



柑桔全爪螨研究概述：从基础到应用*

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摘 要 害螨是世界上公认的难以防治的生物类群, 具有繁殖快、适应性强、突变率高和易产生抗药性等特点。随着种植结构调整和全球气候变化, 以柑桔全爪螨 *Panonychus citri* (McGregor) 为代表的柑桔害螨作为桔园中最常见、最易发生的一类重要有害生物, 在全国柑桔各产区大面积频繁暴发成灾。耕作制度改变和化学农药使用不当等因素导致柑桔害螨的危害加剧, 防治越来越困难。解毒代谢酶系统 (细胞色素 P450 单加氧酶系、谷胱甘肽 S-转移酶和羧酸酯酶等) 在害螨应对植物次生代谢物和杀螨剂的威胁中扮演着重要角色。然而, 由于化学药剂的长期大量不科学使用, 导致害螨抗药性愈发严峻、田间生态受到破坏和农药残留增加。本文以桔园中最常见和最易暴发危害的柑桔全爪螨为对象, 分别从其生长发育调控、抗药性机制和捕食螨应用等方面概述其研究进展, 旨在为害螨基础及应用基础研究提供参考。

关键词 柑桔全爪螨; 发育调控; 抗性机制; 生物防治

An overview of *Panonychus citri*: From fundamental research to field application

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Abstract *Panonychus citri* (McGregor) is one of the most detrimental citrus pest mites worldwide. Its unique developmental characteristics, which include three molts and five developmental stages (egg, larva, protonymph, deutonymph, and adult), high fecundity, and a short developmental cycle, enable it to adapt quickly to environmental changes and stresses. In addition, the efficient detoxification metabolic enzyme system (cytochrome P450 monooxygenase, glutathione S-transferase, and carboxylesterase) of *P. citri* plays an important role in its response to plant secondary metabolites and acaricides. However, the long-term use of chemical control methods can lead to significant pesticide resistance, ecological damage, and an increase in pesticide residues in the environment. Therefore, the biological control strategy of using mites to control mites remains an important approach for future *P. citri* management. This review summarizes the growth and development of *P. citri*, its resistance mechanisms, and the management of predatory mites, to provide a reference for fundamental and applied research on *P. citri*.

Key words *Panonychus citri*; developmental duration; resistance mechanism; biocontrol

柑桔全爪螨 *Panonychus citri* (McGregor) 属节肢动物门 Arthropoda、蛛形纲 Arachnida、蜱螨

亚纲 Acarina、叶螨科 Tetranychidae 的一种植食性螨类。该螨寄主范围广, 多达 112 种寄主植物,

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以取食柑桔类果树为主 (Migeon and Dorkeld, 2019)。通过取食果树叶片、枝杆和嫩果, 导致落叶落果, 降低了品质和产量 (Hu *et al.*, 2022)。其发育周期短, 繁殖力高, 每年多达 19 代, 主要在春秋季节严重为害柑桔类果树 (Faraji, 1992)。

我国柑桔栽培面积超 280 hm², 产量 5 100 万吨, 均居世界首位。目前, 化学防治仍然是防控柑桔全爪螨的最有效措施, 逾 1 319 种杀螨剂在田间被广泛使用 (ICAMA, 2021)。但化学药剂的长期使用造成田间抗性突出问题, 柑桔全爪螨对多种类型杀螨剂均产生严重抗药性, 如: 阿维菌素, 甲氰菊酯, 螺螨酯, 哒螨灵, 联苯肼酯, 丁氟螨酯, 噻螨酮, 唑螨酯和三唑锡等 (Hu *et al.*, 2010; Van Leeuwen *et al.*, 2011; Ouyang *et al.*, 2012; Pan *et al.*, 2020)。田间抗药性的愈发严重致使用药量剧增, 从而引起田间生态失衡及降低了桔园生态多样性 (Livingston *et al.*, 2018)。此外, 产品和环境中的农药残留对食品安全、环境安全和人类健康造成威胁。因此, 本文从柑桔全爪螨的生长发育调控、抗药性机制和生物防治的角度开展综述, 以期为该螨的可持续治理提供参考。

1 柑桔全爪螨的生长发育调控

柑桔全爪螨发育历期短和繁殖力高的特性, 逐渐成为叶螨防控新策略的研究焦点。其中, 几丁质广泛分布于真菌、线虫和节肢动物中, 是外骨骼、气管、前肠、后肠的角质层和中肠上皮的周围膜中最重要的不溶性结构成分之一 (Lehane, 1997)。由几丁质构成的外壳保护节肢动物免受伤害, 同时也阻碍了节肢动物的持续发育。在生长发育过程中, 部分老化的组织和表皮中几丁质的消化伴随着新几丁质的合成和沉淀, 形成新的角质层和表皮 (Zhu *et al.*, 2008b)。在柑桔全爪螨发育过程中, 经历卵、幼螨、前若螨、后若螨和成螨 5 个阶段, 在幼螨和若螨阶段均发生蜕皮现象。通过 RNA 干扰降低柑桔全爪螨幼螨体内几丁质酶 (Chitinase) 的表达量, 能显著降低幼螨的蜕皮率。另外, 蜕皮激素 (Ecdysteroids) 在昆虫生长发育、变态蜕皮和生殖等众多生理过

程中发挥重要的调控作用 (Yamanaka *et al.*, 2013)。20-羟基蜕皮酮 (20E) 可引发昆虫的蜕皮。昆虫体内合成的 20E 通过蜕皮激素转运体 Ecdysone importer (EcI) 进入细胞核内, 与蜕皮激素受体 Ecdysone receptor (EcR) 和超气门蛋白 Ultraspiracle (USP) 结合, 从而引发早期反应基因 (如: *E75*、*E74* 和 *BR-C*) 的表达, 并通过上调 *HR3* 的表达激活下游信号通路级联反应 (Hill *et al.*, 2013; Okamoto *et al.*, 2018)。在柑桔全爪螨中发现, 当抑制蜕皮激素合成基因 (*Spo*) 表达后, 显著影响了前若螨的蜕皮过程并降低了蜕皮率。此外, 有研究表明蜕皮激素类似物 Ponasterone A 可促进前若螨蜕皮, 而 20E 却出现蜕皮延迟现象, 表明 Ponasterone A 是柑桔全爪螨体内蜕皮激素活性物质, 而非 20E (Li *et al.*, 2017)。其受体 *EcR* 与核受体 *PcRXR1/2* 结合可能行使不同功能, 与 *PcRXR1* 结合形成异源二聚体, 参与调控蜕皮过程中新表皮的形成; 而与 *PcRXR2* 结合, 引发与细胞自噬和组织重塑等一系列生理反应 (Li *et al.*, 2021)。*HR3* 作为核受体家族中的一员, 具有典型的保守结构域 DNA 结合域 (DBD) 和配体结合域 (LBD)。*HR3* 通过抑制 20E 早期反应基因 (*E75*、*E74* 和 *BR-C*) 的转录和激活下游反应因子 *Ftz-F1* 调控昆虫的变态发育 (Parvy *et al.*, 2014)。研究发现, *HR3* 在柑桔全爪螨的后若静止期大量转录, 与后若螨的蜕皮期保持一致。另外, 通过 dsRNA 饲喂抑制后若螨 *HR3* 的表达, 柑桔全爪螨出现发育延迟和致死现象 (Li *et al.*, 2020)。可见, 柑桔全爪螨的变态发育受到 20E 通路中多个因子的影响。

在卵生生物中, 卵黄蛋白的合成和发育在生殖过程中起着至关重要的作用。卵黄蛋白 Vitellin (Vn) 是卵子储存的营养来源, 有助于卵黄原蛋白 Vitellogenin (Vg) 和卵黄原蛋白受体 Vitellogenin receptor (VgR) 行使功能。而对于节肢动物卵巢的发育过程, Vg 在脂肪体中合成, 通过血淋巴运输, 随后由 VgR 进行内吞作用进入卵母细胞中 (Sappington and Raikhel, 1998)。相关研究表明, Vg 的生物合成密切联系昆虫的

繁殖或参与繁殖过程 (Sappington and Raikhel, 1998; Kawakami *et al.*, 2009)。譬如, 通过饲喂 siRNA 降低柑桔全爪螨 *Vg* 和 *VgR* 的表达量后, 显著影响了柑桔全爪螨的产卵 (Ali *et al.*, 2017)。柑桔全爪螨卵的发育还需进一步探索。

2 柑桔全爪螨对杀螨剂抗性机制

2.1 田间杀螨剂抗性监测

不考虑化学药剂对生态的影响 (水土污染、天敌减少及抗药性), 化学防治仍然是大部分地区防控害螨最优先考虑的措施。田间柑桔全爪螨杀螨剂抗性在中国、日本、新西兰、土耳其和美国等世界各地被报道 (Gotoh *et al.*, 2004; Hu *et al.*, 2010; Döker and Kazak, 2012; Ouyang *et al.*, 2012; Pan *et al.*, 2020)。多种类型杀螨剂杀螨效率低下, 柑桔全爪螨抗性问题的突出, 使其已成为桔园最普遍的害螨 (Döker and Kazak, 2012)。为确保抗性治理的有效进行, 柑桔全爪螨田间种群的抗性监测是尤为关键的环节。

近年来, Hu 等 (2010) 测定了平河、福州、建阳、临海、重庆和宜都 6 个地区的柑桔全爪螨对 6 种杀螨剂 (螺螨酯、螺虫乙酯、阿维菌素、甲氰菊酯、噻螨酮和哒螨灵) 的敏感性, 发现相较于敏感品系, 平河和福州种群对螺螨酯已产生中等水平抗性 (50.0 和 90.8 倍)。此外, 各地区对几种杀螨剂 (阿维菌素、甲氰菊酯、噻螨酮和哒螨灵) 均产生一定程度抗性, 抗性倍数分别在 1.8-153、5-146.2、2.5-60.6 和 48.2-601.5 倍, 其中对哒螨灵抗性最为严重 (Hu *et al.*, 2010)。丁天波等 (2012) 对重庆北碚、璧山、武隆和忠县的柑桔全爪螨种群开展了阿维菌素、哒螨灵、三唑锡和螺螨酯的毒力测定, 其中三唑锡的毒杀效果最差, 对应 LC_{50} 值在 209.9-370.9 mg/L 之间, 而其余药剂在 4 个监测地区仍保持较好的毒杀效果。韩巧丽等 (2017) 对桂林地区柑桔全爪螨的抗药性进行了评估, 柑桔全爪螨对乙螨唑、四螨嗪、阿维菌素和克螨特等均有较好的敏感性。Pan 等 (2020) 在 2015-2018 年间对中国南方主

要柑桔产区的柑桔全爪螨进行系统性长年的抗性监测, 发现南宁和桂林种群对甲氰菊酯、阿维菌素、丁氟螨酯和联苯肼酯均产生较高水平抗性; 相对于敏感品系, 对甲氰菊酯、阿维菌素和丁氟螨酯的抗性倍数超过 1 000 倍。抗性监测结果反映出柑桔全爪螨抗药性呈现明显的地区差异, 广西地区的种群对杀螨剂的抗性水平普遍高于四川和重庆地区, 但四川和重庆地区柑桔全爪螨田间种群对部分杀螨剂 (联苯肼酯和丁氟螨酯) 的抗性也在逐年增加。

国外柑桔全爪螨抗药性问题同样严峻, 在土耳其库罗瓦地区柑桔全爪螨的暴发及杀螨剂的低效问题引起专家的关注, 对该地区的 10 个柑桔全爪螨田间种群进行抗性监测, 测定发现相对于室内敏感品系, 对阿维菌素、螺螨酯、乙螨唑、螺虫乙酯和哒螨灵的抗性倍数分别为 2.81-34.82、1.23-43.28、1.22-18.35、1.76-27.50 和 2.24-75.06 倍 (Döker *et al.*, 2021)。除此之外, 其余地区未有柑桔全爪螨抗药性的报道。

2.2 杀螨剂对柑桔全爪螨生物特性的影响

田间杀虫 (螨) 剂施用后, 经自然降解、害虫 (螨) 体壁阻隔、体内解毒代谢酶的解毒代谢及人为因素影响后, 仅是亚致死剂量或浓度的药剂能作用于靶标。在亚致死剂量或浓度影响下, 不会直接杀死害虫 (螨), 但可能会影响其生理过程 (生长发育和生殖过程等) 和行为反应 (行动和取食行为等) (Rehan and Freed, 2015)。个体毒理学 (Demographical toxicology) 可用于评估药剂对害虫 (螨) 的亚致死效应, 并对靶标生物长期的影响进行评估 (Stark and Banks, 2003)。最早在 1984 年, Jones 和 Parrella 就对马拉硫磷和氯菊酯对柑桔全爪螨的亚致死效应进行研究, 亚致死浓度的马拉硫磷和氯菊酯能显著提高柑桔全爪螨的生殖力。He 等 (2011) 通过构建生命表观察阿维菌素 LC_{20} 处理柑桔全爪螨后, F_0 、 F_1 和 F_2 代雌成螨的产卵量被显著抑制, 且幼螨期的发育时间显著缩短。另外, 拟除虫菊酯类 (溴氰菊酯、高氰戊菊酯和氯氟氰菊酯) 和新烟碱类 (吡虫啉和噻虫嗪) 药剂施用能够增强柑桔全爪

螨的繁殖力并导致其暴发(Zanardi *et al.*, 2018), 该研究结果与 Gerson 和 Cohen (1989) 的发现一致。联苯肼酯作为一种新型杀螨剂, 作用于叶螨各发育阶段, 近年来在我国被广泛应用。该药剂亚致死剂量对柑桔全爪螨的生物学特性和行为的影响也有报道, 研究发现联苯肼酯导致柑桔全爪螨的产卵力降低及缩短了平均世代周期(T) (Wang *et al.*, 2021)。类似的结果在喹螨醚和灭螨醌(LC_{20} 和 LC_{30}) 处理后的柑桔全爪螨中被发现[繁殖力和净生殖率(R_0)降低](Raoufi *et al.*, 2022)。另外, Khan 等 (2021) 用甲氨基阿维菌素苯甲酸盐 LC_{10} 和 LC_{30} 处理柑桔全爪螨后发现, 其幼螨、前若螨和后若螨的发育历期延长, 且繁殖力降低。综上所述, 不同类型的杀螨剂的亚致死浓度对于柑桔全爪螨生物学特性的影响各异。由此可见, 亚致死浓度对于害虫(螨)生物学影响的研究在田间害虫(螨)防控中至关重要。

2.3 柑桔全爪螨对杀螨剂抗性产生的分子机制

2.3.1 代谢抗性 害虫(螨)抗性形成的分子机制, 主要分为代谢抗性和靶标抗性。代谢抗性的产生通常与体内解毒代谢酶活性的升高相关(细胞色素 P450 单加氧酶系、谷胱甘肽 S-转移酶和羧酸酯酶)。P450s 是一类催化亲脂化化合物的重要代谢酶, 参与大量内源性和外源性化学物质的代谢, 如: 激素、信息素、农药和植物次生代谢物质(Feyereisen, 1999)。P450 基因的上调或下调可显著影响生物体组织中内源性或外源性物质的配置, 从而影响药理/毒理学反应(Liu *et al.*, 2011)。节肢动物体内 P450 活性升高或 P450 基因的组成型过表达, 与其杀虫剂抗性发展密不可分(Cariño *et al.*, 1994; Feyereisen, 2005; Zhu *et al.*, 2008a)。比较分析柑桔全爪螨抗性和敏感品系差异表达的解毒代谢酶基因, 共鉴定获得 46 个 P450 基因(Liu *et al.*, 2011; Jiang *et al.*, 2015)。在噻螨酮抗性品系中发现 CYP307A1 (Y278E) 和 CYP381A2 (T28S) 氨基酸的突变, 可能与噻螨酮抗性相关(Jiang *et al.*, 2015)。以往研究表明, CYP4 家族基因是昆虫中一个重要

的 P450 家族, 该家族基因成员能被外源物质诱导并在抗性品系中过量表达, 参与杀虫剂的解毒过程(Shen *et al.*, 2003; Zhu *et al.*, 2008a)。通过哒螨灵等 4 种杀螨剂的亚致死剂量诱导后, CYP4CF2 和 CYP4CL1 两基因能被显著诱导上调, 可能参与柑桔全爪螨对哒螨灵等杀螨剂的解毒代谢过程(Ding *et al.*, 2013)。另外, Yu 等 (2020) 通过柑桔全爪螨双甲脒抗性和敏感品系间差异基因的鉴定和筛选, 初步明确了 P450s、ABCs 和乙酰胆碱酯酶可能在双甲脒抗性形成过程中起一定作用。相对于昆虫及其他叶螨(二斑叶螨 *Tetranychus urticae* Koch), 柑桔全爪螨 P450 基因的鉴定和功能研究相对较少且滞后, 尚需进一步研究和补充。

谷胱甘肽 S-转移酶 (GSTs) 广泛分布于植物、哺乳动物、昆虫、螨虫和微生物中, 属于一大类解毒酶, 在内源性和外源性解毒代谢过程中起重要作用。同时, GSTs 也参与胞内运输、激素的生物合成和抗氧化应激的保护(Enayati *et al.*, 2005)。在昆虫(螨)体内 GST 活性的上升, 往往与杀虫(螨)剂的抗性相关。在二斑叶螨中, 酶活测定表明, 阿维菌素抗性品系中 GSTs 酶活性显著高于敏感品系(Riga *et al.*, 2014)。而 Liao 等 (2016) 在柑桔全爪螨阿维菌素抗性品系中鉴定获得 PcGSTm5 特异性上调, 并通过体外代谢体系的建立明确了 PcGSTm5 可直接代谢阿维菌素进而参与柑桔全爪螨对阿维菌素的抗性形成。此外, 甲氰菊酯 LC_{10} 处理柑桔全爪螨后, 鉴定到 6 个 GST 基因(PcGSTm1、PcGSTm3、PcGSTm4、PcGSTd1、PcGSTd2 和 PcGSTz1) 显著上调, 它们可能参与柑桔全爪螨对甲氰菊酯的解毒过程(Liao *et al.*, 2013)。进一步比较柑桔全爪螨甲氰菊酯抗性和敏感品系差异表达的 GST 基因, PcGSTd1 在抗性品系中显著上调, 体外抑制和代谢试验显示 PcGSTd1 不能直接代谢甲氰菊酯, 但通过反向遗传学验证了 PcGSTd1 的抗氧化作用减缓了甲氰菊酯引起的氧化应激反应(Liao *et al.*, 2018)。因此, 进一步研究 GSTs 的解毒或抗氧化功能对于阐明 GSTs 杀螨剂抗性过程必不可少。

羧酸酯酶 (CarEs) 属于一个多功能酶的超家族, 广泛存在于包括动物、植物和微生物在内的大多数生物体中。主要涉及昆虫的杀虫剂抗性或激素和半化学代谢 (Ranson *et al.*, 2002; Yu *et al.*, 2009)。作为昆虫重要的解毒代谢系统之一, 有研究表明, 主要通过基因扩增、mRNA 稳定性提高和点突变的形式参与杀虫 (螨) 剂的抗性 (Ranson *et al.*, 2002; Wu *et al.*, 2010)。目前仅在二斑叶螨 (Van Leeuwen *et al.*, 2006; Wei *et al.*, 2019) 和朱砂叶螨 *T. cinnabarinus* (Sun *et al.*, 2010; Feng *et al.*, 2011b; Shi *et al.*, 2016; Wei *et al.*, 2018, 2019) 中有较深入研究。而在柑桔全爪螨中, 相对研究较少。Zhang 等 (2013) 鉴定并克隆出两个柑桔全爪螨 CarEs 基因 (*PcE1* 和 *PcE2*), 且两基因能显著响应阿维菌素胁迫。在随后的研究中发现, *PcE1*、*PcE7* 和 *PcE9* 在甲氰菊酯处理后均显著上调, 并在不同抗性种群中过表达。利用异源表达和体外代谢的技术手段证明 *PcE1*、*PcE7* 和 *PcE9* 均能通过直接代谢甲氰菊酯进而参与柑桔全爪螨对甲氰菊酯的抗性形成 (Shen *et al.*, 2016)。柑桔全爪螨 CarEs 基因表达谱和蛋白功能的研究对于揭示柑桔全爪螨对杀螨剂的抗性产生及解毒过程有重要意义, 但柑桔全爪螨 CarEs 的研究略显不足, 需进一步研究。

2.3.2 靶标抗性 靶标抗性及药剂作用靶标结构变构, 导致药剂不能与靶标有效结合, 影响与杀虫 (螨) 剂的相互作用。近年来, 针对叶螨类靶标抗性的研究逐渐增多, 如: 乙酰胆碱酯酶 (Kwon *et al.*, 2010a; Döker and Kazak, 2012)、钠离子通道 (Kwon *et al.*, 2010b; Feng *et al.*, 2011a; Nyoni *et al.*, 2011; Ding *et al.*, 2015)、氯离子通道 (Kwon *et al.*, 2010c; Dermauw *et al.*, 2012)、细胞色素 b (Van Nieuwenhuyse *et al.*, 2009; Van Leeuwen *et al.*, 2011)、几丁质合成酶 (Van Leeuwen *et al.*, 2012; Tadatsu *et al.*, 2022) 和线粒体复合体 I (Bajda *et al.*, 2017; Alavijeh *et al.*, 2020) 等。其中, Van Leeuwen 等 (2011) 报道了柑桔全爪螨细胞色素 b 中 G126S 和 A133T 突变介导了对联苯腈酯的抗性。拟除虫菊酯类杀螨剂作用的钠离子通道 F1538I 突变在柑

桔全爪螨万州种群被发现 (Ding *et al.*, 2015)。随着技术的革新, Alavijeh 等 (2020) 通过单头提取及 CRISPR/Cas9 技术, 发现并验证了 H92R 和 A94V 突变介导 METI-I 类杀螨剂的抗性。另外, 在日本有学者发现几丁质合成酶 1 (*CHS1*) 中 I1017F 突变是柑桔全爪螨对乙螨唑抗性发展的主要因素 (Tadatsu *et al.*, 2022)。上述研究表明, 靶标相关位点的替换能够给予柑桔全爪螨对杀螨剂不同程度的抗性, 相对于田间柑桔全爪螨抗药性的严重性, 柑桔全爪螨靶标抗性的研究相对滞后。

3 捕食螨防控柑桔全爪螨的应用

生物防治作为害虫 (螨) 综合防治体系中的重要环节, 其利用非作物植物物种和天敌进行生境管理及通过增加农业生态系统中天敌的数量进行有效的害虫 (螨) 控制。生物防治策略在防控柑桔全爪螨方面也备受关注。在中国, 桔园害虫 (螨) 生物防治历史悠久, 发展迅速, 田间应用物种包括 100 多种天敌, 它们属于 72 属 23 科 18 目, 以掠食性为主 (Niu *et al.*, 2014)。加州新小绥螨 *Neoseiulus californicus* 和胡瓜新小绥螨 *N. cucumeris* 作为常用叶螨防治天敌被广泛应用 (Mendel and Schausberger, 2011)。Qayyoun 等 (2021) 比较了加州新小绥螨、胡瓜新小绥螨和纽氏肩绥螨 *Scapulaseius newsami* 3 种捕食螨对柑桔全爪螨种群的控制能力, 结果表明, 胡瓜新小绥螨具有较高的相对控制潜力和最大繁殖潜力, 最适宜用来防控柑桔全爪螨种群。覃贵勇等 (2013) 研究了加州新小绥螨对柑桔全爪螨的控制潜力, 结果显示, 在益: 害比为 5: 30 条件下, 柑桔全爪螨种群能在 4 d 内被有效控制, 具有可观的控制潜力。巴氏新小绥螨 *N. barkeri*, 曾用名巴氏钝绥螨, 是我国生产量及应用范围最大的捕食螨品种。首先, 凌鹏等 (2008) 研究了巴氏新小绥螨对柑桔全爪螨的捕食效能, 表明巴氏新小绥螨对各螨态的柑桔全爪螨的捕食具有选择性, 尤其偏好幼若螨。巴氏新小绥螨在重庆市北碚区和四川省资阳市 (魏洁贤等, 2013), 重庆市万州区 (裴强等, 2014) 及重庆市涪陵区 (王

莉等, 2021) 等地被释放, 有效地控制了柑桔全爪螨种群, 持效期长达 120 d。胡瓜新小绥螨, 在我国东部福州地区和北部陕西地区被应用于防治柑桔全爪螨, 效果显著, 被广泛应用于防控叶螨并实现工厂化生产(张艳璇等, 2003; 李汉一等, 2011; 张光华和邱栋梁, 2013)。通过捕食螨的释放, 有效的实现“以螨治螨”的防控策略, 对环境友好, 有利于维护桔园生态多样性, 前景可观。

4 展望

柑桔全爪螨因其独特的生物学特性, 各种抗药性的形成, 已然成为桔园重要害螨之一。田间抗药性的快速发展, 传统的抗性监测已不能实时快速的反映田间抗性动态。通过挖掘抗性相关基因位点突变(解毒代谢酶基因或靶标基因), 进而开发抗性和敏感基因分子诊断技术, 为高效精准的掌握柑桔产区柑桔全爪螨抗性发展动态和杀螨剂的施用提供技术支撑和指导意见。同时, 利用基因组学、转录组学和蛋白质组学等多组学技术手段, 更加明确柑桔全爪螨变态发育过程中的关键调控因子, 为杀虫(螨)剂的创制提供潜在靶标。针对抗药性产生过程(解毒代谢、药剂转运及靶标结合亲和力降低), 利用差异组学分析, 明确抗性形成关键因子和分子机制, 为田间抗性治理提供理论依据。随着时代的发展, 对害虫综合治理策略也面临革新, 基于田间生物物种间的捕食关系, 将生物防治技术合理的融入到害虫综合治理中, 提高生物防治效果和经济重要性, 统筹协调, 实现杀虫(螨)剂减药减量和维护田间农业生态系统。最终, 从“基础研究”到“田间应用”, 系统有序地实现害螨综合治理。

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