FINAL REPORT

GRDC
GRAINS RESEARCH & DEVELOPMENT CORPORATION

UHS10444

A genetic dissection of screenings and test weight in bread wheat

PROJECT DETAILS

PROJECT CODE:	UHS10444
PROJECT TITLE:	A GENETIC DISSECTION OF SCREENINGS AND TEST WEIGHT IN BREAD WHEAT
START DATE:	29.01.2013
END DATE:	26.11.2013
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Summary

The project consisted of three studies aiming to i) identify quantitative trait loci (QTL) for screenings and test weight; ii) investigate the effect of the Cre1 gene (known to give cereal cyst nematode (CCN) resistance) on screenings; and iii) identify genetic and error correlations between grain morphology related traits and screenings/test weight.

Key results include the identification of five putative QTL for test weight, and eight for screenings, with at least one of these (for test weight) being novel. It was also shown that breeders can improve screenings more effectively by selecting for grain thickness, rather than directly selecting for screenings.

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Conclusions

This study identified five putative QTL for test weight, and eight for screenings, with at least one of these (for test weight) being novel. It is likely that one of the screenings QTL identified is the known grain size gene Gw2; this can be verified once the GW2 marker has been screened in these populations.

No association was found between the Cre1 gene and screenings in two of the populations used, and in the third population resistance was observed to decrease screenings. This is contrast to previous findings, but should be validated in additional environments.

A strong genetic correlation was observed between round grains and high test weight, and between grain thickness and screenings. By analysing the potential for improving screenings and test weight through selection of strongly correlated traits (correlated response to selection), it was shown that improving screenings by selecting for grain thickness would be 1.1 times more effective than directly selecting for screenings itself.

Recommendations

The Gw2 marker has been previously observed to influence screenings in Australian germplasm, and if this gene had a significant effect in this study (to be verified) it adds to existing evidence and further encourages breeders to use this marker in marker assisted selection. Other markers identified in this study provide good candidates for further validation in a range of genetic backgrounds and environments. Pending the results, these could also be adopted for use in breeding programs.

Given the results of the correlation study conducted in this project, it is recommended that breeders use grain thickness to improve screenings, as opposed to directly selecting for screenings.

Achievement/Benefit

Overview of Project Achievements

Nine populations were produced for this project, three to be used in the QTL identification study, four for the Cre1 study, and two for use in validation. High quality DNA was extracted from all lines in each population (~1300 lines total). For each of these populations, phenotype data was produced from 5 environments. 38 markers linked to 10 putative QTL were synthesised in this project, with one from each region being screened over the populations; we aim to have all 38 screened by the end of the project. These populations, along with their DNA and phenotype and genotype data can be used in future studies on a range of traits.