



Egyptian hornet wasp (*Vespa orientalis*) predating on Dermaptera (*Labidura* sp.)  
PHOTO CREDIT: Mohamed Gamal

# A DNA BARCODING REVIEW OF THE ENTOMOFAUNA OF EGYPT

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*From insect diversity to pests to forensics, DNA barcoding plays a vital role in Egyptian biodiversity conservation and legislative protection efforts.*

Egypt has more than 23,587 identified plant and animal species in addition to thousands of algae, bacteria, and viruses<sup>1</sup>, and this unique biodiversity contributes to Egypt's economy and supports the welfare of its citizens. Agricultural production accounts for more than 10 per cent of Egypt's GDP while tourism revenues from marine activities on the Red Sea represent more than 30 billion LE annually.

Protecting threatened species such as dolphins, sharks, and dugong contribute by more than 61 million LE per year and the marine fish production is estimated to be worth 5 billion LE<sup>2</sup>. Therefore, Egypt has paid particular attention to the conservation and legislative protection of its natural heritage.

Joining its International Barcode of Life (iBOL) consortium partners, Egypt has been using DNA barcoding to better understand and plan for protection of biodiversity. So far, Egypt has published 20,980 DNA barcode sequence records, 25 per cent (5,368) of which have species names that represent 695 species.

In this review, we present an overview of the DNA barcoding carried out on the Egyptian entomofauna and introduce current advances of this promising technique. This review focuses on three main areas that highlight studies investigating insect diversity and distribution, insects in forensic applications as well as pest and parasite dynamics.

**Insect diversity and distribution:** DNA barcoding has been used to investigate the genetic diversity of Egyptian wasp populations with a wide geographical range<sup>3</sup>. Three species, *Vespa orientalis*, *Polistes bucharensis*, and *Polistes mongolicus* were accurately identified by their DNA barcodes with the COI phylogenetic signal revealing interesting insights across Jordan, Giza, Cyprus, and Greece. Despite the wide geographical range, only minor genetic diversity was observed among populations of the three wasp species, indicating unrestricted gene flow.

DNA barcoding has also been used in a larger-scale insect diversity investigation in the understudied Sahara-Arabian zoogeographic region, revealing significant heterogeneity between Egypt, Pakistan, and Saudi Arabia<sup>4</sup>. The year-long deployment of Malaise traps in these countries collected 53,092 specimens, including 18,391 from Egypt. The DNA barcode sequences revealed the occurrence of 3,682 BINs belonging to 254 families. These results reflect the high species richness of the area, encouraging further research into biodiversity monitoring for the region.

**Insects in forensic applications:** The Egyptian Forensic Medicine Authority, the leading authority on forensic medicine in Egypt, handles a relatively large number of cases annually and relies on laboratories for assistance with molecular techniques to ensure fast and reliable identification of species of forensic interest (e.g. necrophagous insects). To date, few studies in Egypt have evaluated the use of DNA barcoding in the identification and establishment of reference libraries for insect species of important post-mortem interval indication.

Aly & Wen<sup>5</sup> studied the applicability of a 296-bp cytochrome *c* oxidase I (COI) sequence as a reliable mitochondrial genetic marker for the identification of forensically important flies following previous research showing the efficacy of a short COI marker in this group<sup>6</sup>. The study analyzed 16 species of blow flies (Calliphoridae), flesh flies (Sarcophagidae), and house flies (Muscidae) originating from Egypt and China and concluded that a shorter COI fragment is simple, cheap, and reproducible but lacks agreement with traditional morphological classification. In a follow up investigation, Aly<sup>7</sup> examined the reliability of long (1173-bp) vs. short (272-bp) COI markers for 18 species of the same 3 dipteran families from Egypt and China. The results indicated that the longer COI marker performed better than the shorter marker for dipterous identification due to better monophyletic separation and concordance with taxonomic classifications.



Egyptian records of blow flies (Calliphoridae). Maggots (larva) are scavengers and adults are plant visitors.  
PHOTO CREDIT: Samy Zalot (above), Ramadan Mounir (below)



A more in-depth survey of the genetic diversity of forensically important blow flies (Calliphoridae) revealed numerous haplotypes among 158 specimens collected from four locations in Egypt (Giza, Dayrout, Minya, and North Sinai)<sup>8</sup>. Three particularly important species (*Chrysomya albiceps*, *Chrysomya megacephala*, *Chrysomya marginalis*) were well differentiated using COI supporting its use for subfamily-, genera-, and species-level identification of blow flies.

Most importantly for forensics use, COI is highly effective at identifying different developmental stages of forensically important flies, including larvae, pupae, and even empty puparia, otherwise difficult to identify morphologically. Five different species of Diptera and their immature stages from Alexandria, Egypt including *Chrysomya albiceps*, *Chrysomya megacephala*, *Calliphora vicina*, *Lucilia sericata*, and *Ophyra capensis*, were correctly identified using mitochondrial DNA markers<sup>9</sup>.

**Pest and parasite dynamics:** DNA barcoding has also played an important role in the identification of pests and parasites. Seventeen species of mealybug pests (Hemiptera: Pseudococcidae) have been identified by DNA barcoding specimens collected from pop-

ulations infesting various crops and ornamental plants in Egypt and France. The genetic variation found between populations of the same species using a combination of three markers (28S-D2, COI, and ITS2) and morphological examination indicated cryptic taxa that might respond differently to management strategies.

High diversity and rapid diversification were found in the head louse, *Pediculus humanus* (Pediculidae: Phthiraptera)<sup>10</sup>. *P. humanus* includes two morphologically indistinguishable subspecies: the head louse, *P. humanus capitis* and the body louse, *P. humanus humanus*. By analyzing sequence diversity of two mitochondrial genes (COI, cytb) in 837 specimens of *Pediculus humanus* from Egypt, Pakistan, and South Africa, high diversity and the occurrence of five mitochondrial lineages was revealed with implications for the spread of disease.

**Conclusion:** DNA barcoding of crop pests and pollinators, in addition to disease carrying insect-vectors, will continue to be the top priority for Egyptian government. Egypt actively enacts laws, carries out research, increases public awareness, engages local communities in management of protected areas, and implements projects funded by Egypt and other international donors to protect biodiversity. These motivations place Egypt in a valuable position among other countries joining iBOL in support of BIOSCAN, a project that will build a global monitoring system for the planet.

#### Online:

<https://ibol.org/barcodebulletin/research/a-dna-barcoding-review-of-the-entomofauna-of-egypt/>

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