LTR-retrotransposons of the family *Pseudoviridae* in the genomes of monocotyledonous and dicotyledonous plants.

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LTR-retrotransposons occupy a significant part of the genome of plant (just over 7% of the genome of Arabidopsis thaliana, 25% - of the rice genome, 65% - of the genome of wheat, 75% - of the maize genome. Due to their mobility these elements can cause a variety of mutations and recombinations as well as deletions and translocations as a result of transposition. Taking into account the fact that the induction of transpositions increased under the conditions of environmental changes, transposable elements are an important tool of evolution [1]. We tried to estimate the distribution of inverted sites of LTR-retrotransposons of the family *Pseudoviridae* in the genomes of crop plants using multi-locus genotyping and the possibility of polymorphism obtained by PCR with primers homologous to fragments of these retrotransposons to study the genetic structure of populations of monocots and dicots reproducing in different environmental conditions.

Were chosen representatives of the class of monocots (*Triticum aestivum L.*), and dicots (*Glycine soja Sieb. Et Zucc* and *Glycine max Merrill*) to analyze the possibility of using sites of LTR-retrotransposons as molecular markers in genetic studies of population's structure of plants. Three varieties of wheat were studied: two varieties of winter wheat Moscow 39 (soft winter) - and Mironovskaya 808 (soft winter, derived from the spring) - and a variety of spring wheat Omsk 36 (soft spring), and 5 populations of wild soybean species *Glycine soja Sieb. et Zucc* (Primorsky Region) and representatives of Polukulturnaya C 10 (*Glycine max Merrill*, China). The studies of the genetic structure of populations were carried out on the base of polimorfism of DNA's fragments as results of IRAP-PCR (Inter-Retrotransposon Amplyfied Polymorphism), flanked by inverted sites of LTR-retrotransposon soybean's LTR-retrotransposon LTR SIRE-1 (GCA-GTT-ATG-CAA-GTG-GGA-TCA- GCA), belonging to the family *Pseudoviridae*, genus *Sireviruses*.

We obtained a spectra of clearly replicating DNA fragments as a result of IRAP-PCR with a primer to a terminal site of retroelement LTRSIRE-1 as in soybean (*Glycine soja Sieb. et Zucc* and *Glycine max Merrill*), and in wheat (*Triticum aestivum L.*). The fragments were of the same length (15 loci 350-1010 bp, 26 bp 220-1450 loci respectively. Only one monomorphic locus (700 bp) was detected in soybean (*Glycine soja Sieb.* et Zucc and *Glycine max Merrill*), the share of polymorphic loci (P) on the primer was 93%, $PIC_{average}$ (polymorphic information content) = 0.414. It shows the genetic diversity within the genus *Glycine*, and within a species *Glycine soja Sieb. et Zucc*. At the same *Glycine max Merrill*, locus of 680 bp was absent, whereas the same locus met with varying frequency in representatives of *Glycine soja Sieb. et Zucc.* One of the populations of *Glycine soja Sieb. et Zucc*. was characterized by the absence of locus of 780 bp in the spectrum of DNA, for the other - 540 bp.

The values of the basic population genetic parameters (P, and $PIC_{average}$) of different wheat varieties lower than soybean (69%, 0.120). However, the characteristics of each of the varieties identifies quite clearly. For example, a unique to wheat Moscow 39 locus (790 bp) was present in all the samples of this variety, whereas this fragment was not detected in the spectra of DNA of Myronivska 808 and Omsk 36 varieties. Conversely, the locus of 550 bp was not found only in Moscow 39, and PIC value for this locus was 1 for the other two varieties. A dendrogram was constructed based on the values of genetic distances, calculated by the method of Nej (DN, M.Nej, 1972), corresponding well-known phylogenetic relationships between the studied populations of plants on the basis of the distribution of retrotransposon's fragments LTRSIRE-1.

Spectrum of anonymous DNA fragments of different lengths was obtained as a result of IRAP-PCR. We have chosen one of the most severe clearly reproducing major fragments to determine its nucleotide content. Using the database (http://blast.ncbi.nlm.nih.gov/) and algorithm BLASTn was found the only one region (1900 bp) in the chromosome 1 of *Glycine max Merrill*, flanked by primer highly gomologous to inverted sites of LTR SIRE -1. Next, using a database of repetitive DNA sequences Giri (www.girinst.org / repbase /) the 1922 bp amplicon corresponds to a mobile element SIRE-1 INT was found. Searching a fragment homologous to a mobile element SIRE-1 INT in the database, flanked by inverted sites of retrotransposon LTR SIRE-1 showed that this fragment (SIRE-1 INT) occurs in other chromosomes of *Glycine max Merrill*, and other genomes of plants such as *Medicago truncatula* (bean family), *Sorghum bicolor* (Gramineae family), as well as animals - *Cricetulus griseus*, *Mus musculus* (rodent), *Ovis aries* (toed ungulates). As *Sireviruses* suspected to contain env-like gene [2], there is a possibility of horizontal transfer of these TE from species to species. Due to the broad representation in the genomes of different groups of organisms the sites homologous to the flanks of retrotransposon LTR SIRE-1 such fragments can be successfully used in a multi-locus genotyping in the studies of groups of different taxa.

1. Bohmdorfer G., Tramontano A., Luxa K., Bachmair A. A synthetic biology approach allows inducible retrotransposition in whole plants Syst Synth Biol (2010) 4:133–138;

2. Bousios A. and Darzentas N. Sirevirus LTR retrotransposons: phylogenetic misconceptions in the plant world Mobile DNA 2013, 4:9.