



Scientific note: First report of small hive beetle in South Asia and their potential invasive pathway

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Aethina tumida Murray, also known as the Small Hive Beetle (SHB), is a well-known invasive kleptoparasite of honeybees (Hood 2004; Papach et al. 2023). Native to the sub-Saharan region of Africa, SHB has spread globally, including the other African regions (Mauritius, Reunion), the Americas (Canada, USA, Mexico, Jamaica, Cuba, Guatemala, El Salvador, Nicaragua, Brazil, Costa Rica, Colombia), Europe (Italy), Asia (China, South Korea, Philippines), and Australia (see Papach et al. 2023). While considered a minor pest in its native range, SHB more frequently causes significant damage to apiaries in invaded regions (Hood 2004; Roth et al 2022). Predominantly parasitic on European honeybees, *Apis mellifera* (Hood 2004; Roth et al 2022), its impact on the Eastern honeybee, *Apis cerana*, was unclear until recent verifications in the Philippines (Cervancia et al. 2016) and China

(Zhao et al. 2020), with no recorded impact on *A. cerana* in South Korea (Lee et al. 2017).

Until now, there has been no record of invasion in South Asia. Small hive beetle was first found on 24th June, 2020 in Bangladesh during COVID-19 lockdown. A beekeeper from Pabna District (village-Boroshalikha, Union-Gunaigacha, Upzilla-Chatmohor) informed the Department of Entomology, Sher-e-Bangla Agricultural University about unknown larval infestation in a colony of *A. mellifera*. After visual inspection of different photograph and video clips, we identified it as SHB. In the area of their first discovery, twenty-six out of thirty-four bee hives were severely damaged by the attack of small hive beetle. With the successive survey across the country from 2021 to 2024, SHB have been found widely across the country (Fig. 1).

To infer the evolutionary origin of the invasive population, four geographically distant areas of Bangladesh where SHB infestation occurs were selected (Supplementary online material 1). Subsequently, four DNA-grade samples were collected from each region, totaling 16 adult

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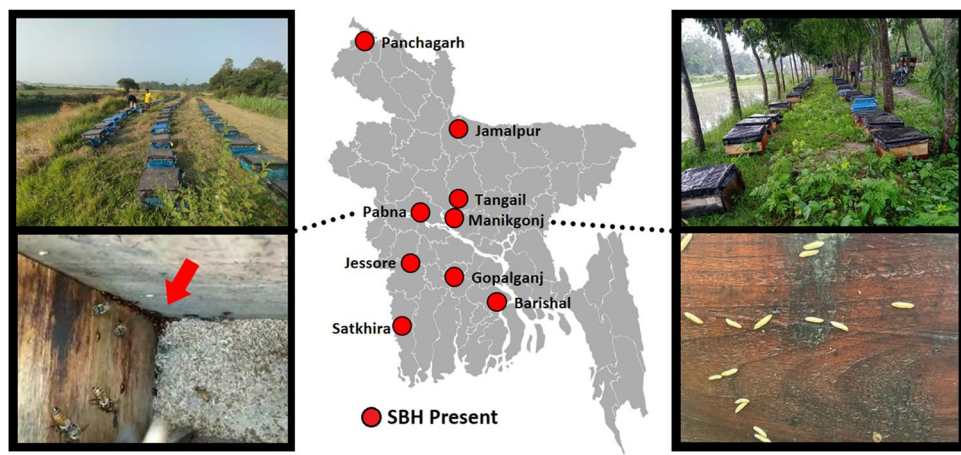


Figure 1. Distribution of *Aethina tumida* in Bangladesh and their infestation.

samples. Genomic DNAs were extracted using Qiagen DNeasy Blood & Tissue Kit following the manufacturer's protocol. It is crucial to get a wide range of genetic data from the species native ranges. Thankfully, the public COI sequences of SHB that were comprehensively generated from their native ranges enable estimating the origin of invaded populations. We downloaded 345 public sequences from 30 countries from the Genbank (Supplementary online material 2). SHB-specific primers and PCR conditions were adopted from Evans et al. (2000). MAFFT ver. 7 online (Katoh et al. 2019) was used for multiple sequence alignment, MEGA X (Kumar et al. 2018) for amino acid translation for the final sequence assessment. To run haplotype networks, TCS algorithm (Clement et al. 2000) was implemented in POPART version 1.7 (Leigh and Bryant 2015). The traits were divided into eight states representing geography (Africa, Australia, Europe, Central America, North America, South America, Asia, and Pacific). The haplotypes were divided into four haplogroups separated by a minimum distance of 20 mutational steps. The sequences obtained in Bangladesh were deposited in NCBI GenBank database with the accession number PP587232 (669 bp in length).

A previous work has demonstrated the presence of two (Cordeiro et al. 2019) or three (Liu et al. 2021) divergent lineages in SHB populations. In our study, SHB has been categorized into four haplogroups, with samples from Bangladesh being classified into haplogroup A, which is characterized by its high genetic diversity (Fig. 2). This haplogroup is native to central and northern Africa and is also found in regions beyond its native range, including areas in Europe where it has invaded. Our study marks the first identification of haplotype A invasion outside of Europe. Haplogroup B, markedly different from Haplogroup A, originates from southeastern Africa, including Madagascar, and has a wide invasive distribution across the globe including the American continent, Australia, and South Korea. Haplogroup D is unique to China and the Philippines and is not found in its native range. Meanwhile, haplogroup C is only found in Burkina Faso, co-occurring with haplogroup B.

A genetic analysis of 16 individuals from four different locations in Bangladesh revealed that they all shared the same haplotype (Fig. 3), indicating a single invasion event and subsequent spread within the country. This specific haplotype has not been identified in public databases, yet haplotypes found in Uganda and Congo, differing by only one to three mutations,

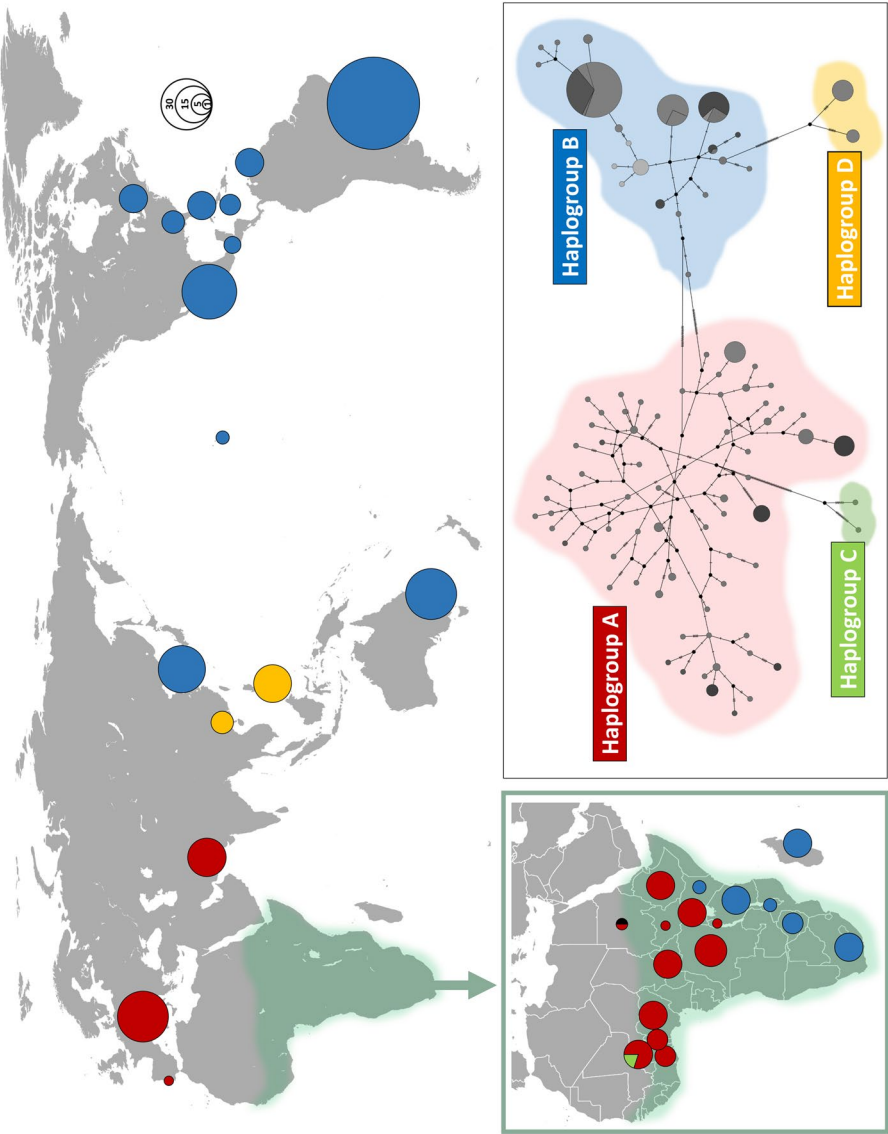


Figure 2. Global distribution of *Aethina tumida* and their genetic clusters inferred from COI data. Haplogroups and corresponding colors are indicated in the lower right. The size of each pie chart represents the number of samples included (see circles in the upper right).

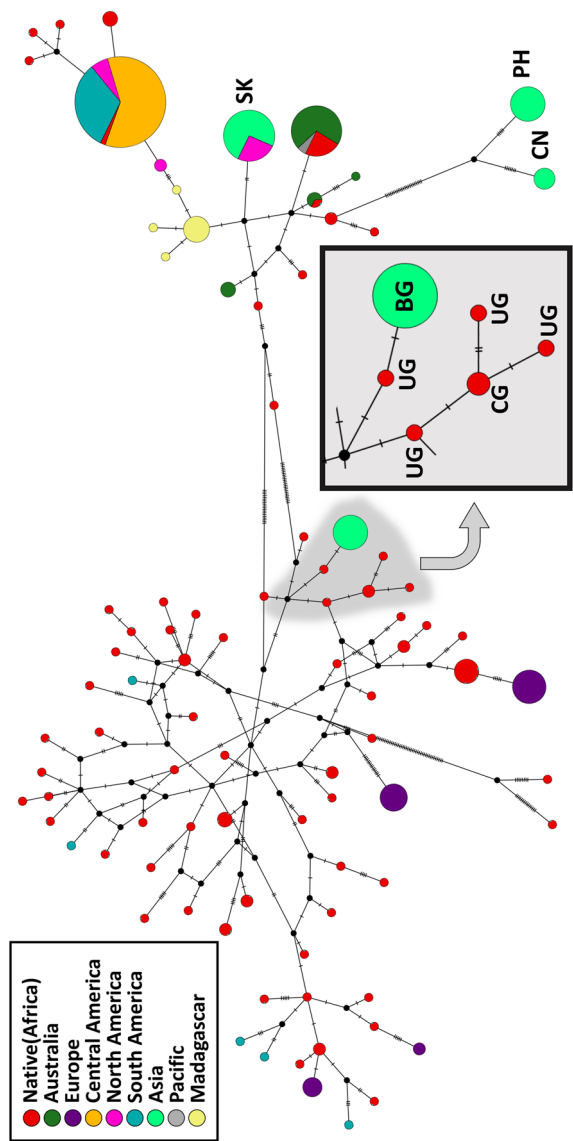


Figure 3. Haplotype network analysis using COI sequences. BG: Bangladesh, CG: Congo, CN: China, PH: Philippines, SK: South Korea, UG: Uganda.

suggest a close genetic relationship (Fig. 3). The absence of an exact matching sequence in the Bangladesh samples suggests that the source population remains unidentified. This makes it unlikely that the invasion in Bangladesh resulted from a recent bridgehead effect across Asia. The only haplotype found in Bangladesh is markedly different from those in South Korea, China, and the Philippines. Interestingly, independent haplotypes have been identified in China, the Philippines, and South Korea—with Korean populations sharing a haplotype with North America—indicating diverse invasive pathways into Asia (Namin et al. 2019; Liu et al. 2021).

This study is the first to document SHB in South Asia, highlighting an independent invasion not linked to other adjacent Asian countries. While the exact origin of the invasion remains uncertain due to the lack of an exact haplotype match, our findings suggest a potential direct source from Uganda or an indirect source through an intermediary region yet to be identified. Additionally, the invasive population in Bangladesh exhibits an identical COI haplotype, indicating the likelihood of a single invasion event. Given the significant population of *A. cerana* in South Asia, understanding the interactions between *A. cerana* and *A. tumida* is crucial, particularly in anticipation of the need for future intervention strategies against SHB.

SUPPLEMENTARY INFORMATION

The online version contains supplementary material available at <https://doi.org/10.1007/s13592-024-01106-3>.

AUTHOR CONTRIBUTION

MSH, MB, and SL designed the research. MSH, MAH, and MMA conducted field surveys. ML and SL performed the experiments and analyses. MSH, MB, and SL wrote the manuscript. All authors read and revised the final manuscript.

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DATA AVAILABILITY

The Bangladesh haplotype is deposited in NCBI GenBank with accession number PP587232.

DECLARATIONS

Conflict of interest The authors declare no competing interests.

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