MASARYK UNIVERSITY

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Kamenice 5, Brno
Entrance from Studentská street

WEDNESDAY

START: 11.00

Hosted by PharmDr. Peter Lukavsky

RNA-protein interactions and the structure of the genetic code

Seminar room 211 building A35

delivered by

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University of Vienna

The relationship between mRNA and protein sequences as embodied in the universal genetic code is a cornerstone of modern-day molecular biology. However, a potential connection between the physicochemical properties of mRNAs and their cognate proteins, with implications concerning both the code's origin and mRNA-protein interactions in general, remains largely unexplored. As our central result, we have recently revealed a robust, statistically significant matching between the composition of mRNA coding sequences and the base-binding preferences of their cognate protein sequences. Consistent results are obtained regardless of how the latter were derived, including:

1) Experimental and computational interaction propensity scales capturing the behavior of amino acids in aqueous solutions of nucleobase analogs,
2) Computational absolute binding free energies between individual aminoacid sidechain analogs and nucleobases in different solvents, and
3) knowledge-based interaction preferences of amino acids for different nucleobases.

As an illustration, purine density profiles of mRNA sequences mirror the knowledge-based guanine affinity profiles of their cognate protein sequences with quantitative accuracy (median Pearson correlation coefficient $|R| = 0.80$ across the entire human proteome). Overall, our results support as well as redefine the stereochemical hypothesis concerning the code's origin, the idea that it evolved from direct interactions between amino acids and the appropriate bases. Moreover, our findings support the possibility of direct complementary interactions between mRNAs and their cognate proteins even in present-day cells, especially if both are unstructured, with implications extending to different facets of nucleic acid/protein biology.

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