## 臺灣金線連品系遺傳標誌之研究

## 中文摘要

臺灣金線連是蘭科(Orchidaceae)金線連屬(Anoectochilus)之小型地生蘭,為 民間藥用植物。依據其外表形態特徵可分爲紅骨、綠骨、長葉和圓葉四個品系, 本實驗利用 DNA 指紋分析技術篩選其特有的分子標誌。rDNA(ribosomal DNA) 序列的分析結果發現,種內各品系間無顯著差異; RAPD(random amplified polymorphic DNA)分析結果,發現 T12+A、T12+T 及 D1+G 引物可產生 對紅骨及綠骨二品系具多型性標誌;在 inter SSR (inter simple sequence repeat)分析中,成功地利用 808、827、835、836、841 及 842 六條引物, 將四個品系完全區分出來。另一方面,利用 AFLP (amplified fragment length polymorphism)分析同一母株在繁殖後代過程可能體細胞變異的結果,我們利 用 17 組引物, 偵測臺灣金線連體細胞變異的程度, 單株 DNA 變異程度介於 0~5.92 %,平均為 2.89 %,本研究結果推薦五組引物組合可效偵測金線連 之體細胞變異。根據本實驗室近年來的實驗結果顯示,臺灣金線連的多醣體具有 提高免疫的功能;雖然總多醣體含量分析結果顯示,各品系之間並無顯著差異, 但根據我們的初步分析結果,各品系之酸性及鹼性多醣含量,具有較明顯的差 異;而各品系多醣體含量的差異,就是提供作爲選擇優良品系植株的參考,配合 本研究所篩選的 RAPD 及 inter SSR 遺傳標誌,及 AFLP 對臺灣金線連體細胞 變異之分析,可建立優良金線連(多醣產量高)品系的篩選模式,並提供在大量 繁殖之過程仍能維持高品質之評估工具。

## 英文摘要

Anoectochilus formosanus Blume, belonging to Orchidaceae, is a perennial herb. It is used as a medicinal plant in folk. There are four lines different lines within the species according to their appearance: red stem, green stem, narrow leaf, and round leaf. The molecular markers screened by fingerprinting techniques are taken as the detectable object to provide complete and abundant genetic information for the researchers. In rDNA sequence analysis, no significant variation was found among the four entried lines. In RAPD analysis, three primers, T12+A, T12+T and D1+G, generated polymorphic markers between the lines of red stem and green stem. However, six screened primers, 808, 827, 835, 836, 841, and 842, were able to completely differentiate the four lines when ISSR analysis was perfomed. In addition, five sets of AFLP primers were recommended in our study to detect the somatic variation among the excised shoots derived from the same individual. Our recent data shown that polysaccharide in A. formosanus exerts immune activity in vivo. No significant difference in total polysaccharide content was found among the four lines, but acidic and basic plysaccharide contents were different. The

polysaccharide content along with RAPD markers and ISSR markers obtained in the study will be employed to set up a model for selection in breeding program.