

28 AGOSTO

at 2.30 p.m.

Room B109, Povo 2



UNIVERSITÀ
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Dipartimento di
Biologia Cellulare, Computazionale e Integrata - CIBIO

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EXTERNAL
seminar

WHAT DO G-QUADRUPLEXES IN VIRAL GENOMES TELL US?

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G-quadruplexes are structural elements that can form in both DNA and RNA molecules. They are formed by guanine-rich sequences that fold into very stable four-stranded structures. G-quadruplexes have been identified in various biological contexts, including genomes of viruses. In viral genomes, G-quadruplexes are proposed as important elements which play a role in viral genome stability (by protecting viral DNA from degradation and recombination events), regulation of gene expression (by affecting transcription and translation processes, in viral genomes, G-quadruplexes can be found in promoter regions and other regulatory sequences), but they are suggested also as antiviral targets (targeting G-quadruplexes can disrupt critical viral processes, such as replication and gene expression, leading to inhibition of viral proliferation). Therefore, the development of small molecules that specifically interact with G-quadruplex structures in viral genomes is a broad research area with therapeutic potential. Using the G4Hunter tool, we have analyzed H1N1 influenza genomes, all Nidovirales genomes, including SARS-CoV2, and all genomes accessible in the NCBI Genome database. Our result shows that G-quadruplex-prone sequences are not distributed randomly in viral genomes, but that they are associated with function regions; moreover, we have shown that the presence of the G-quadruplexes is correlated with the type of viral infection. The presence of G-quadruplex sequences is related to viral life cycles and corresponds to the type of viral infection rather than the type of nucleic acid; while viruses that cause persistent infections are enriched for G-quadruplex-prone sequences, viruses that cause acute infections have a significantly reduced number of G-quadruplexes. Furthermore, we found a significant positive correlation between the frequencies of G-quadruplex-prone sequences in dsDNA viruses and the corresponding hosts of archaea, bacteria and eukaryotes. The strong relationship between the G-quadruplex-prone sequences in the virus and the host indicates a close coevolution and an evolutionarily reciprocal imitation of the genome organization.

Contacts

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