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Beating DNA out of mites

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Details of the methods for the DNA extraction of mites have become more important with an increased interest in whole genome sequencing using next generation sequencing techniques on one side and the advancement of molecular techniques in forensic acarology on the other side. Currently one of the most used methods for homogenisation of microarthropods is bead beating employing small grinding or cutting beads in a shaking microtube homogenizer (BeadBug Benchmark Scientific). A wide variety of bead materials were investigated (glass, garnet, zirconia, steel, and carbide). The influence of different bead sizes (0.1 – 3.0 mm), different densities of the bead material (2.5 – 14.9 g/cm^3), and different shapes of the beads (round balls or sharp-edged particles) on the quantity and quality of DNA extracted from mites was systematically investigated using the Qiagen DNeasy Blood & Tissue kit. The comparison was performed with four mite species: *Tyrolichus casei* (Acaridae) as a future model lab or food mite, *Tyrophagus putrescentiae* (Acaridae) as a model stored-product mite, *Dermatophagoides farinae* (Pyroglyphidae) as a model house dust mite, and *Archegozetes longisetosus* (Trhypochthoniidae) as a model soil mite.

Genome annotation of the flat mite *Brevipalpus yothersi* Baker (Tenuipalpidae)

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The flat mite *Brevipalpus yothersi* Baker, previously erroneously named as *Brevipalpus phoenicis* (Geijskes), was recently resurrected and redescribed into the *B. phoenicis* sensu stricto group. This species is one of the most important pests among the flat mites (Tenuipalpidae); these mites are highly polyphagous and their major importance is due to the transmission of numerous plant viruses- the *Brevipalpus* transmitted virus, BTV`s- which can seriously affect crops such as citrus, coffee, passion fruit and ornamental plants. Among them, the *Citrus leprosis virus* (CiLV) has been considered a key virus for the citrus production in some countries of South and Central America, as well as of the Caribbean. Due of their importance as vectors several studies have been conducted in order to understand the virus-vector interactions, also considering the diversity of species that may be involved. Advances in resources for genomic analyses are essential to the functional biology knowledge, however genomic data about plant mites remains limited. Here we present some features from the initial genomic analyses of assembly of the *B. yothersi* genome. The assembly data was performed from 454 reads and Illumina reads (paired-end and mate-paired). To successful annotation and determine the assembly quality different tools were used- Newbler, CLC genomics, and SSPACE. These analysis resulted in 849 scaffolds and the cumulative size is 72.286 Mb. Comparisons using the spider mite *Tetranychus urticae* Koch genome data showed that 6.4% of the total size of *B. yothersi* scaffolds is homologous to the known repeats from the spider mite library. Although the coding sequence of the flat mite can be considered significantly different from that of *T. urticae* (<80% nucleotide identify), the predicted proteins show good alignment coverage with spider mite genes (~2000). Next steps include collecting more gene models and RNAseq data to further train the splice to gene prediction programs. A relative good quality of *B. yothersi* genome assembly was obtained and the gene prediction quality was improved using evidence from spider mite alignments. The annotated *B. yothersi* genome constitutes a valuable genomic resources to investigate the biology and the rare thelytoky system of the complex mite-virus-plant interaction. Financial Support: CNPq, Fapesp, Embrapa.