

서 수생식물의 생장은 저수지 연안대의 자연 습지보다 저조하였는데, 이러한 이유는 수질 정화습지에서 수문 조건과 토양 특성이 수생 식물생장에 적합하지 않고 교란이 가해지기 때문인 것으로 생각된다. 보다 효율적인 자연형 수질정화시설을 조성하기 위해서는 수생식물 생육에 적합한 습지 환경 조성이 요구된다.

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Variations in Allozyme in *Dictamnus dasycarpus* (Rutaceae) Associated with Heterogeneous Soils.

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Microgeographic allozyme variation was examined in bodenvag plant, *Dictamnus dasycarpus* (Rutaceae), a herbaceous perennial diploid, distributed in both serpentine and adjacent non-serpentine forest soils in Andong, Korea. Total eighty one individuals of *D. dasycarpus* were sampled at each soil type and analyzed using non-denaturing polyacrylamide gel electrophoresis for two enzymes (Peroxidase, Superoxide dismutase). Two alleles per locus were observed for two loci (PER-1, SOD-2) and genotypic frequencies at each locus were significantly different between serpentine and non-serpentine area. At PER-1 locus, the frequency of genotype aa and ab was higher in serpentine than non-serpentine area and bb lower in frequency in serpentine soils. The genotype aa frequency at SOD-2 locus was higher in relatively infertile area and ab, bb genotype were a little higher in non-serpentine than serpentine area. These results suggest that specific genotypes may play an important role in naturally adapting *D. dasycarpus* to heterogeneity in soil type.

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한국산 맥문동 (*Liriope platyphylla*)

WANG et TANG) 과 소엽맥문동 (*Ophiopogon japonicus* KERGAWL.) 의 분포 및 유용성

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한국산 맥문동 (*Liriope. platyphylla*) 과 소엽 맥문동 (*Ophiopogon. japonicus*) 에 관한 분포와 한약자원으로서 유용성에 대해서 조사하였다. 분포지 조사는 전국지역을 대상으로 하였으며, 분포지역을 현지조사와 더불어 서울대학교 표본관 (SNU), 성균관대학교 표본관 (SKK), 강원대학교 표본관 (KWU), 경북대학교 표본관 (KNU) 및 순천대학교 표본관 (SNU) 에 소장된 표본 및 문헌조사를 병행하였다. 현지조사는 1997년 5월부터 2000년 8월 까지 실시하였다. 분포지역으로는 맥문동은 바다에서 가까운 지역 즉 서해안, 남해안, 동해안을 따라 전국적으로 분포하였으며, 소엽맥문동은 남해안과 도서지역에서 그 분포지가 확인되었다. 한약자원의 유용성면에서 맥문동속의 2종 (*L. spicata*, *L. platyphylla*) 과 맥문아재비속의 1종 (*O. japonicus*) 을 각각 이용하고 있으나 우리나라에서는 맥문동속의 맥문동 (*L. platyphylla*) 과 맥문아재비속의 소엽맥문동 (*O. japonicus*) 을 맥문동 (*Liriope Tuber*) 으로 이용하고 있는 반면에 중국과 일본에서는 소엽맥문동 (*O. japonicus*) 을 주로 이용되고 있다. 그 외에 중국에서는 개맥문동 (*L. spicata*) 을 산맥동이라 부르고 있으며 이들의 유용성에 대하여는 실험중이다.

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Allelopathic Potentials of Volatile Essential Oils in *Artemisia scoparia*

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To investigate allelopathic potentials in *Artemisia scoparia* as one of the main weed, and their biological activities, seed germination and seedling growth of receptor plants were examined at different concentrations of essential oil of the donor plant. The treatment of the volatile essential oils of the *A. scoparia* caused significant inhibition in the germination, shoot and radicle growth of the receptor plants. The radicle growth of receptor plants was inhibited more severely than shoot growth. The essential oils of *A. scoparia* extracted by Karlsruher's apparatus was significantly inhibited on several bacteria and fungi. The essential oils of *A. scoparia* inhibited the induction and growth of callus of the receptor plants; *Acyranthes japonica*, *Brassica campestris* subsp. *napus* var. *pekinensis*, *Oryza sativa* and *Sesamum indicum*. The GC/MS was employed for analysis and identification of allelochemicals from *A. scoparia* leaves, i.e. camphene, n-methyl-2,1-borazarene, a-phellandrene, a-terpinene, p-cymene, 1,8-cineole, g-terpinene, l-camphor, endo-borneol, terpinen-4-ol, trans-ocimene, (-)-b-elemene, trans-caryophyllene and ledene. The bioassay with the four commercial compounds was shown from identified chemical compounds was done. 1,8-cineole showed as the strongest growth inhibitor of the chemicals. The results of this experiment on seed germination seedling growth, anti-microbial test and tissue culture indicated that naturally occurring chemical substances of essential oil from *A. scoparia* would be responsible for the phytotoxic and anti-microbial effects.

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**Conservation Genetics and
Fine-Scale Spatial Genetic Structure
of *Leontice microrhyncha*
(Berberidaceae) in Korea.**

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Leontice microrhyncha S. Moore (Berberidaceae), a herbaceous perennial occurs in the deciduous forests of Korea, has been endangered because of small population size and anthropogenic activities. Allozyme variation in six populations using 17 enzyme systems, resolved 33 putative loci, seven (21.2%) loci were polymorphic in at least one population. The mean percent of polymorphic loci (P) was 8.58%, the average number of alleles per polymorphic locus (APs) and effective number of allele (Ae) was 2.33 and 1.04 respectively. Genetic diversity (Hes) was 0.024 and this value was very low relatively compared with other rare taxa. About 62.7% of total variation resided among populations, indicating that gene flow ($N_m=0.149$) among populations was highly restricted. Average genetic identity for all pairs of populations was 0.906, well within the range of values expected for the conspecific population. Populations of *L. microrhyncha* fell into two distinct groups and the genetic similarity of geographically near populations was clearly revealed by a UPGMA phenogram. Spatial autocorrelation analysis was used to explore genetic differentiation at smaller scales; a significant small scale genetic structure was detected in all sampled plots and patch widths were inferred to be approximately 12-14 m. A non-random distribution of genotypes may be a reflection of restricted gene flow, selection and patchy establishment of genetically distinct cohorts. *L. microrhyncha* presented special considerations with respect to conservation because genetic variability was distributed among rather than within populations. Range-wide collections across natural distributions are strongly