



# DISCOVERING A RESILIENT AND HYPERDIVERSE MIDGE FLY FAUNA IN A SINGAPOREAN SWAMP FOREST

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*Researchers uncover a highly unique and diverse chironomid community in a Singaporean swamp forest highlighting the importance of these ecosystems and the power of Next-Generation Sequencing for biomonitoring efforts.*

**B**enthic macroinvertebrates – those animals that live at the bottoms of water bodies - are abundant, diverse, relatively immobile, and responsive to environmental stresses, and these traits make them ideal indicators of the quality of aquatic ecosystems. Our study demonstrates the utility of Next Generation Sequencing (NGS) platforms as an efficient and rapid tool for monitoring efforts.

In freshwater ecosystems, non-biting midges (Diptera: Chironomidae) often constitute the majority of diversity and biomass with different chironomid species varying in their sensitivity to environmental changes. But, when monitoring these habitats, chironomids are either ignored entirely or not studied at a species-level because morphological assessments are expensive and laborious, and the identification literature is based on adults while larvae are most often collected.

The solution? NGS platforms. They allow for fast and effective species-level assessments of large-scale samples at low cost (less than \$0.40 USD/specimen). Moreover, there is a high congruence between molecular and morphological identification, enabling a detailed examination of the composition of taxonomically complex communities<sup>1,2</sup>.

Freshwater swamp forests – the forested wetlands occurring along rivers and lakes – are home to various endemic and endangered species with 33% of birds and 45% of mammals either threatened or endangered on the IUCN Red List<sup>3</sup>, and with most of the insect fauna unknown. These ecosystems are under threat worldwide from habitat destruction, pollution, and climate crisis. Most of the world's tropical swamp forests are found in Southeast Asia's Indo-Malayan region collectively occupying more than 13 million ha<sup>4</sup>



among many geographically separated peninsulas and islands. Nee Soon swamp forest is the largest remnant (90 ha) of its kind in Singapore and thus of high national conservation value.



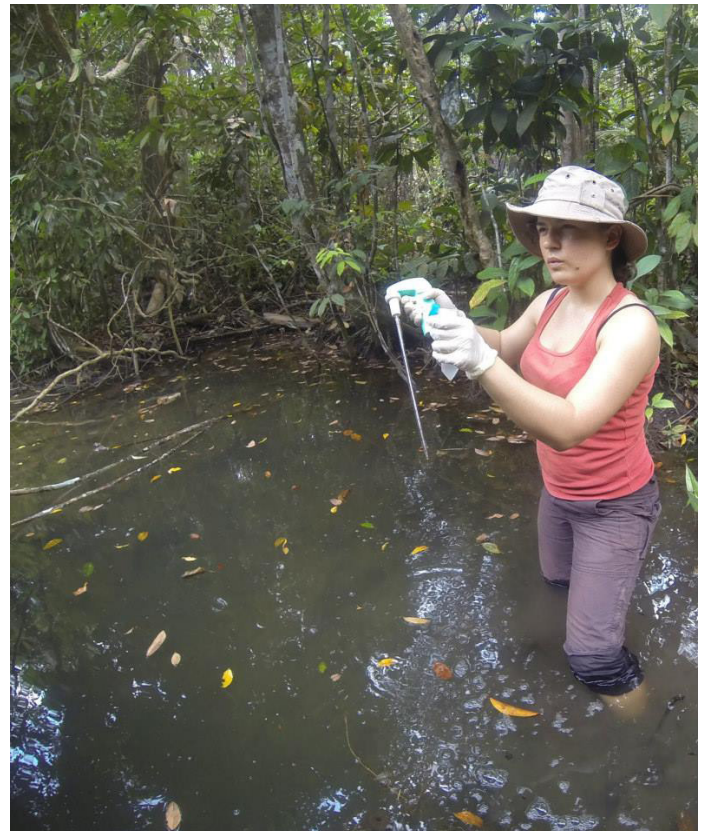
*Chironomid adult collected from Nee Soon Swamp Forest. Different chironomid species vary in their sensitivity to environmental parameters.*

PHOTO CREDIT: Bilgenur Baloğlu

We generated DNA barcodes using NGS to study chironomids among the natural swamp forest Nee Soon and three adjacent man-made reservoirs. We wanted to understand the effects of urbanization and to know whether the chironomid fauna of Nee Soon is resistant to, that is, minimally impacted by, the adjacent reservoirs. We sampled >14,000 chironomid specimens (both adults and larvae) as part of a fresh-water quality monitoring program, and quantified species richness and compositional changes using NGS and DNA barcoding.

Our study showed that Singapore's biggest swamp forest remnant maintains a rich and largely unique fauna of about 350 species. The minimal species overlap between sites indicated that the Nee Soon swamp forest is resistant against the invasion of species from surrounding artificial reservoirs. These findings suggest that even small or fragmented swamp forests can be suitable habitats for chironomids, shedding light on many other swamp forests in Southeast Asia that collectively occupy a much larger area and that are threatened by destruction for oil palm plantations and paper pulp production. Overall, our study exposes the enormous power of NGS and DNA barcoding in ecological research to study ecosystem health, biological diversity, and habitat conservation.

For full details on the study, see Baloğlu et al. 2018 DOI: [10.1186/s12983-018-0276-7](https://doi.org/10.1186/s12983-018-0276-7).



*Bilge Baloğlu sampling water DNA from Singapore's largest swamp forest remnant.*

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#### Online:

<https://ibol.org/barcodebulletin/research/discovering-a-resilient-and-hyperdiverse-midge-fly-fauna-in-a-singaporean-swamp-forest/>