# THE TABANID FLY BIODIVERSITY AND ITS POTENCY AS TRANSMISSION VECTOR OF TRYPANOSOMIASIS TO THE JAVAN RHINO POPULATION WITHIN THE UJUNG KULON NATIONAL PARK

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**ABSTRACT**

Javan rhinos are struggling to survive with only 63 individuals remaining in their last habitat in the world, Ujung Kulon National Park. Infectious disease has been one of the presumably challenges that faced in the Javan rhino conservation due to the unknown cause of Javan rhino die-offs without their horns detached from the body that ruled out the probability of poaching. This study is conducted to investigate the Tabanid fly within the NP as the potential vector for trypanosomiasis on Javan rhino, as they are known as the common trypanosome vector on water buffaloes and cattles.The diversity and the high amount of total Tabanid fly collected showed a high potency of cross infection between the inhabitant's livestock to ungulate sympatric animal in the NP (Javan rhino and banteng). *Tabanus megalops* holds a prominent dominance from the amount of total collected Tabanid fly from this sampling period.

**Keywords:** Javan rhino, biodiversity, Tabanid fly, vector, trypanosome, Ujung Kulon National Park

## 1. INTRODUCTION

Javan rhinoceros is one of the rarest terrestrial mammals in the world. Javan rhinos are struggling to survive with only 63 individuals remaining in their last habitat in the world, Ujung Kulon National Park. Javan rhino used to have a second home in Vietnam, however in 2011, Vietnam lost their last Javan rhinoceros and leaving the Javan rhino's Indonesia group population as the species' last resort of existence. The attempt on actualizing the Javan rhino conservation efforts are facing many complicated challenges; from the geographical location of the Park that prone to natural disaster since it lies nearby the active Mount Krakatoa, the species' small population problem, the species' feeding competition with other ungulate sympatric animal in the Park, and the unknown cause of species deaths reported.

Ujung Kulon National Park consists of two regions; the peninsula region, which is the core habitat of the Javan rhino and the Honje Mountain region that intersect directly with 19 buffer villages. The direct intersection between the NP and the inhabitant's residence cause a concern since the inhabitants are free to entering their water buffaloes in the NP. The inhabitant's main livelihoods lie on the water buffaloes as their livestock. The direct intersect of their villages to the NP allows them to rely solely and freely to shepherd their water buffaloes into the NP. This cause a big concern since the unknown cause of death within the Javan rhino population without any horns detached as a remark, has been one of the challenges that faced the Javan rhino conservation efforts. Disease surveillance study was conducted in 2014 based on this concern towards the water buffaloes' livestock of the 19 UKNP buffer villages. The surveillance study showed that two of the UKNP buffer villages; Rancapinang village (the south border of the NP) and Ujung Jaya village (the north border of the NP) shared the prevalence number of 90% to trypanosomiasis within their water buffaloes livestock (Khairani 2014).

Trypanosomiasis is a vector-borne disease that disrupting blood circulation and causing anemia that will decrease the host's body immune system. *Trypanosoma evansi* is the causative protozoan pathogen of trypanosomiasis. Trypanosomiasis is transmitted by blood sucking insects as its mechanical vector. Tabanid fly is the most common blood sucking insects that transmitted the trypanosomiasis. Trypanosomiasis attacked cattles, water buffaloes, fatal on horses, and other ungulate sympatric animals like elephants, and camels (Desquesnes 2013). *Tabanus* is known to play a significant role in transmitting infectious disease to the cattles through sucking the blood of the host (Chandra *et al.* 2005). It is also reported throughout October-November 2003, there has been case of Sumatran rhino die-offs caused by trypanosomiasis in Peninsular Malaysia (Vellayan *et al.* 2004). Aside from transmitting infectious disease to the host animals, it also caused a persistent irritation to the host's skin due to the blood sucking activity by the Tabanid fly. The infected area can also trigger the occurrence of secondary infection from other pathogens. Since *Trypanosoma evansi* circulating in the blood vessels, its main agenda is by causing anemia so that it will decrease the host's body immune system.

Infectious disease has been one of the presumably challenges that faced in the Javan rhino conservation due to the unknown cause of Javan rhino die-offs without their horns detached from the body that ruled out the probability of poaching. Water buffaloes are known as the reservoir host of the trypanosomiasis. Based on the surveillance report by Khairani (2014) on the high prevalence of the disease occurrence in two buffer villages, the study on the Tabanid fly is imperative to acknowledge the amount of mechanical vectors of the disease in both buffer villages that intersect directly to the NP. The high number of amount Tabanid fly collected in both area presumably leads to a higher risk of the cross infection between the infected water buffaloes to the other ungulate sympatric animals (Javan rhino and banteng) within the NP. This study is conducted to investigate the Tabanid fly within the NP as the potential vector for trypanosomiasis on Javan rhino, as they are known as the common trypanosome vector on water buffaloes and cattles.

## 2. MATERIALS AND METHODS

### Materials

Materials that used in this study are NZI trap, black-painted ball, black funnel, pan, hygrometer and thermometer, clocks, centrifuge tube, labels, pencils, markers, electron microscope, petri dish, collection bottles, and silica gels.

### Sampling Methods

We conduct the sampling with the help of Rhino Health Unit (RHU) team from the UKNP. We adopted the methods on the *Sleeping Sickness* caused by *Trypanosoma gambiense* with Tsetse fly as vector, which is conducted in Africa. We use NZI trap as the sampling media. We set the NZI trap in the open area without any shades from the canopy to gather the much amount of light to lure the Tabanid fly into the NZI trap. NZI trap was set using bamboos or wooden sticks approximately 50 cm from the ground to camouflage NZI trap as the water buffaloes' body to the Tabanid fly. Black-painted funnel is also placed on top of the NZI trap to attract the Tabanid fly into the collection bottle. We set the trap on the ecotone site, which is the intersection between two different environments, such as between the savanna and the forest, to create a optical contrast of the trap that increasing the appeal of the trap for the Tabanid fly. We also ornament the trap with several items, such as black-painted ball hung below the trap, pan full of water to amplify the amount of light into the trap. We collected everyday from 24 hour sampling period.

### Time and Place

We set the trap within the NP (Cidaon and Cibunar) in three sampling period: July, December 2015, and August-September 2016. The three sampling period is considered enough to represents two distinct season; wet and dry season, respectively. We conduct the sampling within the NP for 3-4 days each period. We collected the samples with dry preservation methods using silica gel as the media. All Tabanid fly collected in a centrifuge tube filled with silica gel and tissue to separate the gel and the Tabanid fly. We labeled the sample by time and date of trap setting, time and date of collection, and other variable information such as temperature, humidity, and weather. Identification process is

conducted in the home stay at Polos, Cimanggu Subdistrict, Pandeglang District, Banten Province and at the Entomology Laboratory, Department of Animal Disease Science and Veterinary Public Health, Faculty of Veterinary Medicine, IPB-Bogor.

**Identification Process**

We identify the Tabanid fly using the electron microscope based on taxonomy key guide from Schuurmann and Stekhoven (1926). The identified Tabanid fly is collected per species identified, collection date, and collection site in one centrifuge tube preserved later in the freezer. The identified samples also labeled by the species name, the amount of the species, collection site, time and date of setting and collection, and other variable information.

We sometimes collected samples that in bad condition, such as too dry to be identified. For samples that we have a hard time to identify it, we bring the samples to Entomology Laboratory, Department of Animal Disease Science and Veterinary Public Health, Faculty of Veterinary Medicine, IPB-Bogor, to have a discussion with the lecturer staff regarding the samples' identification process.

**Data Analysis**

The collected Tabanid fly is analyzed descriptively using frequency distribution table. We use the relative abundance value (kn), collected frequency value (ft), and dominance value (dom). We calculate each values by using formulas as followed:

$$\text{Relative Abundance Value} = \frac{\text{Total of specific species collected}}{\text{Total of all species collected}} \text{ x } 100$$

$$\text{Collected Frequency Value} = \frac{\text{Frequency of specific species collected in each collection}}{\text{Total Collection}}$$

Dominance Value = Relative Abundance x Collected Frequency Value

## 3. RESULTS AND DISCUSSION

Based on the Tabanid fly identification collected within the NP, we collected 1266 Tabanid fly from 20 Tabanid fly species. From those 20 tabanid fly species, *Tabanus megalops* holds the prime dominant with the dominance of 39.09952607. *Tabanus striatus* followed it with the dominance of 18.16745656. *Haematopota javana* represents other genus aside Tabanus in the Tabanidae subfamily came in third with the dominance of 8.478146393, followed by *Tabanus atripunctatus* with the dominance of 6.556082148, and *Tabanus rufiventris* with the dominance of 5.687203791. *Tabanus megalops* is shown have a collected frequency value of 1 along with *Tabanus striatus, Tabanus atripunctatus,* and *Tabanus rufiventris.* This means that during the whole sampling period, these species are constantly collected. Based on the data, we obtain the Margalef richness index (R1): 2.659716835 and the Menhinick's richness index (R2) of 711.617875. We also obtain the Simpson's diversity index of 0.215922672. The richness index showed the species quantity in one community. The more species quantity collected from the sampling display the rich quantity species abundance. Based on the Margalef richness index, we obtain a low value of richness due to the constant number of total species collected in the three sampling periods.

Out of 20 species identified from the collected samples, we collected three genus form two subfamilies of Tabanid fly: Chrysops genus (*Chrysops fixissima*) from the Chrysopsinae subfamily, Tabanus and Haematopota (*Haematopota javana, Haematopota fumigata, Haematopota cingulata, Haematopota irregularis*) genus from Tabaninae subfamily. Chrysopsinae subfamily has a distinct feature from the Tabaninae subfamily regarding their relatively small size body. Chrysopsinae subfamily has the body size range of 6-10 mm, whilst Tabaninae has the body size range more than 10 mm. However, despite its small size, Chrysopsinae subfamily recorded as the vector-borne zoonotic disease, such as tularemia and loiasis, whilst Tabaninae subfamily recorded as the vector-borne nonzoonotic disease, such as animal trypanosomiasis or surra and anaplasmosis.

Species Group Classification I from Stekhoven (1926) classification appeared as the most collected species member from the sampling, which placed 5 for its member on the identified species: *Tabanus megalops, T. striatus, T. rufiventris, T. rubidus,* and *T. effilatus.* Species Group Classification I is

classified for their common abdominal markings of three lateral median stripes and their black-brown, brown, blackish, and grayish body color. This species group is distributed all over Indonesia (Stekhoven 1926). *Tabanus megalops* and *T. rubidus* is also reported as the vector for trypanosomiasis in Indonesia (Hadi 2010). Table 1 showed the diversity of identified Tabanid fly species collected within the NP.

The diversity of Tabanid fly collected occurs due to the sampling site is set within the NP. NP consists of primary forest, which naturally contains the multispecies biodiversity. This high amount of total Tabanid fly collected within the NP showed the potency of cross infection of vector-borne transmitted disease from the water buffaloes to the other ungulate sympatric animals (banteng and Javan rhino) within the NP.

Table 1 Compile Sampling Data from Three Sampling Periods (July, December 2015, and August-September 2016)

| No | SPECIES | TOTAL TABANID FLY COLLECTED PER SPECIES IN UKNP | RELATIVE ABUNDANCE | Frequency | | Dominance |
|---|---|---|---|---|---|---|
| | | | | ∑Species Collected | Frequency | |
| 1 | T. megalops | 495 | 39.09952607 | 3 | 1 | 39.09952607 |
| 2 | T. striatus | 230 | 18.16745656 | 3 | 1 | 18.16745656 |
| 3 | T. rufiventris | 72 | 5.687203791 | 3 | 1 | 5.687203791 |
| 4 | T. ceylonicus | 66 | 5.213270142 | 3 | 1 | 5.213270142 |
| 5 | T. rubidus | 4 | 0.315955766 | 2 | 0.66666667 | 0.210637177 |
| 6 | T. albopunctatus | 68 | 5.371248025 | 3 | 1 | 5.371248025 |
| 7 | T. breviusculus | 4 | 0.315955766 | 1 | 0.33333333 | 0.105318589 |
| 8 | T. basalis | 1 | 0.078988942 | 1 | 0.33333333 | 0.026329647 |
| 9 | T. tristis | 9 | 0.710900474 | 2 | 0.66666667 | 0.473933649 |
| 10 | T. ilustris | 1 | 0.078988942 | 1 | 0.33333333 | 0.026329647 |
| 11 | T. aurifer | 5 | 0.394944708 | 1 | 0.33333333 | 0.131648236 |
| 12 | T. atripunctatus | 83 | 6.556082148 | 3 | 1 | 6.556082148 |
| 13 | T. canipus | 1 | 0.078988942 | 1 | 0.33333333 | 0.026329647 |
| 14 | T. immanis | 1 | 0.078988942 | 1 | 0.33333333 | 0.026329647 |
| 15 | T. effilatus | 6 | 0.473933649 | 1 | 0.33333333 | 0.157977883 |
| 16 | H. javana | 161 | 12.71721959 | 2 | 0.66666667 | 8.478146393 |
| 17 | H. cingulata | 43 | 3.396524487 | 1 | 0.33333333 | 1.132174829 |
| 18 | H. fumigata | 11 | 0.868878357 | 1 | 0.33333333 | 0.289626119 |
| 19 | H. irregularis | 1 | 0.078988942 | 1 | 0.33333333 | 0.026329647 |
| 20 | C. fixissima | 4 | 0.315955766 | 1 | 0.33333333 | 0.105318589 |
| TOTAL | | 1266 | 100 | 3 | | |

## 4. CONCLUSION

The diversity and the high amount of total Tabanid fly collected showed a high potency of cross infection between the inhabitant's livestock to ungulate sympatric animal in the NP (Javan rhino and banteng). *Tabanus megalops* holds a prominent dominance from the amount of total collected Tabanid fly from this sampling period.

### Suggestion

More sampling period is needed to investigate the richness and diversity data of the Tabanid fly collected within the NP. We also need to conduct a series of molecular biology for further investigation to confirm the correlation of the Tabanid fly as trypanosomiasis vector within the NP.

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