



## **DNA- Barcode: A Marriage of molecular and traditional taxonomy for effective biodiversity studies**

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DNA-Barcoding is a method that employs short genetic marker of the DNA to identify the organisms taxonomically. Identifying the organisms using morphological description is a traditional way used by the scientist that dates back to Carl Linnaeus during 17th Century. The major imperative inadequacy in traditional taxonomy are the availability of the particular life stages of species, especially organisms like insects, which undergo metamorphisms, difficulty in identification of morphologically similar species and some of the cryptic species, besides in some case identity of the biological breeding individuals to be ascertained. With the advancement in the molecular field, using a short fragment of gens to identify the organism is the very convenient method to overcome all the shortcomings of the traditional taxonomy. DNA barcode can be defined as "Use of short fragment of gene sequence from the standardized region of the genome to establish the taxonomical identity of an organism".

The use of gene sequence to establish the evolutionary relationship was dates back to Carl Woese, who used the ribosomal RNA (rRNA) to discover the Archea, which shaped the new evolutionary tree. In 2003, Paul D.N. Hebert from the University of Guelph, Ontario, Canada, proposed the idea of using ~650 bp of mitochondrial gene sequence as a tool for species identification called as DNA Barcode. The Barcode of Life Database (BOLD) has the compilation of a public library of DNA barcodes that would linked to the specimens, this library would provide a new marker key for identifying species. In recent times, DNA barcode reached a new milestone due to high throughput analysis, wherein the species identity can be done at community level. The major advantages in using DNA barcode are, this method will meet the taxonomic challenges, which can't be addressed by traditional morphology and providing a robust identification of species even at community level across Orders. DNA-Barcoding doesn't require any specialized scientific expert contrary to morphology based taxonomy which demands highly specialized manpower for each group of insects. In recent time due to the dwindling in the availability of taxonomist for each group, DNA- Barcode gains more attention. This method also fit well with the new Nomenclature Law- Phylocode-2012, which is using the uniform platform of naming of organisms across the kingdoms (Animal, Plant).

In India, National Bureau of Agricultural Insect Resources (NBAIR), Bangalore, India, has initiated DNABarcoding of agriculturally important insects. So far more than 2000 insects have been identified and DNA-Barcoded. Some of the taxonomical problem of identifying the species especially the green lace wing bug *Chrysoperla zastrowi sillemi* which was earlier thought to be *C. carnea*. Apart from taxonomical issues, this DNA-Barcode has been used in various aspects viz., biodiversity studies, securing Intellectual Property Rights (IPR) for some of the country's important bio-resources, useful in Bio-security. It can be used to identify the alien invasive pests, so as to undertake any classical biological control if required. In NBAIR, DNA-Barcode has been developed for important alien invasive pests viz., papaya mealybug, coconut leaf beetle etc. This method is useful in identifying endangered animals from smuggling as well as to detect food contamination. One of the major obstacles in DNA Barcode is using single gene strategy; however, this can be overcome by combinations of markers, which will also help to address the issues with the polyphyletic species.

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