# MEG and VAL genes in the *Schistosoma mansoni* genome are enriched for transposable elements.

Philippsen, G.S.; DeMarco, R.

Departamento de Física e Informática, Instituto de Física de São Carlos, Universidade de São Paulo, São Carlos, São Paulo, Brazil

**Introduction:** Micro-Exon Genes (MEGs) and Venon Alergen-Like (VAL) genes are two classes of *S. mansoni* genes for which some members were shown to have protein products located at the host parasite interface. For both classes there are descriptions of multiple gene copies that probably arise from recent gene duplications. **Objectives:** Verify if MEG and VAL genes display differential representation of transposable elements. **Material and methods**: A bioinformatic analysis was performed to verify the frequency of transposable elements in genes from these families and their vicinity. Consensus sequences of known transposable elements was used in a blastn search against *S. mansoni* genome and frequency of alignment in regions corresponding to genes of those two classes were verified. Empirical simulations, where genomic portions having exactly the same profile with regard to size and number as those representing the sampled gene families randomly chosen in the S. mansoni genome, was performed as a control.**Results:** We detected higher than expected frequencies for two SINE elements, Sm-alpha and Sm, and for the LINE Perere-3 in MEGs. Higher than expected frequencies for Sm-alpha and Sm was also found in VAL genes. A more sophisticated analysis utilizing empirical simulations allowed the confirmation of enrichment for all classes at significant levels, except for enrichment of Sm-Alpha in VAL genes. **Conclusions:** The observed enrichment of transposable elements could reflect a preferential targeting of those elements to the regions harboring those genes and the fact that gene rearrangements promoted by those elements in genes that are under pressure from host immune system have a higher chance of producing changes that will be positively selected.

Keywords: Genome evolution, Schistosomiasis,Transposable elements.
Support: FAPESP, PRP-USP and CNPq.