

## **Status of DNA Barcoding of Coccinellidae (lady bird beetles), Trichogrammatidae and Syrphidae (Hover Flies)**

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### **Abstract**

DNA barcode is a genetic signature that occurs naturally within the genome of every living species. One of the gene regions commonly used for all animal groups is a 648 base pair region in the mitochondrial cytochrome oxidase 1 gene (CO1), it has been effectively used in identifying birds, flies, butterflies, fishes and many other animal groups due to the high polymorphisms among species. Paul Herbert (2003) published a paper entitled “Biological Identification through DNA barcodes, which created awareness among scientists on the usefulness of DNA Barcode as an effective technique for identification of species. In the one decade of research after this publication, DNA barcode has evolved rapidly into a tool that can be employed for solving many environmental, agricultural, health and conservation problems around the globe. It also has applications in disease and pest control, market fraud detection and protection of endangered species. This paper reviews current status of DNA Barcoding of Coccinellidae, Trichogrammatidae and Syrphidae.

**Keywords:** Coccinellidae, trichogrammatidae, syrphidae, DNA barcode, mitochondrial cytochrome oxidase 1 gene (CO1)

### **Introduction**

Coccinellids or ladybird beetles belonging to the family coccinellidae, order coleoptera are the most commonly known of all beneficial insects. The family name comes from its genus, *Coccinella*. Adult ladybird beetles are dome shaped, oval or convex, often shiny with short legs and antennae. Coccinellids are commonly yellow, orange or scarlet with small black spots on their wing covers. Such color patterns vary greatly; however, for example, a minority of species, such as *Vibidia duodecimguttata*, a twelve spotted species has whitish spots on a brown background.

Trichogrammatids belong to the family Trichogrammatidae under super family Chalcidoidea (Hymenoptera). These are minute chalcid wasps, endoparasitic and mostly egg parasitoids of more than 200 insect pests belonging to the order Lepidoptera, Coleoptera, Hemiptera, Neuroptera, Diptera, etc. Some also attack on the eggs of spiders and mites. So far more than 80 genera under the family Trichogrammatidae are reported from the world over.

The members of family Syrphidae are also called hover flies as the adults are seen hovering over the flowers for collection of nectar. Hoverflies provide crucial ecosystem services as pollinators, biological control agents and in environmental assessment (Mengual and Thompson 2011). The larvae have a wide spectrum of feeding habits, being Phytophagous, mycophagous, zoophagous and saprophagus. Some of the Syrphid maggots are insectivorous, eating aphids, thrips, and other plant sucking insects. This is beneficial to gardens, as aphids destroy crops, and hoverfly maggots are often used in biological control.

Taxonomic identification of above mentioned families is male oriented. However, this classification has given rise to many controversies. The morphological identification of these families is done by the use of male genitalia in combination with more traditional characters of adult. Earlier, some taxonomists used these characters to identify these families but majority of these names are not valid now. The exact identification up to species, sub species level can be made only with the help of DNA barcoding.

DNA barcoding is the taxonomic method that uses a short genetic marker in an organism's DNA to identify it as belonging to a particular species or strain. Although several loci have been suggested, the most common locus of the animals includes the mitochondrial COI gene (Hebert *et al.*, 2003). It is a technique of sequencing a short fragment of the mitochondrial cytochrome oxidase subunit 1 (COI) gene. The standard sequence used for this purpose is approximately 648 base pair stretch of mitochondrial COI gene fragment amplified by the universal primers.

The classical use of morphological trait for species identification has several limitations. They include, for example, the misidentification of a taxon due to the phenotypic plasticity of the trait studied or the existence of cryptic taxa. Moreover morphological keys are sometimes only effective for a particular life stage or gender. Thus a high level of expertise is often required to correctly identify species with the accuracy required in ecological studies. In addition to the large specialized workforce needed to perform species identifications, morphological taxonomy has other serious challenges. In many species, there are also significant differences in morphology between the genders and different life stages. Cryptic species, by definition, are often impossible to identify by morphological characteristics alone. All of these obstacles in species identification often lead to incorrect identification. Another reason for incorrect species identification is that some researchers attempt to use keys without the appropriate level of expertise. Furthermore, some of the taxonomic keys in use are flawed and such keys are rarely revised since to do so is a major undertaking.

The DNA barcoding approach might correctly present the best solution for identifying species when their morphology is of limited use (Hebert *et al.*, 2003). DNA barcoding has been found promising in the rapid description of biodiversity. Besides adult DNA barcoding also helps in identification of larvae and pupae. DNA barcoding solves the problem of identification of sibling species, cryptic species and sub species. DNA barcoding helps in phylogenetic analysis thus leading to conservation and management.

In DNA barcoding 650 bp stretch of cytochrome oxidase gene 1 from the mitochondrial genome is used. The 650 bp long stretch lies on the 5' end of cytochrome oxidase gene 1. This region acts as a reference to delimit one species from other related ones (Hajibabaei *et al.*, 2007). The Barcoding Project (Hebert *et al.*, 2003) has the potential to revolutionize the process of species identifications and lighten the workload for the diminishing population of Taxonomists.

### **DNA barcoding of three economically important insect families**

#### **1. Coccinellidae**

There are about 6000 known spp. of Coccinellidae (Coleoptera: Insecta) which are worldwide in distribution. The majority of coccinellid species are beneficial because of their predaceous nature, but some are injurious, being Phytophagous on agricultural crops. Ladybird beetles (Coccinellidae: Coleoptera) are important predators in natural and agricultural habitats and prey upon many economically important pests, including aphids, mealy bugs, scale insects, thrips, leaf hoppers, mites, and other soft bodied insects (Khan *et al.*, 2009). They are beneficial for controlling the populations of aphids, scale insects and mealy bugs. *Adalia tetraspilota* (Hope) and *Hippodamia* (Adonia) *variegata* (Goeze) are the predominant species of coccinellids in agro-ecosystems of Kashmir valley (Khan *et al.*, 2007). So far only 192 spp. have been barcoded belonging to about 33 countries (Figure 1).

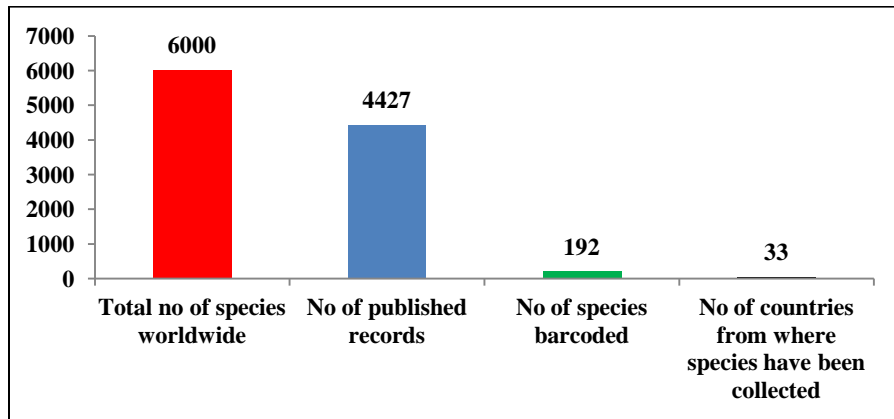


Figure 1: Showing details of DNA barcoding of Coccinellidae worldwide.

## 2. Trichogrammatidae:

*Trichogramma* is the most important genus under this family with over 200 species known from the world. Since all the species under this genus are exclusively egg parasitoids, hence constitute one of the widely used biological control agents against a number of serious insect pests throughout the world. The body length of *Trichogramma* ranges from 0.2 to 1.5 mm. They occur naturally all over the world, in almost every terrestrial habitat, and kill the pests in their egg stage by parasitizing them (Flanders and Quednau, 1960). Today, *Trichogramma* species are the most widely used insect natural enemy in the world, partly because they are easy to mass rear and they attack many important crop insect pests (Hassan, 1993). However, in most crop production system, the number of caterpillar eggs destroyed by native populations of *Trichogramma* is not sufficient to prevent the pest from reaching damage levels (Morrison *et.al.*, 1976). Apart from the potential use of different *Trichogramma* spp. against a number of insect pests attacking rice, maize, corn, cotton, apple, vegetables and pests of forest nurseries and plantations, throughout the world (Jalali and Singh., 1992; Hassan., 1989) their impact on the potentially insecticide resistant species, *Helicoverpa armigera* (Hubner). *Trichogramma* females oviposit inside the hosts eggs whose embryos are quickly killed and parasitized eggs turn black. This visible modification offers the opportunity to easily estimate female realized fecundity without waiting for offspring' emergence (Chiara *et.al.*, 2012). The family Trichogrammatidae has nearly about 840 described spp. out of which only 25 spp. have been successfully barcoded belonging to 14 countries (Figure 2).

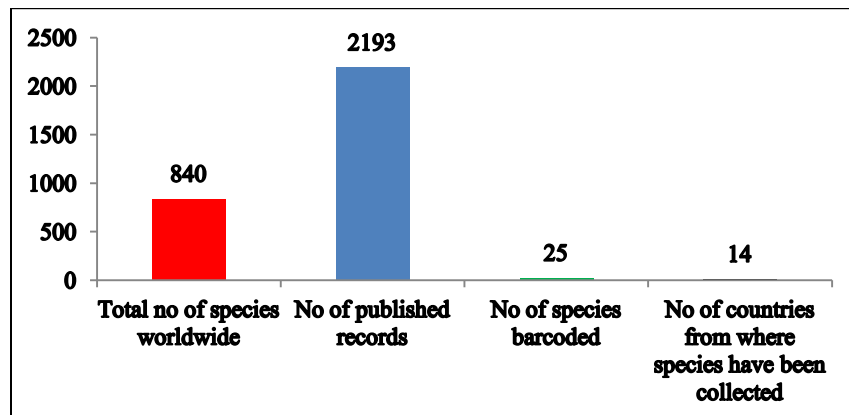
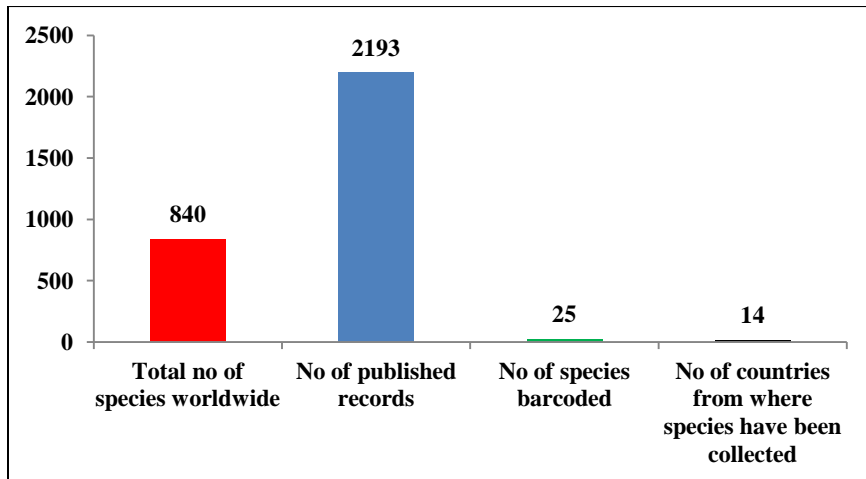


Figure 2: Showing details of DNA barcoding of Trichogrammatidae worldwide.

### 3. Syrphidae:

Syrphidae has a worldwide distribution, with almost 6,000 species described worldwide. Out of these 6000 spp. only 744 spp. have been barcoded so far which belong to 67 countries of the world (Figure 3). Hoverflies warrant attention not only because of their impressive diversity and economic importance, but also for their conspicuous habits and frequently eye-catching appearance (Miranda *et. al.*, 2013).



**Figure 3: Showing details of DNA barcoding of Syrphidae worldwide**

Various studies and analyses of those studies have been performed to determine the success of DNA barcoding for species identification. Meusnier *et al.* (2007) report barcoding Success levels over 97% in studies involving birds, mammals, fishes, and arthropods. Hebert *et al.* (2003) created a profile of one hundred species from seven diverse animal phyla and then attempted to identify newly analyzed taxa using this profile. This experiment resulted in a 96% success rate of correctly assigning the taxa to the appropriate phylum.

### Conclusions

DNA barcoding has become a very important tool for species identification since its adoption in 2003. At present there are about one million species barcodes in BOLD system which is the official depository of DNA barcode data. iBOL, the major barcode project is likely to accelerate the creation of reference barcode libraries. If the DNA barcoding complements with the traditional taxonomy, it will be the major tool in species identification. The DNA barcoding should be supported because of its wide applicability in taxonomy and other branches of biology. DNA Barcoding is as important in developed countries as it is in developing nations for preventing the extinction of endangered species and poaching of our useful biodiversity such as medicinal plants and parts of wild mammals which are taken elsewhere, developed into useful products and exported back for trade at huge costs. With DNA barcoding, processed items can be identified and traced back to place of origin, thereby checking illegal trade and providing opportunity for benefit sharing among nations. Grants such as the Google Impact Award and awareness on the application of DNA barcoding would help developing countries with low technology in biodiversity conservation and management.

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