Journal of General Virology (2015), **96**, 2769–2779

DOI 10.1099/vir.0.000215

Novel parvoviruses in reptiles and genome sequence of a lizard parvovirus shed light on *Dependoparvovirus* genus evolution

Judit J. Pénzes,[1] Hanh T. Pham,[2] Mária Benkö[1] and Peter Tijssen[2]

Correspondence
Judit J. Pénzes
penzes.judit@agrar.mta.hu

[1]Institute for Veterinary Medical Research, Centre for Agricultural Research, Hungarian Academy of Sciences, 21 Hungária krt., Budapest 1143, Hungary

[2]INRS-Institut Armand-Frappier, Université du Québec, 531 Boulevard des Prairies, Laval, QC H7V 1B7, Canada

Here, we report the detection and partial genome characterization of two novel reptilian parvoviruses derived from a short-tailed pygmy chameleon (*Rampholeon brevicaudatus*) and a corn snake (*Pantherophis guttatus*) along with the complete genome analysis of the first lizard parvovirus, obtained from four bearded dragons (*Pogona vitticeps*). Both homology searches and phylogenetic tree reconstructions demonstrated that all are members of the genus *Dependoparvovirus*. Even though most dependoparvoviruses replicate efficiently only in co-infections with large DNA viruses, no such agents could be detected in one of the bearded dragon samples, hence the possibility of autonomous replication was explored. The alternative ORF encoding the full assembly activating protein (AAP), typical for the genus, could be obtained from reptilian parvoviruses for the first time, with a structure that appears to be more ancient than that of avian and mammalian parvoviruses. All three viruses were found to harbour short introns as previously observed for snake adeno-associated virus, shorter than that of any non-reptilian dependoparvovirus. According to the phylogenetic calculations based on full non-structural protein (Rep) and AAP sequences, the monophyletic cluster of reptilian parvoviruses seems to be the most basal out of all lineages of genus *Dependoparvovirus*. The suspected ability for autonomous replication, results of phylogenetic tree reconstruction, intron lengths and the structure of the AAP suggested that a single Squamata origin instead of the earlier assumed diapsid (common avian–reptilian) origin is more likely for the genus *Dependoparvovirus* of the family *Parvoviridae*.

Received 5 March 2015
Accepted 5 June 2015