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CONTENT

TREUBIA

(A JOURNAL ON ZOOLOGY OF THE INDO-AUSTRALIAN ARCHIPELAGO)

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Date of issue: 30 DECEMBER 2020

UDC: 593.4:595.35(594)

Pipit Pitriana

Exploring sponge-inhabiting barnacles of eastern Indonesia using micro-CT scanning

TREUBIA, December 2020, Vol. 47, No. 2, pp. 77–98.

We present a morphological study of Indonesian sponge-inhabiting barnacles using standard light microscopy in combination with micro-CT scanning and computer-aided 3D-reconstruction of the external shell morphology. A taxonomic analysis of the material detected four different genera of sponges inhabited by five different species of balanomorph barnacles, two of which are undescribed. Together with conventional morphological examination by dissection, we provide modern non-destructive imaging methods, using micro-CT scanning to enhance our knowledge of the morphological characters of sponge-inhabiting barnacles from eastern Indonesia. Although there were some methodological limitations regarding the contrast-enhancing technique, this study demonstrates micro-CT as a useful non-destructive technique of integrative taxonomy, for the examination of sponge-inhabiting barnacles.

(Pipit Pitriana, Andreas Wessel, Tina Aschenbach, and Kristina von Rintelen)

Keywords: Cirripedia, Indonesian biodiversity, integrative taxonomy, micro-computer tomography, shell morphology

UDC: 598.89:577.2

Jarulis

Characters of mitochondrial DNA D-loop hypervariable III fragments of Indonesian Rhinoceros Hornbill (*Buceros rhinoceros*) (Aves: Bucerotidae)

TREUBIA, December 2020, Vol. 47, No. 2, pp. 99–110.

The Rhinoceros Hornbill (*Buceros rhinoceros*) genetic characteristics consist of nucleotide polymorphisms, haplotypes, genetic distances, and relationships which are important for their conservation effort in Indonesia. We sequenced mitochondrial DNA D-loop hypervariable III fragments from five Rhinoceros Hornbill individuals at Safari Park Indonesia I and Ragunan Zoo, which were isolated using Dneasy® Blood and Tissue Kit Spin-Column Protocol, Qiagen. D-loop fragment replication was done by PCR technique using DLBuce_F (5'-TGGCCTTTCTCCAAGGTCTA-3') and DLBuce_R (5'-TGAAGG AGT TCATGGGCTTAG-3') primer. Thirty SNP sites were found in 788 bp D-loop sequences of five Rhinoceros Hornbill individuals and each individual had a different haplotype. The average genetic distance between individuals was 3.09% and all individuals were categorized into two groups (Group I: EC6TS, EC1RG, EC2TS and Group II: EC9TS, EC10TS) with a genetic distance of 3.99%. This result indicated that the two groups were distinct subspecies. The genetic distance between Indonesian and Thai Rhinoceros Hornbills was 10.76%. Five Indonesian Rhinoceros Hornbill individuals at Safari Park Indonesia I and Ragunan Zoo probably came from different populations, ancestors, and two different islands. This study can be of use for management consideration in captive breeding effort at both zoos. The D-loop sequence obtained is a

useful character to distinguish three Rhinoceros Hornbill subspecies in Indonesia.

(Jarulis, Choirul Muslim, Dedy Duryadi Solihin, Ani Mardiastuti, and Lilik Budi Prasetyo)

Keywords: Bucerotidae, control region, phylogenetic, Rhinoceros Hornbill conservation, zoo

UDC: 595.773.4(594.59)

Eka Kartika Arum Puspita Sari

Diversity of fruit flies (Tephritidae: *Bactrocera* spp.) in campus C of Airlangga University, Surabaya, Indonesia

TREUBIA, December 2020, Vol. 47, No. 2, pp. 111–122.

This research aims to get information about the species of host plants and fruit flies, composition and structure of community, distribution pattern, and impact of environmental factors to fruit flies in Campus C, Airlangga University. Research was conducted from August to November 2019. A modification of Steiner trap with methyl eugenol 1.5 ml bait was installed in nine sites. Each Steiner trap was placed on a mango tree 1-2 meters above ground level. Trapped fruit fly specimens were collected after one week. Four replications were made, with intervals between two periods of installation. As many as 682 host plants of the fruit flies were found at the study site consisting of 25 species from 15 families. Results showed that 1121 individuals of *Bactrocera* fruit flies were found, consisting of 5 species, namely *B. carambolae*, *B. dorsalis*, *B. minuscula*, *B. occipitalis*, and *B. musae*. The most abundant species was *B. carambolae* (62.8%), followed by *B. dorsalis* (27.3%), *B. minuscula* (8.4%), *B. occipitalis* (1%), and the lowest was *B. musae* (0.5%). *B. occipitalis* has an even distribution pattern, while four other species have aggregated distribution patterns. The diversity index at nine locations ranged from 0.772 (low) to 1.151 (moderate). *B. carambolae* and *B. dorsalis* were the dominant species. The presence of fruit flies was influenced by environmental (humidity, temperature, sunlight intensity, wind) and host plant factors.

(Eka Kartika Arum Puspita Sari, Moch. Affandi, and Sucipto Hariyanto)

Keywords: Dacinae, diversity, fruit flies, methyl eugenol, Steiner trap

UDC: 595.799:598.836:591.5(594.5)

Sih Kahono

First report on hunting behavior of migratory Oriental Honey-buzzard (*Pernis ptilorhynchus orientalis*) towards migratory giant honeybee (*Apis dorsata dorsata*) (Hymenoptera: Apidae) on Java Island, Indonesia

TREUBIA, December 2020, Vol. 47, No. 2, pp. 123–132.

Both migratory Oriental Honey-buzzard (*Pernis ptilorhynchus orientalis*) and migratory giant honeybee (*Apis dorsata dorsata*) can be found in South-east Asia. The Oriental Honey-buzzard is the main predator of the giant honeybee, prey upon its honeycomb, larvae, and honey. Its existence always follows the migration of the giant honeybee. They stay on Java island during the migratory season. The giant honeybee lives in a large colony and has a powerful sting that is useful for defence against its predators. The bee is among the most dangerous animals since its threatening defensive behavior causes severe impact on the eagle and is even frequently fatal for human beings. Data collections on hunting behavior of the Oriental Honey-buzzard were based on irregular observations and interviews between the year 2003 to 2019. We categorized five hunting behaviors during data collections: flying orientation around the bee's nest, attack on living nest, failure to collect the living nest, preying upon the newly empty nest, and transferring attack of the angry bee to people nearby. The safest hunting for the Oriental Honey-buzzard is to prey upon newly empty nest left by the honeybee. When the nest was still occupied by the bee colonies, the eagle should develop a strategy to avoid and reduce the risk of being attacked. It sometimes transfers the attack to people nearby.

(Sih Kahono, Dewi M. Prawiradilaga, Djunijanti Peggie, Erniwati, and Eko Sulistyadi)

Keywords: hunting behavior, Java, migratory giant honeybee, Oriental Honey-buzzard

UDC: 595.798:57.06(594.4)

Fuki Saito-Morooka

Taxonomic notes on the hover wasp genus *Eustenogaster* (Vespidae, Stenogastrinae), with description of two new species from Sumatra Island, Indonesia

TREUBIA, December 2020, Vol. 47, No. 2, pp. 133–154.

Wasps of the genus *Eustenogaster* van der Vecht, 1969, with 17 species currently recognized, are distributed from the Indian subcontinent in the west to the Philippines, Sulawesi Island and Java Island in the east. Two new species of hover wasp genus *Eustenogaster* (*E. multifolia* **sp. nov.**, *E. sumatraensis* **sp. nov.**) are described from specimens collected in Sumatra Island. The female of *E. vietnamensis* occurring in Vietnam are described for the first time. The lectotypes of *Paravespa eva* Bell, 1936 and *Ischnogaster ornatifrons* Cameron, 1902 are designated. The new taxonomic status is proposed for *Stenogaster eximioides* Dover and Rao, 1922 as a good (=valid) species of *Eustenogaster*. The synonymy of *Ischnogaster ornatifrons* Cameron, 1902 with *Eustenogaster micans* (de Saussure, 1852) has been confirmed. A revised key to species and a taxonomic and distributional checklist of all the species of *Eustenogaster* are provided.

(Fuki Saito-Morooka, Hari Nugroho, Alan Handru, and Jun-ichi Kojima)

Keywords: distributional checklist, lectotype, new status, revised key, synonym

Treubia, 47(2): 111–122, December 2020

DOI: 10.14203/treubia.v47i2.3982

DIVERSITY OF FRUIT FLIES (TEPHRITIDAE: *BACTROCERA* SPP.) IN CAMPUS C OF AIRLANGGA UNIVERSITY, SURABAYA, INDONESIA

Eka Kartika Arum Puspita Sari[1], Moch. Affandi[1], and Sucipto Hariyanto[*1]

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ABSTRACT

This research aims to get information about the species of host plants and fruit flies, composition and structure of community, distribution pattern, and impact of environmental factors to fruit flies in Campus C, Airlangga University. Research was conducted from August to November 2019. A modification of Steiner trap with methyl eugenol 1.5 ml bait was installed in nine sites. Each Steiner trap was placed on a mango tree 1-2 meters above ground level. Trapped fruit fly specimens were collected after one week. Four replications were made, with intervals between two periods of installation. As many as 682 host plants of the fruit flies were found at the study site consisting of 25 species from 15 families. Results showed that 1121 individuals of *Bactrocera* fruit flies were found, consisting of 5 species, namely *B. carambolae*, *B. dorsalis*, *B. minuscula*, *B. occipitalis*, and *B. musae*. The most abundant species was *B. carambolae* (62.8%), followed by *B. dorsalis* (27.3%), *B. minuscula* (8.4%), *B. occipitalis* (1%), and the lowest was *B. musae* (0.5%). *B. occipitalis* has an even distribution pattern, while four other species have aggregated distribution patterns. The diversity index at nine locations ranged from 0.772 (low) to 1.151 (moderate). *B. occipitalis* has an even distribution pattern, while five other species have aggregated distribution patterns. The diversity index at nine locations ranged from 0.855 (low) to 1.328 (moderate). *B. carambolae* and *B. dorsalis* were the dominant species. The presence of fruit flies was influenced by environmental (humidity, temperature, sunlight intensity, wind) and host plant factors.

Keywords: Dacinae, diversity, fruit flies, methyl eugenol, Steiner trap

ABSTRAK

Penelitian ini bertujuan untuk mengetahui spesies tanaman inang dan lalat buah, komposisi dan struktur komunitas, pola distribusi, dan faktor lingkungan yang memengaruhi lalat buah di Kampus C, Universitas Airlangga. Penelitian dilaksanakan mulai Agustus hingga November 2019. Modifikasi perangkap Steiner dengan umpan 1.5 ml metil eugenol diletakkan di sembilan titik. Setiap perangkap Steiner digantung di pohon mangga 1-2 meter di atas permukaan tanah. Spesimen lalat buah yang terperangkap dikoleksi setelah satu minggu. Pengulangan dilakukan sebanyak empat kali, dengan interval waktu di antara dua periode pemasangan. Sebanyak 682 tanaman inang lalat buah ditemukan di lokasi penelitian terdiri atas 25 spesies dari 15 famili. Hasil menunjukkan 1121 lalat buah *Bactrocera*, yang terdiri atas 5 spesies, yaitu *B. carambolae*, *B. dorsalis*, *B. minuscula*, *B. occipitalis*, dan *B. musae*. Lalat buah dengan kelimpahan tertinggi adalah *B. carambolae* (62.8%) dan diikuti oleh *B. dorsalis* (27,3%), *B. minuscula* (8,4%), *B. occipitalis* (1%), dan kelimpahan terendah adalah *B. musae* (0,5%). *B. occipitalis* memiliki pola distribusi merata, sedangkan empat spesies lain memiliki pola distribusi mengelompok. Indeks keanekaragaman pada sembilan lokasi berkisar dari 0,772 (rendah) hingga 1,151 (sedang). *B. carambolae* dan *B. dorsalis* adalah spesies yang dominan. Keberadaan lalat buah dipengaruhi oleh faktor lingkungan (kelembapan, suhu, intensitas cahaya, angin) dan faktor tanaman inang.

Kata kunci: Dacinae, diversitas, lalat buah, metil eugenol, perangkap Steiner

INTRODUCTION

There are two genera of fruit flies in Indonesia, namely *Bactrocera* and *Dacus*. *Bactrocera* is a native genus to tropics that can be found in western to eastern Indonesia, while *Dacus* is native to Africa and is mostly found in eastern Indonesia (Siwi & Hidayat, 2006). Fruit flies in the environment act as pollinators, but it can be economically detrimental to humans by attacking 75% of fruiting plant species (Sulis, 2016). The presence of host plants is a main factor influencing the presence and distribution of fruit flies. In addition, the presence of fruit flies is also influenced by the appropriate climates such as temperature (10-30°C), humidity (62-90%), sunlight intensity, and wind speed and direction (Tan & Nishida, 2012; Sayuthi et al., 2019).

Female fruit flies attack the fruit through the oviposition process by inserting the ovipositor into the fruit to lay eggs. The larval phase is the stage with the highest attack intensity on the host plant. Fruit fly larvae damage the fruits by eating the pulp of fruit and causing the fruit falls before it is ripe (Siwi, 2005; Mayasari et al., 2019).

The attractant trap is effective in controlling the fruit flies and eco friendly because it leaves no residue. A commonly used attractant is methyl eugenol (Suputa et al., 2007; Susanto et al., 2017). Fruit flies use visual and chemical cues to find the host, which are based on the color, fruit size, volatile chemical compounds of the host plant, and host nutrients (Siwi, 2005; Khaeruddin, 2015).

The information about fruit flies existence in Surabaya is not widely available. Campus C, Airlangga University is located in Surabaya with a variety of host plants that are suitable for the development of fruit flies. The purpose of this study were to do inventory of the host plants and the fruit fly species, to determine the composition and community structure, distribution patterns, and the influence of environmental factors that affect fruit flies at Campus C, Airlangga University.

MATERIALS AND METHODS

This research was conducted from August to November 2019. Sampling was carried out in the area of Campus C, Airlangga University, Surabaya and the identification process was done in the Biosystematics Laboratory, Faculty of Science and Technology, Airlangga University. The flowering and fruiting conditions of the host plants were recorded at each observation period. Fruit fly traps were applied at nine observation sites based on the presence and distribution of host plants. This type of trap is a modification of Steiner trap with 1.5 ml of methyl eugenol (94.09%) and installed at the tree branch 1-2 m above the ground (Fig. 1).

Traps were installed for one week with a two-weeks interval between installation. The experiment was carried out with four replications. Trapping was conducted in the morning and then after a week were collected in the afternoon. Physical environment variables were measured at each trap installation period, including humidity, temperature, sunlight intensity, and wind speed. Fruit fly samples were identified using the determination key based on the morphological characters of the thorax, wings, legs, and abdomen.

Figure 1. Dry trap modification of the Steiner trap type.

Composition of the fruit flies was calculated as follows (Vere, 2008):

$$\text{Composition} = \frac{ni}{N} \times 100\%$$

The number of individuals in species i is denoted by ni and the total number of all species is denoted by N.

The diversity index was analyzed with *Shannon Index of Diversity* (Pleasants, 1971):

$$H' = - \Sigma\ (ni/N)\ .\ \ln\ (ni/N)$$

Shannon index of diversity is denoted by H', the number of individuals in species i is ni, and the total number of individuals in the community is N. The diversity index assessed by the value of H: >3 = high diversity; H: 1-3 = moderate diversity; H: <1 = low diversity.

The dominance index of fruit flies in Campus C, Airlangga University was analyzed by comparing the obtained dominance value with the frequency (Sa et al., 2012):

$$F = ni/N$$

The frequency is denoted by F, ni represents the number of individuals of species i, and N represents the total number of individuals found. Dominance (D) is obtained by comparing the F result with the 1/S result, S represents the number of species found at study site. If the F value is greater than the 1/S value, the species is dominant (d), but otherwise, it is nondominant (nd).

The distribution patterns of fruit flies were analyzed according to the following Morisita index (Pauley & Hutchens, 2004):

$$Id = n \left(\frac{\sum x^2 - N}{N\ (N-1)}\right)$$

Id is the Morisita index, n represents the number of plots, the number of individuals per plot is denoted by x, and N represents all individuals. The distribution pattern can be assessed by the value of Id: 1 = uniform; Id >1 = aggregated; Id <1 = random.

To determine the correlation between environmental factors and the presence of fruit flies, linear regression equation and the correlation coefficient (R) were analyzed (Gaspersz, 1991). R values range from –1 to +1 (Susanto et al., 2017).

RESULTS

The host plants found in Campus C, Airlangga University consist of 25 species, with 682 individuals (Table 1). Five species of fruit flies were obtained during the study, i.e. *B. carambolae*, *B. dorsalis*, *B. minuscula*, *B. occipitalis*, and *B. musae*, with 1121 individuals consisting of 1119 male and two female (*B. carambolae*) (Table 2, Figs. 1-6).

B. carambolae was the most highly found with a percentage of 62.8% while *B. musae* was only 0.5% (Fig. 7). Based on Shannon index of diversity, H' result at site one, two, seven, and eight can be classified as moderate, meanwhile at site three, four, five, six, and nine can be classified as low. *B. carambolae* and *B. dorsalis* were the dominant species (Table 3). Based on Morisita index (Id), distribution pattern of *B. carambolae*, *B. dorsalis*, *B. minuscula*, and *B. musae* was an aggregate with value of Id 1.3, 1.4, 1.6, and 4.2 respectively. *B. occipitalis* was evenly distributed with a value of Id 1.

During the study, the humidity in Campus C, Airlangga University was 79-90% in the morning and 65-67% in the afternoon. The temperature ranges from 24-25°C in the morning and 28.1-29.4°C in the afternoon. The sunlight's intensity in the morning was 96-413 lx and in the afternoon 128-338 lx. In the morning the wind speed was 0-1 m/s and in the afternoon 0-2 m/s.

The host plant was the main influence of the fruit flies presence and diversity. The results of correlation between the number of host plant species and fruit flies showed a quite strong positive correlation (Fig. 8).

DISCUSSION

A total of 682 individuals from 25 species and 15 families of fruit fly host plants were found at Campus C, Airlangga University. Three species of host plants with the highest number were *Wodyetia bifurcata*, *Manilkara zapota*, and *Musa paradisiaca*.

Five species of fruit flies were found during the study. All fruit flies trapped were male, except for two individuals of *B. carambolae* since methyl eugenol attracts only male fruit flies. *B. carambolae* females that were found at site seven were likely because there were many host plants that start to flower, bear young fruit, even mature fruit. Female fruit flies are attracted to chemical stimuli which influence oviposition preference. Methyl eugenol confuses host selection and thus traps the females. Female fruit flies are attracted to and react strongly to the smell of the host or bait when they have mated and ready to lay eggs (Jang, 1995).

Table 1. Family, species, and number of individual host plants at the study site

Family	Species	Total
Anacardiaceae	*Mangifera indica*	56
Annonaceae	*Annona squamosa*	2
Arecaceae	*Cocos nucifera*	1
	Cocos nucifera var. *eburnea*	3
	Salacca zalacca	4
	Wodyetia bifurcata	309
Caricaceae	*Carica papaya*	20
Gnetaceae	*Gnetum gnemon*	1
Moraceae	*Artocarpus altilis*	2
	Artocarpus camansi	11
	Morus alba	3
Muntingiaceae	*Muntingia calabura*	4
Musaceae	*Musa aromatica*	2
	Musa paradisiaca	77
Myrtaceae	*Psidium guajava*	22
	Syzygium aqueum	15
	Syzygium cumini	3
	Syzygium malaccense	2
Oxalidaceae	*Averrhoa bilimbi*	6
	Averrhoa carambola	6
Rubiaceae	*Morinda citrifolia*	1
Rutaceae	*Citrus aurantifolia*	2
Sapotaceae	*Manilkara zapota*	124
Solanaceae	*Capsicum annuum*	5
Strelitziaceae	*Ravenala madagascariensis*	1
Number of individuals		682
Number of species		25

Table 2. Abundance of fruit flies at each observation site

Site	Species					Total
	B. carambolae	*B. dorsalis*	*B. minuscula*	*B. occipitalis*	*B. musae*	
1	40	21	12	1	-	74
2	33	23	9	1	-	68
3	54	40	3	1	-	98
4	103	44	4	4	-	155
5	60	16	5	1	-	82
6	65	29	4	1	-	99
7	68*	38	9	1	2	116*
8	109	31	15	1	4	160
9	172	64	33	-	-	269
Total	704*	306	94	11	6	1121*

Note: *= include 2 female individuals

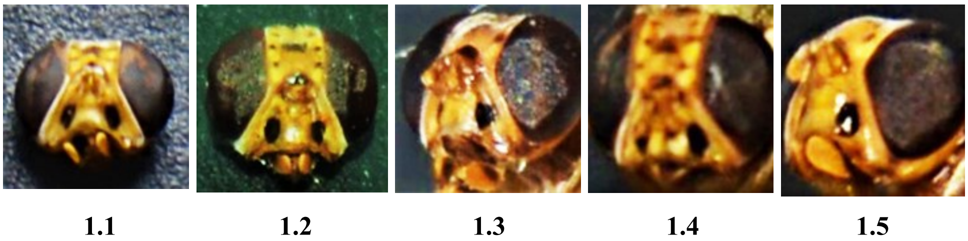

Figure 1. The head of *Bactrocera* spp.: 1. *B. carambolae*, 2. *B. dorsalis*, 3. *B. minuscula*, 4. *B. occipitalis*, 5. *B. musae*.

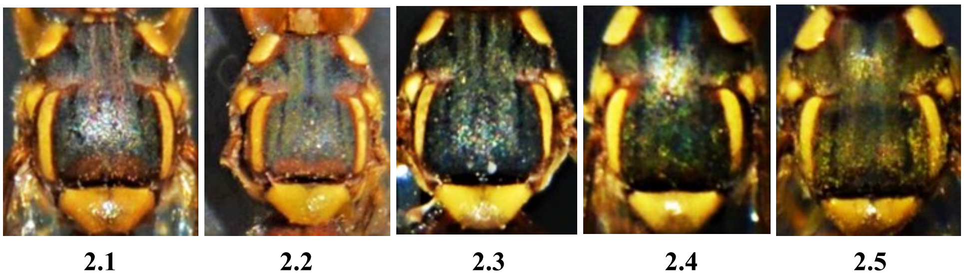

Figure 2. The thorax of *Bactrocera* spp.: 1. *B. carambolae*, 2. *B. dorsalis*, 3. *B. minuscula*, 4. *B. occipitalis*, 5. *B. musae*.

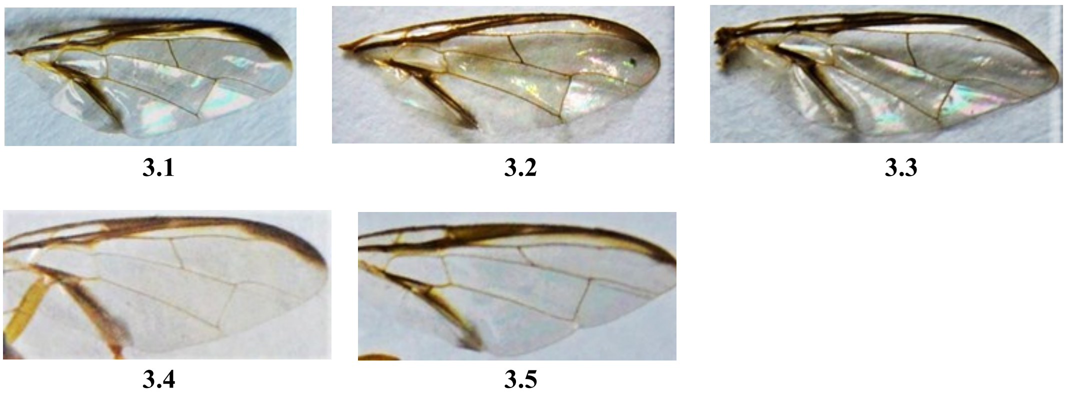

Figure 3. The wings of *Bactrocera* spp.: 1. *B. carambolae*, 2. *B. dorsalis*, 3. *B. minuscula*, 4. *B. occipitalis*, 5. *B. musae*.

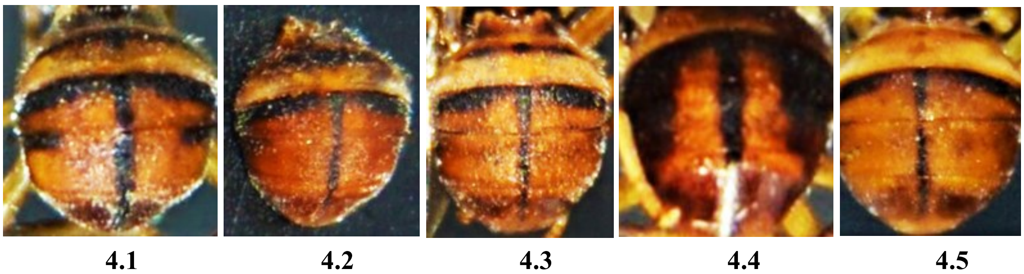

Figure 4. The abdomens of *Bactrocera* spp.: 1. *B. carambolae*, 2. *B. dorsalis*, 3. *B. minuscula*, 4. *B. occipitalis*, 5. *B. musae*.



5.1 **5.2** **5.3**


5.4 **5.5**

Figure 5. The legs of *Bactrocera* spp.: 1. *B. carambolae*, 2. *B. dorsalis*, 3. *B. minuscula*, 4. *B. occipitalis*, 5. *B. musae*.


6.1 **6.2**

Figure 6. *Bactrocera carambolae*: 1. Male, 2. Female (with ovipositor).

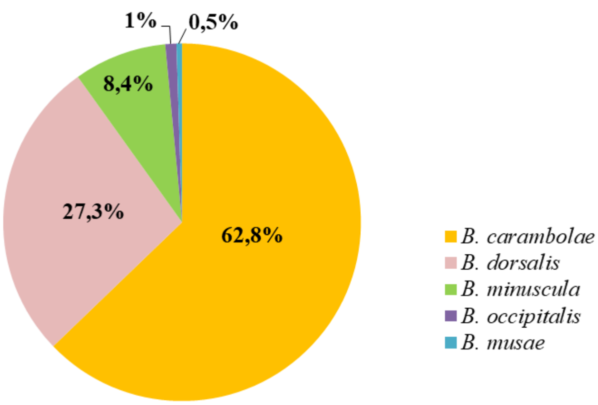

Figure 7. Composition of fruit fly species found during the study.

Table 3. Dominance index of fruit flies at Campus C, Airlangga University

Species	Abundance (ni)	F	d/dn
B. carambolae	704	0.628	d
B. dorsalis	306	0.273	d
B. minuscula	94	0.084	nd
B. occipitalis	11	0.009	nd
B. musae	6	0.005	nd
Total Individuals (N)	1121		
S	6		
1/S	0.167		

Note: F = frequency; d = dominant; nd = non-dominant

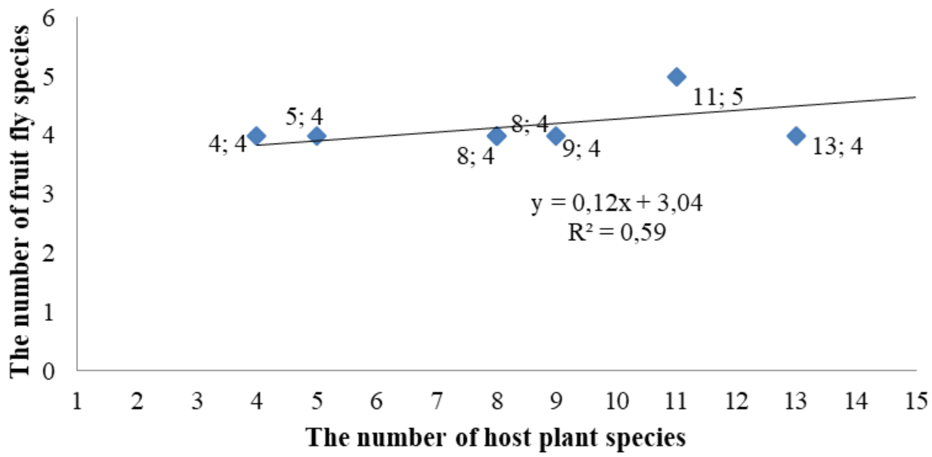

Figure 8. Correlation between the number of host plant species and fruit flies.

However, only two female individuals were trapped, most likely because the females happened to be near the bait.

The community structure at sites one, two, seven, and eight was less stable with a moderate level of individual distribution, meanwhile the community structure at sites three, four, five, six, and nine was unstable with a low level of individual distribution. The diversity level was low to moderate because there was a dominant species and make a competition. The diversity levels of fruit flies at Campus C, Airlangga University were consistent with the report from Aceh market using a modified Steiner trap showing low and moderate levels of *B. carambolae* and *B. dorsalis* from four locations (Sayuthi et al., 2019). *B. carambolae* and *B. dorsalis* were the two dominant species found with the highest number of individuals because they were the most widely spread and polyphagous with the highest number of host plants. The number of *B. dorsalis* individuals was fewer than *B. carambolae*, even it has more host plant species due to competition factor. *B. carambolae* is more competitive than *B. dorsalis*. The flowering and fruiting factors of the host plant also contributed to the abundance of *B. carambolae* and *B. dorsalis* compared to the the other three species. The host plants of *B. carambolae* and *B. dorsalis* produce flowers and fruits continuously, while the host plants of other species are seasonal. A report from Bali showed that *B. dorsalis* dominated because the research was conducted in papaya gardens (Suartini et al., 2015). The results of this research are in accordance with the research in Bogor which showed that *B. carambolae* was the most dominant species, because *B. carambolae* is a polyphagous fruit fly that can attack the most of hosts (Larasati et al., 2013).

The small number of individuals of *B. minuscula*, *B. papayae*, *B. occipitalis*, and *B. musae* which were found at Campus C, Airlangga University, perhaps because the flowering and fruiting conditions of the host plant were not synchronous (Zida et al., 2020). The results of this study are in line with several studies which showed that *B. carambolae* was the most dominant species (Pranowo et al., 2009; Sodiq et al., 2015; Suwarno et al., 2018). *B. dorsalis* was also found with a total of 155 individuals in another report (Robson et al., 2019). Based on the research that has been done and related research, it is confirmed that the distribution of *B. carambolae* and *B. dorsalis* is very wide, and very competitive with an abundant number of host plants (Saputra et al., 2019).

The distribution pattern of fruit flies in Campus C, Airlangga University tends to be aggregated. The distribution pattern of aggregates is most common in nature due to various environmental conditions, even though the location is not very wide (Pleasants, 1971). The aggregated distribution pattern of fruit flies is caused by similarities of the environment, climate, the existence of associations, the presence of food sources that are concentrated in certain locations, and the specificity of fruit flies in selecting host plants. Another factor that can influence aggregated distribution patterns is that fruit flies have trace pheromones as a signpost so that fruit flies are able to follow previous fruit fly trails leading to trap (Kardinan, 2019). *B. occipitalis* has an evenly distributed pattern with a small number of individuals due to the intense competition. In addition, the host plant of *B.occipitalis* in the study site was limited.

Humidity, temperature, sunlight intensity, and wind speed at Campus C, Airlangga University are suitable and optimal to support the existence of fruit fly populations. Temperature can affect the development of fruit flies (Solomon et al., 2018). However, this contradicts other studies which have shown that fruit fly abundance is not influenced by temperature (Susanto et al., 2017). The main factor that affects the presence and diversity of fruit flies is the host plant (Ardiyanti et al., 2019; Sayuthi et al., 2019). The diversity of fruit flies increases with the number of host plant species (Larasati et al., 2013; Khaeruddin, 2015; Susanto et al., 2017; Sayuthi et al., 2019). The results showed that the number of host plant species had a strong correlation with the number of fruit flies at Campus C, Airlangga

Universty. The variation in fruit fly species is influenced by the presence of the host plant, host plant species, and adaptation to the environment (Astriyani et al., 2016). The host plants are a source of food and a place for laying eggs. It plays a role in the development of the fruit fly population (Susanto et al., 2017). The presence of the host is followed by flowering and fruiting factors (Montoya et al., 2000; Sodiq et al., 2016). Fruit flies search for the source of the scent of methyl eugenol through chemical and visual cues in the form of yellow trap. Chemical and visual cues are used to find food sources. Therefore, host plants that produce seasonal fruit are a limiting factor.

B. dorsalis has 305 host plant species from 50 families and *B. carambolae* 26-45 families (Pramudi & Rosa, 2016; Tape et al., 2016; CABI, 2018; Kardinan, 2019). Star fruit and guava are the main host plants for *B. carambolae* (CABI, 2018; Suwarno et al., 2018; Sahetapy et al., 2019; Susanto et al., 2019). The main host plants of *B. dorsalis* are chili, tomato, banana, orange, star fruit, guava, mango, jackfruit, apple, watermelon, and melon. Banana is the main host of *B. musae* (Sunarno & Popoko, 2013). Guava and mango are the main host plants of *B. occipitalis* (Plant Health Australia, 2016). The host plant of *B. minuscula* is still unknown (Suputa et al., 2010).

For humans, fruit flies are economically significant pests for vegetable and fruit farming. Fruit flies cause fruit to rot and fall prematurely (Follett et al., 2019). It is necessary to control the fruit fly population and maintain the balance of the ecosystem so that the quality and quantity of plant production remain good. To control the pests, the use of yellow traps with methyl eugenol as bait can be applied because it does not leave harmful residues (Han et al., 2017; Kumbara et al., 2018; Hodiyah et al., 2019).

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VOL. 47, NO. 2, DECEMBER 2020

CONTENT