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論文名稱(外文):	Genetic diversity and phylogenetic relationships analyses of Taoyuan, Lanyu, and other exotic pig breeds based on mitochondrial sequences
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中文摘要:	<p>桃園豬於 1877 年自廣東地區被引進，並成為臺灣早期主要飼養之豬種。為了改進性能，於 1896 年後，盤克夏、約克夏、漢布夏、藍瑞斯、杜洛克等外來豬種陸續被引入臺灣。由於純種桃園豬的經濟性狀較外來豬種差，造成飼養意願降低，使得其數量遽減。為了進行保種，桃園豬在 1974 年後被隔離飼養於臺灣省畜產試驗所。蘭嶼豬為蘭嶼島上之在地豬種，並於 1975 年與 1980 年分別自蘭嶼島引種至國立臺灣大學與臺東種畜繁殖場，隔離飼養作為發展實驗用豬種之研究。由引種時間推論，外來豬種之基因有滲入桃園豬與蘭嶼豬之可能。然而桃園豬與蘭嶼豬這兩個保種族群內部的遺傳結構，迄今仍未知。瞭解保種族群的遺傳多樣性，將有助於建立往後保種工作之方針，故有其重要性。</p> <p>本研究乃根據粒線體序列之多型性，探討下列主旨：(1) 計算桃園豬以及蘭嶼豬保種族群內部粒線體序列的遺傳變異程度；(2) 確認外來豬種的粒線體遺傳資訊是否曾經滲入保種族群當中；(3) 分析桃園豬、蘭嶼豬保種族群與全世界豬種間之親緣關係。收集藍瑞斯、約克夏、杜洛克、盤克夏、梅山豬、保種桃園豬、保種蘭嶼豬共 129 隻的粒線體樣本，並以聚合酶鏈反應增幅其控制區域與細胞色素 b 片段，再進行純化與定序。另外 43 筆來自 NCBI 資料庫</p>

的歐亞豬種控制區域序列，亦被收集並納入計算。根據基因型歧異度 ( $h$ ) 與核苷酸歧異度 ( $\pi$ )，分析桃園豬與蘭嶼豬保種族群內部的遺傳歧異度。另根據 Hasegawa-Kishino-Yano 85 (HKY85) 之演化模式，將粒線體控制區域與細胞色素  $b$  序列變異之多型性資訊，轉換成為遺傳距離，最後利用兩兩序列間的遺傳距離，建構 Maximum Likelihood (ML) 樹狀圖。桃園豬保種族群的控制區域與細胞色素  $b$  序列，皆僅出現一種基因型，並且由  $h$  值 (0.000) 與  $\pi$  值 (0.000%) 顯示出低度的歧異度；蘭嶼豬保種族群的控制區域與細胞色素  $b$  序列，皆可被分為兩種基因型 (第一型與第二型)，並且由  $h$  值 (0.384) 與  $\pi$  值 (0.510%) 顯示其歧異度的嚴重流失。在控制區域與細胞色素  $b$  序列的親緣關係分析中，第一型蘭嶼豬序列與其他豬隻序列分離，並形成一獨特類群；第二型蘭嶼豬則與約克夏、盤克夏、梅山豬以及桃園豬歸類於同一類群。在包含 184 頭歐亞豬隻控制區域序列的 ML 樹狀圖中，第一型蘭嶼豬序列仍然與其他歐亞豬隻序列分離，形成一獨特類群；第二型蘭嶼豬與桃園豬序列則同樣被歸類於亞洲豬種序列。

綜合上述結果，桃園豬與蘭嶼豬保種族群皆出現低度的遺傳歧異度，顯示瓶頸效應或是創始者效應在這些族群中，有曾經發生過之可能。桃園豬保種族群序列被歸類於亞洲類群，顯示歐洲豬種的母方遺傳資訊，未滲入受測桃園豬保種族群當中。第一型蘭嶼豬序列與其他歐亞豬隻序列分離，並形成一獨特類群，可能是由於第一型蘭嶼豬具有與其他歐亞豬種不同起源之母方遺傳資訊。第二型蘭嶼豬序列被歸類於亞洲主類群中，可能是由於亞洲主類群中的豬種，其母方遺傳資訊曾經滲入蘭嶼豬當中，所造成之結果。

#### 外文摘要:

Taoyuan pigs were introduced from Guangdong area in 1877 and were a major breed in early Taiwan. For improving their performance, Berkshire pigs were introduced into Taiwan by Japanese in 1896. Then according to their poor economic efficiency and lower willing of rearing, the number of pure Taoyuan pigs decreased dramatically after the exotic pig breeds (Yorkshire, Hampshire, Landrace, and Duroc) were introduced. For animal conservation, Taoyuan pigs were reared isolately in Taiwan Livestock Research Institute after 1974. Lanyu pigs, an indigenous breed in Lanyu Islet were transferred to National Taiwan University and Taitung Animal Propagation Station for developing laboratory swine in 1975 and 1980, respectively. Two herds of Lanyu pigs were reared in isolation and performed natural mating until 2004 and 1991. The genes of exotic pig breeds might introgress into Taoyuan and Lanyu pigs after exotic breeds introduced into Taiwan. The genetic diversity within conserved Taoyuan and Lanyu herds and whether the genetic introgression had previously occurred were currently unknown, so it is important identifying the genetic diversity of conserved herds for the orientation of conservation.

The aims of the study were to investigate: (1) the genetic variation within conserved herds of Taoyuan and Lanyu pigs. (2) Whether the maternal genetic introgression from exotic pig breeds into the conserved herds (3) the phylogenetic relationships of two conserved breeds to worldwide pig breeds. The polymorphisms of mitochondrial sequences were applied for those studies. Mitochondrial DNAs of 129 individuals from Landrace, Yorkshire, Duroc,

Berkshire, Meishan, and conserved herds of Taoyuan and Lanyu pigs were obtained. Their control region and cytochrome b fragments were amplified by polymerase chain reaction then sequenced. Genetic diversities within conserved herd sequences of Taoyuan and Lanyu pigs were examined based on the relationships of haplotype diversity ( $h$ ) and nucleotide diversity ( $\pi$ ). The Hasegawa-Kishino-Yano 85 (HKY85) substitution model was used to obtain the genetic distances based on the polymorphisms of substitution sites of control region and cytochrome b sequences. The Maximum Likelihood (ML) tree of different sequences was constructed according to the pairwise genetic distances. To determine the phylogenetic relationship among Taoyuan, Lanyu, and other Eurasian pig breeds, 55 control region sequences of Eurasian pig breed obtained from NCBI database were included.

The control region and cytochrome b sequences of conserved Taoyuan only remained one haplotype, and shown absence of diversity by low  $h$  (0.000) and low  $\pi$  (0.000%) value; conserved Lanyu sequences were divided into two haplotypes (type I and type II), and shown severe loss of diversity by low  $h$  (0.384) and high  $\pi$  (0.510%) value. In the phylogenetic relationship of control region and cytochrome b sequences, type I Lanyu formed a unique clade different from all other pigs while type II Lanyu sequence was clustered with Yorkshire, Berkshire, Meishan, and Taoyuan. In ML tree containing 184 control region sequences of Eurasian pigs, type I Lanyu sequence still formed a unique clade different from Asian and European pig sequences, while type II Lanyu and Taoyuan sequences were clustered within the Asian clade.

In conclusion, low genetic diversity observed both in conserved Taoyuan and Lanyu pigs indicates recent population bottleneck or founder event might happen in these herds. Taoyuan sequence was clustered in Asian clade indicate that maternal lineage introgression from European clade pigs wasn't found. Type I Lanyu sequence formed a unique clade different from other Asian and European sequences suggesting that the origin of Lanyu pigs have maternal lineage distinct from other Asian and European pigs. Type II Lanyu sequence was clustered within the Asian clade, it might be the result of maternal lineage introgression from Asian clade pigs into Lanyu pigs.