Dynamics of Transposable Elements and Small RNA in Polyploidization Events

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Transposable elements (TEs) are DNA sequences with the ability of independently self-replicating within a genome. They are present in the genome of most species, and can constitute a large part the genome, for plants in particular. As an example, 85% of the sequence of the maize genome derives from past transposition events [1]. Their proliferation is controlled by RNA interference, mediated by *small-interfering* RNA (siRNA), short RNA sequences (22-24nt) that can be transcribed from the TEs themselves.

The so-called "genomic shock" events can alter significantly this control mechanism, possibly enabling a burst of Transposable Elements. One of such possible events is polyploidization, by which the whole genome can be doubled. It is known that such events are common among many species, leading to very large genomes, such as the one from wheat.

In order to understand the proliferation and the epigenetic control of TEs, a model was built that accounted for the deactivation (*silencing*) of TEs, the production of different kinds of siRNA and the replication of active TEs [2] (see Fig. 1). The model compared well with experimental studies and highlighted the importance of silenced TEs as a source of siRNA.

In the case of a polyploidization event, the model needs to be extended to account for the extra copies of the genome. Here we address the development of such a model and distinguish between two cases, one in which the polyploidization event involves the same species (autopolyploid) and the case in which hybridization with a different species is present (allopolyploid).

The equilibria and stability of both cases are studied, in the general case where n copies of the genome are present (n-ploidy). The model allows to study how is siRNA partitioned among the different copies of the genome. Two cases have been considered, one in which siRNA is homogeneously distributed among the different copies and another in which siRNA is distributed according to the specific abundances of active TEs among the different copies of the genome. We study these two regimes and explore the inequivalent dynamical regimes using dynamical system theory.

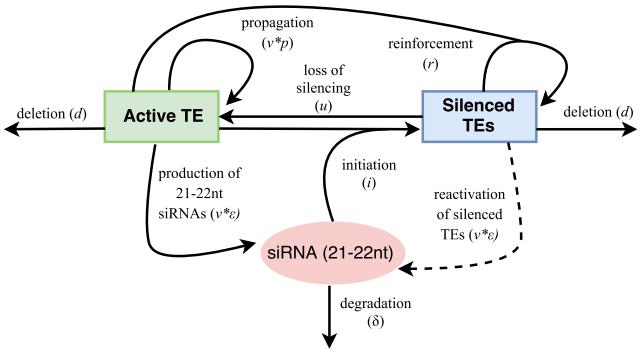

Fig. 1. Block diagram of the model from Roessler et al. [2]

This model has allowed us to uncover a very rich phenomenology, which depends very strongly on the partitioning of siRNA. This can help elucidate standing questions in hybridization dynamics, such as subgenome dominance or whether siRNA is additively expressed by the different copies of the genome.

[1] M. C. Stitzer, S. N. Anderson, N. M. Springer, and J. Ross-Ibarra, PLOS Genetics **17**(10): e1009768 (2021).

[2] K. Roessler, A. Bousios, E. Meca, and B. S. Gaut, Genome Biology and Evolution **10**, 803–815 (2018).