

Accepted Manuscript

Title: The Splicing Code

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PII: S0303-2647(17)30321-0

DOI: <https://doi.org/10.1016/j.biosystems.2017.11.002>

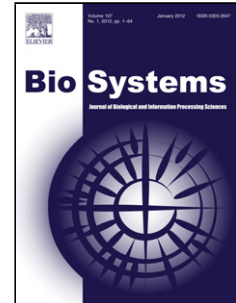
Reference: BIO 3806

To appear in: *BioSystems*

Received date: 10-8-2017

Revised date: 2-11-2017

Accepted date: 3-11-2017



Please cite this article as: Baralle, Marco, Baralle, Francisco Ernesto, The Splicing Code. *BioSystems* <https://doi.org/10.1016/j.biosystems.2017.11.002>

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*The Splicing Code***Marco Baralle and Francisco Ernesto Baralle****International Centre for Genetic Engineering and Biotechnology, Padriciano 99****Abstract**

This issue dedicated to the code of life tackles very challenging and open questions in Biology. The genetic code, brilliantly uncovered over 50 years ago is an example of a univocal biological code. In fact, except for very few and marginal variations, it is the same from bacteria to man, the RNA stretch: 5' GUGUUC 3' reads as the dipeptide: Val-Phe in bacteria, in yeast, in Arabidopsis, in zebra fish, in mouse and in human. A degree of ambiguity is possible if mutations are introduced in the tRNAs in a way that the anticodon reads one amino acid but the aminoacyl-transferase attaches a different one onto the tRNA. These were the very useful suppressor genes that aided greatly the study of bacterial genetics. Other biological codes however, are more akin to social codes and are less amenable to an unambiguous deciphering. Legal and ethical codes, whether we like it or not, are flexible and depend on the structure and history of the society that has produced them, as well as a specific point in time. The codes that govern RNA splicing have similar characteristics. In fact, the splicing code depends on a myriad of different factors that in part are influenced by the background in which they are read such as different cells, tissues or developmental stages. Given the complexity of the splicing process, the construction of an algorithm that can define exons or their fate with certainty has not yet been achieved. However a substantial amount of information towards the deciphering of the splicing code has been gathered and in this manuscript we summarize the point reached.

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