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A NEW MAIZE *TASSEL SEED* MUTANT IS UNDER THE CONTROL OF A TWO-LOCUS SYSTEM

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Unisexual maize flowers originate through selective abortion of female primordia in the tassel and of male stamens in the ear from bisexual inflorescences. Tassel seed mutations are known to alter the usual sex fate allowing carpel survival in the male inflorescence. Objective of the present research is to describe and map a novel tassel seed phenotype shown by an inbred line, Rig7, identified among a set of lines derived from in vitro regeneration. Genetic mapping was carried out using a B73 x Rig7 F2 population (genotyped with 15K SNP array) and by SNP-based bulk segregant analysis using two additional populations (BC1 and F2). Both approaches clearly indicated that the tassel seed phenotype is under the control of two loci mapping on chromosomes 2 and 6. A strong and unexplained recombination suppression across chromosome 2 precluded the characterization of the locus on such chromosome. On the contrary, the chromosome 6 locus was mapped to a < 2 Mb region on bin 6.07. Further fine mapping analysis using 2,000 F2 recombinants and corresponding F3 and F4 families enabled us to narrow down the tassel seed 6.07 locus to a 130 kb region which included three genes based on B73 genome annotation. Candidate genes are being further characterized and tested by comparison of allele sequences and gene expression analysis.