

# The analysis of genetic diversity of *Pueraria montana* in Taiwan revealed by ISSR method <sup>(1)</sup>

Pei-Hua Tsia <sup>(2)</sup> Shin-Lon Ho <sup>(2)</sup> Chin-Jin Hou <sup>(2)</sup> Jeng-Bin Lin <sup>(3)</sup> and Tzu-Rung Li <sup>(3)(4)</sup>

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## Abstract

*Pueraria montana* is widely in Taiwan area. Which roots can be used for food and make wine, stem can make ropes and leave can feed animals. This study investigated the genetic diversity among 91 samples collected from 18 areas in Taiwan. UBC inter-simple sequence repeat (ISSR) of the markers to distinguish gene structure for using. According to ISSR analysis, 15 primers were polymorphic from the results. The results of AMOVA showed those of the variance component between population regions, variance component between population within regions and the variance component among individuals within the population were 10.02%, 14.05% and 75.92%, respectively. The value of total gene diversity (H), genetic differentiation index (Gst) and gene flow index (Nm), were 0.3634, 0.4401 and 0.636 respectively. Cluster analysis and principal coordinate analysis revealed that the population could be divided into five groups by genetic distance 0.23. First group includes Taipei, Taoyuan, Hsinchu and Yilan. Second group includes Taichung, Pingtung, Yunlin, Kaohsiung, Hualien, Taitung, Chiayi and Tainan. Third group includes Miaoli, Nantou, Changhua and Alishan. Fourth group includes Keelung, and the last one includes Kinmen. There is not significant relationship between genetic and geographical distance of populations. In conclusion, *Pueraria montana* has been the trend of differentiation, and genetic drift played an important role on the differentiation between groups.

Key word: Cluster analysis, Genetic diversity, ISSR, *Pueraria montana*.

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(1) Contribution no. 2562 from Livestock Research Institute, Council of Agriculture, Executive Yuan.

(2) Agronomy Department National Chiayi University, Chiayi, 600, Taiwan, R.O.C.

(3) Division of Forage Crops, COA-LRI, Hsinhua, Tainan, 712 Taiwan, R.O.C.

(4) Corresponding author, E-mail: trli@mail.tlri.gov.tw.