

Identification of Genes Encoding for Substances Interfering with Blood Clotting
in the Midgut of *Rhodnius prolixus*

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R. prolixus is an obligate hematophagous triatomine and a Chagas disease vector. ESTs from a cDNA library of *R. prolixus* midgut were analyzed and 17 sequences were found that have Kazal type serine protease inhibitors domains, which prevent blood clotting in this organism. An attempt to cluster these sequences using CAP3 returned 5 different contigs, regardless the criteria used for clusterization. Upon the release of *R. prolixus* trace sequences we identified 19 putative exons, some of which present in more than one contig. Some contigs found could be either the product of alternative splicing of one or more genes or the transcription product of different genes sharing local similarities, as it would be expected as the result of gene duplication followed by divergent evolution. Two approaches to clarify this hypothesis were used: bioinformatics and PCR cDNA amplification/sequencing. GenSeed was used to assemble trace sequences that match our ESTs. We found two separate genomic sequences in which the putative exon organization presented in our longer EST could be confirmed. Yet, we didn't succeed in corroborating the complete exon order of this EST in an uninterrupted genomic sequence. Other assemblies of trace sequences partially confirmed the exon order of other ESTs. Using PCR and specific oligonucleotides we amplified four DNA fragments which sequences would reveal the full sequence of two transcripts from two different genes. This data showed that *R. prolixus* differs from other triatomine as *T. infestans* and *T. brasiliensis*, which have only one transcript having Kazal type domains.

Keywords: Bioinformatics, Hematophagous, Kazal, PCR, *R. prolixus*.

Acknowledgments: FAPERJ, CNPq.