detail about each cross combination. This design requires seed of the six basic generations (two parents, F1, F2, and backcrosses of the F1 to both parents of the F1). This design enables estimates of additive and dominance components of variance and heritability for each cross (Kearsey and Pooni, 1996).

Previous work using a diallel crossing design looked at 36 F1 hybrids. The six basic generations were produced for all 36 of these. Twenty-nine of the 36 cross combinations were phenotyped in the glasshouse, using the specific combining ability information of the diallel work to guide population selection.

Of the bread wheat genotypes studied, two of these (Puseas and Kennedy) are susceptible; the remaining seven (2-49, CPI133814, IRN497, Lang, QT10162, Sunco, and W21MMT70) have a level of partial resistance. The parent 2-49 is considered one of the best sources of resistance to crown rot currently available (Wildermuth *et al.* 2001).

The seedlings were phenotyped for crown rot resistance in a glasshouse test, following a modification of the Wildermuth and McNamara (1994) method, as described below. This method closely mimics field infection, and is highly correlated with field results.

In summary of this method, this seedling phenotyping is a three week duration experiment where seeds are planted in steam-sterilised soil below a banded layer of inoculum (consisting of a mixture of five *F. pseudograminearum* isolates grown on colonised wheat and barley grain, and milled through a 2 mm sieve). Through control of moisture, the seedlings grow for a week without fungal activation, then the remaining two weeks with the actively growing fungus. After three weeks the seedlings are washed free of soil and the percentage of lesioning on the first three leaf sheaths visually assessed.

The standard glasshouse procedures have evolved since the 1994 paper, with modifications in the ratio of soil in the three pot layers, and a changed weight of inoculum per pot. The category rating system has been replaced by the actual percentage of lesioning for this genetics work, however the original system is still used for routine screening.

## RESULTS

Twenty-nine of the available cross combinations were tested in the glasshouse (a simplified summary is presented in Table 1). The majority of the combinations with better crown rot resistance also had a more complex genetic model of resistance (eg an epistatic model, or failure to fit a model). This does not mean improved resistance is unobtainable, as detailed knowledge of the genetics of each cross enables the optimal combinations to be pursued, with the highest heritability, lowest number of genes, combined with the highest resistance. From this shortlist, those which already contain agronomic advantages can be favoured (those with an adapted parent, such as QT10162, Sunco or Lang in the cross), as they will increase the speed of releasing a variety with improved crown rot resistance.

Table 1. A simplified summary of twenty-nine glasshouse crown rot 'generation means analysis' genetics experiments

Population	Genetic Complexity <sup>1</sup>	Ranked Disease Level <sup>2</sup>
CPI133814 - IRN497	7	1
W21MMT70 - IRN497	8	2
2-49 - CPI133814	7	3
QT10162 - IRN497	2	4
QT10162 - W21MMT70	8	5
Puseas - IRN497	8	6
CPI133814 - Puseas	8	7
CPI133814 - Sunco	9	8
2-49 - IRN497	8	9
CPI133814 - Lang	9	10
Sunco - IRN497	8	11
2-49 - Sunco	9	12
2-49 - W21MMT70	6	13
W21MMT70 - Kennedy	7	14
Puseas - QT10162	8	15
CPI133814 - Kennedy	4	16
QT10162 - Sunco	6	17
Sunco - W21MMT70	8	18
2-49 - Lang	6	19
IRN497 - Lang	3	20
W21MMT70 - Lang	5	21
Puseas - W21MMT70	6	22
QT10162 - Lang	1	23
2-49 - Kennedy	8	24
2-49 - QT10162	8	25
Puseas - Sunco	7	26
2-49 - Puseas	8	27
Puseas - Lang	8	28
QT10162 - Kennedy	9	29

<sup>1</sup> Genetic complexity. An indication of the ease of transferring resistance from this cross combination into a fixed line, where '1' is the best and the simplest to transfer.

<sup>2</sup> Ranked disease level. A standardised measure of the level of disease found in each cross combination, where '1' is the best with the lowest level of disease.

Results from fourteen cross combination populations tested in the field in 2005 and 2006 indicate there are some differences in the genetics behind seedling resistance and field resistance.

The genetic complexity of the adult plant resistance was generally greater than that for seedling resistance, although QT10162-Sunco and W21MMT70-Lang showed a simple model of inheritance in both seedling and field testing.

The highest field resistance was seen in W21MMT70-Lang and 2-49-CPI133814 in 2005, and 2-49-W21MMT70 and QT10162-Sunco in 2006.

## DISCUSSION

Many of the crosses in this study had complex epistatic models controlling crown rot resistance. A number were controlled through additive gene model or additive x additive epistasis, which will be captured in a fixed line. A number of other crosses with strong resistance were controlled with dominance or dominance x dominance epistasis, meaning the resistance will not carry through to a fixed line (Kearsey and Pooni, 1996).

This information is able to guide selection of populations to go forward with, and explains why resistance in parent lines or segregating material alone will not guarantee resistance will be found in a fixed line. Further work is underway to compare selection in crosses with these two types of epistatic control.

Field evaluation is needed of the better performing crosses identified from the seedling testing, as seed has not been available for field evaluation of crosses based on IRN497 or many of CPI133814 crosses.

Further work is underway with the CPI133814 - IRN497 cross, which was identified as the optimal cross for crown rot resistance. This cross will be of use to produce a parental line for further development with elevated resistance levels beyond those currently available, rather than a variety for release, as the parents lack adaptation characteristics.

Pre-breeding selection work has commenced with the better performing crosses that have an adapted parent on at least one side of the cross.

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