Acta Tropica 142 (2015) 89–95

Contents lists available at ScienceDirect

Acta Tropica

journal homepage: www.elsevier.com/locate/actatropica

Study of mosquito fauna in rice ecosystems around Hanoi, Northern Vietnam

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ARTICLE INFO

Article history:
Received 12 September 2014
Received in revised form 30 October 2014
Accepted 1 November 2014
Available online 7 November 2014

Keywords:
Agriculture
Culex vishnui subgroup
Integrated vector management
Mosquito control

ABSTRACT

Species of the *Culex vishnui* subgroup, *Cx. fuscocephala* and *Cx. gelidus*, which are known Japanese encephalitis (JE) vectors, are distributed in rice agroecosystems in Asian countries. Hence, although ecological studies of rice agroecosystems in northern Vietnam are necessary, very few integrated studies of breeding habitats of mosquitoes, including JE vectors, have been conducted. We carried out a field study and investigated the mosquito fauna in six rice production areas in northern Vietnam during the rainy and dry seasons of 2009. Mosquitoes and potential mosquito predators were collected from aquatic habitats by using larval dippers. We collected 1780 *Culex* individuals (including 254 *Cx. tritaeniorhynchus*; 113 *Cx. vishnui*, 58 *Cx. vishnui* complex, consisting of *Cx. vishnui* and *Cx. pseudovishnui*; 12 *Cx. gelidus*; 1 *Cx. bitaeniorhynchus*; and 1 *Cx. fuscocephala*), 148 *Anopheles* individuals (including 5 *An. vagus*), 1 *Mansonia annulifera*, and 1 *Mimomyia chamberlaini* during the rainy season. During the dry season, we collected 176 *Culex* individuals (including 33 *Cx. vishnui*, 24 *Cx. tritaeniorhynchus*, 8 *Cx. vishnui* complex, and 1 *Cx. gelidus*) and 186 *Anopheles* individuals (including 9 *An. tessellatus*, 2 *An. kochi*, and 2 *An. barbumbrosus*). We found mosquitoes in all aquatic habitats, namely, rice fields, ditches, ponds, wetlands, irrigation canals, and rice nurseries, and *Cx. tritaeniorhynchus* and *Cx. vishnui* complex were found in all the above six areas. Heteroptera such as *Micronecta*, Veliidae, and Pleidae were abundant and widely distributed in both the seasons. The abundance of mosquito larvae was higher in the rice fields, ditches, and ponds during the rainy season than during the dry season. *Cx. tritaeniorhynchus*, *Cx. vishnui* complex, *Cx. fuscocephala*, and *Cx. gelidus* were abundant in rice agroecosystems (rice fields, ditches, ponds, and wetlands) in northern Vietnam, and their abundance was high during the rainy season. These findings deepen our understanding of mosquito ecology and strengthen mosquito control strategies to be applied in rice ecosystems Vietnam in the future.

1. Introduction

Mosquito-borne diseases such as malaria and Japanese encephalitis (JE) are major public health threats in Asian countries. JE has spread throughout Asia and may have originated in the Indo-Malaysian region of Asia (Solomon et al., 2003). JE cases have been reported in India, Nepal, Sri Lanka, Bangladesh, Myanmar, Laos, Cambodia, Thailand, Vietnam, Malaysia, China, Philippines, Indonesia, Korea, Japan, Papua New Guinea, and most recently, in the southern parts of Australia. In Asian countries, *Culex tritaeniorhynchus* Giles, *Cx. vishnui* complex, *Cx. fuscocephala* Theobald, and *Cx. gelidus* Theobald are JE vectors (Van Peenten et al., 1975; Gingrich et al., 1992; Reuben et al., 1994; Vythilingam et al., 1997; Stoops et al., 2008; Van den Hurk et al., 2009). The *Cx. vishnui* subgroup species, viz., *Cx. tritaeniorhynchus*, *Cx. pseudovishnui*, and *Cx. vishnui*, are the vectors of JE in Southeast Asia (Van den Hurk et al., 2009), and they breed in a wide range of aquatic habitats (Stoops et al., 2008). The common breeding habitats of these vector mosquitoes are rice fields, furrow pits, puddles, cisterns, and permanent and transient ground pools. Of these, the most important breeding habitat is the rice field ecosystem (Mogi, 1978; Victor and Reuben, 1999), and their population abundance is closely related to rice agroecosystems (Lacey and Lacey, 1990; Takagi et al., 1995, 1997; Keiser et al., 2005).

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http://dx.doi.org/10.1016/j.actatropica.2014.11.002
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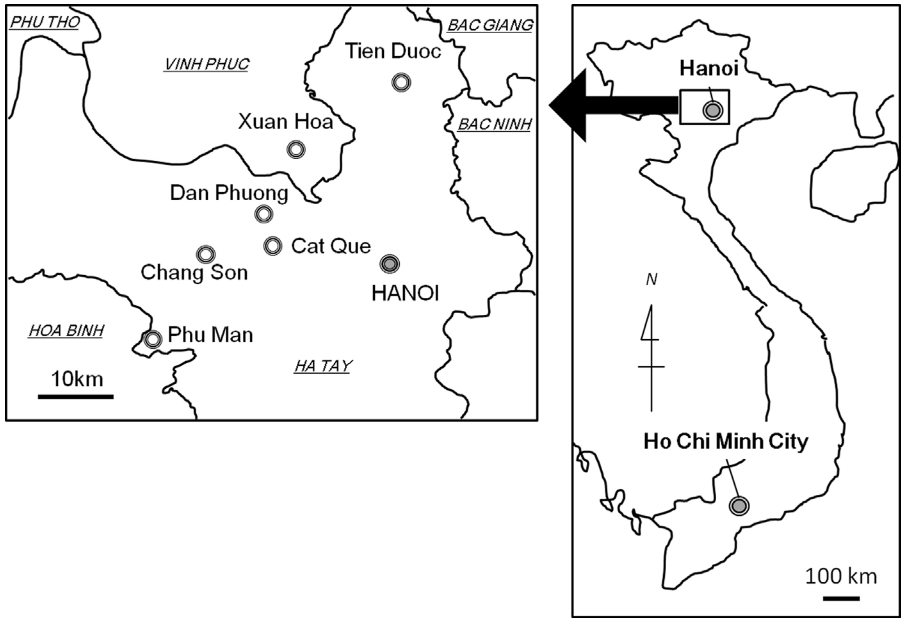

Fig. 1. Map showing the study sites (districts and towns) in southern Vietnam.

In Vietnam, JE has been recognized as an important public health problem since 1951 (Okuno, 1978; Nguyen and Nguyen, 1995). *Cx. tritaeniorhynchus*, *Cx. gelidus*, *Cx. vishnui* complex, and *Cx. quinquefasciatus* Say are the JE vectors distributed in this country (Nguyen et al., 1974; Ohba et al., 2011; Kuwata et al., 2013). A previous study (Hasegawa et al., 2008) showed that the proximity of hosts to breeding sites in a rice-cultivating village in northern Vietnam positively affected the abundance of *Cx. gelidus*, but not of *Cx. vishnui* complex. However, very few integrated studies of the breeding habitats of mosquitoes in rice agrosystems, including JE vectors, have been conducted in Vietnam.

Wetlands, including rice fields, have a wide variety of natural enemies of mosquitoes (Sunahara et al., 2002; Ohba and Nakasuji, 2006; Mogi, 2007). The impact of natural enemies on *Cx. tritaeniorhynchus* larvae was determined in several ecological studies in rice agroecosystems (Mogi and Miyagi, 1990; Mogi, 1993; Takagi et al., 1996). Fish, aquatic insects, and spiders are predators of *Cx. tritaeniorhynchus* (Watanabe et al., 1968; Mogi, 2007), and these predators are expected to contribute to the integrated vector control management.

In the present study, we conducted an ecological study on mosquito fauna and its potential predators associated with rice agrosystems in six rice production areas around Hanoi in northern Vietnam, during the rainy and dry season of 2009.

2. Materials and methods

2.1. Study site

We conducted this study from June 29 to July 1, 2009 (rainy season) and from October 19 to 21, 2009 (dry season, after the rice-harvesting period) in six districts around Hanoi in northern Vietnam (Table S1; Fig. 1). Farmers cultivate rice two times a year in these areas, February to May and June to September. Rice fields and adjoining aquatic habitats such as ponds (water depth >1 m), rice nurseries, wetlands (water depth <1 m), ditches (width <1 m), and irrigation canal (width >1 m) were selected as potential mosquito breeding sites (Fig. S1). The aquatic habitats for sampling in each district were selected based on the relative area of each aquatic habitat.

2.2. Sampling methods

We monitored the abundance of mosquito larvae and other insects by a dipping method as described in Ohba et al. (2011). The dipper used for collection was 12 cm in diameter and 5 cm deep. We collected one sample from each study plot; each sample consisted of 30 dips made at 30 points at more than 1 m intervals. If it was not possible to collect 30 dips due to the small size of an aquatic habitat, we made 10 or 20 dips and converted them to 30 dips. By using this method alone, we may have missed a number of predatory insects and fish resting on foliage. We stored and studied all the samples at the laboratory of the National Institute of Hygiene and Epidemiology in Hanoi. Insects, excluding mosquito larvae, were identified to the order, family, or genus level using a binocular. Based on the literature (Mogi, 2007; Shaalan and Canyon, 2009), potential predators were classified into invertebrate (Coleoptera, Hemiptera, and Odonata) and vertebrate predators (fish and anuran larvae).

We preserved the collected mosquito larvae in 70% ethanol until identification, and identified all larvae, excluding damaged and/or first- to third-instar larvae, using taxonomic keys (Rattanarithikul et al., 2005a,b, 2006a,b). Pupae were reared until emergence for species identification. Larvae smaller than the fourth instar were identified to the genus level and counted. Because adults emerged from pupae of *Cx. vishnui* and *Cx. pseudovishnui* were difficult to identify certainty, they were categorized as *Culex vishnui* complex.

2.3. Data analysis

Similar to previous studies (Yasuoka et al., 2006; Yasuoka and Levins, 2007), niche width was calculated for each species using the formula: niche width = number of habitat types at a species collection site divided by six, which is the total number of habitat types included in this study. The knowledge of the environmental factors affecting mosquito abundance in main aquatic habitats in rice ecosystems (rice fields, ponds, and ditches) is indispensable for future mosquito management, because rice ecosystems are the most common and widespread wetlands in Vietnamese agroecosystems. We used a general linear model (GLM) with negative binomial ("glm.nb" package) in R version 2.12.1 (R Development Core Team, 2011) to determine mosquito abundance in rice