Short Report

ASSESSMENT OF THE GENETIC DIVERSITY OF *XANTHOMONAS* AS THE CAUSAL AGENT OF ALDER ANGULAR SPOT IN MAZANDARAN AND GOLESTAN PROVINCES USING BOX-PCR AND REP-PCR

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Alder (*Alnus subcordata subsp. Subcordata*) is one of the most important tree species in northern forests of Iran and is economically considered as the fourth commercial tree. A leaf spot disease of alder caused by ***Xanthomonas*** sp. has been reported from several forest regions of Mazandaran province (Rahimian *et al*. 1383. 16th Iran. Plant Protec. Cong., 439). According to a recent genomic study, the bacterial agent of this disease has the highest similarity to *Xanthomonas arboricola* (Rahimian *et al*. 1387. 18th Iran. Plant Protec. Cong., 428). Though limited studies have been performed about the homology of isolates and the distribution of the disease (Rahimian *et al*. 1383. 16th Iran, Plant Protec. Cong., 439), detailed information is not available about the genetic diversity of isolates from different regions. This study was conducted to evaluate the genetic similarity or diversity among the isolates obtained from different regions of Mazandaran and Golestan provinces. Phenotypic characteristics of isolates were very similar and they were different only in utilization of carbon sources including L- Serin, Leucine Dextrin, Quinate, Tyrosine. The population genetic diversity analysis of the bacterial pathogen of alder angular leaf spot was performed using BOX-PCR and REP-PCR. Genomic DNA was extracted from isolates using alkaline lysis, and PCR was performed as recommended by Versalovich *et al*., but by reducing the deneturing time (Versalovich *et al*. 1991. Nucleic Acids Res, 24: 6823 -6831). PCR products were electrophoresed in 2 percent agarose gel and the gel was stained with ethidium bromide. Similarity, matrix of the isolates was obtained using Jaccard's coefficient and cluster analysis by employing the UPGAMA method and NTSYS software. Cluster analysis by BOXAIR primer showed that the isolates were divided into 24 groups at 80 percent level. However, the isolates of alder showed the same similarity with standard isolate *Xanthomonas arboricola pv. coryli*. At 63 percent level, alder isolates were divided into 15 groups, but with the same amount of similarity they were clustered with *Xanthomonas arboricola pv. pruni*. At 40 percent level, alder isolates were divided into seven groups and showed similar homology with reference isolate of *Xanthomonas arboricola pv. juglandis*. According to these findings, it can be concluded that isolates inciting alder angular leaf spot have high variability, while BOX-PCR was unable to differentiate *X. arboricola* pathovars. Results obtained with REP1R and REP2I primers showed that at 78 percent level, isolates were divided into 14 groups. In contrast, the isolates showed the same level of similarity with *X. arboricola pv. juglandis* and *X. arboricola pv. coryli* pathovars. At 57 percent similarity level, the isolates were divided into seven groups and were clustered *with X. arboricola pv. pruni* with the same amount of similarity. The data show that alder isolates have high variation and REP-PCR has a better efficiency for grouping causal agent of angular leaf spot of alder isolates.