

REAL TIME PCR ASSAY TO ASSESS RETROELEMENTS AMOUNT IN *TRITICUM* AND *AEGILOPS* SPECIES AND ITS PHILOGENESIS IMPLICATIONS

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The assess of variation among related taxa allows geneticists to understand phylogenetics relationships and plant breeders to exploit wider pools of diversity. The genetic variation and genetic structure of a species reflects not only the patterns of its genetic exchange, but also its history in term of gene flow, range fragmentation and isolation among population. In present work, we have employed Real-Time PCR technique to analyze the amount of WIS2-1A retrotransposon in some *Triticum* and *Aegilops* species. WIS 2-1A is the first retrotransposon found in wheat, it was primarily observed as an insertion of 8 Kb into Glu-1 locus, a High-Molecular-Weight (HMW) storage protein gene, in *Triticum aestivum* (AABBDD). WIS 2-1A has a high presence of homologous sequences showing high levels of interspecific variability and almost no intraspecific differentiation, moreover it represents a recently evolved region unique to *Triticeae* genomes. To understand the molecular evolution of this locus used as an index of genetic differentiation, we have compared the amount of retrotransposons WIS2-1A revealed in three ploidy level of wheat: *Triticum monococcum* ($2n = 2x = 14$, AA), *T. dicoccum* ($2n = 4x = 28$, AABB), *T. spelta* ($2n = 6x = 42$, AABBDD), with the corresponding D genome donor, *Aegilops tauschii* ($2n = 2x = 14$, DD), B genome donor *Aegilops speltoides* and other two species of *Aegilops* (*sharonensis* and *bicornis*). The obtained polymorphism in retrotransposon number has been used to model the temporal sequence of insertion events in a lineage and to establish phylogenetic hypotheses. The obtained results show the presence of WIS2-1A retrotransposon not only in the *Triticum* species examined, but also in the *Aegilops* ones in accord with previous work (Moore *et al.*, 1991) where it has been observed that WIS2-1A is a very ancient element present probably in the common ancestors; infact the presence of this retroelement it has been confirmed in all *Triticeae* tested (Moore *et al.*, 1991). Moreover, the highest number of retrotransposon was found in *Ae. Speltoides* and *T. spelta*, followed, in decreasing order, by *T. dicoccum*, *Ae. Tauschii*, *Ae. Bicornis*, *Ae. sharonensis* upon the lowest *T. monococcum*. These results confirm previous studies where it has been observed that genome B contain a major number of retrotransposons compared with the D genome.