3D MODELS OF PROTEINS AND PUTATIVE G-QUADRUPLEXES IN PORCINE

CIRCOVIRUS TYPE 3 SINGLE-STRANDED CIRCULAR DNA

The problem

now, there is no Until about 3D information structure of proteins and G-quadruplexes putative (G4s) in porcine circovirus 3 (PCV-3) genome.

Methods

motifs of G4s. 3D models of The goal of the present G4s and proteins were built study was 3D modelling of by the AlphaFold 3 (J. the replicase and capsid Abramson et al, 2024). For a protein structure for the two reliability of the 3D model evolutionarily most distant prediction in AlphaFold 3 PCV-3 isolates as well as the pIDDT parameter was search and identification of used. A pIDDT value for a perfect G-quadruplexes in confidence should be over AlphaFold 3. 90 on a scale from 0 to 100.

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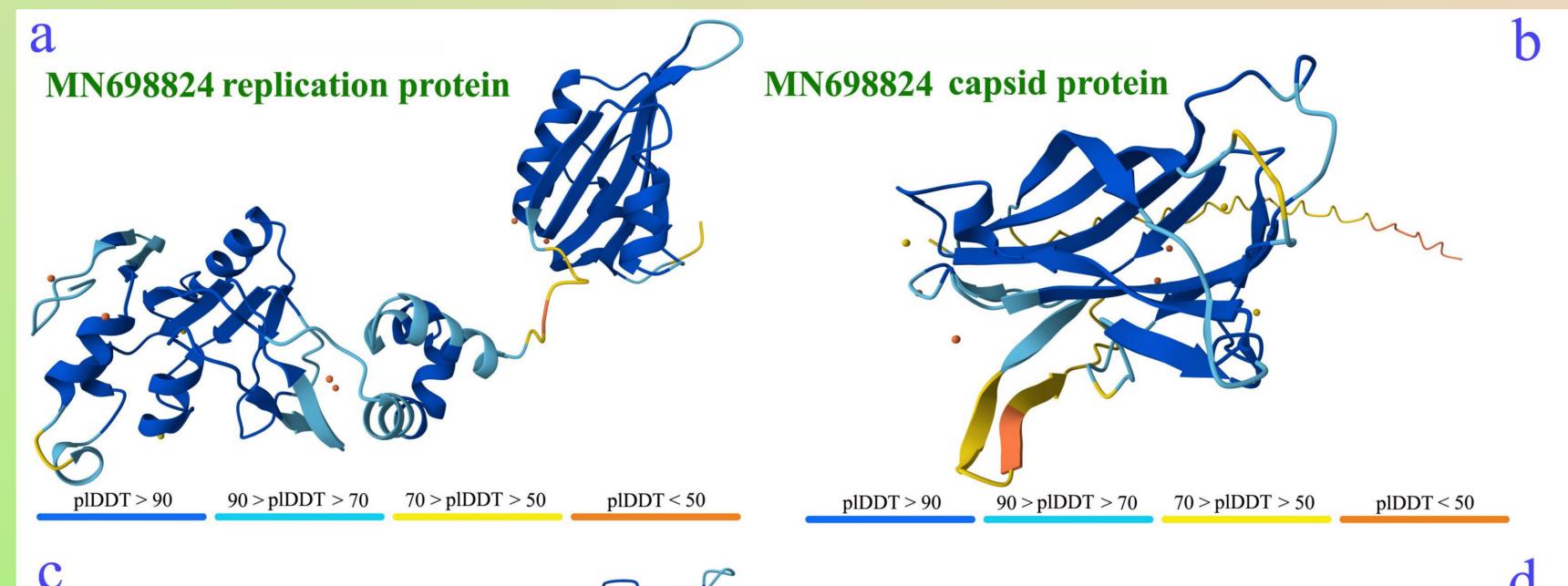
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Introduction

3D models of biopolymers artificial by predicted intelligence AlphaFold have the same accuracy as their structures determined searching by experimental methods.

model the PCV-3 genome Results

4 conserved putative G-quadruplexes formed by three G-tetrads were found in the DNA of PCV-3 PP067099 isolate with complete genome (Table 1).



MT075518 replication protein

MT075518 capsid protein

Fig. 3. 3D models of replication and capsid proteins for two phylogenetically most distant PCV-3 isolates. Number of βsheets is 17 for MT075518 PCV-3 isolate comparing with 10 ones for MN698824 isolate.

Fig. 4. Intramolecular anti-parallel Gquadruplex structure formed by stacking of three G-quartets with length of 15 nt in 1164-1178 position of PP067099 PCV-3 isolate.

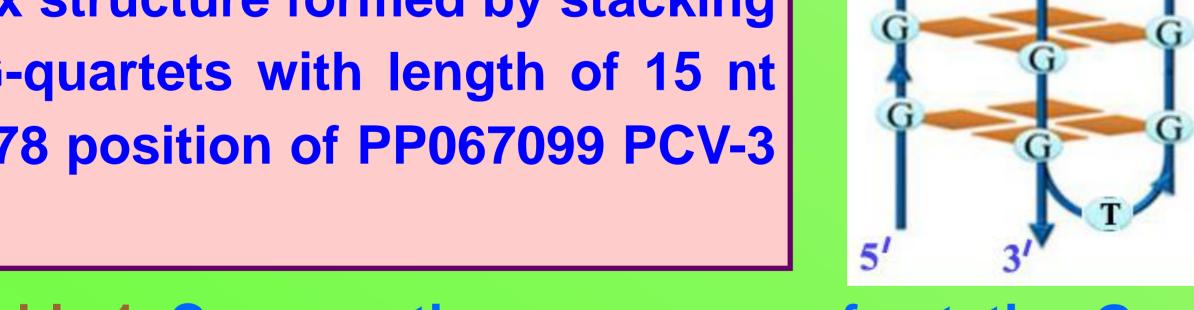


Table 1. Conservative sequences of putative G-quadruplexes in DNA of the *Porcine circovirus* 3 PP067099 isolate. G-rich fragments of sequences for G4s are underlined.

Position	Gene/ Product	G-quadruplex motif	G-score	pIDDT	Number of PCV-3 isolates with 100% identity by BLAST
645	Replicase	GGGTTTGCGTGATTTTTGCGGGGTGATGGGGGTTGGG	59	90 > pIDDT > 70	1172
802	Replicase	GGG CCTTGGT <u>GGG</u> ATGGTTATAAT <u>GGG</u> GA <u>GGG</u>	63	70 > pIDDT > 50	1117
893	Replicase	GGGACAGGTACCCTCTGAGGGTTCCTGTTAAGGGGTGGG	58	70 > pIDDT > 50	1011
1164	Intergenic region	GGGTGGGTGGG (Fig. 4)	72	pIDDT > 90	1998

P067102.1 Porcine circovirus 3 strain HeN-7C complete genome MN698824.1 Porcine circovirus 3 strain K-2019-3 complete genome

Fig. 1. Phylogenetic tree of 51 PCV-3 isolates with complete genome for determination of the most distant isolates.

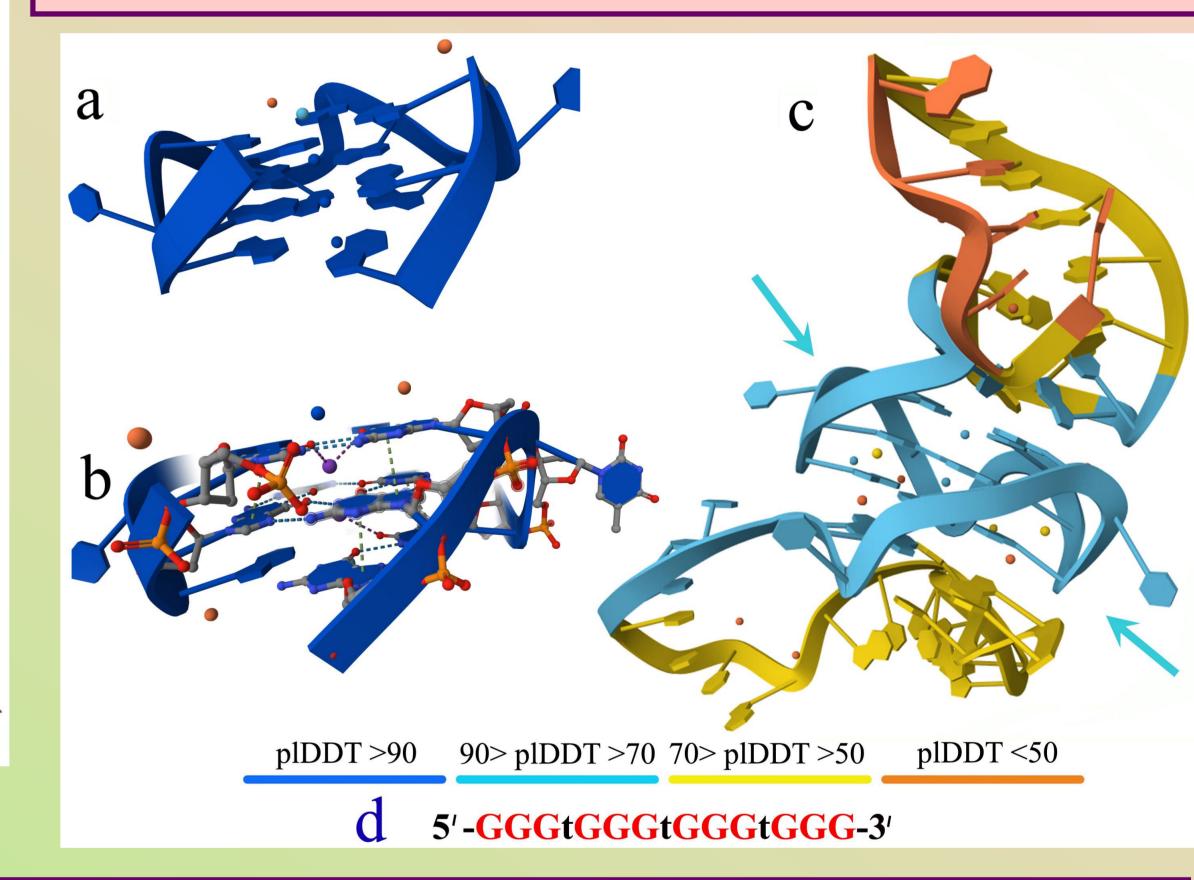


Fig. 2. 3D models of G-quadruplexes formed by three G-tetrads in single-stranded DNA of PP067099 isolate of the PCV-3 for a fragment of 15 nucleotides (nt) at positions 1164-1178 for 8 Na+ (a, b) and 57 nt at positions 1144-1200 for 20 Na+ (c; arrows indicate G4) in the intergenic region. (a, b) - pIDDT > 90, (c) - 90 > plDDT > 70. (d) – G4 motif.

Conclusion

Main difference between two phylogenetically distant PCV-3 isolates is the number of β-sheets of capsid proteins.