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Mobile Genetic Elements in Trematode Himasthla Elongata Clonal Polymorphism

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Abstract : Animals that reproduce asexually were thought to have the same genotypes within generations for a long time. However, some refuting examples were found, and mobile genetic elements (MGEs) or transposons are considered to be the most probable source of genetic instability. Dispersed nature and the ability to change their genomic localization enables MGEs to be efficient mutators. Hence the study of MGEs genomic impact requires an appropriate object which comprehends both representative amounts of various MGEs and options to evaluate the genomic influence of MGEs. Animals that reproduce asexually seem to be a decent model to study MGEs impact in genomic variability. We found a small marine trematode Himasthla elongata (Himasthlidae) to be a good model for such investigation as it has a small genome size, diverse MGEs and parthenogenetic stages in the lifecycle. In the current work, clonal diversity of cercaria was traced with an AFLP (Amplified fragment length polymorphism) method, diverse zones from electrophoretic patterns were cloned, and the nature of the fragments explored. Polymorphic patterns of individual cercariae AFLP-based fingerprints are enriched with retrotransposons of different families. The bulk of those sequences are represented by open reading frames of non-Long Terminal Repeats containing elements(non-LTR) yet Long-Terminal Repeats containing elements (LTR), to a lesser extent in variable figments of AFLP array. The CR1 elements expose both in polymorphic and conservative patterns are remarkably more frequent than the other non-LTR retrotransposons. This data was confirmed with shotgun sequencing-based on Illumina HiSeq 2500 platform. Individual cercaria of the same clone (i.e., originated from a single miracidium and inhabiting one host) has a various distribution of MGE families detected in sequenced AFLP patterns. The most numerous are CR1 and RTE-Bov retrotransposons, typical for trematode genomes. Also, we identified LTR-retrotransposons of Pao and Gypsy families among DNA transposons of CMC-EnSpm, Tc1/Mariner, MuLE-MuDR and Merlin families. We detected many of them in H. elongata transcriptome. Such uneven MGEs distribution in AFLP sequences' sets reflects the different patterns of transposons spreading in cercarial genomes as transposons affect the genome in many ways (ectopic recombination, gene structure interruption, epigenetic silencing). It is considered that they play a key role in the origins of trematode clonal polymorphism. The authors greatly appreciate the help received at the Kartesh White Sea Biological Station of the Russian Academy of Sciences Zoological Institute. This work is funded with RSF 19-74-20102 and RFBR 17-04-02161 grants and the research program of the Zoological Institute of the Russian Academy of Sciences (project number AAAA-A19-119020690109-2).

Keywords : AFLP, clonal polymorphism, Himasthla elongata, mobile genetic elements, NGS

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