INTRODUCTION
Crown rot of wheat, predominantly caused by Fusarium pseudograminearum in the northern grain belt of Australia, has become an increasingly important issue for the cereals industry due to the application of conservation tillage practices. The use of partially resistant germplasm is the most economically and environmentally sound means to overcome losses caused by this disease. Our group has previously identified a range of QTL from various sources of partial resistance. This paper reports on recent work that assessed the effectiveness of pyramiding QTL from partially resistant germplasm to improve resistance to crown rot.

MATERIALS AND METHODS
A doubled haploid population (n=207) was produced from a cross between two previously characterised sources of partial resistance (2-49 and W21MMT70). Line 2-49 is widely recognised as a superior source for crown rot resistance and W21MMT70 also displays a useful level of resistance. The population was phenotyped in 2006 and 2007 for seedling resistance to crown rot as per the method of Wildermuth and McNamara (1). Linkage maps of chromosomal regions of interest were constructed, and Windows QTL Cartographer (2) was used to conduct composite interval mapping (CIM) in order to identify QTL.

RESULTS AND DISCUSSION
The average disease severity of the 2-49 x W21MMT70 population was skewed towards resistance (Figure 1). A number of the offspring performed significantly better than both parents, with the best recording a disease severity rating of only 4% of the susceptible check cultivar Pusesas.

Figure 1. Disease severity histogram of the 2-49 x W21MMT70 population. Parental means are indicated by filled (2-49) or unfilled (W21MMT70) arrows.

Previous work (3,4) identified QTL inherited from 2-49 on chromosomes 1A, 1D, 4B, and 7B in a 2-49 x Janz population, and from W21MMT70 on chromosomes 2D, 3B, and 5D in a W21MMT70 x Mendos population. Three QTL were detected by CIM in the 2-49 x W21MMT70 population (Table 1). Two were inherited from 2-49 (chromosomes 1A and 1D) and one from W21MMT70 (chromosome 3B). No QTL were detected on chromosomes 2D, 4B, 5D, and 7B. Overall, the 3B QTL inherited from W21MMT70 had the greatest effect on reducing levels of disease.

Table 1. QTL identified in the 2-49 x W21MMT70 population. Chromosome location (Chr.), likelihood ratio statistic (LRS), significance level (Sg, suggestive; HS, highly significant), and % phenotypic variation explained (% P.E.) shown.

<table>
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<tr>
<th>Chr.</th>
<th>2006</th>
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<td></td>
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<td>1D</td>
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<td>HS</td>
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<tr>
<td>3B</td>
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SUMMARY
Of seven QTL detected in the source mapping populations (2-49 x Janz and W21MMT70 x Mendos), only three were detected with additive effect in the 2-49 x W21MMT70 population. This finding suggests that the expression of some of the previously detected QTL may be dependent upon the background into which they are introgressed. Nonetheless, the pyramiding strategy proved successful in increasing the level of resistance to crown rot, and the identification of markers which flank major QTL will be useful for marker-assisted selection.

ACKNOWLEDGEMENTS
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REFERENCES