

長臂猿種緣關係之完整細胞色素 *b* 基因分析

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摘要：進行物種繁殖的保育工作時，首先需確認物種的種別，以免產生雜交種的子代。目前長臂猿的種別鑑定，有外觀、聲音及 DNA 分析等三種主要方法。前兩種方法快速簡單，但是均需經驗豐富的專家方可獲致信賴的結果。而 DNA 的鑑定，已證實可有效提供種別鑑定的依據。本研究的主要目的，係利用 DNA 分析技術，確定長臂猿的種緣關係。我們分析 35 隻長臂猿細胞色素 *b* 全長 1141 鹼基序列，且與 252 鹼基序列所得種緣分析結果一致，不僅鑑定出外觀無法確定的種別，且解決了先前 NADH 脫氫酵素 ND4/ND5 基因段無法分辨的種別。因此日後進行長臂猿種別的 DNA 分析時，可先利用細胞色素 *b* 基因 252 鹼基做初步快速分析的目標基因。此外，外觀上疑似黑手長臂猿與灰長臂猿雜交種之春花(G2)，由其聲音及上述基因的綜合分析，顯示春花(G2)可能是由雄性黑手長臂猿與雌性同屬的白手長臂猿雜交的後代，且可能在卵子受精過程中發生父系粒線體基因滲出的現象。本研究顯示長臂猿的圈養繁殖，選擇外觀分類與基因分類一致的個體，應可避免雜交子代的產生。

關鍵字：長臂猿、細胞色素 *b*、種緣關係、定序

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Phylogenetic analysis of gibbons based on the complete cytochrome *b* gene

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Abstract : Correct species identification is crucial for zoo officials in order to find suitable partners when carrying out breeding programs and preventing the accidental breeding of hybrids. Currently, the identification of gibbon species are based on fur coloration data, vocal data, and DNA sequence data, respectively. Although, the first two approaches are simple and fast, with these, only experienced experts can reliably identify gibbon species. DNA analysis has been proven to be an effective way for taxonomic studies of organisms. Thus, the main purpose of this study is to apply molecular level analysis to identify the gibbon species. In this study, we have sequenced the complete cytochrome *b* gene of 35 gibbons. The phylogenetic relationships inferred from the 1141 base-pair (bp) cytochrome *b* gene are consistent with those derived from 252 bp segment of the same gene. The result not only successfully distinguishes the gibbon species of those that were doubtful based on fur coloration data, but also resolve the species identities that were not able to be determined based on the 896 bp fragment of ND4 and ND5 (NADH dehydrogenase complex) genes. Thus, in the future, phylogenetic relationships derived from the 252 bp segment of cytochrome *b* gene can be served as a preliminary and quick identification of gibbon species. Besides, in addition to fur coloration, vocal, and genetic data in this study have suggested that the previously unidentified gibbon (Chun-hua, G2) could be a hybrid of a female *H. lar* and a male *H. agilis*. In addition, during their hybridization, paternal leakage of mitochondria might have occurred. To prevent the accidental breeding of hybrids, results from this study indicate that gibbons with consistent genetic and fur coloration characteristics should be given priority in the zoo's breeding program.

Key words: gibbon, cytochrome *b*, phylogeny, and sequencing.

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