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Título: RNAi in Piezodorus guildinii (Hemiptera - Pentatomidae): Transcriptome assembly, machinery analysis and in-vivo response towards the development of new pest control strategies.

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Body

Red-banded stink bug *Piezodorus guildinii* (*P. guildinii*) has been described as the most damaging stink bug regarding soybean crops, leading to seed injury, low germination percentages and foliar retention, even at low population densities. In recent years, RNA interference (RNAi), a conserved eukaryote mechanism of post-transcriptional silencing, has been explored to develop species-selective pesticides. In this work the first *P. guildinii* transcriptome from a pool of all developmental stages was assembled, annotated and RNAi components were analyzed. Putative sequences encompassing siRNA, miRNA and piRNA pathways were identified, leading to a total of 56 sequences related to the silencing process. In addition, to evaluate the functionality of RNAi machinery, *P. guildinii* adults were injected with 28ng per mg of body weight of dsRNA targeting vATPase A, A mortality of 35% and 51.6% was observed after 7 and 14 days, respectively, and a downregulation of vATPase A gene of 84% 72h post injection. In addition, Dicer-2 and Argonaute-2 genes, core RNAi proteins, were upregulated 1.8-fold 48h after injection. These findings showed for the first time that RNAi is functional in *P. guildinii* and the silencing of essential genes has a significant effect in adult viability. Taken together, the work reported here shows that RNAi could be an interesting approach for the development of red-banded stink bug control strategies **Acknowledgements**

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