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Low Levels of Genetic Diversity Within Populations of
Hosta clausa (Liliaceae)

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Genetic diversity of Korean populations in Hosta clausa was investigated using starch gel electrophoresis. Hosta clausa is widespread, and grows only along streamsides and has both sexual and asexual reproduction. Populations of the species are small, isolated. Thirty-two percent of the loci examined were polymorphic, and mean genetic diversity within populations ($H_{\text{P}} = 0.082$) was lower than mean estimates for species with very similar life history characteristics (0.131), particularly for its congener H. yingeri (0.250). Mean number of multilocus genotypes per population was 8.7 and genotypic diversity index (D_{G}) was 0.84. Significant differences in allele frequencies among populations were found at all seven polymorphic loci ($P < 0.001$). About one-fifth of the total allozyme variation was among populations ($G_{\text{ST}} = 0.192$). Indirect estimate of the number of migrants per generation ($N_{\text{M}} = 0.48$, calculated from mean G_{ST}) and nine private alleles found indicate that gene movement among populations was low. The low levels of genetic diversity within populations and the relatively high levels of genetic diversity among populations indicate that strong moist habitat preferences, clonal reproduction, low level of gene flow among populations, genetic drift, and historical events may play roles in the genetic structuring of the species.

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**Pyrolysis Mass Spectrometry as a Method for the
Classification of Actinomycetes**

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Pilot experiments were designed to determine the potential of Curie-point pyrolysis mass spectrometry (Py-MS) in the classification of acidophilic actinomycetes. The results formed the basis of mathematically derived characterization of individual strains and clusters. Those were compared with the results of conventional methods such as numerical taxonomy and fatty acid profiles analyzed by gas chromatography mass spectrometry (GC-MS). Py-MS was shown to be a rapid, relatively inexpensive and reproducible method for the classification and discrimination of acidophilic actinomycetes.