

Analysis of natural variation for seed dormancy and preharvest sprouting tolerance in wheat

F.C. Ogbonnaya^{1*}, M. Imtiaz¹, R.F. Eastwood², J. Wilson³, P. Hearnden⁺, J. Oman⁺, K. Gatford⁺, and M. van Ginkel¹.

Email: F.Ogbonnaya@cgiar.org

¹International Centre for Agricultural Research in the Dry Areas, PO Box 5466, Aleppo, Syria.

²Australian Grain Technologies, Grains Innovation Park 110 Natimuk Rd, PB 260, Horsham Vic. 3401, Australia.

³Department of Primary Industries (DPI), Primary Industries Research Victoria (PIRVic), Private Bag 260, Horsham, Victoria 3401, Australia; ⁺ previously at DPI, PIRVic, Private Bag 260, Horsham, Victoria 3401, Australia.

Preharvest sprouting (PHS) is one of the most important factors affecting wheat quality in many wheat producing areas especially in environments characterized by late season rainfall during grain maturation and high humidity prior to harvest. In such environments, the incorporation of sufficient levels of PHS tolerance is necessary to minimize losses associated with Preharvest sprouting damage often results in down-grading of premium milling quality wheat to feed quality, which results in seriously reduced pay-outs to farmers. Preharvest sprouting is a complex trait that is affected by many environmental and genetic cues. To identify loci that determine natural variation for seed dormancy and PHS tolerance in wheat, we carried out comprehensive quantitative trait loci (QTL) analyses of two BC₁F₇ synthetic backcross (SBLs) populations. These populations were derived from crosses involving Syn36 (synthetic hexaploid with moderate seed dormancy) and Syn37 (synthetic hexaploid with high seed dormancy) and Janz (Australian prime hard wheat cultivar, PHS-susceptible) respectively and a set of F₈ recombinant inbred lines (RILs) population derived from the cross between “CN19055” (PHS-resistant) with locally adapted Australian cultivar “Annuello” (PHS-susceptible). Assessment for seed dormancy was based on germination index (GI7) while PHS tolerance was based on whole head assay (sprouting index, SI) and visibly sprouted seeds (VI), the latter two following artificial weathering in a controlled environment chamber. Genomic regions on chromosomes 1D, 2D, 3D, 4A, 5D and 6D were found to have significant impact on seed dormancy and PHS tolerance in wheat. We report for the first time identification of new loci on chromosomes 1D and 2D that control PHST. Coincident QTLs were identified for GI7, SI and VI on chromosomes 4A, 3D and 5D. Molecular markers associated with these traits explained 9 to 43% for GI7, 7 to 13% for SI and 13 to 45% for VI depending on the population. QTL associated with red grain color of *Ae. tauschii* was also separated from seed dormancy to develop white PHS-tolerant wheat germplasm. These results confirmed the role of major loci including 4A and 3D that had previously been reported which that confer seed dormancy and PHS tolerance in wheat. This indicated that the QTLs found in this study are reliable, thus it would be worthwhile to target these conserved loci including the novel loci on 1D and 2D for further molecular characterization, cloning and use in breeding.