

Pigeon circoviruses from feral pigeon in Australia demonstrates extensive recombination and genetic admixture with other circoviruses

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Pigeon circovirus (PiCV) have been known to be genetically diverse and has a circular ssDNA genome of ~2 kb and reported as the likely aetiological agent of young pigeon disease syndrome. PiCV have been found to be infecting pigeons in various parts of the world. However, limited availability of PiCV genome sequence data in Australia has hindered phylogeographic studies. In this study, we screened 17 swab samples sourced from feral pigeon in New South Wales, which didn't show any recognisable pathology, and recovered 13 complete genomes of PiCV using PCR optimised with different combinations of primers followed by direct amplicon sequencing. Phylogenetic analyses revealed that the Australian PiCV circulating in wild feral pigeon formed two strongly supported monophyletic clades; one grouped with others PiCV sequences isolated from Poland, Australia, United Kingdom, Belgium, China, and Japan, and other clade showing distant relationship to the PiCV isolated from Poland. Interestingly, one of the novel PiCV isolated in this study made a solitary clade that have very weak posterior support. To investigate the relatedness of the novel PiCV discovered in this study, we further analysed the PiCV genome sequences isolated in this study with other selected circoviruses genome sequences, and demonstrated a likely spillover of a novel PiCV from a wild canary circovirus, which has been strongly supported by the recombination and circovirus population genetic structure analysis. The potential for such findings suggest that the high degree of genetic variation within the PiCV species as a whole is reflected in evolutionary dynamics within Australia, indicated the likely possible route of genetic admixture with other circoviruses.

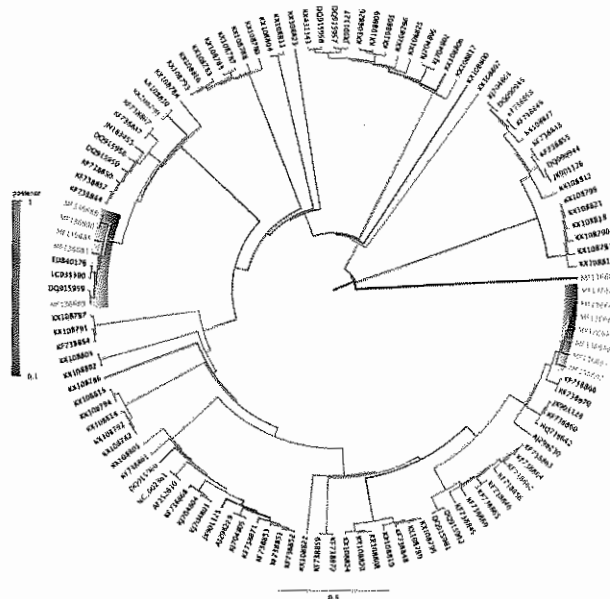


Figure 1 full genome picv.png