

Characterization of satDNAs in *Mahanarva quadripunctata* (Cercopidae) through high-throughput and chromosomal analysis

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Abstract/Resumo

Spittlebugs (Auchenorrhyncha) are a group of insects best known to cause losses in agricultural and pasture grasses by feeding plant fluids. Despite the great karyotypic variability described for organisms with holocentric chromosomes, as observed in Auchenorrhyncha, genomic organization of repetitive DNA sequences, such as Satellite DNAs remains poorly studied. Due to its abundance in the eukaryotic genomes, the obtaining of markers based in satDNAs could improve the understanding of karyotype evolution. Here using Illumina next-generation sequencing and graph-based clustering we performed the characterization of satDNA families prospected from the genome of *Mahanarva quadripunctata* ($2n=19, X0♂$). Moreover, we tested the occurrence of the two most abundant satDNA in *M. quadripunctata* in other species of Auchenorrhyncha. A total of 30 satDNA families were found through Illumina NGS and RepeatExplorer analyses, representing 4.53% of the *M. quadripunctata* genome. The eight successfully isolated satDNAs were labeled and used as probes for fluorescent *in situ* hybridization, resulting in several distribution patterns as follows: (I) two satDNAs spread to the whole chromosome complement, forming band-like pattern; (II) two satDNAs with clusters in one autosomal bivalent; (III) three satDNAs interspersed across the whole genome without observation of conspicuous bands; (IV) one satDNA with no signals detected by FISH. Dot blot using genomic DNA from six *Mahanarva* and other eight Auchenorrhyncha species revealed positive hybridization only against the genomic DNA of *Mahanarva* species for the two most abundant satDNAs, indicating common origin, at least, in *Mahanarva* genus in accordance to "Library hypothesis". The data suggest complex organization for distinct families of satDNAs, at chromosomal level, suggesting divergent patterns of clusterization and evolution.

Keyword/Palavras-chave: FISH; Next-generation Sequencing; Spittlebugs; Satellite DNA