

O25-5. Museum data validates change of crabronid wasp diversity at Delhi

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Crabronidae (Hymenoptera: Sphecoidea) includes over 200 genera and 9000 species worldwide. Subfamily Crabroninae, the most diverse group of family Crabronidae, includes around 100 genera and 9,000 species around the world. However, the Indian fauna is poorly known. During the current global warming, collection data of museums have proved to be valuable sources of information indicating changes in diversity and distribution of species. As isotherms shift away from a particular location, warming at the location may occur, but the spatial context of temperature change will influence the regional setting of species diversity change. This study focuses on the effect of climatic variables on species diversity. Long term annual and monthly trends for maximum and minimum temperature of North West Region of India were used for trend analysis with Sen's slope estimator and Mann-Kendall Statistics for assessing differences, if any. Intensive surveys for collecting these wasps were made during 2017 to 2018 at IARI, New Delhi. The current data were compared with the collection data of 1959 to 1960 housed at National Pusa Collection. Changes in abiotic conditions affected the diversity of species. Maximum temperature showed significant increasing trends during the months of February, April, August, November and December while minimum temperature showed significant negative trends in January and June. In response the crabronid wasps shifted their time of occurrence from summer to winter, which might be due to the presence of optimum temperature. Thus museum data can validate observation based species occurrence data.

O25-6. Barcoding and Phylogenetic analysis of delphacid plant hopper complex in rice

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Delphacid planthoppers constitute the economically important planthopper complex in rice. They cause inevitable damage directly by feeding and indirectly as vectors. Delphacidae is the largest family of the Fulgoroidea superfamily and most economically important group feeds on graminaceous crop plants. The Delphacids are easily distinguished at family level by the presence of a large, movable spur on the apex of the hind tibiae. In rice, the major pests viz., brown planthopper *Nilaparvata lugens* (vector of grassy stunt and ragged stunt viral diseases); small brown planthopper, *Laodelphax striatellus* (Fallen) (vector of rice stripe and black streaked dwarf); white backed planthopper like *Sogatella furcifera*, *S. kolophon*, *S. vibix* and minor pests, viz., *Toya propinqua*, *Tagosodes pusanus*, *Coronacellas inhalana*, *Sardia rostrata*, *Peregrinus maidis*, *Nycheuma cognatum*, *Cemus sauteri*, etc. These species are known for their complexity like cryptic species, wing polymorphism, sexual dimorphism etc, which hinders their identification. The conventional taxonomy combined with molecular tools will give explicit identification. In this regard, we generated DNA barcodes by targeting four gene loci mtCOI, 28srDNA- D2 region, 28srDNA- D9-10 region and Histone gene. The molecular phylogeny analysis has been made to give the evolutionary relationship among these pest species. This will give a comprehensive account on identification, which in turn helps in the survey, monitoring and early warning of the major Delphacid pests of rice.

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