

Breeding wheats with enhanced crown rot resistance

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Crown rot (CR), caused by species of *Fusarium*, is the most significant biotic constraint to wheat production in Australia. Since the same *Fusarium* pathogens also cause Fusarium head blight (FHB), our initial approach was to seek sources of CR resistance amongst genotypes with known FHB resistance. This work did not show any correlation between CR and FHB resistance. Subsequently we embarked on a screening of more than 2,200 genotypes of wheats and their close relatives using a high throughput CR bioassay. This showed that genotypes with high levels of CR resistance are available in hexaploids. None of the several hundred tetraploid and diploid genotypes assessed showed high level of CR resistance. Current research is aimed at identifying loci conferring CR resistance from two of the best sources by QTL mapping. Single-seed-descendent populations between resistant sources and elite local varieties are being generated to validate QTL effects and to transfer this resistance into locally adapted varieties. As durum (*T. durum* L.) genotypes are more susceptible than hexaploid wheat (*Triticum aestivum* L.), an additional aim is to transfer CR resistance from hexaploids into durum genotypes via a backcrossing program. Latest results from these projects will be presented.