GENETIC VARIABILITY OF IRANIAN BYDV-PAV ISOLATES

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INTRODUCTION
Barley yellow dwarf viruses (BYDV's) cause serious losses to cereal crops worldwide. These viruses are phloem-limited, belong to Luteoviridae and are transmitted by aphids in a circulative manner (1).

Previous results have revealed the wide distribution of these viruses throughout Iran. Among them, BYDV-PAV is the most prevalent virus. However there is not enough information in regards to its genetic variability.

The present study was carried out to analyze the genetic diversity of PAV isolates in central and southern provinces of Iran, using some parts of ORF1 and ORF5.

MATERIALS AND METHODS
Collected wheat, barley and oat samples were tested by enzyme-linked immunosorbent assay (ELISA) and tissue print immunoassay (TPIA) to insure their infection with PAV.

Total RNA was extracted from infected tissues. RT-PCR was carried out using BYDV-PAV specific primers for polymerase gene (903bp) and read-through domain (575bp). The amplified fragments were inserted into PTZ28R/T vector, cloned in Escherichia coli (DH5α) and sequenced.

RESULTS
Sequence analysis of ORF5 region at nucleotide and amino acid levels revealed a high identity between Iranian isolates and those in the GenBank. However, in regards to ORF1 the results showed a high genetic variability among Iranian and GenBank isolates at both amino acid and nucleotide levels.

According to phylogenetic analysis of ORF1 sequences, Iranian BYDV-PAV isolates fall in two groups. The first group comprises the isolates of Boushehr, Rostagh, Esfandaghe, Abas Abad, Kermanshah, Saveh, Ilam and some BYDV-PAV isolates of Australia, Japan and America with more than 90% similarity at amino acid level. The second group consisted of Kahnouj, Arak, Karaj and Yazd isolates with more than 93% similarity at amino acid level.

However, the similarity between these two groups at amino acid level was only 77-86%.

DISCUSSION
According to the ICTV Sixth Report, that more than 10% differences at amino acid level for each gene product can be considered as two distinct species in the Luteoviridae family. Thus the second group of Iranian PAV isolates can be proposed as a new species (2).

REFERENCES