

Fine Mapping and Characterization of the *tassel-less4* Mutant in Maize

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Tassel-less4 (Tls4) is a mutant in *Zea mays* (maize) which is characterized by its deficiencies in inflorescence resulting in a smaller tassel, the male reproductive structure in maize. The *tls4* mutant is also characterized by its reduced plant height and narrow leaves. Both fine mapping and bioinformatic methods have been used to locate the causative gene for the *tls4* phenotype. Through the utilization of bulked segregant analysis (BSA) and next generation sequencing (NGS) the causative gene was found to be on the long arm of chromosome 4. Fine mapping was then performed using publicly available markers. After exhausting the publicly available markers, new simple sequence repeat (SSR) and derived cleaved polymorphic sequence (dCAPS) markers were created by utilizing differences in the B73 and MO17 maize backgrounds. The utilization of these techniques has narrowed the possible location for *tls4*'s gene to a 200kbp region containing 6 remaining genes. The remaining candidate genes include genes involved in endocytosis and protein folding. The *tls4* phenotype is characteristic of mutants containing defects in the plant growth hormone auxin. Auxin is involved in the regulation of plant growth and differentiation. One specific function of auxin is the control of organ formation. By studying *tls4* a more complete picture of how auxin functions in plants can be produced and utilized to increase future agricultural productivity.