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Biochemical studies of the *Euphorbia esula* complex

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Pyrolysis mass spectrometry (PYMS) and starch gel electrophoresis were used to determine patterns of biochemical variation in the *Euphorbia esula* complex. These patterns of biochemical variation are being used to elucidate underlying patterns of genetic variation.

Pyrolysis mass spectrometry is a method that has been used for the determination of overall patterns of biochemical variation in several types of complex biological materials. Other workers have used PYMS in taxonomic studies of microorganisms and in studies of the relationship between the biochemical constitution of host plants and their susceptibility to herbivorous insects. We have conducted studies aimed at determining the feasibility of using PYMS to elucidate patterns of biochemical variation in the *Euphorbia esula* complex. These patterns of variation should provide information relative to the taxonomy of this group and their susceptibility to potential biocontrol agents. Analysis of spectral data by factor analysis, discriminate analysis and graphical rotation showed several distinct biochemical differences between *E. cyparissias*, *E. esula* (from Austria), and the 'Gallatin' and 'Teton' accessions from Montana. It was not possible to correlate these differences with differential preference of biological control agents because quantitative indices of the susceptibility of these accessions to biocontrol agents were not available.

Electrophoresis, the separation of proteins in an electric field, is being used to determine patterns of genetic variation of the *E. esula* complex. This procedure involved producing starch gel zymograms for several accessions within each of several populations of leafy spurge and then doing genetic analysis to determine the allelic basis for the observed banding patterns. This genetic data can, in turn, be used to calculate indices of genetic similarity within populations and genetic distance between populations.