

Rapid Communication

A noteworthy step on a vast continent: new expansion records of the guava fruit fly, *Bactrocera correcta* (Bezzi, 1916) (Diptera: Tephritidae), in mainland China

Xiaofei Liu^{1,2,3}, Liyun Zhang^{1,2}, Robert A. Haack⁴, Jiang Liu^{1,2} and Hui Ye^{5,*}

¹Asian International Rivers Center, Yunnan University, Kunming 650091, China

²Yunnan Key Laboratory of International Rivers and Transboundary Eco-Security, Yunnan University, Kunming 650091, China

³Department of Ecology, Peking University, Beijing 100871, China

⁴USDA Forest Service, Northern Research Station, Lansing, Michigan 48910, USA (emeritus)

⁵School of Agriculture, Yunnan University, Kunming 650091, China

Author e-mails: xiaofei.liu@outlook.com (XL), zhangliyun@ynu.edu.cn (LZ), robert.haack@usda.gov (RAH), liujiang@ynu.edu.cn (JL), yehui@ynu.edu.cn (HY)

Liyun Zhang and Xiaofei Liu contributed equally to this work as co-first authors.

*Corresponding author

Citation: Liu X, Zhang L, Haack RA, Liu J, Ye H (2019) A noteworthy step on a vast continent: new expansion records of the guava fruit fly, *Bactrocera correcta* (Bezzi, 1916) (Diptera: Tephritidae), in mainland China. *BioInvasions Records* 8(3): 530–539, <https://doi.org/10.3391/bir.2019.8.3.08>

Received: 10 February 2019

Accepted: 25 May 2019

Published: 16 July 2019

Handling editor: Oliver Pescott

Thematic editor: Stelios Katsanevakis

Copyright: © Liu et al.

This is an open access article distributed under terms of the Creative Commons Attribution License ([Attribution 4.0 International - CC BY 4.0](https://creativecommons.org/licenses/by/4.0/)).

OPEN ACCESS

Abstract

Bactrocera correcta (Bezzi, 1916), commonly known as the guava fruit fly, is of concern as an invasive pest in tropical and subtropical countries. It was first recorded in China in 1982 in Yuanjiang, in southern Yunnan Province. We monitored the spread of *B. correcta* in the field during 2017 and 2018, and found that it had moved about 300 kilometers eastward from its known range in 2011 in Yunnan and has now entered the neighboring Guangxi Province. A species distribution model used to predict the potential distribution of *B. correcta* in China revealed that southern China provides the most suitable habitat for *B. correcta*, and that further eastward expansion threatens large areas of southeastern China. Results from this study suggest that the rapid eastward migration of *B. correcta* is related to improved highway and high-speed railway systems in China that transport fruits and vegetables to eastern markets. This paper also discusses methods to slow the expansion of *B. correcta* in China.

Key words: tephritid fruit fly, range expansion, Guangxi, geographic barrier, human-assisted spread

Introduction

The guava fruit fly, *Bactrocera correcta* (Bezzi, 1916) (Diptera: Tephritidae), is an important insect pest that infests more than 70 species of tropical and subtropical fruits and melons, representing 35 plant families, such as guava, mango, cashew, cherry, jujube, orange, banana, carambola, and wax apple (Allwood et al. 1999; Maynard et al. 2004; USDA 2014). In Thailand, *B. correcta* along with *Bactrocera dorsalis* (Hendel, 1912) are considered the main fruit pests, seriously affecting production of mango and guava (Kunprom et al. 2015). In India, damage rates to tropical fruits caused by *B. correcta* can reach 80%, ranking it as the country's most serious fruit fly pest (Jalaluddin et al. 1999).

Bactrocera correcta is currently a serious pest in tropical and subtropical areas of Asia, being first recorded in Bihar, India in 1916 (Bezzi 1916), followed by Nepal, Pakistan, Sri Lanka and Thailand (White and Elson-Harris 1992). It has since expanded to Bangladesh, Bhutan, China, Laos, Malaysia, Myanmar and Vietnam (Wang 1996; Drew and Raghu 2002; Liu et al. 2013; Qin et al. 2015). Possibly through trade of infested fruit, small numbers of *B. correcta* have been detected multiple times in California and Florida, USA, which were followed by active eradication programs (USDA 2014). Given the above, *B. correcta* is considered highly invasive, and is therefore targeted as a quarantine pest in many countries (White and Elson-Harris 1992; Qin et al. 2016).

Bactrocera correcta was first detected in Yunnan, China, in 1982 (Wang and Zhao 1989). In the following decades, it gradually expanded inland, but was confined to various mountain valleys in southwestern Yunnan, displaying a patchy geographical distribution in Yunnan (Liu et al. 2013). Southern China, including Fujian, Guangdong, Guangxi, Hainan, and Taiwan, are considered the most suitable areas for *B. correcta* in China (Qin et al. 2015). In the past decade, the transportation systems connecting Yunnan and Guangxi in western China to Guangdong in eastern China have been dramatically improved (Liu et al. 2014), which have increased the frequency and volume of goods being transported eastward within China as well as the potential spread of pests. If *B. correcta* were to expand throughout southern China it would cause severe negative impacts on fruit and vegetable production in this region (Lu et al. 2010, 2013; Qin et al. 2015). Thus, understanding *B. correcta* dispersal and spread is a core component for developing prevention and control programs for this fruit fly in China.

During 2017 and 2018, we surveyed for *B. correcta* in areas around its known range in southwestern China to determine if there had been any spread eastward within China. Furthermore, we used the species distribution model to analyze future spread potential of *B. correcta* in China and thereby provide updated information for setting internal quarantines and management guidelines.

Materials and methods

Study area and field monitoring

Within China, *B. correcta* was only known to occur in Yunnan prior to this study. However, since 2006, the distribution of *B. correcta* in China has expanded eastward to the Nanpanjiang River basin that borders Yunnan and the neighboring provinces of Guangxi to the south and Guizhou to the north (Liu et al. 2013). Therefore, our investigation was carried out in the three provinces of Yunnan, Guangxi, and Guizhou.

Field monitoring was conducted from March 2017 to July 2018 for a total of 17 months. At times, we expanded the monitoring area eastward in response to positive detections of *B. correcta*. We first established monitoring sites in Funing, Guangnan, and Qiubei in Yunnan Province, Baise in Guangxi Province, and Xingyi in Guizhou Province. Later in 2017, based on initial results of the investigation, we expanded the sampling area to include five additional counties in Guangxi Province, including Bama, Chongzuo, Longan, Pingguo, and Tianyang (Supplementary material Table S1). The sampling region covered a total area of nearly 90,000 square kilometers. All of these areas have been affected by other invasive fruit flies in recent years, with *B. dorsalis* being the dominant fruit fly species present; however, *B. correcta* was never detected in any earlier monitoring efforts.

At each survey site, one fruit orchard was selected, and three traps were deployed. We used Steiner traps baited with methyl eugenol to attract male fruit flies as described in Chen et al. (2010). The traps were suspended from branches in the fruit trees at a height of 1.5–2 m above the ground. All fruit fly specimens were collected at 15-day intervals, returned to the laboratory in Yunnan University, and identified to species using the morphological characters proposed by Drew and Romig (2013). All sampling sites were georeferenced by GPS (MG768W, UniStrong, Beijing, China) and the corresponding distribution map was drawn using GRASS GIS 7.2.2 (GRASS Development Team 2017).

Species distribution modeling

We used species distribution modeling to better understand the distribution pattern of *B. correcta* in China and to provide a theoretical basis when developing pest management strategies for this fruit fly. The occurrence data of *B. correcta* in Asia were obtained from the GBIF database (<http://www.gbif.org/>), genetic sample information (Kunprom et al. 2015; Qin et al. 2016), and field survey results (Satarkar et al. 2009; Liu et al. 2013) (Table S2).

Environmental data were obtained from the Bioclim Database (WorldClim Version2, <http://www.worldclim.org/>). We used seven bioclimatic variables (2.5' spatial resolution) to develop a *B. correcta* distribution model, which included Annual Mean Temperature (bio1), Temperature Seasonality (bio4), Max Temperature of Warmest Month (bio5), Min Temperature of Coldest Month (bio6), Temperature Annual Range (bio7), Mean Temperature of Warmest Quarter (bio10), and Mean Temperature of Coldest Quarter (bio11). All of the above selected variables have been regarded as important environmental factors affecting the distribution of *B. correcta* (Liu et al. 2013).

A Maxent model was used to predict the potential distribution of *B. correcta* in China because of its excellent performance in ecological niche

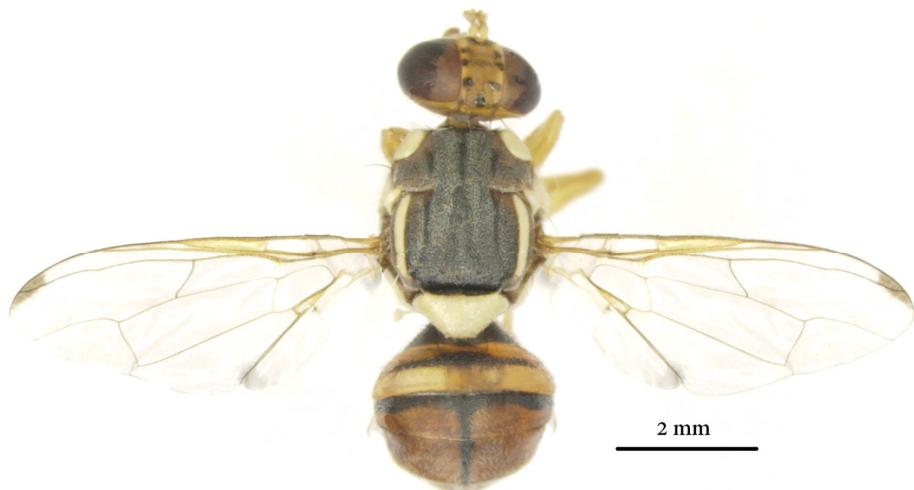


Figure 1. Guava fruit fly *Bactrocera correcta* (Bezzi, 1916) (δ) collected from Baise, Guangxi, China. Photo by Xiaofei Liu.

modeling (Phillips et al. 2006). We randomly sampled 10,000 points in buffer areas around occurrences as the background samples. The buffer size was 0.5 degrees. When selecting the model parameters, we used models with regularization multiplier (RM) values ranging from 0.5 to 4.5 (with increments of 0.5) with six feature class (FC) combinations (L, LQ, H, LQH, LQHP, with L = linear, Q = quadratic, H = hinge, and P = product). According to the lowest delta AICc score, the FC = LQH and RM = 3 were used in the final modeling effort (Figure S1). All analyses were conducted using the Wallace Package in R (R Core Team 2018) (Warren and Seifert 2011; Kass et al. 2018).

Results

We detected *B. correcta* in a mango orchard in March 2017 in Baise, Guangxi, which was the first time that this fruit fly was detected outside of Yunnan in China (Figure 1). The sampling site in Baise is about 300 km further east from where it had last been recorded in Yunnan in 2011 (Liu et al. 2013). As a result of the positive detection in Baise, we extended the monitoring eastward to Bama, Pingguo, and Tianyang in Guangxi Province in April 2017. Of these three new districts, we discovered *B. correcta* in Tianyang, which is located 38 km east of Baise.

In August 2017, we added two more monitoring sites to the south and east of Tianyang, one in Longan County about 100 km southeast of Tianyang, and the other in Chongzuo County about 140 km south of Tianyang. There were no *B. correcta* adults collected at these two sites during the subsequent monitoring period.

These data revealed that the eastern boundary of *B. correcta* range in China extended at least to Baise and Tianyang. However, neither of these two locations were contiguous with the known range of *B. correcta* in Yunnan.

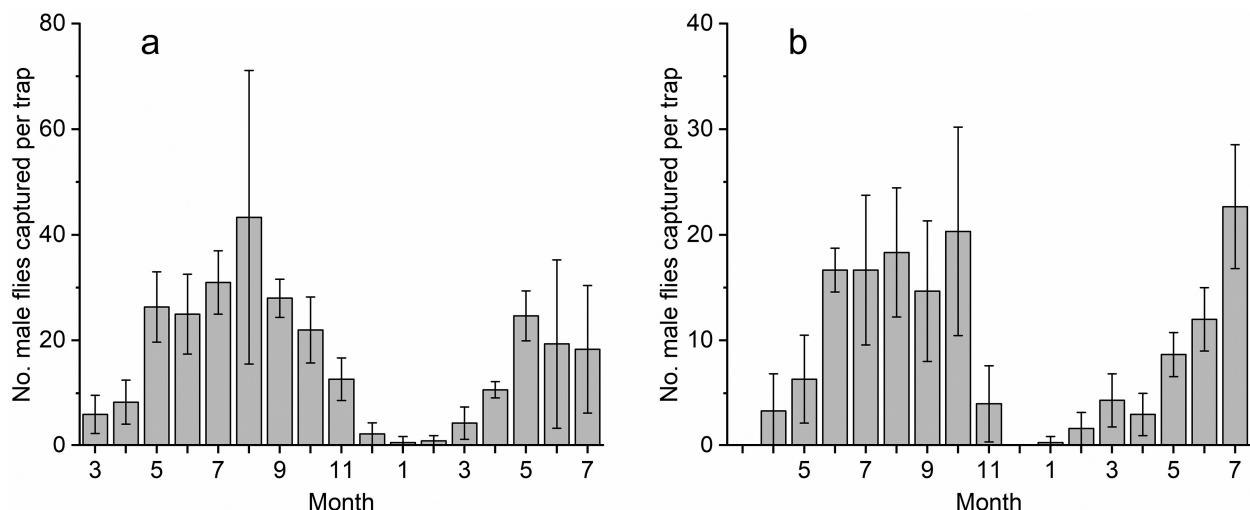


Figure 2. The average number of *Bactrocera correcta* male adults captured per trap (baited with methyl eugenol) in 2017 and 2018 in Baise (a) and Tianyang (b), Guangxi, China. Numbers on the X-axis correspond to months of the year, and error bars represent ± 1 standard deviation.

Bactrocera correcta populations peaked during the summer months and fell during the winter months at all monitoring sites based on trap catches. For example, at the Baise site, of the 852 *B. correcta* male adults collected during March 2017 to July 2018, 495 (58%) were trapped in summer (June–September 2017) compared with only 12 individuals trapped in winter (December 2017–February 2018) (Figure 2). Similarly, at Tianyang, the vast majority of the 459 *B. correcta* males collected were trapped during the months of June through October in 2017 and 2018 (79.3%) compared with 1.3% during December 2017–February 2018 (Figure 2). In addition, the trapping results indicated that *B. correcta* was active throughout the year at both Baise and Tianyang, suggesting that *B. correcta* is well established in Guangxi.

The species distribution model predicted highly suitable areas for establishment of *B. correcta* in the tropical and subtropical regions of China south of 25°N Latitude (Figure 3). The area suitable for *B. correcta* in Yunnan comprises about 20% of the total land area of Yunnan, resulting in a patchy distribution due to the many mountain chains in Yunnan. By contrast, the area suitable for *B. correcta* in southeastern China is generally contiguous and extensive, indicating that southeastern China would be very suitable for invasion by *B. correcta*. The current distribution of *B. correcta* in southwestern China (Figure 3) suggests that the mountains of Yunnan have largely hindered natural spread from west to east, whereas the current disjunct populations found in Baise and Tianyang likely resulted from human-assisted movement and thus pose a higher risk for invasion of *B. correcta* to the east.

Discussion

Yunnan Province, in southwest China, borders Laos, Myanmar, and Vietnam and is believed to be the main entry site for invasive organisms entering China from the Indochina Peninsula, as well as an important transit

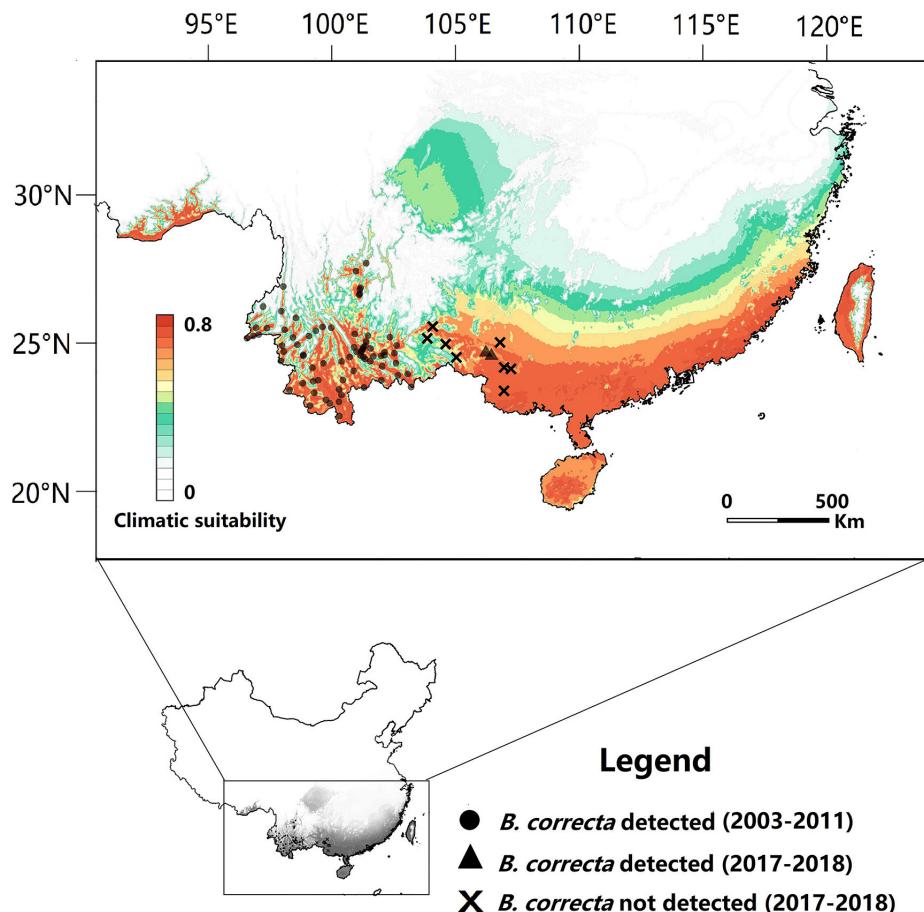


Figure 3. Sites where *Bactrocera correcta* has been detected in the past or during the present study in China, as well as predictions of climatic suitability for *B. correcta* in China based on Maxent model (0 = low, 1 = high).

point for alien species to enter the interior of China (Wan et al. 2017). Examples of harmful exotic plants and insects that have entered China through Yunnan include crofton weed (*Ageratina adenophora* (Sprengel) King and Robinson), siam weed (*Chromolaena odorata* (L.) King and Robinson), and pea leafminer (*Liriomyza huidobrensis* (Blanchard)) (Xu et al. 2012; Wan et al. 2017). As for the exotic species of *Bactrocera* in China, many species, such as *B. dorsalis* and *B. thailandica* Drew and Hancock, 1994, entered China through Yunnan (Liu et al. 2009; Shi et al. 2012). This pattern of invasion has led to Yunnan becoming the richest area for fruit fly biodiversity in China. For example, Yunnan has 67% of the total number of Dacini fruit fly species found in all of China and of the 83 Dacini species known to occur in Yunnan, more than 50 were introduced (= 60%) (Wang 1996; Doorenweerd et al. 2018).

Although many exotics have entered Yunnan, the northern plateau and the complex series of longitudinal mountain ridges and valleys in southern Yunnan form a natural barrier for the eastward spread of many alien organisms into the interior of China (He et al. 2005; Gan and He 2006). Of all the Dacini fruit flies that have been reported in China, about one third are still confined to Yunnan, suggesting that the unique geography of

Yunnan plays an important role in slowing natural spread both northward and eastward (Wang 1996; Chen et al. 2010).

As stated above, *B. correcta* was first reported in Yunnan in 1982 in the Yuanjiang River valley and was generally restricted to that region for more than 30 years (Wang and Zhao 1989; Liu et al. 2013). Several laboratory and field studies have confirmed that *B. correcta* is poorly adapted to low temperatures and long-range dispersal (Liu and Ye 2009; Liu et al. 2015), and therefore the Yunnan-Guizhou Plateau and Hengduan Mountains in northern Yunnan have effectively prevented natural spread of *B. correcta* northward toward Sichuan (Liu et al. 2013; Qin et al. 2016). By contrast, the geographic barriers that restrict natural eastward spread of *B. correcta* from Yunnan are relatively narrow mountain chains in Yunnan and therefore have been the main focus for pest surveys by regional plant health specialists.

In the present study, our field surveys revealed for the first time that *B. correcta* had expanded beyond Yunnan and entered Guangxi to the east. The newly invaded sites in Guangxi were more than 300 kilometers further east than the last historical distribution record in Yunnan made in 2011 (Liu et al. 2013). This discovery indicates that the geographic barriers in Yunnan to eastward spread of *B. correcta* have been breached, and now many agricultural crops in southeastern China are threatened.

What was responsible for the eastward jump of *B. correcta* to Guangxi? It was likely not natural spread given that there is no valley connection between the newly invaded sites in Guangxi and the historical known range in Yunnan, and moreover no *B. correcta* adults were detected in any of the four monitoring sites between the historical range in Yunnan and the newly invaded sites. In addition, although some studies have shown that *B. correcta* can adapt quickly to the new environments (Liu 2010; Liu et al. 2013), there is no evidence that *B. correcta* has adapted sufficiently to disperse naturally eastward over the high-altitude mountains in Yunnan.

The movement of people and goods is reasonably regarded as one of the main factors in the spread of exotic agricultural and forest organisms both within and between countries (Haack 2006; Colunga-Garcia et al. 2009, 2013; Mazzi and Dorn 2012). Within a country, the rate at which invasive organisms can spread is often enhanced by transportation improvements (Ding et al. 2008; Hu et al. 2013), such as the new modern highway and high-speed railway links that were opened between Yunnan and Guangxi in 2012 and 2016, respectively, both of which run through Baise and Tianyang. These transportation improvements have shortened the travel time between Yunnan's historical *B. correcta* eastern outbreak areas and Guangxi's newly infested sites from 15 hours to 6 hours by highway and from 10 hours to 3 hours by high-speed rail. Similarly, the railway freight capacity between Yunnan and Guangxi has increased from 27 million tons

to 110 million tons per year after completion of the high-speed rail system (Liu et al. 2014; Zhu 2015). These increases in the rate and volume of goods transported along these improved highways and high-speed railways could easily have served as the pathway for eastward movement of *B. correcta* into Guangxi.

Bactrocera dorsalis is one of the most damaging fruit flies worldwide and is similar to *B. correcta* in many life-history attributes, including sharing many of the same host plants (Gu et al. 2019). Evidence based on population genetics suggests that Yunnan was the main channel by which *B. dorsalis* entered China from more southern countries and expanded to the north and east within China, although this inference cannot be conclusively confirmed due to the lack of historical expansion records (Shi et al. 2012; Zeng et al. 2019). The invasion pattern so far demonstrated by *B. correcta* in China is very similar to that of *B. dorsalis* in that *B. correcta* entered China through Yunnan, and is now spreading eastward within China.

Given the potential for pests to move more readily within China as transportation networks improve indicates a need for China to adjust its monitoring efforts and internal quarantine regulations against pests like *B. correcta*. For example, a network of monitoring sites, using traps baited with attractant lures, could be established throughout southern China in major areas of fruit production and along major transportation routes. Second, given the apparent restricted range of *B. correcta* in Guangxi, it may be possible to attempt an eradication program to prevent further spread of this pest. And third, additional training on *B. correcta* identification and management could be provided to growers and inspectors throughout the known range of *B. correcta* and in neighboring provinces, with a special focus on vital transportation hubs and major fruit distribution centers. Such actions could enhance early detection of *B. correcta* populations, which would allow for rapid control efforts, and thereby slow the eastward invasion of *B. correcta* to southeastern China.

Acknowledgements

We would like to thank the anonymous reviewers and the editor for their comments, which helped to improve the manuscript. We thank our many cooperators throughout southwestern China who cared for the fruit fly traps used in this project. We thank Mrs. Xue Fan (Science and Technology Development Research Center of Chengdu) for her encouragement and inspiration. This research was supported by the National Key R&D Program of China (2017YFC0505200), Natural Science Foundation of China (No. 41401065; No. 41461009), and Natural Science Foundation of Yunnan Province (No. 2015FB109).

References

- Allwood AJ, Chinajariyawong A, Kritsaneepaiboon S, Drew RAI, Hamacek EL, Hancock DL, Hengsawad C, Jipanin JC, Jirasurat M, Krong CK, Leong CTS, Vijaysegaran S (1999) Host plant records for fruit flies (Diptera: Tephritidae) in Southeast Asia. *Raffles Bulletin of Zoology* 47: 1–92
- Bezzi M (1916) On the fruit-flies of the genus *Dacus* (s. l.) occurring in India, Burma, and Ceylon. *Bulletin of Entomological Research* 7: 99–121, <https://doi.org/10.1017/S0007485300017430>

- Chen X, Liu XF, Ye H (2010) The major fruit fly (Diptera: Tephritidae) pest species and their geographic distribution in Yunnan Province. *Acta Ecologica Sinica* 30: 717–725
- Colunga-Garcia M, Haack RA, Adelaja AO (2009) Freight transportation and the potential for invasions of exotic insects in urban and periurban forests of the United States. *Journal of Economic Entomology* 102: 237–246, <https://doi.org/10.1603/029.102.0133>
- Colunga-Garcia M, Haack RA, Magarey RD, Borchert DM (2013) Understanding trade pathways to target biosecurity surveillance. *NeoBiota* 18: 103–118, <https://doi.org/10.3897/neobiota.18.4019>
- Ding JQ, Mack RN, Lu P, Ren M, Huang H (2008) China's booming economy is sparking and accelerating biological invasions. *AIBS Bulletin* 58: 317–324, <https://doi.org/10.1641/B580407>
- Doorenweerd C, Leblanc L, Norrbom AL, San Jose M, Rubinoff D (2018) A global checklist of the 932 fruit fly species in the tribe Dacini (Diptera, Tephritidae). *ZooKeys* 730: 19–56, <https://doi.org/10.3897/zookeys.730.21786>
- Drew RAI, Raghu S (2002) The fruit fly fauna (Diptera: Tephritidae: Dacinae) of the rainforest habitat of the Western Ghats, India. *Raffles Bulletin of Zoology* 50: 327–352
- Drew RAI, Romig MC (2013) Tropical Fruit Flies of South-East Asia, CAB International, Wallingford, UK, 664 pp
- Gan S, He DM (2006) Assessment on eco-environment background of Yunnan plateau mountain region. *Journal of Yunnan University Natural Sciences* 28: 161–165
- GBIF (2018) Global Biodiversity Information Facility. <http://www.gbif.org> (accessed 10 December 2018)
- GRASS Development Team (2017) Geographic Resources Analysis Support System (GRASS) Software, Version 7.2. Open Source Geospatial Foundation. <http://grass.osgeo.org>
- Gu XY, Zhao Y, Su Y, Wu JJ, Wang ZY, Hu JT, Liu LJ, Zhao ZH, Hoffmann AA, Chen B, Li ZH (2019) A transcriptional and functional analysis of heat hardening in two invasive fruit fly species, *Bactrocera dorsalis* and *Bactrocera correcta*. *Evolutionary Applications* 12: 1147–1163, <https://doi.org/10.1111/eva.12793>
- Haack RA (2006) Exotic bark-and wood-boring Coleoptera in the United States: recent establishments and interceptions. *Canadian Journal of Forest Research* 36: 269–288, <https://doi.org/10.1139/x05-249>
- He DM, Wu SH, Peng H, Yang ZF, Ou XK, Cui BS (2005) A study of ecosystem changes in longitudinal range-gorge region and transboundary eco-security in Southwest China. *Advances in Earth Science* 20: 338–344
- Hu SJ, Ning T, Fu DY, Haack RA, Zhang Z, Chen DD, Ma XY, Ye H (2013) Dispersal of the Japanese pine sawyer, *Monochamus alternatus* (Coleoptera: Cerambycidae), in mainland China as inferred from molecular data and associations to indices of human activity. *PLoS ONE* 8: e57568, <https://doi.org/10.1371/journal.pone.0057568>
- Jalaluddin SM, Natarajan K, Sadakathulla S, Balasubramaniyan S (1999) Discovery of the guava fruit fly *Bactrocera correcta* (Bezzi). *Entomon* 24: 195–196
- Kass JM, Vilela B, Aiello-Lammens ME, Muscarella R, Merow C, Anderson RP (2018) Wallace: A flexible platform for reproducible modeling of species niches and distributions built for community expansion. *Methods in Ecology and Evolution* 9: 1151–1156, <https://doi.org/10.1111/2041-210X.12945>
- Kunprom C, Nanork Sopalaadwan P, Pramual P (2015) Population genetics and demographic history of guava fruit fly *Bactrocera correcta* (Diptera: Tephritidae) in northeastern Thailand. *European Journal of Entomology* 112: 227–234, <https://doi.org/10.14411/eje.2015.033>
- Liu XF (2010) Studies on the occurrence, distribution and migration of *Bactrocera correcta* (Bezzi) in Yunnan. PhD Thesis, Yunnan University, Kunming, China, 115 pp
- Liu XF, Ye H (2009) Effect of temperature on development and survival of *Bactrocera correcta* (Diptera: Tephritidae). *Scientific Research and Essays* 4: 467–472
- Liu XF, Wang XJ, Ye H (2009) One newly recorded species of the genus *Bactrocera* Macquart (Diptera, Tephritidae) from China. *Acta Zootaxonomica Sinica* 34(3): 661–663
- Liu XF, Jin Y, Ye H (2013) Recent spread and climatic ecological niche of the invasive guava fruit fly, *Bactrocera correcta*, in mainland China. *Journal of Pest Science* 86: 449–458, <https://doi.org/10.1007/s10340-013-0488-8>
- Liu BL, Lee SJ, Xiao JH, Wang L, Jiao ZL (2014) Contemporary Logistics in China. Springer, Berlin, Heidelberg, 232 pp, <https://doi.org/10.1007/978-3-662-47721-2>
- Liu T, Li L, Zhang FH, Gong SR, Li TX, Zhan GP, Wang YJ (2015) Effect of low-temperature phosphine fumigation on the survival of *Bactrocera correcta* (Diptera: Tephritidae). *Journal of Economic Entomology* 108: 1624–1629, <https://doi.org/10.1093/jee/tov150>
- Lu WG, Deng YL, Li ZH, Lin W, Wan FH, Wang ZL (2010) A prediction of potential geographical distribution of guava fruit fly, *Bactrocera* (*Bactrocera*) *correcta* (Bezzi) in China. *Acta Phytotaxonomica Sinica* 37(6): 529–534
- Maynard GV, Hamilton JG, Grimshaw JF (2004) Quarantine-phytosanitary, sanitary and incursion management: an Australian entomological perspective. *Australian Journal of Entomology* 43: 318–328, <https://doi.org/10.1111/j.1326-6756.2004.00441.x>
- Mazzi D, Dorn S (2012) Movement of insect pests in agricultural landscapes. *Annals of Applied Biology* 160: 97–113, <https://doi.org/10.1111/j.1744-7348.2012.00533.x>

- Phillips SJ, Anderson RP, Schapire RE (2006) Maximum entropy modeling of species geographic distributions. *Ecological Modelling* 190: 231–259, <https://doi.org/10.1016/j.ecolmodel.2005.03.026>
- Qin YJ, Ni W, Wu J, Zhao Z, Chen H, Li ZH (2015) The potential geographic distribution of *Bactrocera correcta* (Diptera: Tephritidae) in China based on eclosion rate model. *Applied Entomology and Zoology* 50: 371–381, <https://doi.org/10.1007/s13355-015-0344-9>
- Qin YJ, Buahom N, Krosch MN, Du Y, Wu Y, Malacrida AR, Deng YL, Liu JQ, Jiang XL, Li ZH (2016) Genetic diversity and population structure in *Bactrocera correcta* (Diptera: Tephritidae) inferred from mtDNA cox1 and microsatellite markers. *Scientific Reports* 6: 38476, <https://doi.org/10.1038/srep38476>
- R Core Team (2018) R: a language and environment for statistical computing. r foundation for statistical computing. Vienna, Austria. <https://www.R-project.org>
- Satarkar VR, Krishnamurthy SV, Faleiro JR, Verghese A (2009) Spatial distribution of major *Bactrocera* fruit flies attracted to methyl eugenol in different ecological zones of Goa, India. *International Journal of Tropical Insect Science* 29: 195–201, <https://doi.org/10.1017/S174275840999035X>
- Shi W, Kerdelhué C, Ye H (2012) Genetic structure and inferences on potential source areas for *Bactrocera dorsalis* (Hendel) based on mitochondrial and microsatellite markers. *PLoS ONE* 7: e37083, <https://doi.org/10.1371/journal.pone.0037083>
- USDA (2014) Provisional list of host plants of guava fruit fly, *Bactrocera correcta* (Bezzi) (Diptera: Tephritidae). USDA Animal and Plant Health Inspection Service, Raleigh, NC, 64 pp. https://www.aphis.usda.gov/plant_health/plant_pest_info/fruit_flies/downloads/host-lists/bactrocera-correcta-provisional-host-plants.pdf
- Wan FH, Jiang MX, Zhan A (2017) Biological invasions and its management in China, Springer, Dordrecht, 369 pp, <https://doi.org/10.1007/978-94-024-0948-2>
- Wang XJ (1996) The fruit flies of the East Asian region. *Acta Zootaxonomica Sinica* Supplement 21: 1–338
- Wang XJ, Zhao MZ (1989) Notes on the genus *Dacus* Fabricius in China with descriptions of five new species. *Acta Zoologica Sinica* 14: 209–219
- Warren DL, Seifert SN (2011) Ecological niche modeling in Maxent: the importance of model complexity and the performance of model selection criteria. *Ecological Applications* 21: 335–342, <https://doi.org/10.1890/10-1171.1>
- White IM, Elson-Harris MM (1992) Fruit flies of economic significance: their identification and bionomics, CAB International, Wallingford, UK, 600 pp
- Xu HG, Qiang S, Genovesi P, Ding H, Wu J, Meng L, Han ZM, Miao JL, Hu BS, Guo JY, Sun HY, Huang C, Lei JC, Le ZF, Zhang XP, He SP, Wu Y, Zheng Z, Chen L, Jarošík V, Pyšek P (2012) An inventory of invasive alien species in China. *NeoBiota* 15: 1–26, <https://doi.org/10.3897/neobiota.15.3575>
- Zeng Y, Reddy GVP, Li, ZH, Qin YJ, Wang, YN, Pan, XB, Jiang F, Gao F, Zhao ZH (2019) Global distribution and invasion pattern of oriental fruit fly, *Bactrocera dorsalis* (Diptera: Tephritidae). *Journal of Applied Entomology* 143: 165–176, <https://doi.org/10.1111/jen.12582>
- Zhu SX (2015) Current situations and problems of logistics for Guangxi fresh agricultural products in new period and recommendations. *Asian Agricultural Research* 7(10): 39–43

Supplementary material

The following supplementary material is available for this article:

Table S1. Monitoring sites, sampling duration, and *Bactrocera correcta* occurrence at each sampling site in China during 2017–2018.

Table S2. Occurrence data in Asia for *Bactrocera correcta* records used in the Maxent modeling effort in this paper.

Figure S1. Values for delta AICc based on different Maxent model settings (L = linear, Q = quadratic, H = hinge, and P = product) used to predict the potential distribution of *B. correcta* in China.

This material is available as part of online article from:

http://www.reabic.net/journals/bir/2019/Supplements/BIR_2019_Liu_etal_SupplementaryTables.xlsx

http://www.reabic.net/journals/bir/2019/Supplements/BIR_2019_Liu_etal_Figure_S1.pdf