

台灣豬口蹄疫病毒變異性之研究

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摘要

本計畫將純化的口蹄疫 O/TW/97 病毒連續在倉鼠腎臟細胞株繼代 150 代，其 VP1 核酸序列共有 10 個位置發生變異，在第 1 至第 15 代的繼代病毒均未出現變異，從第 16 代至 150 代間，繼代病毒的 VP1 之核酸變異率分佈於 0.2 至 1.3 之間，而該等病毒的 VP1 胺基酸共有 7 個位置發生變異，從第 16 代至 150 代間之變異率則介於 0.5 至 2.9 之間，但都不在主要的抗原位上。另一方面，各繼代病毒株與臺灣歷年分離之口蹄疫病毒株之 VP1 基因核酸序列的演化樹分析顯示，所有繼代病毒株與疫苗株(O/TW/205/98)最為接近，而臺灣歷年分離病毒株與繼代病毒株則差異較多。而由各繼代病毒株的 r1 值檢測結果均落在 0.4 至 0.81 之間，顯示口蹄疫 O/TW/205/98 疫苗株對各繼代病毒株均具有保護的潛力。可見口蹄疫病毒在無抗體壓力存在下，即使像細胞培養時供給較拮据的環境，仍無法與有免疫壓力存在下所發生之變異性相提並論。所以未來應就高低不同抗體存在下，探討其變異率。

Study on the genetic variation of porcinophilic foot and mouth disease virus in Taiwan

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Abstract

A purified foot-and-mouth disease virus (FMDV) was passaged serially in baby hamster kidney (BHK) cells for 150 passages. Totally 10 and 7 mutations occurred in VP1 nucleotide and derived amino acid sequences of passaged FMDV respectively. The mutations happened between the 16th generation and the 150th generation of passage. In passaged FMDV, the variation rates of nucleic acid and amino acid were 0.2 to 1.3 and 0.5 to 2.9 respectively. However, the mutations did not occur at the major antigenetic sites. On the other hand, basing on the VP1 sequences of passaged FMDVs and FMDV isolates of Taiwan, the phylogenetic tree analysis was performed. The result showed that the passaged FMDVs were the closest to the FMDV O/TW/205/98 vaccine strain and away from the FMDV isolates of Taiwan. Furthermore, the result of r_1 values of passaged FMDVs, between 0.4 and 0.81, indicated that the FMDV O/TW/205/98 vaccine strain would give a certain protection against the passaged FMDVs. It was obvious that the occurrence of FMDV variation was quite different in vitro and in vivo. Therefore, the investigation on the variation rate of FMDV should base on the existence of different levels of neutralization antibodies against FMDV in the future.