ESCOLA GAÚCHA DE BIOINFORMÁTICA

17 A 21 DE JULHO DE 2017

AULAS PALESTRAS MINI-CURSOS SESSÃO DE PÔSTERES

LIVRO DE RESUMOS

Dorn, Marcio
EGB 2017 - Livro de Resumos / Marcio Dorn, Rodrigo Ligabue Braun, Hugo Verli. -- Porto Alegre, 2017.
39 f.

Anais/Livro de Resumos - Universidade Federal do Rio Grande do Sul, Instituto de Informática e Centro de Biotecnologia - UFRGS, 2017.

1. bioinformática. 2. biologia computacional. 3. escola. I. Ligabue Braun, Rodrigo. II. Verli, Hugo. I. , . II. Título.

DOI: 10.13140/RG.2.2.34681.77929

AGRADECIMENTO E APOIO

CAPES
FAPERGS
Fundação de Amparo à Pesquisa do Estado do Rio Grande do Sul
CNPq
Conselho Nacional de Desenvolvimento Científico e Tecnológico
pro pesq
Pró-Reitoria de Pesquisa - UFRGS
INF INSTITUTO DE INFORMÁTICA UFRGS PPGC
PPGBCM CBiot/UFRGS

REALIZAÇÃO

UFRGS UNIVERSIDADE FEDERAL DO RIO GRANDE DO SUL
INF INSTITUTO DE INFORMÁTICA UFRGS
CBiot Centro de Biotecnologia da UFRGS

LOCAL

Centro de Eventos do Instituto de Informática da UFRGS

SITE › WWW.UFRGS.BR/EGB

DETECTION OF LTR RETROTRANSPOSONS IN THREE *Hamiltosporidium* lineages

ALBUQUERQUE, NATHALIA RAMMÉ MEDEIROS[1]; SILVEIRA, JULIANO DE OLIVEIRA[1]; HAAG, KAREN LUISA[1].
[1]Laboratório de Genômica Evolutiva, Departamento de Genética, Universidade Federal do Rio Grande do Sul.

Microsporidia have one of the smallest genomes among eukaryotes, due to their obligate intracellular parasitism that resulted in an extensive reduction in genome size and complexity. Transposable elements (TEs) compose a high fraction in eukaryotic genomes, the vast majority being retrotransposons, due to their "copy-paste" transposition mechanism. TEs are able to mutate genes, alter gene regulation and generate new genes. Transposition events can be deleterious when TEs integrate in active coding regions and disrupt important genes. Due to the absence of recombination, TEs may accumulate in asexual genomes and contribute to extinction of asexual organisms. However, there is no evidence showing different TE densities between sexual and asexual lineages. We assessed the genomes of three Hamiltosporidium lineages for TE content. Two genomes of H. magnivora lineages (BEOM2 and ILBN2) that reproduce sexually and are vertically transmitted, and one genome of an H. tvaerminnensis lineage (FIOER33) that reproduces asexually and is both vertically and horizontally transmitted. The RepeatMasker software was used for initial screening of TE content. A set of core protein domains encoded by LTR retrotransposons was used in BLASTp searches in the proteomes of BEOM2, ILBN2 and FIOER33. Finally, LTRharvest was used to detect full-length elements. No copies of DNA transposons larger than 80 pb long and with >80% identity to the reference elements were found in the genomes. Nevertheless, LTR retrotransposons copies were detected in all three genomes. BLASTp identified 31 core protein domains in BEOM2, 199 in ILBN2 and 15 in FIOER33 predicted proteomes with *e-values* >1e-10. LTRharvest found 40 elements in BEOM2, 41 in ILBN2 and 23 in FIOER33 genomes. However, only two potentially active LTR retrotransposons, with pair of LTRs 5' and 3', and the presence of at least 3 key protein domains (reverse transcritase, RNAseH and integrase) were found in the genomes. Both elements are shared between all three lineages, indicating fixed insertions that occurred before the divergence of the species. The genomes of sexual lineages (BEOM2 and ILBN2) have increased TE load compared with the asexual lineage (FIOER33). These results indicate that the H. tvaerminnensis (FIOER33) were able to eliminate deleterious TEs, but the underlying molecular mechanism that eliminates TE insertions remain unknown.

Key words: Microsporidia, Transposable elements, LTR retrotransposons.