Plum pox virus (PPV) 

Sharka ya pimmari Aiheyo Alloyo Bousile (PPV) 

Susan Jhans (Povovirus)

emaatit acchisad yi ke zahb 31. 

Bithis geyewa rayeens eegal dakh. 

Aa amm Alloyo dakh.

P1/P2

Mrqal

ppv

Bioreba

plum

Ghabin Alloyo dakh. 

Yeeal Alloyo dakh. 

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plum
Association of Plum Pox Virus Strain M with Plum Fruit Dropping in Mazandaran Province; E. Mohammadi1, F. Goharzad1 and A. Zaghi2; 1- Plant Protection Organization of Iran (elham54m@yahoo.com); 2- Jihad Agriculture Organization of Mazandaran Province.

Sharka (plum pox disease) is caused by Plum pox virus (PPV) a member of the genus Potyvirus (1). It is considered one of the most devastating diseases of stone fruits in terms of economic importance. The disease causes reduced quality and premature dropping of fruit and is one of the limiting factor of apricot, peach, plum and certain other stone fruit production in Iran. The disease has progressively spread to a large part of the European continent, Mediterranean basin and some of Middle East countries.

Severe fruit dropping was recently observed in some plum orchards of Mazandaran province. In order to investigate possible involvement of PPV, 75 leaf and shoot samples collected during the late summer and autumn of 2010. Sampling was based on typical PPV symptoms. Virus infection was confirmed by serological and molecular testing. Serological diagnosis was made by DAS-ELISA using a commercial PPV polyclonal antiserum (Bioreba, Switzerland). Molecular detection was made by trapping virus particle with the above polyclonal antiserum and IC-RT-PCR was performed by using the general pair of primers P1/P2. Total RNA were extracted from dormant buds and barks (2) using RNeasy Plant Mini Kit (Qiagen, Germany) according to the manufacturer’s instructions.

The results showed that 48 out of 75 plum samples were found to be infected with PPV. One-step RT-PCR (Qiagene One-Step RT-PCR Kit) was performed using the general primer pair (P1/P2). The P1/P2 primers revealed and confirmed the presence of the virus by amplifying the expected 243 bp fragment located at the C-terminus of PPV CP gene (3). The results of RT-PCR analysis were in complete agreement with the DAS-ELISA and IC-RT-PCR results.

Since, the severity of symptoms depends largely on plant species and virus strain, the type of strain determined by RT-PCR targeting (Cter) CP, using P1/PD and P1/PM pair of primers that distinguish two major and PPV-D strains PPV-M, respectively; The RT-PCR analyses confirmed that all 48 samples were infected with PPV-M type and no samples were positive for PPV-D. Subsequently, molecular strain typing was confirmed by Restriction Fragment Length Polymerase (RFLP) of 243 bp amplicon using Rsal and Alul restriction endonucleases digestion (4). In this study, the pattern after enzyme digestion showed all of PCR products contained the Alul site.