【附錄三】麗莎病毒演化分析圖

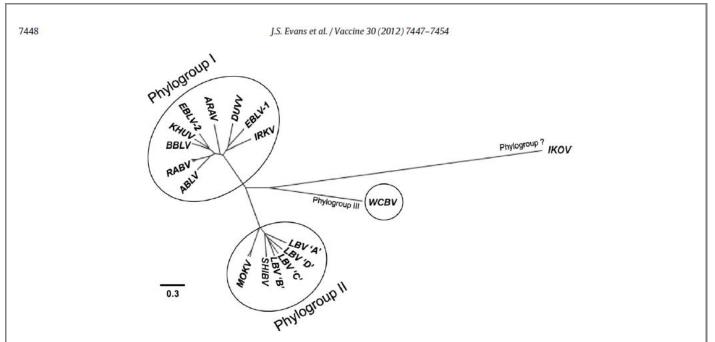說明：遵照 OIE 的要求所生產且可上市疫苗，能夠抵抗所有「第一型遺傳譜系麗莎病毒」（Lyssavirus phylogroup 1）。

Fig. 1. Bayesian phylogenetic analysis of glycoprotein ectodomain sequences from representative lyssavirus species, implemented in BEAST (v1.4.8). The GTR+I model of nucleotide substitution and a chain length of 5 million were used. The maximum clade credibility tree was chosen using Treeanotator (v1.4.8) and viewed using Figtree (v1.1.2) estimated samples sizes were >100 and posterior probabilities at key nodes are shown. Scale bar represents substitutions per site. Accession numbers for each of the lyssavirus species analysed in this study are: ABLV AF801020, RABV CVS-11 EU352767, RABV Pitman Moore AJ871962, RABV Flury-HEP GU565704, BBLV JF311903, KHUV EF614261, EBLV-2 EF 157977, ARAV EF614259, DUVV EU293119, EBLV-1 EU293109 and EU293120, IRKV EF614260, MOKV HM623780 and EU293118, SHIBV GU170201, LBV 'B' EF547431, LBV 'C' EF547425, LBV 'D' GU170202, LBV 'A' EF547432, WCBV EF614258 and IKOV JN800509.