烟粉虱成灾机制与绿色精准防控研究进展

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摘要：烟粉虱*Bemisia tabaci*是全球性重大刺吸式害虫，可通过取食植物造成直接危害，亦可传播多种植物病毒间接影响植物正常生长。在中国，该虫成灾风险主要受隐种替代、寄主适应性、媒介传毒、抗药性演化和栽培环境共同影响。近年来，烟粉虱地中海隐种在多个调查地区优势化，且以烟粉虱为唯一已知传播媒介的番茄黄化曲叶病毒扩散态势加剧。同时，烟粉虱地中海隐种田间种群对多类药剂的敏感性下降，削弱了单纯依赖化学药剂压低虫口策略的稳定性。该文围绕烟粉虱重要隐种在中国的发生发展历程，系统综述其危害性、隐种替代、寄主适应性、与病毒互作、抗药性机制及绿色防控技术，旨在为烟粉虱的绿色防控提供参考。

关键词：烟粉虱；成灾机制；地中海隐种；抗药性；绿色精准防控；综合治理

Research progress on outbreak mechanisms and green precision control of tobacco whitefly *Bemisia tabaci*

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Abstract: Tobacco whitefly *Bemisia tabaci* is a globally significant piercing-sucking pest that causes direct damage to plants by feeding and also indirectly affects normal plant growth by transmitting various plant viruses. In China, the outbreak risk of this pest is primarily influenced by cryptic species replacement, host adaptation, virus transmission, insecticide resistance evolution, and cultivation environments. In recent years, the Mediterranean cryptic species (MED) has become dominant in multiple surveyed regions, and the spread of tomato yellow leaf curl virus, which is transmitted by *B. tabaci*, has intensified. Meanwhile, field populations of MED have shown reduced sensitivity to multiple classes of insecticides, weakening the stability of control strategies that rely solely on chemical pesticides to suppress pest populations. This article systematically reviews the occurrence and development of important *B. tabaci* cryptic species in China, focusing on their damage, cryptic species replacement, host adaptation, interactions with viruses, insecticide resistance mechanisms, and green control technologies, aiming to provide a scientific basis for the sustainable management of *B. tabaci.*

Key words: *Bemisia tabaci*; outbreak mechanism; Mediterranean cryptic species; insecticide resistance; green precision control; integrated management

烟粉虱*Bemisia tabaci*隶属半翅目粉虱科，是全球性重大农业害虫。烟粉虱成虫和若虫通过刺吸植物韧皮部汁液直接造成植株产量下降，其排泄的蜜露可诱发煤污病，另外烟粉虱还可传播多种植物病毒，因此其在较低种群密度的情况下仍可造成重大经济损失（Navas-Castillo et al.，2011；王雨蒙等，

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2020)。烟粉虱是由多个形态相近、但生态适合度和传播能力存在显著差异的隐种组成的复合体,其隐种命名和识别标准也经历了持续修订(Dinsdale et al.,2010;De Barro et al.,2011;Boykin,2014)。在众多隐种中,中东–小亚细亚1(Middle East-Asia Minor 1,MEAM1)隐种(也称B生物型)和地中海(Mediterranean,MED)隐种(也称Q生物型)是我国入侵性最强、对农业生产影响最严重的两个隐种。目前,我国烟粉虱的发生发展阶段大致分为本土隐种发生、MEAM1隐种入侵暴发和MED隐种扩散替代等阶段。在上述过程中,设施农业全年生产、带虫种苗调运、长期高频用药等多重因素共同驱动了烟粉虱隐种格局的动态变化(Chu et al.,2006;褚栋等,2012;Guo et al.,2021)。部分蔬菜作物在苗期对病毒侵染极为敏感,即便有少量带毒烟粉虱成虫迁入,也会显著增加作物后期病害暴发风险;同时,MED隐种较强的抗药性演化能力导致化学防治的效果大幅下降(Li et al.,2022;Wang et al.,2023)。因此,在降低化学药剂依赖和生态风险的前提下,科学集成应用适配性强的物理、生物、生态和低风险化学防治措施,开展烟粉虱绿色精准防控工作迫在眉睫。本文从烟粉虱发生发展、隐种替代、寄主适应性、与病毒互作、抗药性机制及绿色防控技术等方面进行阐述,系统综述我国烟粉虱的研究进展与绿色可持续治理方法,以期为烟粉虱后续基础研究深化与田间绿色防控技术落地应用提供理论参考与实践依据。

1 我国烟粉虱的发生发展过程

我国烟粉虱的发生发展大致可概括为3个阶段。第一阶段是隐种识别与入侵种群建立。早期研究通过线粒体细胞色素氧化酶I(mitochondrial cytochrome oxidase I,mtCOI)基因序列建立了我国烟粉虱生物型或隐种鉴定基础(罗晨等,2002)。其中MED隐种最初在河南、北京等省市被报道,并随观赏植物和多作物系统在全国范围内扩散(Chu et al.,2006;Pan et al.,2011)。第二阶段是MED隐种优势化。2003—2014年烟粉虱的动态监测表明,MED隐种在田间种群中的比例显著上升;到2018年前后,MED隐种已成为我国大部分地区田间的优势隐种(Zheng et al.,2017;Wang et al.,2023;Ji et al.,2024)。第三阶段是因粉虱传播的植物病毒病流行风险增加。目前,由烟粉虱作为唯一传播媒介的番茄黄化曲叶病毒(tomato yellow leaf curl virus,TYLCV)扩散态势加剧。TYLCV于2006年在上海市田间番茄*Solanum lycopersicum*中被检出,相关报道显示田间病株率高达90%(王冬生等,2006);截至2021年底,Li et al.(2022)梳理了当时可获得的公开资料和序列信息,明确了我国已报道99种双生病毒的1 600余个分离物,其中TYLCV全长序列分离物415个,分布于多数省份,其中云南、山东、河南、北京和河北等省市分离或报道的TYLCV分离物数量较多,证实了设施番茄和露地番茄种植区是烟粉虱及其传播病毒风险管理的重要区域。因此,持续开展烟粉虱田间隐种动态监测与传播病毒的协同预警,是保障烟粉虱寄主作物安全的关键措施。

2 烟粉虱隐种替代与寄主适应性

隐种替代不应简单理解为某一隐种在所有生态条件下均具备绝对的适合度优势,而应将其视为寄主作物结构、温度背景、设施栽培条件、种群迁飞输入和化学药剂选择压力等多因素共同作用下的动态结果。烟粉虱MEAM1和MED隐种在取食效率、发育历期、产卵量、低温或高温耐受性、病毒传播能力和药剂敏感性上均表现出明显差异,使得不同隐种在不同寄主作物、季节和田间用药制度下的竞争中可能出现差异(Wang et al.,2023)。近期基于线粒体与微卫星标记的群体研究进一步证实,烟粉虱MED与MEAM1隐种在我国的遗传多样性和种群结构存在差异,其入侵来源、遗传变异储备以及局部扩张过程均会影响隐种的替代进程(Xue et al.,2024)。

烟粉虱的寄主适应性首先体现在成虫产卵和若虫生长发育两个环节。寄主植物叶片茸毛、表皮蜡质、叶色、叶片厚度和叶背微环境等均可影响成虫着陆、刺探取食和产卵位置;萜类、酚类、黄酮类、生物碱、芥子油苷、酰基糖和蛋白酶抑制剂等化学防御物质则可通过趋避、拒食、降低蜜露排泄、抑制产卵或延缓若虫发育等多种途径显著降低烟粉虱适合度(Bleeker et al.,2011;Marchant et al.,2020;Li et al.,2023)。上述研究结果提示寄主抗性不能仅通过单一指标进行评价,需要把成虫寄主选择性、若虫存活率、群体增长率和传毒效率等关键指标纳入其中进行综合评估。

近年来,随着分子生物学技术的快速发展,烟粉虱寄主适应性的研究已从表型差异分析深入到效应因子、解毒代谢网络和水平基因转移等分子机制层面。烟粉虱在与寄主互作相关基因家族上存在较强可塑性,这为解析烟粉虱寄主适应性的分子基础提供了重要前提(Chen et al.,2016;Campbell et al.,

2023）。研究发现，唾液效应因子BtE3可影响烟粉虱在寄主植物上的取食表现，保守小RNA效应因子则能通过跨界沉默效应来抑制植物的免疫防御反应，这些发现均揭示了烟粉虱并非被动适应寄主，而是在取食过程中主动重塑植物防御状态（Peng et al.，2023；Han et al.，2025）。同时，烟粉虱丙二酰基转移酶1（malonyltransferase 1，MaT1）基因*BtPMaT1*能有效中和部分植物酚苷类防御物质，而来源于植物的碳水化合物活性酶则可能参与植物细胞壁的降解或糖类营养物质的利用（Xia et al.，2021；Gilbert & Maumus，2022；Colinet et al.，2025）。综上所述，烟粉虱的隐种替代、寄主适应及抗药性演化三者并非相互独立，植物次生代谢物长期选择所塑造的广谱解毒能力，可能为烟粉虱抗药性的演化提供了重要基础。

3 媒介传毒与病毒–媒介互作

烟粉虱传播病毒本质上是病毒连续突破媒介昆虫生理屏障的过程。以双生病毒为例，病毒颗粒随韧皮部汁液被烟粉虱取食后进入消化道，穿过中肠上皮进入血淋巴，再被识别后进入初级唾液腺，最终随唾液排出并侵染新的寄主植物（Ghosh & Ghanim，2021）。烟粉虱植物病毒受体蛋白Cubilin（BtCUBN）和Amnionless（BtAMN）可形成受体复合体，介导双生病毒侵入中肠细胞（Zhao et al.，2020）；在唾液腺阶段，网格蛋白介导的内吞作用和早期内体运输对双生病毒穿越初级唾液腺屏障具有关键作用（Guo et al.，2023）。TYLCV还能在烟粉虱唾液腺中利用宿主DNA合成系统进行复制，这使得对媒介传毒过程的理解从传统的病毒被动循回运输扩展为更复杂的媒介组织嗜性、细胞转运和病毒复制的互作体系（He et al.，2020）。

在烟粉虱传毒研究中，需要特别区分TYLCV与番茄褪绿病毒（tomato chlorosis virus，ToCV）的传播生态学特征。前者为双生病毒科菜豆金色花叶病毒属*Begomovirus*成员，主要由烟粉虱以持久循回方式传播；后者为长线形病毒科毛形病毒属*Crinivirus*成员，可由烟粉虱属*Bemisia*和温室白粉虱属*Trialeurodes*的粉虱以半持久方式传播（Fiallo-Olivé & Navas-Castillo，2019；Fortes et al.，2020）。二者常在番茄产区共同发生，但病毒类别、媒介体内保留时间、侵染的关键媒介组织和阻断窗口期并不相同。另外，TYLCV与ToCV复合侵染可提高烟粉虱MED隐种体内组织蛋白酶cathepsin B的表达，进而促进ToCV传播，这表明混合侵染并非两个病害风险的简单叠加，可能通过改变媒介生理状态和取食行为放大病毒病的流行风险（代惠洁等，2017；Lu et al.，2023）。因此，制订田间诊断标准和防控策略需要关注病毒种类、带毒率、混合侵染比例和媒介隐种组成。

植物病毒还会反向调节寄主植物和媒介昆虫行为，进而促进自身传播扩散。感染植株的叶色、挥发物、营养状态和防御反应改变后，可能更易吸引非带毒烟粉虱取食；当感染植株质量下降后，带毒成虫可能转移至健康植株，从而提高传播效率（Navas-Castillo et al.，2011；Li et al.，2022）。不同隐种或本土种在TYLCV经卵传播能力上存在差异，提示隐种组成可能影响病毒越冬、初侵染来源和区域病毒病的流行规律（Guo et al.，2019）。烟粉虱共生菌系统同样参与病毒–媒介互作：初级共生菌*Portiera*提供必需营养，而汉密尔顿菌*Hamiltonella*、立克次体*Rickettsia*和沃尔巴克氏体*Wolbachia*等次级共生菌可能通过调控伴侣蛋白表达、免疫调节或营养代谢途径，影响病毒稳定性和传播效率，但其作用方向往往取决于特定病毒株系、烟粉虱隐种和环境条件（Andreason et al.，2020；李娜娜等，2024）。此外，沉默*TOB1*（*transducer of erbB2.1*）基因和Toll样受体（Toll-like receptor，TLR）基因*TLR3*会降低烟粉虱的适合度并抑制双生病毒的传播，这揭示了媒介昆虫的免疫和细胞内转运通路也是潜在防治靶点（Thesnim et al.，2023）。

4 烟粉虱的抗药性演化

烟粉虱抗药性演化是其在药剂强选择压力下由遗传变异、诱导表达、适合度代价和种群迁移共同驱动的进化过程。抗药性机制包括代谢抗性、靶标抗性、穿透抗性和行为抗性。目前，已获得了烟粉虱参考基因组、比较基因组和转录组数据，这为抗性基因的筛选提供了基础（Chen et al.，2016；Horowitz et al.，2020；Campbell et al.，2023）。细胞色素P450单加氧酶（简称为P450）、谷胱甘肽*S*-转移酶、羧酸酯酶和ABC转运蛋白可通过氧化代谢、共价结合、水解或外排作用降低昆虫体内的有效药量，其中关于P450在烟粉虱抗药性中的作用研究较系统（Yang et al.，2020）。烟粉虱*CYP6CM1*是介导对新烟碱类药剂抗性的代表基因，其过表达和点突变均可影响对吡虫啉等药剂的代谢（Karunker et al.，2008；Pym et al.，2023）。烟粉虱*CYP6DPx*可同时参与对尼古丁和新烟碱类药剂的抗性形成，揭示植物源毒素适应与人工药剂抗性之间可能存在功能桥接（Pym et

al.,2024)。

我国烟粉虱田间种群已对氨基甲酸酯类、拟除虫菊酯类、新烟碱类和部分新型药剂表现出不同程度的抗性,全国年度监测结果显示烟粉虱抗药性水平具有普遍的地区差异和药剂类别差异(Zheng et al.,2021)。北京、山东、湖南等省市的烟粉虱抗药性监测结果及相关分子机制研究证实田间化学药剂使用史会影响其抗性倍数和分子机制(杨鑫等,2014)。烟粉虱抗药性演化还表现为不同药剂之间的交叉抗性和新型药剂抗性风险。在我国烟粉虱田间种群中,*CYP4v2*、*CYP6CX1*等P450基因被证实与其抗药性相关(Yang et al.,2013;杨鑫等,2014);丝裂原活化蛋白激酶–环磷腺苷效应元件结合蛋白(mitogen-activated protein kinase-cAMP-responsive element-binding protein,MAPK-CREB)调控通路可通过激活P450基因表达参与其对吡虫啉的抗性形成(Yang et al.,2020);*CYP6CX4*过表达与其对丁烯内酯类药剂氟吡呋喃酮的抗性形成相关,提示即使作用机制较新的药剂,在高频使用背景下也可能迅速进入代谢抗性通道(Zhang et al.,2024)。谷胱甘肽*S*-转移酶、羧酸酯酶和ABC转运蛋白的表达变化也可提供候选抗药性分子线索,但其功能解析需要结合协同剂、生物测定、诊断剂量、异源表达或遗传连锁等证据协同验证,最终为烟粉虱的田间抗药性治理提供理论基础。

害虫抗药性治理的核心是降低药剂选择强度并延缓抗药性等位基因在区域种群中的扩散。烟粉虱的田间抗药性水平具有明显的地区差异和年度波动,说明单一地区经验不能替代本地种群的敏感性监测(Zheng et al.,2021)。在实际应用中,应把隐种鉴定、成虫与若虫生物测定、用药种类、用药次数控制和非化学措施共同纳入决策,特别是在病毒病危害风险较高的苗期,需要快速压低带毒成虫基数,但连续使用同一作用机制药剂会强化烟粉虱的抗药性选择,因此应联合应用种苗检疫、防虫网、清除病株、保护天敌和低风险药剂精准干预等措施进行防控。

5 烟粉虱的绿色防控技术

绿色防控并非是以单一产品替代化学药剂,需根据害虫发生阶段和技术成熟度进行协同防控。基于烟粉虱现有防控措施,采取健康种苗、防虫网、残株处理和杂草寄主管理属这些成熟度较高的防控措施,可有效降低带虫带毒种苗和周边虫源输入风险;黄板诱集适合监测成虫迁入动态并辅助降低成虫数量,但不能替代叶背卵和若虫的系统调查,也不能单独作为病毒病高风险区的防控依据。生物防治是绿色防治的重要一环,其中天敌如寄生蜂(赵悦等,2024),以及虫生真菌如白僵菌*Beauveria* spp.、绿僵菌*Metarhizium* spp.和蜡蚧轮枝菌*Lecanicillium* spp.等,目前均已用于烟粉虱生物防治,具有作用机制多样和抗性风险较低等优点(Mascarin et al.,2013;Sani et al.,2020)。但其田间防效受温湿度、紫外线、菌株毒力、制剂稳定性和喷雾覆盖度的影响较大,不同作物和设施条件下的防效不宜直接横向比较,更适合作为低虫量或中低虫量阶段的预防性措施。

植物源药剂和内生菌资源可作为综合治理中的辅助措施,纳米递送可提高这类药剂活性成分或dsRNA在叶面的附着、缓释和抗降解能力,RNA干扰(RNA interference,RNAi)则适合靶标功能验证和未来精准干预储备(Jain et al.,2021;2022)。然而,在田间应用前需要解决dsRNA降解、递送效率、沉默持续期、非靶标风险、成本和登记监管等问题。

6 结论与展望

综上所述,烟粉虱成灾风险通常受隐种替代、寄主适应、媒介传毒、共生菌互作和药剂选择压力等多因素共同影响,并在具体作物和栽培场景中表现出差异。在我国,烟粉虱MED隐种优势化、TYLCV等病毒快速传播扩散和烟粉虱区域抗药性积累共同加剧了设施蔬菜和重要经济作物上烟粉虱的治理难度。今后应在3个层面推进烟粉虱防控研究与应用:一是构建覆盖育苗、移栽和采收期的区域连续监测网络,统一隐种鉴定、带毒率检测、病株率调查和抗药性检测的标准与方法;二是系统开展绿色技术的场景化组合评价,形成不同作物、不同隐种和不同病毒病风险等级下的技术清单;三是推进RNAi、纳米递送和共生菌调控等前沿技术的安全性、成本和监管可行性评估。通过将基础机制、本土监测和田间可操作技术结合,推动烟粉虱治理从传统经验性压制转向可复制、可评价、可推广的绿色精准防控。

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