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ICGEB International SEMINAR PROGRAMME 2018

Thursday, 26 April 2018 | 12:00 noon | ICGEB Seminar Room, W building | Padriciano, 99, Trieste, ITALY

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Genome segmentation offers certain evolutionary benefits to a number of pathogenic RNA viruses, including rotaviruses and influenza viruses. However, as the number of RNA segments per virion increases, the task of a non-random selection of a full set of distinct genomic RNAs poses a formidable challenge to maintaining the integrity of segmented genomes. Recently we have identified sequence-specific inter-segment interactions between rotavirus (+)ssRNA genome segment precursors. We have shown that binding of the rotavirus-encoded non-structural protein NSP2 to viral ssRNAs results in the remodeling of RNA, which is conducive to formation of inter-segment contacts. These protein-RNA interactions result in the stabilisation of extended intermolecular RNA-RNA contacts, potentially underpinning transient inter-segment interactions prior to genome encapsidation and replication. Using this approach we have identified a number of RNA-RNA interaction sites in the rotavirus genome, which are likely to be involved in genome segment assortment process.

Having established the role of NSP2 in promoting inter-segment RNA-RNA contacts, we are developing super-resolution imaging tools for direct visualization of the RNA assortment complexes in rotavirus-infected cells. To unravel the mechanisms by which NSP2 controls the formation of inter-molecular RNA helices we have applied RNA structure probing methods that allowed us to monitor conformational rearrangements, which are prerequisite for formation of the RNA assortment complex. Our findings open up unique avenues for understanding the challenges for further improvement of the recently developed fully plasmid-based reverse genetics systems for rotaviruses.

"These can go up to eleven': shedding light on the molecular mechanisms of genome segment counting in rotaviruses"

Host: E. Buratti

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