

## عنوان مقاله:

Phylogeny and genetic diversity of *Fusarium graminearum* species complex associated with *Fusarium* head blight of (wheat in Moghan plain (Iran

## محل انتشار:

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## خلاصه مقاله:

Thirty-seven isolates of *Fusarium graminearum* species complex obtained from wheat heads with *Fusarium* head blight symptoms were selected and used for phylogenetic studies. They were collected from different localities of Moghan plain (Ardebil province, Iran). Partial sequences of translation elongation factor 1-alpha (TEF), putative reductase (RED) and UTP-ammonia ligase (URA) genes were amplified using specific primers and sequences were analyzed using Maximum Parsimony method. Almost all strains of *F. graminearum* species complex belonged to *F. graminearum* sensu stricto. The results indicated homogeneity within *F. graminearum* species complex. Inter-simple sequence repeat markers (ISSR) were employed to study the genetic structure of *F. graminearum*s. populations collected from five localities in Moghan plain. The ISSR markers were generated by five primers and data analysed using UPGMA method with Jaccard's coefficient. Cluster analysis showed that all isolates were divided into four clades with 82% similarity level. The analysis of molecular variation indicated that most of the gene diversity (97%) was distributed within populations, whereas 3% of the variation was found among populations. Phylogenetic species identification and genetic diversity knowledge of major agent of FHB disease will be useful in defining the risk of pathogen evolution as well as benefiting disease management strategies.

## کلمات کلیدی:

Microsatellite markers, RED, TEF, URA, wheat scab

## لینک ثابت مقاله در پایگاه سیویلیکا:

