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Poster Abstract – D.51

TOWARD MAP-BASED CLONING OF THE *REDUCED GRAIN FILLING* 1 GENE IN MAIZE

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The grain filling is an important trait associated with the yield of crop. The reduced grain filling (*rgf*1) phenotype in maize is caused by a dominant mutation and presents final grain weight reduced to 30% of that of the wild type. Its pericarp is partially unfilled, while the embryo and somatic tissues are viable and indistinguishable from wild type. Respect to other small size seed mutants, *rgf*1 shows dosage-dependent reduction. This aspect makes *rgf*1 a good candidate for understanding endosperm development and seed filling. Using back-cross populations *rgf*1 was mapped to bin 2.04 of chromosome 2 between two SSR markers, bnlg1613 and bnlg1140, at a distance of 4.4cM. The region between the 2 markers was enriched using interval mapping pools: the mapping interval was reduced to 0.5cM with the aid of AFLP markers. These results were confirmed by testing an F3 population consisting of 1406 individuals obtained from the cross B37 x *rgf*1. Two single copy AFLP markers co-segregated with the mutant locus and were used as probes for screening a BAC library. Additional *rgf*1 alleles were generated by transposon insertion. Out of 650,000 F1 seeds obtained from the cross of *rgf*1/*rgf*1, *Mu* to wild type, 6 independent insertions were isolated. Genetic and molecular evidences are reported to sustain the recessive, wild type and lethal nature of the new alleles.