



Malaise trap deployed in Carajás National Forest in Brazil  
PHOTO CREDIT: Christina Lynggaard

# INSECTS DON'T TALK, BUT NEW DNA-BASED TECHNOLOGIES ARE HELPING TO TELL THEIR STORIES

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## *Researchers unlock clues about vertebrate diversity by examining arthropod samples*

The study of arthropod diversity often uses primers solely targeting arthropod DNA, ignoring those originating from non-arthropod sources. Yet, some arthropods (e.g. sand flies, blowflies, mosquitoes) feed on vertebrates and vertebrate remains. By specifically targeting these vertebrate-feeding arthropods, invertebrate derived DNA (iDNA) can be used to understand vertebrate diversity as well. Our study has found that by using samples collected for arthropod diversity research, we can tap into a rich information source of vertebrate diversity.

Arthropods are highly abundant and provide vital ecosystem services such as pollination, decomposition

of organic matter, and they serve as a food source for other animals. Because of this, hundreds to thousands of arthropod samples are collected globally every year for monitoring programs, conservation efforts, and ecosystem assessments.

However, identifying arthropod species based on physical characteristics is difficult, requiring specific expertise and a significant amount of time. Due to this, molecular analyses, such as DNA metabarcoding, are being used to identify the arthropods present in bulk samples, speeding-up the otherwise time-demanding identification process by screening the contents of hundreds of samples simultaneously.

In this study, bulk arthropod samples were collected using pitfall and Malaise traps deployed at the Carajás National Forest in Brazil and in the Udzungwa Mountains in Tanzania. Our aim was to study the arthropod diversity in these areas by using metabarcoding primers targeting arthropod DNA. Nevertheless, we conducted an additional analysis targeting vertebrate DNA remains in the bulk samples by using metabarcoding vertebrate primers.



*Bulk arthropod sample.*

PHOTO CREDIT: Christina Lynggaard

We were able to detect vertebrate DNA in 19 per cent of our 265 analysed samples, identifying more than 30 vertebrate taxa including mammals, amphibians and birds. For example, we found South American tapir (*Tapirus terrestris*), chirinda screeching frog (*Arthroleptis xenodactyloides*), velvety free-tailed bat (*Molossus molossus*), Zanzibar bushbaby (*Paragalago zanzibaricus*) and honeyguide greenbul (*Baeopogon indicator*). The presence of some species was further confirmed through visual observations during the sample collections.

Some cases represent the first time those vertebrate species have been detected in the area. This could indicate that we are detecting vertebrates that live in different areas to where the arthropods were collected or that with this method it is possible to detect local animals that are difficult to observe.

The sensitivity of new DNA-based technologies is changing the way we explore and understand the relationships between species. Approaches like DNA metabarcoding can not only tell us about the different types of insects in our environment, but also what

they eat and where they have been. Our study is the first to not target a specific invertebrate group to detect vertebrate DNA but instead to use bulk arthropod samples. We encourage others to consider bulk samples during environmental monitoring not only as a source for arthropod diversity information, but one for vertebrate diversity as well.

This study is published in the [eDNA Journal](#).



*Tapir footprint found in one of the Brazilian study sites during bulk arthropod sample collection confirmed the presence of some of the detected vertebrate taxa.*

PHOTO CREDIT: Christina Lynggaard



*Bushbaby (*Paragalago zanzibaricus*) found in the Udzungwa Mountains in the Tanzanian study site during bulk arthropod sample collection confirmed the presence of some of the detected vertebrate taxa.*

PHOTO CREDIT: mnielsenphotography

#### **Online:**

<https://ibol.org/barcodebulletin/research/insects-dont-talk-but-new-dna-based-technologies-are-helping-to-tell-their-stories/>