Abstract:

LEA protein as a kind of accumulative protein at the late embryo period,for the first time, are identified and introduced to overcome environmental tensions imposed to wheat and cotton. Dehydrine proteins of the second group are among extremely hydrophilic proteins of LEA family which are stable against dryness. In order to provide a general identification and evaluation of molecular evolution of nucleotide sequence of DHN5 Gene location , this Gene was first separated and then its sequence in three wild species of Diploeed(Aegilops speltoides, Aegilops tauschii,and Tricticum urartu), two wheat species of tetraploid (Behrang,Shabrang),and two wheat hexaploid species of wheat cultivars(Bollani and Sistan) was identified. This Gene was identified for the first time during this study and obtained results from sequencing of the gene in cultivars species and their wild ancestors were recorded in NCBI database. The results demonstrate that transformative replacement happens more than cross replacement.DN/DS proportion equals to 1/13 which shows positive DHN5 Gene selecting process among cultivar and wild species of wheat during the evolution. Protected regions represent small part of DHN5 Gene sequence which shows its capability for mutation and nucleotide changes. Phylogenetic tree related to wheat dehydrine gene sequence along with 28 other varieties are depicted based on Neighbor-Joining method which shows different evolution forms of DHN5 gene. Obtained results from phylogenetic analysis show that Sistan cultivar, due to its compatibility to to draught tension, has been imposed so many mutations,therefore, it's sequence has been extremely changed which invoked us to separate it from other species in phylogenetic studies. Based on obtained results from all studied species, it will be concluded that this Gene is probably located in all three A,B,and C wheat genomes.

Keywords: Protein, Sequencing, Gene, Phylogeny, Wheat

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