

鄱阳湖地区扶桑绵粉蚧发生及其寄生性天敌鉴定

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摘要: 扶桑绵粉蚧 *Phenacoccus solenopsis* (半翅目: 粉蚧科) 是重要的入侵性害虫, 对棉花危害严重。为明确扶桑绵粉蚧在鄱阳湖地区发生危害情况, 掌握其寄生性天敌的种类、寄生特点及生态控害功能, 对鄱阳湖周边地区扶桑绵粉蚧及寄生天敌概况进行随机抽样调查, 采用形态学结合 *mtCO I* 基因序列分析对寄生蜂鉴定分析。结果显示: 该地区扶桑绵粉蚧发生较为普遍, 寄主植物种类较多, 共涉及 26 科 59 种, 棉花、胡麻等大田经济作物发生较重, 辣椒等部分蔬菜、马齿苋等部分杂草类也是该虫的偏好性寄主; 扶桑绵粉蚧寄生蜂共有 2 科 4 种, 分别为跳小蜂科的班氏跳小蜂 *Aenasius bambawalei*、南京刷盾跳小蜂 *Cheiloneurus nankingensis*、原长缘跳小蜂 *Prochiloneurus* sp. 和蚜小蜂科的豹纹花翅蚜小蜂 *Marietta picta*, 中班氏跳小蜂是初级寄生蜂的优势种, 其余 3 种均为重寄生蜂, 而南京刷盾跳小蜂为重寄生蜂的优势种。班氏跳小蜂与南京刷盾跳小蜂寄生的僵蚧所占比例分别为 47.91%、32.89%, 孵化出的寄生蜂数占全部寄生蜂总量的 13.26%、79.05%, 且南京刷盾跳小蜂始终伴随班氏跳小蜂的发生而发生, 对后者控害功能具有巨大的干扰作用。通过 Kimura2-Parameter (K_2P) 计算 4 种寄生蜂的 *mtCO I* 序列的遗传距离为 0.060 2~0.335 5, 平均遗传距离为 0.1026。基于鄱阳湖地区扶桑绵粉蚧发生的普遍性, 利用班氏跳小蜂的寄生功能, 是控制扶桑绵粉蚧种群数量的重要方法, 但降低南京刷盾跳小蜂的重寄生干扰, 是发挥班氏跳小蜂生态控害功能的关键。

关键词: 扶桑绵粉蚧; 生物防治; 班氏跳小蜂; 南京刷盾跳小蜂; DNA 条形码

Investigation of mealybug *Phenacoccus solenopsis* and identification to its parasitoids in Poyang Lake area

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Abstract: *Phenacoccus solenopsis* (Hemiptera: Pseudococcidae) is an important invasive pest, which seriously harms cotton. The study was conducted to confirm the occurrence, distribution of *P. solenopsis*, characteristics and control potential of parasitoids' species in Poyang Lake area. Random sampling investigations were conducted in the field, and the parasitoids of mealybug were identified by the analysis of morphological and mitochondrial cytochrome c oxidase 1 (*mtCO I*) gene sequence. The result showed that the occurrence of the mealybug was common in Poyang Lake area. It had many host plants including 59 species belonging to 26 families. The pest occurred seriously in cotton, flax and other cash crops in the field. Some vegetables such as pepper and some weeds such as purslane were also the preferred host plants for the mealybug. The occurrence of parasitoid wasps accompanied with the mealybug. The parasitoid wasps of *P. solenopsis* were categorized into 2 families and 4 species, *Aenasius bambawalei*, *Cheiloneurus nankingensis*, *Prochiloneurus* sp. and *Marietta picta* (Hymenoptera: Aphelinidae). Among these wasp species, *A. bambawalei* was the primary parasitoid and the dominant taxon, while the other three species were hyperparasitoids and the *C. nankingensis* was the most prevalent species. The proportion of the mummy for *A. bambawalei* and *C. nankingensis* was 47.91% and 32.89%, respectively. The number of

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hatched parasitoid respectively accounted for 13.26% and 79.05% of the total number of parasitic wasps. In addition, the occurrence of the two wasps was always accompanied with each other, which had a huge interference on pest control. Kimura2-Parameter (K_2P) calculated that the genetic distance of mtCO I sequence of four parasitoids was 0.060 2~0.335 5, and the total average genetic distance was 0.102 6. Based on the occurrence of mealybug in Poyang Lake area, making full use of the ecological control function of *A. bambawale* is an important method to prevent outbreak of *P. solenopsis*, but reducing the interference of hyperparasitoids *C. nankingensis* is the key to exert the ecological function of *A. bambawale*.

Keywords: *Phenacoccus solenopsis*; biological control; *Aenasius bambawalei*; *Cheiloneurus nankingensis*; DNA barcode