

Ecotypic variation of *Imperata cylindrica* populations in Taiwan : I. Morphological and molecular evidences

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摘要.

Abstract

Imperata cylindrica L. Beauv, a common C4 grass, is widely distributed in various habitats in Taiwan. Among 55 populations in various habitats, six sites were selected for the study. These sites are namely, Chuwei (an estuary mangrove forest area with high salinity), Sarlun (in a coastal saline area), Kengting (at Taiwan's southern tip with a drought season in winter), Penghu (an islet about 100 km from the west coast that is droughty in most seasons), and Nankang and Hoshe (both inland control sites with mild weather). Leaves of *I. cylindrica* sampled from these sites were examined under light microscope and scanning electron microscope for anatomic study in order to see their difference. The results showed that the grass leaves collected from the Chuwei site exhibited a clear difference from those of other sites, revealing a hollow structure in the midrib of leaves and villous trichomes on the abaxial leaf surface. The rhizomes of the grass were also collected from each site, brought back to the laboratory, and were transplanted into pots and grown in a greenhouse of the Academia Sinica. The phenotypic characters, such as plant height and leaf width, of the grasses collected from the field and from the greenhouse were compared. The results showed that plants collected from Chuwei, Sarlun, and Penghu were significantly shorter than those of the remaining three sites. The grass leaves collected from both the field and greenhouse were analyzed by means of random amplified polymorphic DNA. Forty 10 base pair primers were employed, and only 31 primers were adequate. Of them, 82 distinguished bands resulted from the RAPD study, showing the difference among populations of the six sites. Furthermore, using an Euclidean distance method, the phylogenetic relationship among the six populations was obtained. The findings revealed that the Nankang and Hoshe populations evolved into an ecotype, which was significantly different from another cluster of the remaining 4 populations. However, populations at Chuwei and Sarlun formed into a unique ecotype although they were also closer to other populations Penghu and Kengting. The phenotypic, morphological, and molecular data are correlated to each other.