Zoosymposia 22: 247–248 (2022)
https://www.mapress.com/j/zs

Correspondence

ISSN 1178-9905 (print edition)
ZOOSYMPOSIA
ISSN 1178-9913 (online edition)

https://doi.org/10.11646/zoosymposia.22.1.149

Status of abamectin resistance and mechanisms in *Tetranychus urticae* in China*

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**In*: Zhang, Z.-Q., Fan, Q.-H., Heath, A.C.G. & Minor, M.A. (Eds) (2022) *Acarological Frontiers: Proceedings of the XVI International Congress of Acarology (1–5 Dec. 2022, Auckland, New Zealand)*. Magnolia Press, Auckland, 328 pp.

The two-spotted spider mite, *Tetranychus urticae* Koch, is an important agricultural pest worldwide. It is prone to evolve resistance to pesticides, including organophosphates, pyrethroids, and some newly developed compounds (Xu *et al.*, 2018; Alpkent *et al.*, 2020), due to the frequent pesticide spray and the biological characteristics of *T. urticae*, such as short life cycle and parthenogenesis, etc. There is no doubt that the development of pesticide resistance and unclear resistant mechanisms have impeded the chemical control and resistance management of *T. urticae* in the field.

Abamectin is a widely used insecticide and acaricide in the field, showing a broad spectrum of toxic activities against arthropods and some mites including *T. urticae*. Currently, a series of documents reported that *T. urticae* field populations have developed different levels of resistance to abamectin in China (Xu *et al.*, 2018; Zhang *et al.*, 2022b) and other countries (Çağatay *et al.*, 2018; Döker *et al.*, 2020; Xue *et al.*, 2020; Papapostolou *et al.*, 2021). Target mutations in glutamate-gated chloride channels (GluCls) have been shown to be associated with abamectin resistance (mutation G314D in GluCl1, G326E in GluCl3) (Kwon *et al.*, 2010; Dermauw *et al.*, 2012; Mermans *et al.*, 2017). In Chinese *T. urticae* field populations, G314D and G326E were present at different mutation frequencies, which were not correlated significantly with the resistance levels (Xu *et al.*, 2018). Except for the target resistance, P450 genes were also suggested to be involved in abamectin resistance based on the synergism experiments and transcription sequence analysis for the resistant populations (Xu *et al*., 2021). Also, abamectin resistance was found to be governed by multi-genes based on a near-isogenic resistant strain (NIL-Aba) (Zhang *et al*., 2022a). Over-expression of the CYP392A16 gene was found in European *T. urticae* populations leading to abamectin resistance (Riga *et al.*, 2014; Papapostolou *et al.*, 2022); however, the CYP392A16 gene was not highly or differently expressed in Chinese *T. urticae* field populations. In the meanwhile, the CYP392D8 gene was found to be not directly associated with abamectin resistance, even though it was highly expressed in two resistant *T. urticae* populations from China (Xu *et al*., 2022). To elucidate the resistant mechanisms of *T. urticae* in the field in China, extensive studies on those potential candidate P450 genes possibly related to abamectin resistance need to be further explored.

Acknowledgements. This research was funded by the National Natural Science Foundation of China (32072458), the earmarked fund for China Agriculture Research System (CARS-25), and the Beijing Key Laboratory for Pest Control and Sustainable Cultivation of Vegetables.

Keywords: *Tetranychus urticae*, abamectin, resistant mechanism, target mutation, P450

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Submitted: 29 Sept. 2022; Accepted by Zhi-Qiang Zhang: 8 Oct. 2022; published: 30 Nov. 2022

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