

Allele-specific primer based identification of dimeric *alpha*-amylase inhibitor genes in wheat

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ABSTRACT

Wheat is one of the most important staple food crops cultivated over 200 mha in the range of environment throughout the world. Wheat production must continue to increase by 2% annually, more particularly in developing world including south-east Asia. Besides increasing the inherent productivity of wheat, it is important to minimize the losses caused to production by various abiotic and biotic factors. Alpha-amylase inhibitors are attractive candidates for the control of seed weevils as these insects are highly dependent on starch as the energy source. They play an important role in the carbohydrate metabolism of many heterotrophic and autotrophic organisms. In this study, we aimed to make sequence comparison and phylogenetic relationship among dimeric alpha-amylase inhibitor genes. These genes were clustered into two major groups based on phylogenetic analysis. Multiple alignments show at least 24 candidates single nucleotide polymorphisms in inhibitor genes, which could further be exploited for SNPs based haplotype diversity among Indian released wheat genotype. We have detected dimeric alpha-amylase inhibitor genes in cultivated and wild ancestors of wheat using genome specific primers. Genes encoding dimeric alpha-amylase belong to the family of 24 kDa alpha-amylase inhibitors. In this study, specific primer pairs were designed based on SNPs of these genes and chromosome locations of inhibitor genes confirmed by amplification in accession of *T. urartu*, *A. tauschii*, and *A. speltoides*. Results obtained under this study support that inhibitor genes amplified with primer PSWDAIAF1/PSWDAIAF2 and PSWDAIBF1/PSWDAIBF2 is present on genome B. These results further support evidence at molecular level that dimeric alpha-amylase inhibitor in cultivated wheat is encoded by a multigene family.