

Opportunistic sampling of yellow canary (*Crithagra flaviventris*) has revealed a high genetic diversity of detected parvoviral sequences

ABSTRACT

Parvoviruses are known to be significant viral pathogens that infect a wide range of species globally. However, little is known about the parvoviruses circulating in Australian birds, including yellow canaries. Here, we present four parvoviral sequences including three novel parvoviruses detected from 10 yellow canaries (*Crithagra flaviventris*), named canary chaphamaparvovirus 1 and -2 (CaChPV1 and CaChPV2), canary dependoparvovirus 1 and -2 (CaDePV1 and CaDePV2). The whole genome sequences of CaChPV1, CaChPV2, CaDePV1, and CaDePV2 showed the highest identity with other parvoviruses at 76.4%, 75.9%, 84.0%, and 59.1%, respectively. Phylogenetic analysis demonstrated that CaChPV1 and CaChPV2 were clustered within the genus Chaphamaparvovirus. Meanwhile, CaDePV1 and CaDePV2 fall within the genus Dependoparvovirus and have the closest evolutionary relationship to the bird-associated dependoparvoviruses. Overall, this study enriched our understanding of the genetic diversity among avian parvoviruses within the Parvoviridae family.