

## The genetic diversity of *Herba Houttyniae* in Taiwan

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### ABSTRACT

Lots of species of medical plants have found in Taiwan because of the special climate and geographic condition. Most of traditional herb medicine was derived from wild species. The genetic diversity of some herb species has gradually eroded owing to biological destruction and ultra utilization by people. Selection of best variety or genotype is the first step aiming to the good quality of Chinese herb medicine. Enlarging genetic diversity of inter- and intra- species is very important for breeder to preserve some useful germplasms, and then have more opportunities to develop new varieties and search new drugs for controlling disease. In order to enhance the gene pool of herb medicine, collection, identification, conservation and evaluation to genetic resources of herbs would be an urgent task.

The genetic variations of 10 wild populations and 24 cultivated lines of *Houttuynia cordata* Thunb were tested by morphological characters and RAPD markers. The results of principal component analysis (PCA) and Cluster analysis by using UPGMA method showed that 10 populations can be classified as 3 groups, and all the tested lines can be classified as 2 groups, of which, 17 lines was classified as one group. The results also showed that the genetic diversity in wild population based on RAPD genetic similarity was corrected with geographic distribution. The genetic diversity of wild population groups was higher than that of cultivated ones. Considering variation of chemical component, the content of flavonoids involving rutin, hyperin, isoquercitrin and quercitrin had significant difference in populations and lines. In view of breeding, population of Suao and line of Kouhu were the noticeable germplasms.

**Key words:** *Herba Houttyniae*; genetic diversity; RAPD; flavonoids