

Short Communication: Tabanid and muscoid hematophagous flies as potential vectors of Surra Disease in Yogyakarta, Indonesia

NILA QUDSIYATI¹, RADEN WISNU NURCAHYO^{2,*}, DWI PRIYOWIDODO²,
SOEDARMANTO INDARJULIANTO³

¹Veterinary Science Doctoral Program, Faculty of Veterinary Medicine, Universitas Gadjah Mada. Jl. Fauna No. 2, Karanggayam, Caturtunggal, Depok, Sleman 55281, Yogyakarta, Indonesia

²Department of Parasitology, Faculty of Veterinary Medicine, Universitas Gadjah Mada. Jl. Fauna No. 2, Karanggayam, Caturtunggal, Depok, Sleman 55281, Yogyakarta, Indonesia. Tel./fax.: +62-274-6411525, *email: wisnu-nc@ugm.ac.id

³Department of Internal Medicine, Faculty of Veterinary Medicine, Universitas Gadjah Mada. Jl. Fauna No.2, Karanggayam, Caturtunggal, Depok, Sleman 55281, Yogyakarta, Indonesia

Manuscript received: 9 July 2022. Revision accepted: 1 February 2023.

Abstract. Qudsiyati N, Nurcahyo RW, Priowidodo D, Indarjulianto S. 2023. Short Communication: Tabanid and muscoid hematophagous flies as potential vectors of Surra Disease in Yogyakarta, Indonesia. *Biodiversitas* 24: 675-680. As a tropical country, Indonesia provides disease vectors and various kinds of parasitic diseases, such as surra disease caused by *Trypanosoma evansi*, which is transmitted by blood-sucking insects (flies), with a suitable environment. The disease is responsible for economic losses due to the decrease in beef production, and it can also be a potential zoonosis threatening human health. Disease prevention with vaccines is still unavailable. Therefore, treatment and prevention are carried out to eradicate flies with insecticides that can be hazardous to both humans and the environment. The present study aims at identifying the species and the phenology of potential surra fly vectors based on habitat differences. It was conducted from April to June 2022 in the Andini Mulyo farmer group, lowland Bantul and Maju Jaya farmer group, highland Kulon Progo, Daerah Istimewa Yogyakarta (DIY). The flies were caught using the NZi trap placed randomly or adjacent to *Trypanosoma*-positive cattle pens. The results showed that there were eight species of flies found in the Maju Jaya group, namely *Tabanus megalops*, *T. rubidus*, *Tabanus* sp., *Stomoxys indica*, *S. calcitrans*, *S. sitiens*, *Haematobia irritans*, and *Musca domestica*. Of them, except *Tabanus megalops* and *Tabanus* sp. were also recorded in Andini Mulyo group. The dominant vegetation found in Andini Mulyo and Tani Maju, respectively, are rice plants and wild plants, so the abundance of flies and the species richness of flies had a positive correlation with the Tani Maju group's vegetation. The potential flies as surra disease vectors in the area found in surra disease cases were biting flies such as *T. megalops*, *T. rubidus*, *Tabanus* sp., *S. indica*, *S. calcitrans*, *S. sitiens*, *Haematobia irritans*. In addition, the hematogenous flies in Bantul and Kulon Progo could potentially cause the wider spread of surra disease and the decrease cow weight.

Keywords: Cow, flies, *Trypanosoma*

INTRODUCTION

As a tropical country, Indonesia serves as a suitable host for disease vectors and various kinds of parasitic diseases, such as surra disease, which is still unresolved, with a suitable environment. Surra disease is caused by the blood protozoan *Trypanosoma evansi*, which is transmitted by vectors such as *Tabanus* spp., *Stomoxys* spp., *Haematobia* spp., fleas, ticks, and other hematophagous species. The disease has a variety of hosts and is geographically widely distributed. The spread of surra disease cases in Indonesia is supported by rainy weather that can increase the vector (Nurcahyo 2017). Its zoonotic potential was demonstrated in 2004 when the first reported parasite *T. evansi* infecting an Indian cattle farmer was followed by other human case reports. The first report of human trypanosomiasis of 24 serum samples from farmers in the Southwest Sumba district showed that there were 4 (16.7%) seropositive for antigen *T. evansi* (Sawitri et al. 2019).

Farmers in surra outbreak areas are at high risk of trypanosomiasis cases due to the presence of a vector that enables farmers to come into contact with surra vectors (Sawitri et al. 2019). Another casual factor is the location of the cattle pens close to residential areas, which is very potential to spread zoonotic parasitic diseases to humans (Novita 2019). Efforts to prevent surra disease have been made in Indonesia, such as maintaining environmental sanitation and immediately going to the nearest healthcare service facility in the case that someone is affected by the disease for a week (Novita 2019). However, the treatment becomes ineffective because of the resistance of drugs such as isometamidium chloride and diminazene aceturate (Nuryady et al. 2019). Additionally, the efforts to treat the disease have not managed to overcome the problem of the economic losses resulting from it. Therefore, it is necessary to prevent and control it in order to avoid a decrease in beef production. All of the efforts should be supported by the information related to biodiversity as an agent for the spread of the surra disease that affects Yogyakarta and

Brebes, Central Java. The flies caught in Yogyakarta were *Stomoxys calcitrans* (51.2%), *Haematobia irritans* (19.6%), *Tabanus rubidus* (16.9%), *Hippobosca* sp. (6.9%), and *T. striatus* (5.4%) (Nurcahyo et al. 2017). Unfortunately, the previous study of flies in Yogyakarta did not provide the general public with pictures and detailed morphology of every fly species.

The present study puts emphasis on the urgency of the prevention of the disease in the newly affected areas. It is necessary to conduct a further and more integrated study of the vectors in the affected areas considering that play an important role in the transmission of surra cases. This study aimed at identifying and analyzing the diversity and the phenology of potential surra fly vectors based on habitat differences in Bantul and Kulon Progo, Daerah Istimewa Yogyakarta (DIY). It was conducted in Bantul and Kulon Progo, in which positive surra disease was detected in cows. The strength of the study compared to the previous study is that there has not been any information and data of the infestations of beef cattle by fly species in Bantul. It is expected that it could reduce the risk factors and break the chain of distribution of the disease. Based on the background above, it is necessary to study the diversity of beef cattle so that policies of surra disease vector control can be made and implemented, especially in DIY. The pre-study of *Pendidikan Magister Menuju Doktor untuk Sarjana Unggul* (PMDSU) or The Master Education for Doctoral Study of Excellent Scholars identified and collected flies' potential to spread surra in DIY before molecular analyses were performed.

MATERIALS AND METHODS

Study areas

The study areas were selected by considering a large number of cases in the areas (Owino et al. 2021). The study was conducted in areas with repeated outbreaks of Surra disease or an increasing number of cases in cattle. It used two altitude-based habitat types, which were Maju Jaya group of Kulon Progo representing highland (161 above sea level/asl) and Andini Mulya group of Bantul representing lowland (32 asl) in DIY (Figure 1).

Procedures

Ethics statement

The methods for flies collection in the study was certified by the institutional animal care and use committee (IACUC) of the Faculty of Veterinary Medicine of Gadjah Mada University, with reference number 028/EC-FKH/Eks./2022 and informed consent from Kulon Progo and Bantul service and cattlemen of the cattle pens of the Andini Mulyo and Tani Maju groups.

Trap planning

The NZi fly traps were placed randomly or adjacent to the *Trypanosoma*-positive cattle pens, approximately 10 cm above the ground level, amid the forage, and about 5 m from the cattle pens. Cow dung and urine were placed at the bottom of the fly traps. Previous studies used 1,8-octanol attractant or cow urine and acetone (Mugasa et al. 2018). The traps were placed in the location by paying good attention to the ecotone site, the border between two different environments (pens near positive cows and forage lands such as rice fields or puddles) so that the blue color of NZi to attract *Tabanus* flies into the traps (Kalbuadi et al. 2016).

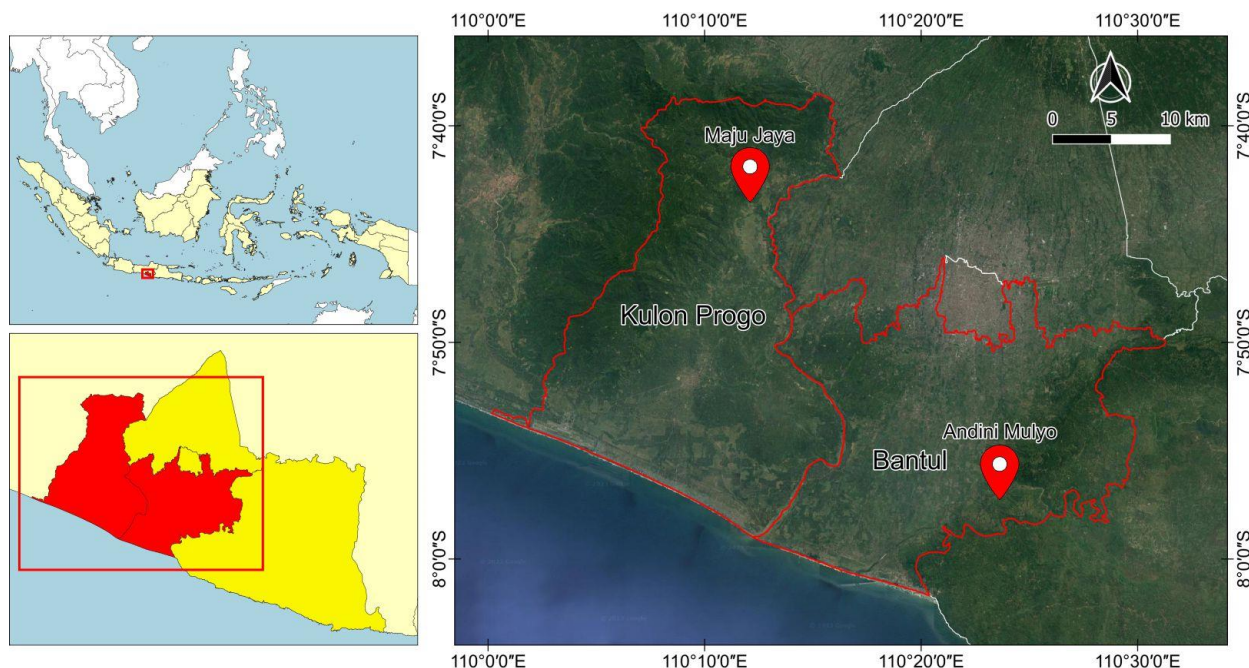


Figure 1. The study locations: Maju Jaya group (7°43'44.3\" S, 110°11'52.2\" E), Andini Mulyo group, Bantul (7°56'29.0\" S, 110°22'38.7\" E), Yogyakarta, Indonesia

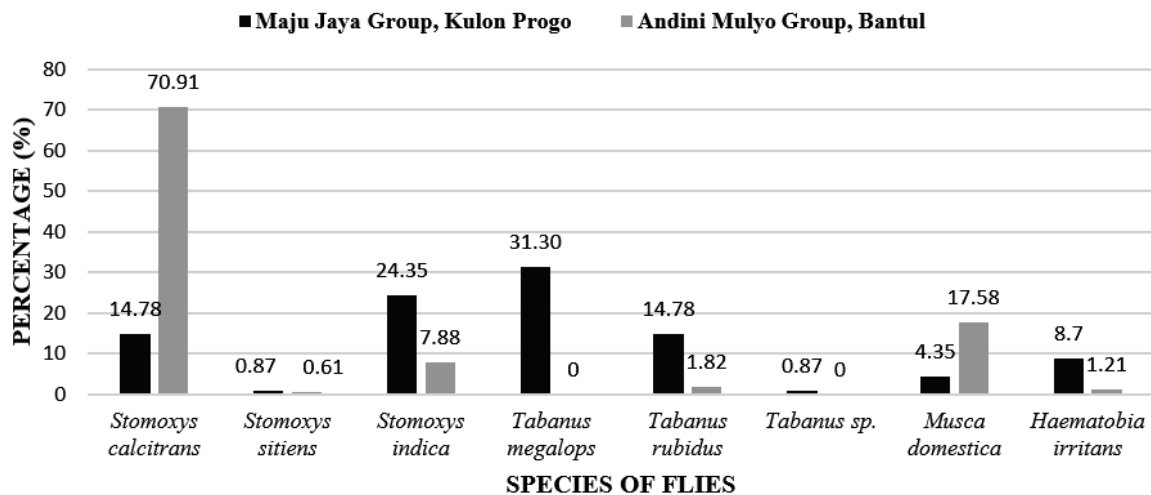


Figure 2. The percentage of the flies in “Maju Jaya” group, Kulon Progo and “Andini Mulyo” group, Bantul, Yogyakarta, Indonesia

Flies’ collection

The study was conducted from April to June 2022. The flies were caught using an NZi trap every weekend (on Saturday in Bantul and on Sunday in Kulon Progo). Samples were drawn using a purposive sampling technique in sunny weather from 08.00 a.m. to 04.00 p.m. every hour in insecticide-free conditions. The caught flies were placed in a plastic bag and then stored in a cooler box containing 4°C ice cubes. All of the in-field specimens were labeled (location, date, and time of collection).

Flies’ identification

The flies were identified using important characteristics, such as wing venation, abdomen pattern, and eye distance. The identification of flies is based on journals and identification books. For the genus *Stomoxys*, we referred to Tumrasvin and Shinonaga (1978); Masmeatathip et al. (2006); Phasuk et al. (2013); Lorn et al. (2019); Soviana et al. (2019); Prihandono et al. (2021); Rochon et al. (2021); Makhahlela et al. (2022). The identification of the *Tabanus* was based on journals and books such as Desquesnes et al. (2018); Mugasa et al. (2018); Wongthangsiri et al. (2019); Changbunjong et al. (2021). The identification of *Musca domestica* was based on Masmeatathip et al. (2006); Geden et al. (2021); Rochon et al. (2021), while *Haematobia irritans* referred to Brewer et al. (2021). The photos of flies were taken using a Sony A6000 camera, Sony E 30mm lens, and Lightning YN 600.

Data analysis

Data were analyzed descriptively. The population of the diverse flies from Andini Mulyo group, Bantul and Tani Maju group, Kulon Progo, DIY was expressed as percentages using Microsoft Excel.

RESULTS AND DISCUSSION

Results

There were 8 fly species found in the cattle of the Tani Maju group, including *Stomoxys calcitrans*, *S. indica*, *S.*

sitiens, *Tabanus megalops*, *T. rubidus*, *Tabanus sp.*, *Musca domestica*, and *Haematobia irritans*. Six of the species were found in the cattle of the Andini Mulyo group, while the *Tabanus megalops* and the *Tabanus sp.* were not found. The *T. megalops* had the biggest percentage in Maju Jaya (31.30%), followed by *S. indica* (24.35%), and the smallest was *S. sitiens* and *Tabanus sp.* (0.87%). The *S. calcitrans* and the *Musca domestica* had the biggest percentages in Andini Mulyo group (70.91% and 17.58%, respectively), and the smallest was the *S. sitiens* (0.61%) (Figure 2).

Discussion

The *Stomoxys calcitrans* had a blade-like trunk close to the head, the thorax had a checkerboard pattern, and the abdomen had a checkered pattern, one middle spot, and two parallel round spots on the dorsal side of the second and third segments (Figure 3A). The morphology of *S. calcitrans* in the study was consistent with previous studies (Prihandono et al. 2021; Makhahlela et al. 2022). The hallmark of the m1+2 wing venation was slightly forward and met the ribs just behind the wing apex (Rochon et al. 2021). The data group of the *S. calcitrans* flies had different meanings in the two study sites. The average fly species to the humidity of *S. calcitrans* was found higher in the “Andini Mulyo” group than in the “Maju Jaya” Group because of its compatibility with the environment (relative humidity and light intensity).

It was consistent with a study (Phasuk et al. 2013) showing that weather parameters such as relative humidity and light intensity were significantly correlated with the abundance of the *S. calcitrans*. The results of the analysis of the data of the Andini Mulyo group were also consistent with previous studies showing that the most common *Stomoxys* species was *S. calcitrans*, followed by *S. indicus* and *S. sitiens* (Lorn et al. 2019; Soviana et al. 2019). Another study of the diversity of the *Stomoxys* spp. at dairy cattle farms in Pangalengan, Bandung district, which was caught by using Vavoa and NZi traps every month, also showed that *S. calcitrans* was the dominant fly population (Kusumastuti et al. 2022).

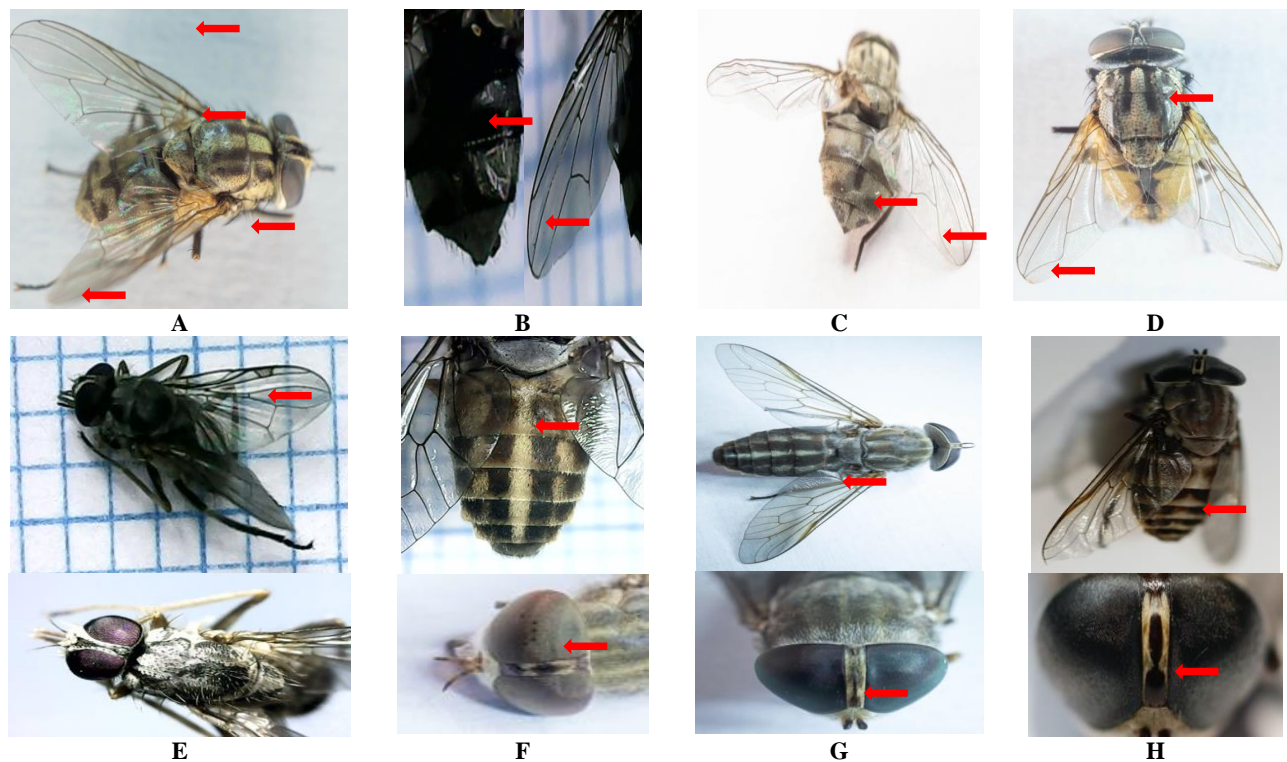


Figure 3. The characteristics and the morphology of flies indicated by red Arrow. A. *Stomoxys calcitrans*; B. *S. sitiens*; C. *S. indica*; D. *Musca domestica*; E. *Haematobia irritans*; F. *Tabanus megalops*; G. *T. rubidus*; H. *Tabanus* sp.

The species *Stomoxys* caught in Bantul, and Kulon Progo were *S. sitiens* and *S. indica*. The *Stomoxys sitiens* had an abdominal pattern of two distinct lateral black spots extending over the second and third abdominal segments (Tumrasvin and Shinonaga 1978; Masmeatathip et al. 2006). The characteristics of the *S. sitiens* indicated by red arrows can be seen in Figure 3B. It differed from the *Stomoxys indica*, which had a gray-brown abdomen with distinct spots or transverse bands (Figure 3C). The characteristics were consistent with the studies by Tumrasvin and Shinonaga (1978) and Masmeatathip et al. (2006).

The morphology of the *Musca domestica* was almost similar to that of the *S. calcitrans*, but both species could be distinguished by the pattern of their abdomen, thorax, and wings (Masmeatathip et al. 2006). The unique morphology of the *M. domestica*, especially its wing venation, was characterized by a sharp m1+2 characteristic forward and meeting the ribs in the anterior position to the wing crest (Rochon et al. 2021). The characteristics of *M. domestica* were red eyes, a spongy mouth, four dark lines on the thorax, an upward notch in the fourth wing vein (m1+2), an abdomen along the sides, the dark longitudinal band along the dorsal median anterior segment, and space. The eyes of female flies were farther apart than that of males, and male flies showed greater lateral yellowing than females (Geden et al. 2021). The hallmark of wing venation of the *M. domestica* was an upward indentation on the fourth wing vein (m1+2), a spongy mouth, four dark

lines on the thorax, and the abdominal pattern could be seen in Figure 3D indicated by red arrows.

Haematobia irritans was an external ectoparasite in cattle. Adult flies were 3-5 mm long and had a piercing/sucking proboscis. Wing vein m1 with forward curvature (Figure 3E). The chest was black, and the belly had a brown midline with a dark posterior border. An egg length of 1 mm was deposited at the bottom of cow dung (Brewer et al. 2021).

The morphology of the *Tabanus* genus was characterized by an inherited brown antenna (Mugasa et al. 2018). The *Tabanus* was a livestock pest because it had a large body, a mouth capable of carrying a lot of blood, very high productivity, and the behavior of moving from one house to another to transmit pathogens (Wongthangsiri et al. 2019). The tabanids were very effective bait for NZi traps in catching flies (Baldacchino et al. 2014). It was used in the NZ1 trap in the form of volatile urine from ungulates (horses, sheep, and cows) (Baldacchino et al. 2012). The species of *Tabanus* found in Andini Mulyo group and Maju Jaya group was *T. rubidus*. The average number of the species differed in the two study sites, while the *T. megalops* and the *Tabanus* sp. were found only in the Maju Jaya group during the study.

The typical morphology of the *T. megalops* was characterized by a brownish dorsal abdomen, no dark median line on the yellowish abdomen, and a basal callus close to the eye (Figure 3F). The belly line generally had a lighter dark color, from black to brown (Wongthangsiri et al. 2019). The midline of the second tergite was crossed by a

pale tomentum and hairline (Changbunjong et al. 2021). The biggest percentage of *T. megalops* (31.30%) was found in the Maju Jaya group, Kulon Progo, because the habitat had more complex plants than that of Andini Mulyo group, Bantul. The previous studies showed that *T. megalops* held a prominent dominance in the total number of collected Tabanid flies in the sampling period in National Park (NP). The NP consisted of a primary forest, which naturally contained multispecies biodiversity (Alvernita et al. 2016). It was also consistent with Changbunjong et al. (2018), stating that the species diversity of horse flies in primer forests was higher than in other habitats (villages and secondary forests).

The morphology of *T. rubidus* was characterized by a basal callus that was triangular than rectangular (Changbunjong et al. 2021), as indicated by the red arrow in (Figure 3G). Another species of *Tabanus* was characterized by the dorsal abdomen with median and sub-lateral lines and the left-wing indicated by the red arrow at the base of the hexagonal disc cells (Figure 3H). However, we have not been able to identify it at the species level. It was caught in the Maju Jaya group, but it was not found in the Andini Mulyo group during the study period. Therefore, it was necessary for an entomologist to be aware of it and to further test it using a molecular test (PCR) to determine the species of the fly.

The community in the composition of tabanids correlated significantly with the slope, altitude, and size of unforested patches. The altitude could have a negative or positive effect on the species. The abundance of flies and the species richness were negatively correlated with large open habitats and positively correlated with patch-shape complexity (Baldacchino et al. 2013a). The results of the study showed that the Maju Jaya group was situated in a highland area and had a complex environment with a variety of plants, so the abundance of the *Tabanus megalops* and *Tabanus* sp. increased at the Andini Mulyo group in lowland Bantul.

Flies, as the mechanical non-cyclic vectors of *T. evansi*, caused surra disease (Radwanska et al. 2018). The flies were also mechanical vectors of pathogens in livestock and occasionally in humans. They inflicted direct losses to livestock in the form of skin lesions, disturbances, reduced food intake, stress, blood loss, and immunosuppressive effects. The indirect effect of pathogen transmission was interrupted feeding, and *Stomoxys* restarted their blood feeding on other hosts. At the time of injecting saliva before sucking blood, it injected some of the infected blood remaining in its mouth (Baldacchino et al. 2013b).

In conclusion, the more complex the plants in a habitat, the higher diversity of flies and the more potentially hematophagous as surra disease vectors such as *Tabanus* sp., *T. megalops*, *T. rubidus*, *S. calcitrans*, *S. sitiens*, *S. indica*, and *Haematobia irritans*.

ACKNOWLEDGEMENTS

The study was supported by the Ministry of Research, Technology, and Higher Education of the Republic of

Indonesian through Pendidikan Magister Menuju Doktor Untuk Sarjana Unggul (PMDSU), Master Education for Doctoral Study of Excellent Scholars with contract number (089/E5/PG.02.00.PT/2022) and derivative contract number (1988/UN1/DITLIT/DitLit/PT.01.03/2022). Thanks to April Hari Wardhana, Ph.D. (Indonesian Research Center for Veterinary Sciences, Bogor); Dr. drh. Irkham Widiyono (Department of Internal Medicine, Gadjah Mada University); Dr. drh. Joko Prastowo, Dr. drh. Ana Sahara, drh. Lintang Winantya Firdausy, drh. Vika Ichsanita Ninditya (Department of Parasitology, Gadjah Mada University), drh. Shabrina Riztia Kusumastuti, and drh. Nabilah Putroe Agung, who has helped us and given us advice for this article. We would also like to thank Jocelinda Wibisono Oey and Roza Febria Diniah Putri, who have helped us with assistance in the flies sampling. We would like to express our gratitude to BBVET Wates employees (Rochmadiyanto, drh. Nining, Koeswari, Nurrahman, Suci, Bayu), Kulon Progo service employees (drh. Arfian, drh. Haryadi, drh. Estu, and drh. Wisnu), and Bantul service employees (drh. Sunari and Harsana) for information of surra case data, assistance, and advice related to this research.

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