台灣地區人口DNA型別分佈在刑事鑑定應用之研究

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摘要

本研究建立台灣地區族群人口之 DNA 型別分佈，研究族群包含布農、排灣、賽夏、雅美、阿美、魯凱、泰雅、鄒、巴宰、卑南、客與漢族等十二個族群，多型基因均爲 STR 基因位，包含 D3S1358、vWA、FGA、D8S1179、D21S11、D18S51、D5S818、D13S317、D7S820、D16S539、TH01、TPOX 與 CSF1PO 十三種。以高嚴謹的卡方檢定進行 Hardy-Weinberg 平衡的適合度檢驗，除了六個基因位的八個族群外，其餘均符合 Hardy-Weinberg 平衡。以漢族爲例，在十三個基因位中，隨機兩個樣品相符機率(Pm)最高的是 TPOX(0.2254)，最低的是 FGA(0.0354)。在突變率的篩檢上，在 250 個親子配對遺傳的對偶基因型(allele)中僅發現 D8S1179 基因位出現一個突變，從對偶基因型 16 突變爲 15。本研究計算出各族群的近親係數 f、隨機兩個樣品相符機率 Pm、父母子三人組之親子鑑定排除率 PE(3)、單親與子二人組之親子鑑定排除率 PE(2)、及所有族群之近親總係數 F 與族群差異 θ，提供刑事鑑定在 STR 基因位的選擇或數據引用的參考。最後，依據十二個族群在十三個 STR 基因位的基因距離數據，進行聚類分析所得的 Neighbor-joining 親緣圖亦可提供人類學研究族群親緣關係之參考。

Population study on forensic application of STR loci in Taiwan

ABSTRACT

This study established the population data of STR loci in Taiwan. The populations included Bunun, Paiwan, Saisiat, Yami, Ami, Rukai, Atayal, Chou, Pazeh, Puyuma, Haka and Han. And the STR loci were D3S1358, VWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, D16S539, TH01, TPOX and CSF1PO. In this study the chi-square test was used to test the Hardy-Weinberg equilibrium. No deviations from the Hardy-Weinberg equilibrium were observed for the 13 STR loci, except 8 populations in 6 loci. This may caused by small sample size or many rare alleles. In Han population, the highest probability of matching is TPOX(0.2254), and the lowest is FGA(0.0354) among 13 loci. There was only one mutation event revealed in 250 meiosis alleles in the mutation screening. The only mutation event was found in D8S1179 locus from allele 16 to 15. This study also established the data of inbreeding coefficient (f), probability of matching (Pm), power of exclusion on trio and duo cases in parentage testing, total inbreeding coefficient (F) and variation among populations(θ), which can be helpful in forensic application. Finally, the Neighbor-joining trees of cluster analysis by the genetic distance of 12 populations were established, which may be useful in anthropology on phylogenetic study.

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