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Molecular studies on Indian Muscid flies (Diptera: Muscidae): A review

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Abstract
One of the remarkable achievements of modern biology has been the development of accurate and reliable technologies for the rapid screening of DNA sequence variations. Molecular identification and DNA barcoding is a taxonomic method that can be used to identify a species, including an unknown one. Mitochondrial genome is most extensively studied genomic system in insects. In this review, we describe the various molecular works that have been done on Indian Muscidae. It can be concluded that, the molecular studies are not common for the Indian muscid species and only few studies have been conducted. A lot of work still has to be done in India with more species and molecular markers.

Keywords: mitochondrial DNA, Muscidae, India, review

1. Introduction

Flies belonging to the order Diptera have enormous medical and veterinary importance. They are important as they come in contact with humans and animals directly or indirectly. Due to their association with feces or decomposing organic materials, which are used for the development of their immature stages, muscid flies are potential carriers of diseases (Souza and Linhares, 1997) [47].

Family Muscidae includes about 5000 described species under 170 genera and is amply represented in all the biogeographical regions of the world (Kutty *et al.*, 2008) [24]. Of these, 263 species under 35 genera are known from India (Bharti, 2008) [6]. Members of this family have considerable medical and veterinary importance because of their capacity to transmit diseases to humans and animals. Adults of many species are mechanical carriers for pathogens of various diseases like typhoid, leprosy, tuberculosis, dysentery, anthrax, cholera, poliomyelitis etc. (Greenberg, 1971, 1973) [15, 16].

The house fly, *Musca domestica*, plays an important role as a disease carrier and has negative impacts on livestock, humans and poultry. It has been reported to be a potential vector of metazoan parasites found in pig pens (Forster *et al.*, 2009) [13]. Larvae of *Musca domestica* cause accidental myiasis in man and animals (Lane and Crosskey, 1993) [25]. House flies can also be mechanical carriers of *Vibrio cholera*, thus increasing its dissemination (Fotedar, 2001) [14]. Approximately 497 fungal spores of 15 genera were recorded from the external surfaces of both male and female house flies, which indicate their role as a carrier for fungal spores (Phoku *et al.*, 2014) [30]. House flies are also effective vectors of *Escherichia coli* in cattle, as well as from cattle to humans and vice-versa (Ahmad *et al.*, 2007; Sasaki *et al.*, 2000) [1, 33]. The immature stages of several species are occasionally found in association with decaying human cadavers and can be helpful as forensic indicators (Sukontason *et al.*, 2007; Preativatanyou *et al.*, 2010) [50, 31]. Biting stable flies of the genus *Stomoxys* are considered major pests of pasture cattle and livestock (Hogsette and Farkas, 2000; Hogsette *et al.*, 2008) [17, 18]. Both male and female adults require three to five blood meals for successful mating, inflicting painful bites and subsequent bleeding which can result in lower average weight and decreased milk production, with enormous economic losses worldwide (Bruce and Decker, 1958; Campbell *et al.*, 1987, 2001) [8, 10, 11].

The horn fly, *Hematobia irritans* (L.) is also one of the most damaging ectoparasites of pastured cattle. Annual losses in cattle production owing to reduced weight gain, poor feeding efficiency, and decreased milk production are estimated at $730 million per year (Campbell 1976, Drummond *et al.* 1981, Kinzer *et al.* 1984, Kunz *et al.* 1991) [9, 12, 22, 23]. Many species of genus *Atherigona* are well known as major economic pests of various grasses and cereals.

Classification of insect species is critical for both basic and applied research, which is primarily done on the basis of morphological attributes. However, the identification exclusively based on morphological features poses problems in the case of many groups because of their small size, morphological attributes that alter as task of environment and commonness of biotypes and species that cannot be easily distinguished by morphological criteria. Similarly, damaged or incomplete specimens and immature stages are difficult to identify by conventional methods. Sometimes it is difficult to identify many species of the muscid flies because of their similar morphological characters (Benecke and Wells, 2001) [5]. To solve these problems Deoxyribonucleic acid (DNA) based methods for species identification are used, especially for scientists not properly trained in taxonomy and can be applied on all life stages including old or damaged samples when anatomical characteristics may be destroyed (Sperling *et al.*, 1994; Wells and Stevens 2008) [48, 52]. There have been many attempts to use the molecular taxonomy techniques to insects with good results (Xiang and Kochar, 1991; Kambhampati, 1995; Tang *et al.*, 1996) [53, 19, 51]. DNA Sequencing is a far more informative and useful technique in comparison to other molecular techniques (for identification and for studying interspecific and intraspecific variations).

2. Molecular identification of Muscid flies in India

Malviya *et al.* (2011) [26] conducted a study on genetic relatedness among three populations of *Musca domestica* from the Arial, Allahabad city and Jhunsi regions of district Allahabad on the basis of RAPD-PCR. The study revealed low level of genetic diversity among the populations.

Malviya *et al*. (2012) [27] further investigated genetic relationship between 2 muscid spp. Musca domestica and Lispe orientalis by using Random Amplified Polymorphic DNA-Polymerase Chain Reaction Technique (RAPD-PCR) and revealed that the two species were distantly related as shown by low genetic identity values.

Malviya *et al.* (2015) [28] conducted a study on genetic relationship between 2 muscids flies using RAPD-PCR marker. The high value of genetic identity showed close relationship between *M. domestica* and *A. orientalis*.

Ojha *et al.* (2016) [29] used the COI gene to delineate putative insect species associated with the salt lake of Great Rann of Kutch in western India. The quantification of biodiversity revealed that 80% of specimens belonged to Diptera and 10% to each of Hymenoptera and Coleoptera.

Srivastava (2016) [49] conducted a study on genetic variation in house fly (*Musca domestica*) populations from Mirzapur and analysed five gene enzyme systems namely acid phosphate, alkaline phosphate, malate dehydrogenase, malic enzyme and aldehyde oxidase. The study revealed that almost all the polymorphic loci were highly differentiated with high degree of inbreeding among the population.

Archana *et al.* (2016) [4] confirmed identification of 5 different fly species on the basis of morphological characters as well as by DNA barcoding to prove their correct identity. Even the immature stages were identified up to species level by using barcoding. The study concluded that interspecific variation in DNA sequences of COI genes was much higher than intraspecific and provided an opportunity to use DNA sequences for exact species identification.

Singh and Achint (2017) [46] identified 5 muscid species on the basis of mitochondrial gene COII from Punjab and concluded that, COII gene can be used as a genetic marker to differentiate medically and veterinary important muscid flies.

It can easily be inferred from this discussion that almost negligible molecular work has been done on Indian Muscidae though other dipteran families like Calliphoridae and Sarcophagidae have been studied extensively from this angle because of their forensic importance. Sharma and Singh (2014, 2016) [34, 41], Singh and Khullar (2014, 2015) [42, 43], Singh *et al.* (2015) [44], Priya and Sebastian (2015) [32], Khullar *et al.* (2016, 2017) [20, 21], Bharti and Singh (2017) [7] and Algalil and Zambare (2017a) [2] have contributed towards molecular studies on Indian Calliphoridae while Singh *et al. (*2014) [45], Sharma *et al.* (2015a, 2015b, 2015c, 2016a, 2016b) [36, 37, 38, 39, 40], Sharma and Singh (2016) [35] and Algalil and Zambare (2017b) [3] did the same for the family Sarcophagidae.

3. Conclusion

It can be concluded on the basis of the foregoing discussion that the references about molecular studies are not common for the Indian muscid species and only few studies have been conducted. A lot of work still has to be done in India with more species and molecular markers. Thus, upcoming research workers with determination should push to choose this magnificent but neglected field in their own research activities.

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