Sites homologous to helitron family and their polymorphism in mammal genomes

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The diversity of genome elements and their polymorphism allows researchers best choice of conserved and variable spectra for polyloci genotyping (genome scanning). In case of using anonymous sequences (DNA fragments flanked by short inverted repeats used as primer in PCR) one can compare different DNA markers on example of the same object and also compare the same marker on example of different objects. That allows investigation patterns of distribution and polymorphism of different marker types, studying relations of their variability with phylogeny features of different animal groups.

Helitron flanks are considered as a new type of DNA markers which is suitable for such surveys. Helitrons belong to DNA transposon family and utilize a unique replication mechanism called rolling-circle. On a 5'-end there is TC dinucleotide and on a 3'-end there are CTRR nucleotides, also in 3'-region there is often a sequence capable to form DNA hairpins. These mobile elements usually insert in AT dinucleotide and then may create their nonautonomous copies, which differ by interior nucleotide sequence. It has been showed that helitrons may capture DNA fragments without distinguishing its intron-exon structure and carry them to new places in genome (Dong Y. et al., 2011). It turned out that many mobile elements described earlier now are considered to belong to helitron family, for example Aie, AthE1, Basho and ATREP elements found in *Arabidopsis thaliana*.

Moreover, search in genome sequences allowed finding helitrons in lots of eukaryotes: fungi, plants and animals. In cattle and horse genomes we found presence of certain fragments with homology to 3'-ends of helitrons. Then we constructed a primer homologous to rather conserved fragment of helitron families HeligloriaA and HeligloriaB observed in animals.

Using of that sequence as PCR primer in cattle, musk oxen and horses allowed an achievement of polyloci spectra of DNA fragments flanked by its inverted repeat. Those spectra contained amplicons from 100 to 2000 bp, and in total there were about 20 amplicons in every specter with specie and breed specific features. We also observed amplicons of the same length in spectra acquired from different species. Musk oxen provided differences in spectra according to habitat and also differences between modern and ancient individuals.

Data acquired evidence that mammalian genomes contain nucleotide sequences homologous to helitron fragments in different strands on short distances. These sequences can be utilized as PCR primers providing polymorphic polyloci amplification spectra, and that can be used for investigation of gene pools of various organisms as well as other known DNA markers.

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