



**1** Article

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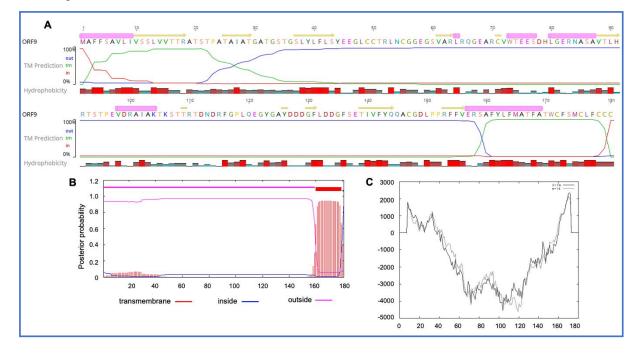
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## Molecular Characterisation of a Novel and Highly Divergent Passerine Adenovirus 1

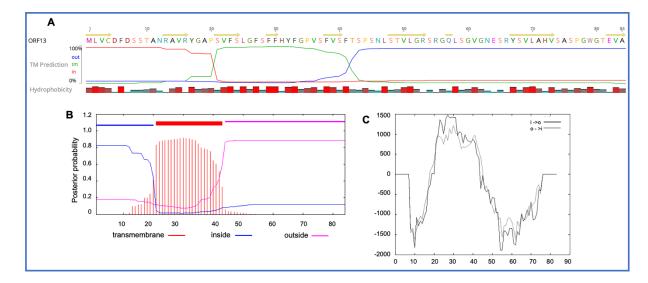
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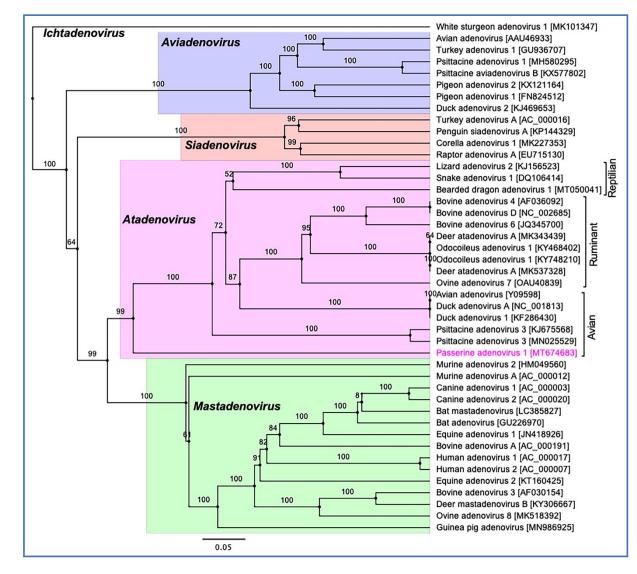
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15 Figure S1. Predicted structure of the unique PaAdV1-ORF09. (A) prediction of transmembrane helices 16 (TMHs) in unique PaAdV1-ORF10 gene using EMBOSS 6.5.7 tool in Geneious (version 10.2.2) (A), 17 TMHMM (B) and TMpred (C). All the programs consistently predicted two TMHs. (A) TMHs 18 detected by EMBOSS also showed the presence of alpha-helices within TMHs predicted region that 19 has been dominated by highly hydrophobic residue (red colour). (B and C) The X-axis represents the 20 position of residue, whereas Y-axis represents the posterior probability (B) and scores (above 500 are 21 considered significant) (C) for the predicted TMHs. (C) solid and dashed black lines indicated protein 22 orientation as inside to outside, and outside to inside, respectively.



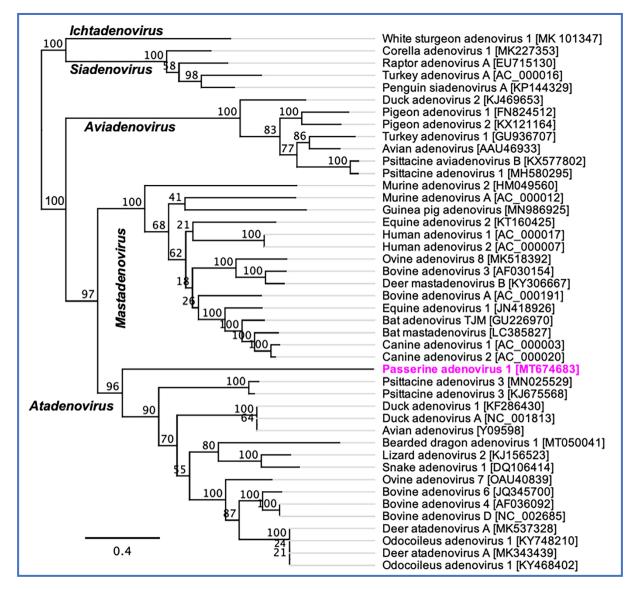


24 Figure S2. Predicted structure of the unique PaAdV1-ORF13. (A) prediction of transmembrane helices 25 (TMHs) in unique PaAdV1-ORF10 gene using EMBOSS 6.5.7 tool in Geneious (version 10.2.2) (A), 26 TMHMM (B) and TMpred (C). All the programs consistently predicted two TMHs. (A) TMHs 27 detected by EMBOSS also showed the presence of alpha-helices within TMHs predicted region that 28 has been dominated by highly hydrophobic residue (red colour). (B and C) The X-axis represents the 29 position of residue, whereas Y-axis represents the posterior probability (B) and scores (above 500 are 30 considered significant) (C) for the predicted TMHs. (C) solid and dashed black lines indicated protein 31 orientation as inside to outside, and outside to inside, respectively.



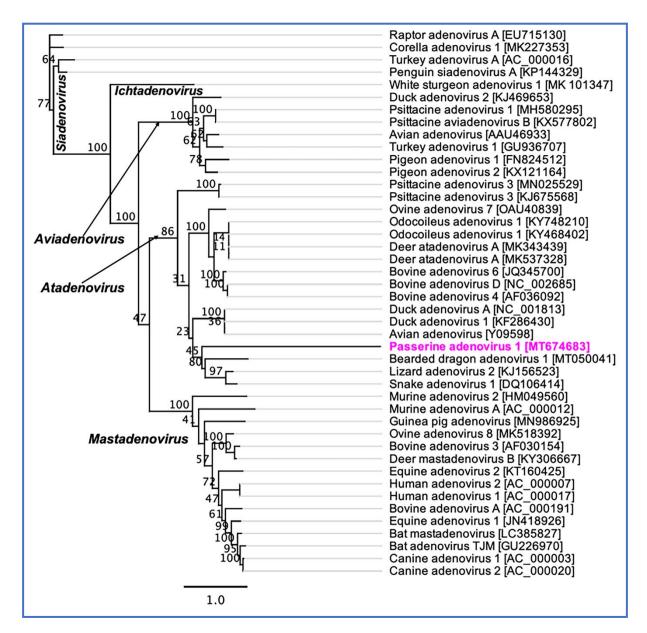
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33 Figure S3. Phylogenetic tree showed the possible evolutionary relationship of novel passerine adenovirus 1 34 with other selected AdVs. Neighbor-Joining (NJ) tree was constructed using concatenated amino acid sequences 35 of the complete DNA-dependent DNA polymerase, pTP, penton and hexon genes. Concatenated protein 36 sequences were aligned with MAFTT (version 7.388) (Katoh and Standley, 2013) in Geneious (version 10.2.2) 37 under the BLOSUM62 scoring matrix and gap open penalty =1.53. The gap >30 residues deleted from the 38 alignments. The unrooted NJ tree was constructed using Jukes-Cantor genetic distance model with 1000 39 bootstrap resamplings in Geneious (version 10.2.2). The numbers on the left shown bootstrap values as 40 percentages and the labels at branch tips refer to original AdVs species name followed by GenBank accession 41 number in parentheses. The final tree was visualised with FigTree (version 1.4.4). The five official genera were 42 highlighted as different background colours and novel passerine adenovirus 1 was shown as pink colour.

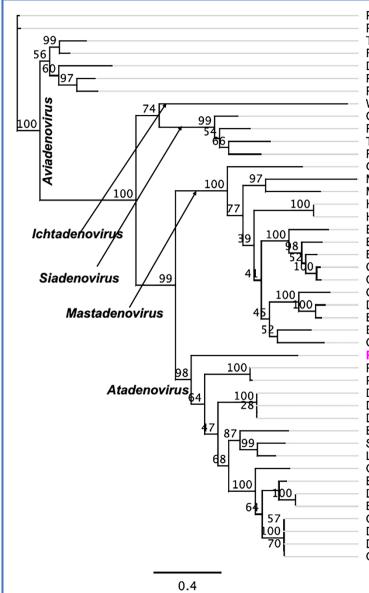




44 Figure S4. Phylogenetic tree showed the possible evolutionary relationship of novel passerine adenovirus 1 45 with other selected AdVs. Maximum likelihood (ML) tree was constructed using amino acid sequences of the 46 complete DNA-dependent DNA polymerase gene. Selected protein sequences were aligned with MAFTT 47 (version 7.450) (Katoh and Standley, 2013) in Geneious (version 10.2.2) under the BLOSUM62 scoring matrix 48 and gap open penalty =1.53. The unrooted ML tree was constructed with PhyML (Guindon et al., 2010) under 49 the LG substitution model, and 100 bootstrap resamplings were chosen to generate ML trees using tools 50 available in Geneious (version 10.2.2). The numbers on the left shown bootstrap values as percentages and the 51 labels at branch tips refer to original AdVs species name followed by GenBank accession number in parentheses. 52 The novel passerine adenovirus 1 was shown as pink colour.



**Figure S5.** Phylogenetic tree showed the possible evolutionary relationship of novel passerine adenovirus 1 with other selected AdVs. Maximum likelihood (ML) tree was constructed using amino acid sequences of the complete pTP gene. Selected protein sequences were aligned with MAFTT (version 7.450) (Katoh and Standley, 2013) in Geneious (version 10.2.2) under the BLOSUM62 scoring matrix and gap open penalty =1.53. The unrooted ML tree was constructed with PhyML (Guindon et al., 2010) under the LG substitution model, and 100 bootstrap resamplings were chosen to generate ML trees using tools available in Geneious (version 10.2.2). The numbers on the left shown bootstrap values as percentages and the labels at branch tips refer to original AdVs species name followed by GenBank accession number in parentheses. The novel passerine adenovirus 1 was shown as pink colour.

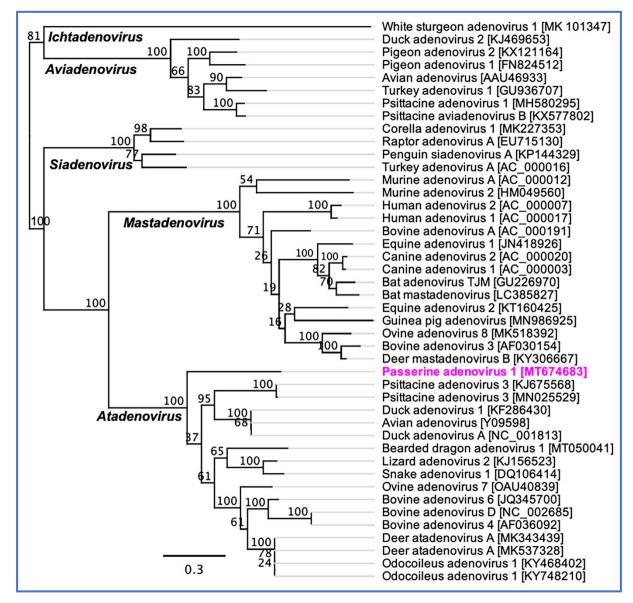


Psittacine aviadenovirus B [KX577802] Psittacine adenovirus 1 [MH580295] Turkey adenovirus 1 [GU936707] Fowl aviadenovirus 1 [AAU46933] Duck adenovirus 2 [KJ469653] Pigeon adenovirus 2 [KX121164] Pigeon adenovirus 1 [FN824512] White sturgeon adenovirus 1 [MK101347] Corella adenovirus 1 [MK227353] Penguin siadenovirus A [KP144329] Turkey siadenovirus A [AC\_000016] Raptor adenovirus 1 [EU715130] Guinea pig adenovirus [MN986925] Murine mastadenovirus A [AC\_000012] Murine adenovirus 2 [HM049560] Human adenovirus 2 [AC\_000007] Human adenovirus 1 [AC\_000017] Equine adenovirus 1 [JN418926] Bat adenovirus [GU226970] Bat mastadenovirus [LC385827] Canine adenovirus 2 [AC\_000020] Canine adenovirus 1 [AC\_000003] Ovine adenovirus 8 [MK518392] Deer mastadenovirus B [KY306667] Bovine adenovirus 3 [AF030154] Equine adenovirus 2 [KT160425 Ovine mastadenovirus A [AC\_000001] Psittacine adenovirus 3 [MN025529] Psittacine adenovirus 3 [KJ675568] Duck adenovirus 1 [KF286430] Duck adenovirus 1 Y095981 Duck atadenovirus A [NC\_001813] Bearded dragon adenovirus 1 [MT050041] Snake adenovirus 1 [DQ106414] Lizard adenovirus 2 [KJ156523] Ovine adenovirus 7 [OAU40839] Bovine adenovirus 6 [JQ345700] Deer atadenovirus A [NC\_002685] Bovine adenovirus 4 [AF036092] Odocoileus adenovirus 1 [KY748210] Deer atadenovirus A [MK537328] Deer atadenovirus A [MK343439] Odocoileus adenovirus 1 [KY468402]

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**Figure S6.** Phylogenetic tree showed the possible evolutionary relationship of novel passerine adenovirus 1 with other selected AdVs. Maximum likelihood (ML) tree was constructed using amino acid sequences of the complete penton gene. Selected protein sequences were aligned with MAFTT (version 7.450) (Katoh and Standley, 2013) in Geneious (version 10.2.2) under the BLOSUM62 scoring matrix and gap open penalty =1.53. The unrooted ML tree was constructed with PhyML (Guindon et al., 2010) under the LG substitution model, and 100 bootstrap resamplings were chosen to generate ML trees using tools available in Geneious (version 10.2.2). The numbers on the left shown bootstrap values as percentages and the labels at branch tips refer to original AdVs species name followed by GenBank accession number in parentheses. The novel passerine adenovirus 1 was shown as pink colour.



**Figure S7.** Phylogenetic tree showed the possible evolutionary relationship of novel passerine adenovirus 1 with other selected AdVs. Maximum likelihood (ML) tree was constructed using amino acid sequences of the complete hexon gene. Selected protein sequences were aligned with MAFTT (version 7.450) (Katoh and Standley, 2013) in Geneious (version 10.2.2) under the BLOSUM62 scoring matrix and gap open penalty =1.53. The unrooted ML tree was constructed with PhyML (Guindon et al., 2010) under the LG substitution model, and 100 bootstrap resamplings were chosen to generate ML trees using tools available in Geneious (version 10.2.2). The numbers on the left shown bootstrap values as percentages and the labels at branch tips refer to original AdVs species name followed by GenBank accession number in parentheses. The novel passerine adenovirus 1 was shown as pink colour.