



## Biological control potential of *Pyemotes zhonghuajia* Yu, Zhang & He (Prostigmata: Pyemotidae)\*

YAN-FEI SONG, SHUAI YE, TAI-AN TIAN, YI-CHAI CHEN, MAO-FA YANG & JIAN-FENG LIU<sup>1</sup>

Institute of Entomology, Guizhou University; Guizhou Provincial Key Laboratory for Agricultural Pest Management of the Mountainous Region; Scientific Observing and Experimental Station of Crop Pest in Guiyang, Ministry of Agriculture, Guiyang 550025, P. R. China

<sup>1</sup>Corresponding author: [✉ jfliu3@gzu.edu.cn](mailto:jfliu3@gzu.edu.cn)

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**Summary:** *Pyemotes zhonghuajia* Yu, Zhang & He is an ectoparasitic mite of various pests. Our studies found that *P. zhonghuajia* could kill *Spodoptera frugiperda* (Smith), *Mythimna separata* (Walker), and *Spodoptera litura* (Fabricius) at different developmental stages. Through an integrated approach of lipidomics, transcriptomics, and proteomics, we explored the immune response of *S. frugiperda* parasitized by *P. zhonghuajia*. In order to explore toxin proteins of *P. zhonghuajia*, we mined toxin genes by combining genome and transcriptome.

*Pyemotes zhonghuajia* Yu, Zhang & He (Prostigmata: Pyemotidae) is a highly efficient domestic venomous ectoparasitic mite against various of Lepidoptera, Coleoptera, and Hemiptera pests (Li *et al.*, 2019; Lu *et al.*, 2019; Liu *et al.*, 2020). *Pyemotes zhonghuajia* could paralyze and kill various stages of *Spodoptera frugiperda* (Smith), *Mythimna separata* (Walker), and *Spodoptera litura* (Fabricius), including, eggs, larvae, prepupae, pupae or even adults, but could only successfully lay offspring adults on their eggs, prepupae or pupae of hosts (Liu *et al.*, 2020; Tian *et al.*, 2020a; Chen *et al.*, 2021; Song *et al.*, 2022a). Recently, we found that *Phthorimaea operculella* (Zeller) fourth instar larvae is a highly suitable host to conduct the mass rearing of *P. zhonghuajia* (Figure 1). This mite had the highest lethal weight ratio to paralyze and kill a third instar *S. litura* larva—680,000 times its own weight (Chen *et al.*, 2021). A shorter period of starvation (24 h) could improve the movement rates and lethal efficiency of *P. zhonghuajia* against *S. frugiperda* larvae (Tian *et al.*, 2020b). The parasitism of 40 (lethal densities) and 10 (sublethal densities) *P. zhonghuajia* mites significantly influenced the cellular immune response and humoral immune response of *S. frugiperda* fifth instar larvae. Lethal and sublethal mechanisms of *S. frugiperda* induced by 40 and 10 *P. zhonghuajia* mites were a complex process involving signal transport and immune resistance through an integrated approach of lipidomics, transcriptomics, and proteomics. The complete mitogenome of *P. zhonghuajia* is 14, 772 bp, containing 13 PCGs, 22 tRNAs, two rRNAs and one control region (Ye *et al.*, 2022). The genome size of *P. zhonghuajia* is 71.943 Mb, and 68.51 Mb is subsequently assigned to three chromosomes. Neurotoxin and dermonecrotic toxin gene families are found with significant expansion within *P. zhonghuajia* genome (Song *et al.*, 2022b). To elucidate the insecticidal mechanism of the mite toxins, future studies should focus on the identification of structure and target of insecticidal proteins, and then identify and clone the receptor for *P. zhonghuajia* toxins. *Xenopus laevis* oocytes are used to express the receptors and the inhibition of the receptors by toxins is detected by two-electrode voltage-clamp to clarify the regulatory mechanism of toxin proteins on the host.

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**Keywords:** *Pyemotes zhonghuajia*, lethal, genome, toxin genes, proteins



**FIGURE 1.** Mass rearing of *Pyemotes zhonghuajia* on *Phthorimaea operculella* fourth instar larva.

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