

Genetic dissection of agronomically important traits in bread wheat (*Triticum aestivum* L.) using a chromosome 3A specific RICL population

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Wheat feeds most of our nutritional demands, and now is emerging as an attractive alternative to feed our demands for biofuel and energy. In view to satisfy these demands, it is important to understand the balance between grain yield and plant biomass (harvest index). This result is possible only by understanding the genetic/molecular basis of both of these complex traits. We initially identified wheat chromosome 3A as a major determinant of grain yield, plant biomass, and other agronomically important traits including plant height, preharvest sprouting tolerance, earliness *per se*, etc. To dissect these traits to their components, a recombinant inbred chromosome line (RICL) population of 95 individuals was developed by crossing Cheyenne with Cheyenne carrying chromosome 3A from Wichita [CNN×CNN(WI3A)]. The above population was genotyped for 43 chromosome 3A specific markers (including RFLPs and SSRs) and phenotyped for grain yield, root and shoot biomass, plant height, kernel weight, kernel number per spike, tiller number m⁻¹, days to flowering, etc. QTL interval mapping using these lines allowed identification of at least one major QTL for each of these traits. Major QTLs identified for grain yield, root and shoot biomass explain 21%, 32% and 42% of the variation, respectively. Rice-wheat synteny was used to identify candidate genes (CGs) underlying these QTLs. Some of the interesting CGs (e.g., *BASI*, *DOG1*, *GID2*, *ABI8*, *GA3ox2*, *GA2ox5* and *CKX2*) identified through comparative analysis are being tested by virus induced gene silencing (VIGS) and RNAi.