Editorial
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Impact of Telomerase RNAs in land plants

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Editorial

The origin of direct chromosomes associated with divergence of eukaryotes led to the elaboration of mechanisms neutralizing the deficient replication of chromosome ends the telomeres. The most common medium to overcome the end- replication problem involves a ribo nucleoprotein complex enzyme telomerase. Telomerase elongates the 3 '- end of telomeric DNA using the catalytic exertion of its core protein subunit telomerase rear transcriptase (TERT)-which can constantly add a short DNA stretch to telomeric DNA. The sequence added by telomerase is directed by a template region in telomerase RNA (TR), the other core telomerase subunit. In addition to these two core subunits, the complex of telomerase involves several other associated proteins which affect colorful way of telomerase function in vivo, as,e.g. telomerase assembly, trafficking, localisation, processivity, or its reclamation to telomeres.

Due to the medium of their extension by telomerase, telomere DNAs are formed by tandemly repeated arrays of short DNA sequence units, which are generally well conserved through large taxa of advanced eukaryotes, as,e.g. (TTAGGG) in invertebrates. Lower eukaryotes show more expansive diversity in telomere DNA, as can be instanced in incentive or algal telomeres. Eventually, organisms which had acquired some of the telomerase-independent mechanisms of telomere conflation, either during elaboration or due to targeted dislocation of telomerase, can retain entirely different telomeres composed of retrotransposons or tandem reprises.

Among land shops, telomeres of (TTTAGGG) sequence were first characterized in Arabidopsis and also linked in numerous other land factory species. Still, multitudinous exceptions were plant as well, first in Allium and affiliated Allioidae factory species, also among the other Asparagales rubrics and other factory taxa. In our former studies, we demonstrated that changes in telomere sequences correspond to the phylogenetic divergence of factory families and rubrics. Therefore, in monocotyledonous shops, telomere DNAs evolved from (TTTAGGG) (common also in shops of the Asparaguses order up to the family Doryanthaceae) and a switch to (TTAGGG) passed with the divergence of the family Iridaceae. Eventually, (CTCGGTTATGGG) telomeres surfaced with the divergence of the Allium rubric. With characterizations of Allium telomeres, we illustrated the last given exception from canonical telomeres among land shops and demonstrated that all these unusual factory telomeres are synthesized by telomerase. The story of unusual factory telomeres could, thus, finish nearly symbolically at the Allium genus, where it began in 1995. Still, this would leave some abecedarian questions open. The first of these is the molecular base of the evolutionary switches in telomere DNA sequences. In this work, we approach this question and consider the following possible scripts (i) TR remained basically the same across the Asparagales phylogeny, and the observed switches in telomere conflation passed either as a result of mutations in the template region of TR or mutation in the vicinity of the template sequence which could change the boundaries of the region honored as a template; (ii) different RNA motes took over the TR function. Generally, characterization of TRs is complicated by their extreme divergence in size (from 159 nt in Tetrahymena to 2200 nt in Plasmodium), nucleotide sequence, and pathways of biogenesis among organisms. A certain position of conservation can be seen only at the position of the secondary structure motifs in TRs. This complicates an in silico TR identification, and the only TR sphere of at least incompletely predictable sequence is the template region which contains a permutation of the telomere reprise unit in a given organism stretched by at least one nucleotide.

To characterise TRs and their changes underpinning evolutionary transitions of telomeres in Asparagales, we take advantage of the surprisingly large length of the Allium telomere reprise unit (12 nt) to identify seeker TRs in transcriptomes depleted of ribosomal RNA (rRNA) in multiple Allium species in parallel, and examine the seeker TRs by reconstitution trials. Importantly, grounded on the Allium TRs, we identify their orthologs in the other land shops and find their template regions corresponding to their telomere reprise sequences. Interestingly, we also identify the corresponding homolog in Arabidopsis thaliana, where a different seeker TR, TER1, has been reported before to be suitable to give a templating function in telomerase in vitro reconstitution trials. Still, we demonstrate then by in vitro and in vivo trials that the recently linked TR is the natural templating subunit of telomerase in Arabidopsis, as well as are its orthologs in other flowering shops.

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