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## Putative G-quadruplexes in the genome of unconventional retrovirus bovine foamy virus

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G-quadruplexes (G4s) are guanine-rich DNA structures, which play essential regulatory role in key steps of the viral life cycle (replication, transcription regulation, translation). There is currently no relevant information about putative G4s in the bovine foamy virus (BFV) genome. The **goal** of the present study was the determination of such conservative non-B-DNA structures as conservative G-quadruplexes, which can be formed by two and three G-quartets in the mRNA, sense and antisense strands of the bovine foamy virus proviral DNA. **Methods.** Bioinformatics analysis was used for searching the motifs of intramolecular G-quadruplexes in BFV mRNA and proviral DNA, as well as for determining the G-score (a parameter that characterizes the stability of the G-quadruplex in relative units). QGRS Mapper software was used for searching motifs of G-quadruplexes on the web-server <http://quadruplex.ramapo.edu/qgrs/app/start>. BioEdit software (version 7.2.5) was used for obtaining consensus sequence of BFV isolates with complete genome. The search for GGG motifs in the BFV mRNA and proviral DNA, manipulation with nucleotide sequences and multiple alignment were performed by MEGA software (version 6.06). In addition, putative G4s were identified by G4Hunter software on the web-server <http://bioinformatics.ibp.cz>. **Results.** On the basis of multiple alignment of 27 BFV isolates 26 putative conservative G-quadruplexes from two G-quartets were found in mRNA and sense strand

of BFV proviral DNA with G-score from 30 to 36. 32 G4s formed by two G-quartets with G-score from 30 to 36 and 2 G4s formed by three G-quartets were found in antisense strand of BFV proviral DNA with G-score of 53. These two G4s are direct repeats and are localized in U5 5'-LTR and in U5 3'-LTR. A feature of one of the G4 in the sense strand is the presence of G4 in the i-motif (C-rich fragment of the complementary strand). Both of these G4s, which are localized in the *pol* gene, are the most stable among the G4s formed by two tetrads. The density of G4s was 2.1/kbp in sense strand of BFV proviral DNA and 2.8/kbp in antisense strand. A localization map of putative conserved intramolecular G-quadruplexes formed by two and three G-tetrads on the BFV genome was created, which made it possible to reveal the details of the structural organization of the “+” strand compared to the “-” strand of the BFV proviral DNA. **Conclusions.** Conservative G4s are unevenly distributed throughout the BFV genome. A distinctive feature of the BFV genomic organization is the fact that the antisense strand of the BFV proviral DNA is characterized by a significantly higher density of G-quadruplexes compared to one of the sense strands. The QGRS Mapper software detects a significantly higher number of potential G4s (34 G4s in antisense strand of BFV proviral DNA) compared to the G4Hunter software (7 G4s).

**Keywords:** bovine foamy virus, BFV, G-quadruplex, i-motif, non-canonical structure, antisense strand.