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AFLP analysis on individuals from leafy spurge populations characterized as resistant or susceptible to flea beetle biocontrol agents

DAVID P. HORVATH

Research Plant Physiologist, USDA-ARS, Biosciences Research Laboratory, State University Station, Fargo, ND 58105-5674

Abstract

Biocontrol agents are becoming a major part of integrated pest management. However, since the pest is a living organism, selection for resistance to the biocontrol agent will occur. A pest with more genetic variability is expected to evolve resistance mechanisms faster than a pest with less genetic variability. Several species of flea beetles (of the *Aphthona* genus) have been employed as biocontrol agents to help control leafy spurge. However, resistance to these beetles has been observed in some populations of leafy spurge. It is not known if the resistance is the result of environmental factors or genetic differences in the resistant populations. Also, the level of genetic variability present in wild populations of leafy spurge is unknown. Knowing the level of genetic variability present in leafy spurge and understanding the mechanisms by which this pest is adapting resistance strategies will aid in predicting the long term success of the flea beetles as a bio-control agent on leafy spurge. We have initiated an analysis of the genetic variability present in wild populations of leafy spurge and have begun to look for specific genetic markers that could be linked to genes involved in resistance to the flea beetles. Dr. Bob Nowerski, a researcher at Montana State University, provided us with dried leaf material for five individual leafy spurge plants each from 50 different populations. These populations were treated with various *Aphthona* species and Dr. Nowerski has characterized the populations as being either susceptible or resistant to these biocontrol agents. We extracted DNA from individual plants and initiated their genetic characterization using the small genome AFLP kit from Gibco/BRL (AFLP Analysis System II). An appropriate number of bands (20 to 100) were generated with the EcoRI (AA) and each of the seven different MseI primers tested. These data are consistent

with previous studies suggesting leafy spurge has a relatively small genome. Amplification generated an average of 41 bands per primer set of which 10 were major bands. There was an average of 1.6 clearly polymorphic bands between individuals from a single population per primer set. This average compares with three to five polymorphic bands per primer set from two closely related barley varieties (Foster and ND9712). These data are consistent with the hypothesis that the level of polymorphism is very low within a given population of leafy spurge.