Investigating Plant Telomere Motifs Using Bioinformatics

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Telomeres are nucleoprotein complexes protecting ends of eukaryotic chromosome from damage. Plant telomeres consist of the typical tandemly repeated motif TTTAGGG(n), but rare changes of telomere motif are known. Because of the great importance of the telomere protective system, it is highly conserved and any alteration is peculiar from an evolutionary perspective. In this work, I used bioinformatics to search publicly available sequence data in hopes to confirm the classical telomeric motif or identify new motifs in a variety of plant species. Sequence data from Short Read Archive database from NCBI were downloaded and processed on Galaxy computational platform. Quality control, read trimming and data conversion were carried out. These data were analysed in Tandem Repeats Finder, bioinformatics software for finding tandem repetitions in sequence data. I inferred candidate telomeric motifs in each examined species based on data outputted by TRF. Obtained results were put into the context of current plant phylogeny. I confirmed the typical plant telomeric motif in the majority of plants species examined. From the thirty datasets, three showed promising results for discovering a new altered telomeric motif: In the sea grass species Zostera marina I found a dominant motif TTAGGG(n), while the species Zostera muelleri has the standard motif, pointing to a mutation within a genus. Species Alnus glutinosa and Utricularia gibba don’t possess the typical plant telomere motif, however I wasn’t able to infer a candidate motif from sequence data alone. Molecular biology analyses are needed to confirm the altered telomere motifs in these species.

Awards Won:

Third Award of $1,000