In silico analysis reveal high variability in RNAi machinery of five different insect orders

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Insects are the most diverse class of living organisms on Earth, and most of them can be considered pest to the major crops. RNA interference (RNAi) refers to the process of post-transcriptional silencing of cellular mRNA. RNAi strategies have been widely employed to regulate gene expression in plants, animals and insect-pests. According to what has been broadly described for *Drosophila melanogaster*, the main small RNA–based silencing pathways used as a biotechnological tool to insect control are the microRNA (miRNA) and small interference RNA (siRNA) pathways. Even with advances in the characterization of insect RNAi machinery, little is known about the particularities of this molecular pathway in insects. Thus, the present study aims to evaluate *in silico* the canonical and non-canonical RNAi machinery elements in five different insect orders (Coleoptera, Diptera, Hemiptera, Hymenoptera, and Lepidoptera). Twenty gene families related to the biogenesis and presentation of small RNAs in insects were searched in several different databases containing genomic and transcriptomic data from 168 different insect species. After candidate selection using BLASTP and TBLASTN tools, each predicted protein sequence was analyzed for characteristic protein domains (PFAM and PROSITE) and putative tertiary structure (SWISS-MODEL). Specific characteristics were observed for each insect orders analyzed, such as the absence of some non-canonical elements, and structural peculiarities. Thus, the present study contributes to elucidate obscure points of the RNAi-based gene silencing in insects and assists in the development of biotechnological tools for insect pests control.