

STUDY OF GENETIC DIVERSITY OF *Puccinia triticina* PATHOTYPES, THE CAUSAL AGENT OF WHEAT LEAF RUST IN IRAN BASED ON rDNA IGS1 SEQUENCING *

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Abstract

To identify pathotypes, phenotypes and genetic diversity of Iranian wheat leaf (brown) rust (*Puccinia triticina*) isolates, eleven samples were collected from different geographical regions. Pathotype and phenotype of each isolate was identified and the intergenic spacer of rDNA (IGS1) was sequenced. One PCR product (870 bp) was recovered from all isolates. Multiple sequence alignments showed 0.0 to 1.2 % difference indicating that IGS1 sequences were highly conserved among all analyzed isolates. The unrooted phylogenetic tree of sequences was drawn based on neighbor joining (NJ) procedures. Based on NJ tree, all sequences were grouped into six different clades. The results showed no direct relationship between *P. triticina* pathotypes and rDNA IGS1 sequence differences.

Keywords: Rust phenotypes, Sequence alignments, Dot matrix, Phylogenetic tree, Neighbor joining.

See Persian text for figures and tables (Pages ۱۵۷-۱۶۹).

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