Reprinted with permission from: Proceedings and Progress Reports of the Leafy Spurge Symposium. Gillette, WY. July 10-12, 1990. p. 14.

Published by: Great Plains Agricultural Council: Leafy Spurge Symposium.

Evaluation of genetic diversity in leafy spurge (*Euphorbia esula*) using chloroplast DNA sequence variation

SCOTT NISSEN¹, MARTHA ROWE¹, DON LEE¹ and ROBERT MASTERS²

Department of Agronomy¹ and USDA-ARS², University of Nebraska-Lincoln, NE 68563-0915.

Understanding the genetic diversity within the North American leafy spurge complex is essential for increasing the success of biocontrol efforts. Multiple introductions of leafy spurge into North America has led to a population of intra-specific hybrids or biotypes often having distinct morphological characteristics. Defining specific North American biotypes and relating them to Eurasian progenitors would be useful in biocontrol efforts. Restriction fragment length polymorphorism (RFLP) analysis of chloroplast DNA (cpDNA) was used to determine the existence and extent of cpDNA sequence variation among collections of morphogically, and geographically diverse *Euphorbia* spp. Accessions from Russia, Italy, Austria, Nebraska and Montana were used in the initial phase of this research. Total DNA was extracted and digested with restriction endonucleases Eco RI, Hind III, Pst I and Xho I. DNA fragments were then separated by electrophoresis on agrose gels. Southern blot analyses were performed using labeled mung bean cpCNA probes. Preliminary data suggests that cpDNA sequence variation does exist among the accessions examined and could provide a means of determining relationships between North American biotypes and Eurasian progenitors.