A STEPWISE MODEL FOR THE ORIGIN OF THE RNA WORLD.
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One of the open issues in the RNA world model for the origin and early evolution of life is how a template-dependent RNA polymerase ribozyme emerged from short RNA oligomers obtained by random polymerization. Indeed, a minimum size of 165 nt is experimentally found for such a ribozyme, a length three to four times that of the longest RNA oligomers obtained by polymerization on clay mineral surfaces. We have performed computational studies to investigate the structural repertoire present in large pools of 12 to 40-mer random ssRNA sequences. Topologically simple RNA modules turn out to be the most abundant ones, especially hairpin structures and stem-loops [1]. A fraction of the ubiquitous hairpin modules could have displayed RNA ligase activity, as they do in certain current ribozymes, and catalyze the assembly of larger, eventually functional RNA molecules. We demonstrated that such ligation processes allow a fraction of the population to retain their previous modular structure. Therefore, structural and functional complexity can progressively increase even in the absence of template replication [2].

This allows us to build up a stepwise model of ligation-based, modular evolution that could pave the way to the emergence of a ribozyme with RNA replicate activity [3]. Our evolutionary model shows two main advantages with respect to previous hypotheses put forward for the origin of the RNA world: i) short RNA modules polymerized on different microenvironments might suffice to produce the first functional RNAs; ii) modular evolution shortens adaptation times and allows attaining complex structures that could not be otherwise directly selected. Therefore, ligation-based modular evolution might have bridged the gap between the first random RNA oligomers and a template-dependent RNA polymerase ribozyme that triggered information-driven evolution.

References