

simplistic assumptions. The new rates of molecular evolution presented here will advance our ability to date recent evolutionary events in the marine realm and will expand our understanding of the impacts of prior climatic changes upon the history of life.

### Assessing a DNA mini-barcode strategy for species identification in neotropical necrophagous blow flies (Diptera: Calliphoridae) of forensic importance

Andrés López-Rubio, Eduardo Amat, Adriana Pérez, Giovan F. Gómez, and Luz M. Gómez

<sup>1</sup>Facultad de Derecho y Ciencias Forenses, Tecnológico de Antioquia, Colombia.  
Corresponding author: Andrés López-Rubio (email: alopezru@tdea.edu.co).

**Background:** Higher Diptera exhibit overwhelming variety in terms of morphology, habits, and species diversity. Among dipterans, the necrophagous Calliphoridae (blow flies) are the most important insects commonly used in the forensic entomology framework. Because of underestimated assessed diversity in the Neotropical region, species identification, and delimitation of biological entities become a difficult task based on morphological characters alone. Studies using the standard COI barcode region have given rise to controversial results and challenges in obtaining amplicons from blow flies and old specimens. **Results:** A 331-bp fragment was analyzed and used as an alternative mini-barcode in 150 specimens, including species from 12 genera of forensic importance: *Calliphora*, *Blepharicnema*, *Chlorobrachycoma*, *Chloroprocta*, *Chrysomya*, *Comptosomyops*, *Lucilia*, *Paralucilia*, *Hemilucilia*, *Cochliomyia*, *Sarconesiopsis*, and *Roraimomusca*. Distance matrix and dendrograms revealed useful polymorphisms to cluster specimens at the generic, and in some cases at the species, level. Clusters confirmed the currently proposed classification at the generic level based on morphological characters. Some species of *Lucilia*, *Paralucilia*, and *Hemilucilia* were not monophyletic. For the first time, molecular data for *Chlorobrachycoma* were obtained. **Significance:** The use of DNA mini-barcode is an alternative to achieve COI sequences from blow flies, including those from specimens with more than 50 years of storage. The short COI sequences allowed a reliable assignment mostly at the generic level, and partially at species level. Our approach provides a useful backbone to DNA mini-barcode dataset for Neotropical flies.

### Advancing DNA barcoding applications: monitoring environmental, agricultural, and public health outcomes

Andrew Lowe, Eleanor Dormontt, Kor-Jent van Dijk, Jennifer Young, Martin Breed, Nick Gellie, and Jacob Mills

University of Adelaide, Adelaide, Australia.  
Corresponding author: Andrew Lowe (email: andrew.lowe@adelaide.edu.au).

DNA barcoding has come a long way in a relatively short period of time. Some of the most exciting applications of DNA barcoding are the potential to identify species and biological products across a broad range of previously intractable situations. However, we still have some way to go to further develop the approach to harness the latest sequencing capabilities and ensure that DNA barcoding remains at the cutting edge. This talk will outline a range of DNA barcoding applications through case study examples and the steps that are now being taken to embed DNA barcoding in standardised screening frameworks and policy, including (i) control of illegally logged and non-conforming timber products in global supply chains, (ii) monitoring the return of ecological function to restored ecosystems, (iii) revealing ecological relationships between taxa to augment agricultural decision making, (iv) understanding the benefits of green space exposure to the human microbiome and public health, and (v) development of a human microbiome fingerprint. The talk will finish by outlining recent advances and options for cheap, quick multi-locus DNA barcoding approaches along with the challenges this will bring to the barcoding community in terms of standardisation and data management.

### Assessing the efficacy of DNA barcoding in Protura (Arthropoda: Hexapoda)

Yun-Xia Luan,<sup>1</sup> Yun Bu,<sup>2</sup> and Chang-Yuan Qian<sup>1</sup>

<sup>1</sup>Key Laboratory of Insect Developmental and Evolutionary Biology, Shanghai Institute of Plant Physiology and Ecology, Chinese Academy of Sciences, China.

<sup>2</sup>Natural History Research Center, Shanghai Natural History Museum, Shanghai Science & Technology Museum, China.

Corresponding author: Yun-Xia Luan (email: yxluan@sibs.ac.cn).

**Background:** Protura, a poorly known group of tiny soil animals, is one of the most primitive hexapods. Based on morphological taxonomy, there are more than 800 known species in Protura that have been described in 10 families of 3 orders. However, most diagnostic characters are difficult to recognize due to their small body size (~1 mm), and only a select number of scientists can identify the proturan species in the world, which has seriously impeded the studies on the phylogeny and ecology of Protura. This study aimed to examine if the DNA barcoding (COI gene) is a useful approach for determining proturan species. **Results:** The study sequenced and analyzed DNA barcodes of 265 proturan specimens from 61 species belonging to 26 genera, 8 families, and 3 orders. For most species, the molecular clusters are well consistent with the morphological determination. However, some unusually large intraspecific genetic distances (up to 25%) may indicate the presence of cryptic species. In addition, our data show low genetic variation within populations, but reveal high genetic differentiation among different geographic populations, with a notable correlation between geographic and genetic distances. **Significance:** The study clearly demonstrates that the standard DNA barcoding is effective but not enough for species discrimination of Protura. The taxonomy and biogeography of Protura are worth further studies by using more molecular markers.

### Using DNA metabarcoding to reveal the role of hoverflies (Syrphidae) in pollen transport

Andrew Lucas,<sup>1</sup> Owen Bodger,<sup>2</sup> Col R. Ford,<sup>3</sup> Laura Jones,<sup>3</sup> Dan W. Forman,<sup>1</sup> Matthew Hegarty,<sup>4</sup> Penelope J. Neyland,<sup>1</sup> and Natasha de Vere<sup>3</sup>

<sup>1</sup>Department of Biosciences, Swansea University, United Kingdom.

<sup>2</sup>Institute of Life Science, Swansea University, United Kingdom.

<sup>3</sup>National Botanic Garden of Wales, United Kingdom.

<sup>4</sup>Institute of Biological, Environmental and Rural Sciences, Aberystwyth University, United Kingdom.

Corresponding author: Andrew Lucas (email: andrew.lucas@cyfoethnaturiolcymru.gov.uk).

**Background:** Pollination by insects is a key ecosystem service, but there is concern about the decline in pollinators, caused by habitat degradation, diseases and parasites, and climate change. There are key gaps in the pollination science evidence-base, particularly relating to which insects pollinate which plants, and how pollination networks are structured. Most research has focused on bee populations. However, hoverflies (Syrphidae) also feed exclusively on nectar and pollen, making them potential pollinators of a wide range of wild plants and crops. **Results:** Using DNA metabarcoding to identify pollen, we investigated pollen transport by a range of hoverfly species in conservation grasslands in Wales, UK. It was possible to assign over 98% of sequences to species, genus, or family level. Hoverflies transport pollen from more plant species than previously appreciated. Networks are generalised at the site and species level, but at the individual level varied from specialised to relatively generalised. This suggests that generalised networks may result from a series of short-term specialised feeding bouts by individual insects. Most pollen recorded came from common plant taxa. However, differences in the proportions of various plant taxa in pollen loads between hoverfly species demonstrate some functional complementarity. **Significance:** We show the value of DNA metabarcoding in investigating plant-pollinator interactions. It allows the systematic investigation of pollination networks, from individual insects to whole communities. Our results show how generalised networks can emerge from the short-term specialisation of individuals, thus reconciling generalised network structures with effective plant pollination. Treating hoverflies as a single functional group underestimates the range of pollination function within this ecologically diverse guild. This study is one