

FIGURE 1 Predicted genome organization of Po-Circo-like virus GD06 and Po-Circo-like virus GD09

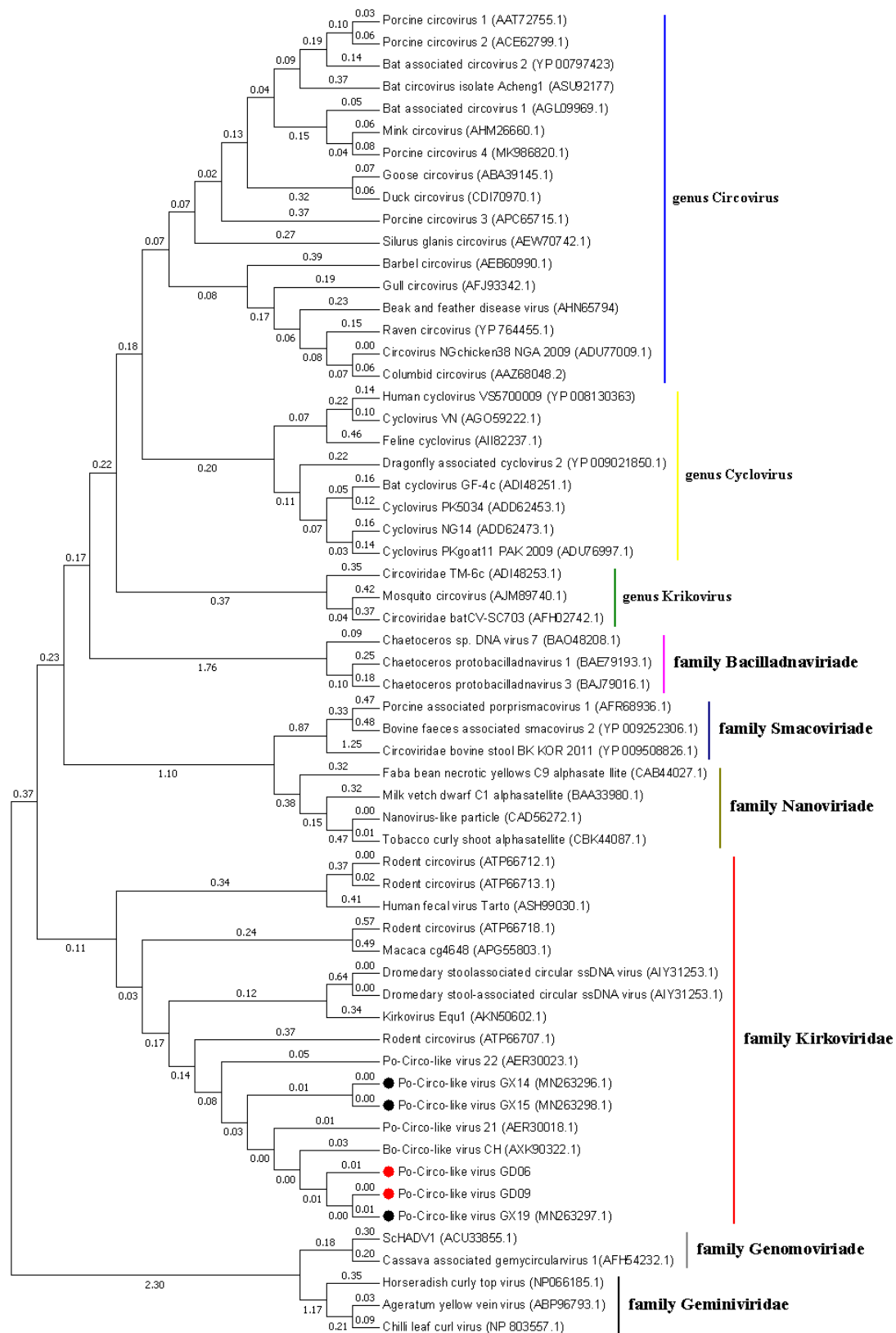


Fig 2 A Phylogenetic tree was constructed based on amino acid sequence of the Rep protein. The tree was built using the maximum-likelihood method and 10 bootstrap replicates. The strains in

the present study are marked with red circles. Black circles indicate the three strains of the Po-Circo-like virus (GX19, GX15 and GX14).

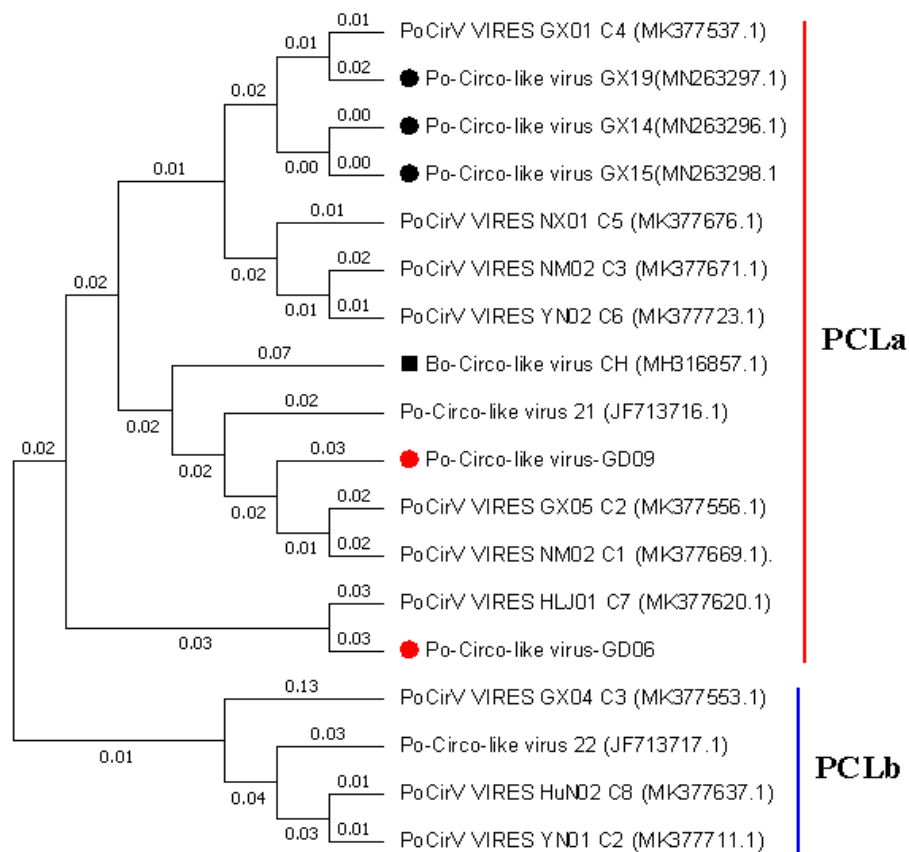


Fig 3. A phylogenetic analysis based on the nucleotide sequences of rep gene. The strains in the present study are marked with red circles. Black box indicates the Bo-Circo-like virus, and black circles indicate the three strains of the Po-Circo-like virus (GX19, GX15 and GX14).