

学位論文要旨 Dissertation Abstract

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学位論文題目 :

Title of Dissertation

Chloroplast DNA structure, diversity and genetic variation of *hosta*, and analysis of their essential macro-micro mineral content (ギボウシ属植物の葉緑体DND構造, 多様性と遺伝的変異及び主要な多量・微量ミネラルの分析)

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Hostas are major ornamental plants for perennial shady nurseries. They have striking foliage with attractive flowers, and their leaves are sometimes used as vegetables in Japan and Korea. Hosta is a widely grown ornamental plant.

Experiment 01: Diversity studies are now a key tool in genetic conservation work. Hostas appear with frequent species variation in mountains and riversides around the Shikoku Island, Japan. We sequenced *trnS-trnG* regional cpDNA in 81 populations comprising 399 individuals of 11 *Hosta* taxa collected from Shikoku area to evaluate *trnS-trnG* regional cpDNA diversity, divergence and genetic structure variation among taxa for hosta populations. The significant negative neutrality test values are the evidence of expansion of the total population. *H. sieboldiana* and *H. kiyosumiensis* are more widely distributed than other species, having greater opportunity for intra specific gene flow. *H. sieboldiana*, *H. alismifolia*, *H. longipes* var. *gracillima* and *H. kikutii* var. *polyneuron* showed the excessive low frequency variants. The genetic structures of the *H. tardiva* with *H. kikutii* var. *caput-avis* and *H. sieboldiana* with *H. tardiva* populations were greatly differentiated (F_{ST} value: >0.15 to 0.25). We found maximum evolutionary divergence (0.009) between *H. alismifolia* and *H. kikutii* var. *polyneuron* populations. The different numbers of haplotypes was found in different taxon. The highest number of haplotypes (14) was found in *H. longipes* var. *gracillima*.

Experiment 02: The objective of the second experiment was to estimate the genetic identity and genetic distance of twelve hosta taxa and to build a UPGMA cluster for them using RAPD. We amplified the cpDNA of twelve

hostas by means of 20 RAPD 10mer markers (Kit A: OPA-01 to OPA-20). Out of 20 RAPD markers, the genomic cpDNA was successfully amplified for fourteen. Fourteen markers generated a total of 102 fragments. We found maximum genetic distance (0.655) and minimum genetic identity (0.520) between *H. sieboldiana* - *H. longissima* and between *H. sieboldii* - *H. longissima*. Estimated minimum genetic distance (0.071) and maximum genetic identity (0.931) were found between *H. kikutii* var. *polyneuron* - *H. longipes* var. *caduca*. The UPGMA dendrogram revealed the relationship among the 12 hosta. The results confirmed our hypothesis of large genetic variability among the taxa, which distinguishes the genotypes clearly. The RAPD 10mer markers were found useful in application to the evaluation of the genetic variability and diversity within taxa.

Experiment 03: Hosta is a perennial ornamental herb, sometimes consumed as a vegetable in Japan. We analyzed the leaf mineral content of twelve hosta plant taxa. The leaf K content of 12 hosta plant taxa ranged from 2.85 to 4.05%; the P content from 0.13 to 0.34%; Ca from 0.02 to 1.15%; Mg from 540.00 to 794.12 ppm; Mn 26.93 to 133.77 ppm; Zn 115.39 to 334.52 ppm; Cu 1.78 to 5.95 ppm and Fe 26.43 to 251.95 ppm. Our results indicate that *H. alismifolia* is the best source of K; *H. sieboldii* the best sources of Ca and Fe; *H. nakaiana* of P, Mg and Zn; and *H. longissima* of Mg and Cu. The K content value for *H. montana* was statistically identical to that for *H. alismifolia*. The Cu content values for *H. montana* and *H. nakaiana* were statically identical to that for *H. longissima*. *H. alismifolia*, *H. sieboldii*, *H. longissima*, *H. nakaiana*, and *H. montana* were found to be richer in the minerals studied than the other species studied here.

Experiment 04: Hybridization of hostas is frequently done by home gardener. The aim of our last experiment was to analyze the morphological traits based hierarchical cluster, euclidean distance and PCA with a view to provide necessary information to the hosta breeders. *H. sieboldiana* and *H. montana* had similar morphological characters while *H. longipes* var. *gracillima* and *H. kiyosumiensis* had mostly similar morphological characters as well. It was found that the dissimilarity distance between *H. alismifolia* and *H. montana* was maximum (452.2) which was closely followed by *H. longissima* and *H. montana* (447.6) whereas minimum dissimilarity distance between *H. sieboldii* and *H. nakaiana* (36.2). Leaf area was found as a unique morphological trait. PCA indicated that two important components accounted for 97.76% of the total variation among traits in of hosta taxa. The first and second component contributed 81.92% and 15.84% of the total variation, respectively.