# Bat ectoparasites in Hong Kong and Their Specificity of Host-parasite Interaction

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### 1. Abstract

The variety of bat flies, an obligate ectoparasite of bat, in Hong Kong as well as the specificity of host-parasite association are investigated in this study. In the 344 bat fly individuals collected, a total of 9 taxon groups is identified based on morphological observation and DNA barcoding results, with the most abundant ones being *Phthiridium* sp. and *Brachytarsina kanoi*. Host specificity of the bat flies greatly varies among different species, with some of them being associated with only one hosts while some are found to be infesting multiple bat genera.

### 2. Introduction

#### **Bat flies (Diptera: Hipposboscoidea)**

- Highly specialized bat ectoparasites in two families: Nycteriibidae and Streblidae<sup>1</sup>.
- Spend most their lifetimes on the fur or wing membrane of a bat and feed only on bat's blood<sup>1</sup>.

## 3.Methodology

#### **Step 1: Morphological characterization**

Specimens were separated into morphospecies using a compound microscope with reference to literatures and taxonomic keys of other regions<sup>4,5</sup>.

#### Host specificity of bat flies

- Considered to infest a wide range of host species due to multiple bat species in a single roost and the flight ability of Streblid flies<sup>1,3</sup>.
- Shown in recent controlled studies that bat flies are highly host-specific, with most of them only associated with a narrow range of congeneric bat species<sup>3</sup>.
- Degree of specificity varies with bat fly or host morphology, ecology and behaviour<sup>3</sup>.

#### **Objectives**

- To investigate the variety of bat flies in Hong Kong.
- To investigate the host-parasite association between bat flies and their hosts bats, and hence the host specificity of bat flies.



**Figure 1**: *Hipposideros armiger;* Credit: Hon Shing FUNG

5

1.9

5

1.9

5.9

50

15.1

50

25

26.8

44

35

75

50

1.7

4

24.4

52

### **Step 2: DNA barcoding**

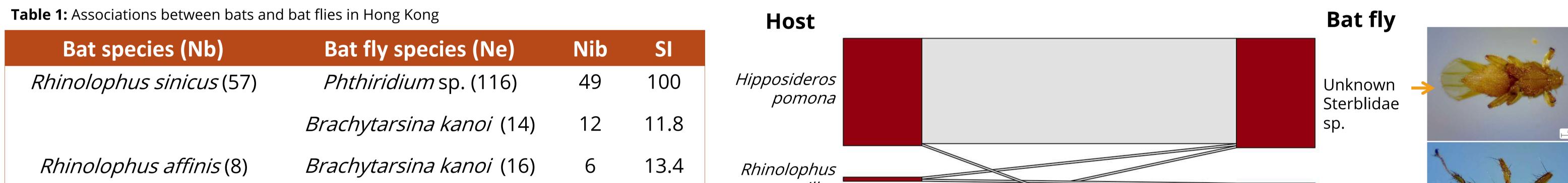
DNA was extracted from whole specimen of individuals of selected groups. A region of the mitochondrial cytochrome *c* oxidase subunit I (COI) gene was targeted and amplified for sequencing.



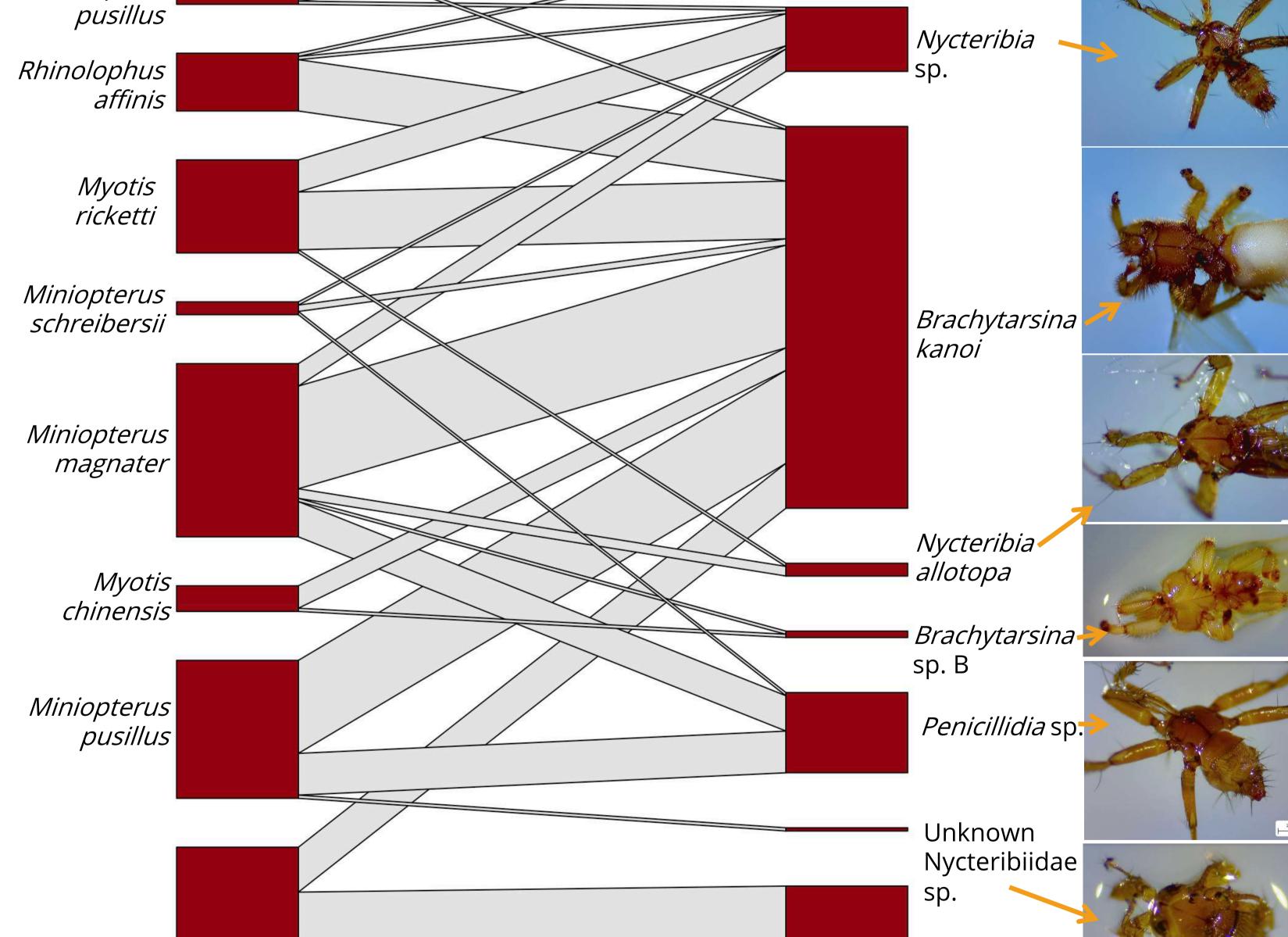
Figure 2: Lateral (left) and dorsal (right) view of a mounted bat fly (Nycteribiidae); Credit: Dr. Simon SIn

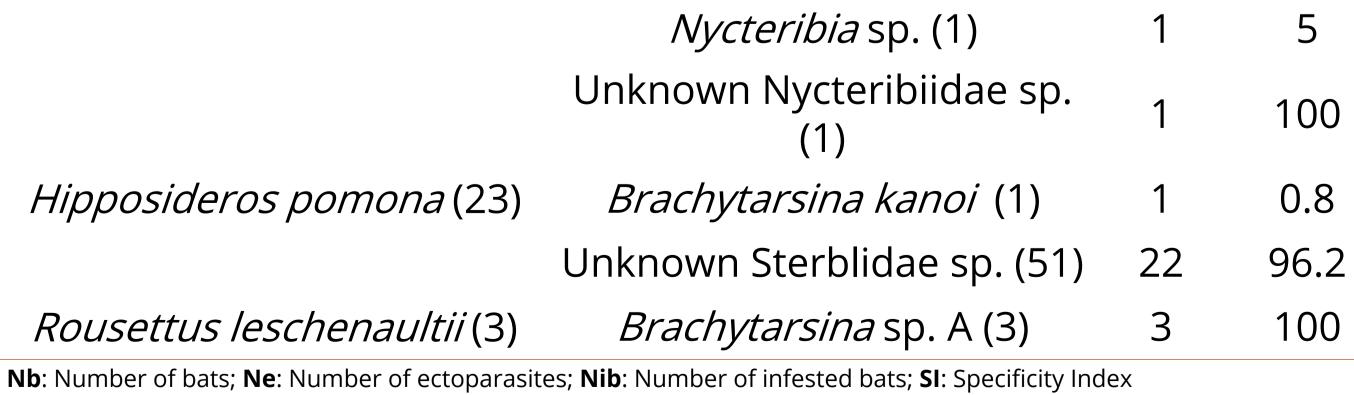
### 4. Result

X



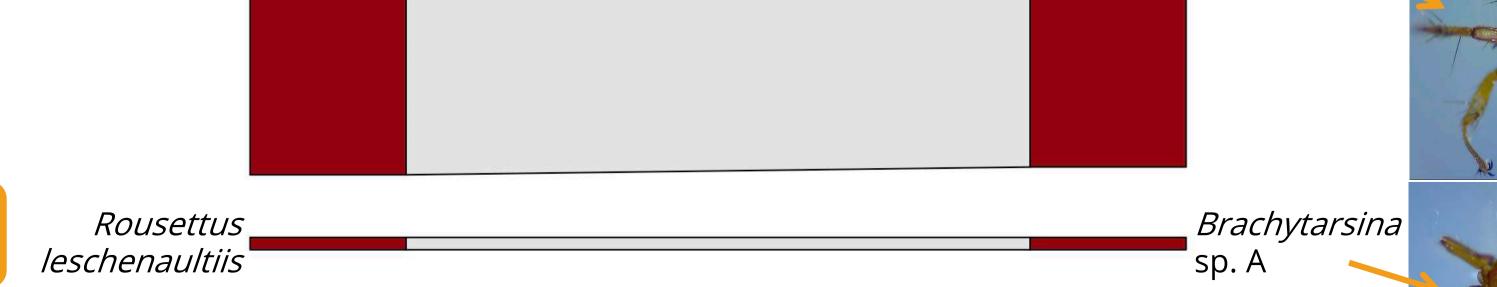
	<i>Nycteribia</i> sp. (1)	1
	Unknown Sterblidae sp. (1)	1
<i>Rhinolophus pusillus</i> (2)	<i>Nycteribia</i> sp. (1)	1
	Unknown Sterblidae sp.(1)	1
<i>Myotis chinensis</i> (5)	<i>Brachytarsina kanoi</i> (7)	4
	<i>Brachytarsina</i> sp. B (1)	1
<i>Myotis ricketti</i> (17)	<i>Brachytarsina kanoi</i> (18)	11
	<i>Nycteribia</i> sp. (10)	5
	<i>Nycteribia allotopa</i> (1)	1
<i>Miniopterus magnater</i> (24)	<i>Brachytarsina kanoi</i> (32)	17
	<i>Penicillidia</i> sp. (11)	9
	<i>Nycteribia</i> sp. (7)	7
	<i>Nycteribia allotopa</i> (4)	3
	<i>Brachytarsina</i> sp. B (1)	1
<i>Miniopterus schreibersii</i> (1)	<i>Brachytarsina kanoi</i> (2)	1
	<i>Penicillidia</i> sp. (1)	1
<i>Miniopterus pusillus</i> (19)	<i>Brachytarsina kanoi</i> (29)	18
	<i>Penicillidia</i> sp. (13)	7





### 5. Discussion and Conclusion

- A total of 9 taxon groups of bat flies were discovered from 10 bat species, with most of these genera are well known from the old world and nearby regions<sup>6</sup>.
- Host specificity of bat flies was found to be varying with different species. Different from previous studies, some groups were found be infesting multiple bat species from different genera, suggesting a possibility in behavioural difference or accidental infestation.



**Figure 3:** Interaction web between bats and bat flies in Hong Kong. Bar widths are proportional to the number of individual for each group. Photos of the bat fly groups are presented next to their names.

#### Reference

Rhinolophus

sinicus

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Phthiridium

sp.

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