

A Phylogenetic survey of Polygalacturonase-inhibiting protein1 (PGIP1) in different plant orders

Majid Shouri^{1*}, Samin Seddigh², Mahnaz Hourshad¹, Mehran Zolfaghari¹

1. Department of Plant Pathology, Varamin-Pishva Branch, Islamic Azad University, Varamin, Iran

2. Department of Plant Protection, Varamin-Pishva Branch, Islamic Azad University, Varamin, Iran

Abstract

Polygalacturonase inhibiting protein 1 (PGIP1) is a protein that is found in plants and plays a major role in plant defense against fungal infections. Phylogenetic analysis of PGIP1 in plants have shown this protein is highly conserved among different plant species. However, there is also evidence of genetic variation in PGIP1 among certain plant species, possibly as a result of the ongoing competition between plants and fungal pathogens. Understanding the evolutionary relationships of PGIP1 can help in the selection of plant species with specific genetic variations that confer enhanced resistance to fungal infections. In current study, the PGIP1 protein reference sequences (RefSeq) belonging to various plant species of different orders including Asterales, Brassicales, Caryophyllales, Cucurbitales, Fabales, Malvales, Nymphaeales, Poales, Rosales, Sapindales and Vitales were retrieved from NCBI. Phylogenetic analyses were done using Molecular Evolutionary Genetic Analysis (MEGA; version 11.0). The phylogenetic tree was constructed with the Maximum-Likelihood method, ClustalW algorithm, JTT Matrix-based model and 1000 bootstrap replications. The results showed that all PGIP1 proteins were divided into six different groups, designated as Groups I–VI. Most of the designated groups were supported by more than 30 bootstrap values. Based on the tree, all the samples categorized in different groups. All the species of Brassicales, Cucurbitales and Fabales orders were predominantly found in groups II, III and IV, respectively. Interestingly, species from the same order tended to cluster together within the same sub-branches of the phylogenetic tree. Rosales species were separated in a sub-branch in group I while Poales species were separated as a sub-branch in group V. Phylogenetic analysis showed that evolutionary relationships among different groups of PGIP1 were inevitable. Moreover, within each group, similar amino acid sequences suggested strong evolutionary relationships among different orders. These results indicated that, in plants, PGIP1 are possibly inherited from a common ancestor.

Keywords: MEGA; Phylogenetic analysis; Plants; PGIP1