

5. SUMMARY AND CONCLUSIONS

The results obtained in the present investigation entitled “Biodiversity of fruit flies (Tephritidae: Diptera) and utilization of gut bacteria in their management” are summarized here under:

- In Himachal Pradesh, *Bactrocera cucurbitae* and *Bactrocera tau* were observed to be serious on cucurbits. However, cucurbits sample collected from other states indicated infestation of *B. cucurbitae* only.
- In Himachal Pradesh, mean per cent infestation was recorded to be 65.88 per cent. The maximum infestation of 80.00 per cent was recorded at Palampur (Kangra) and minimum of 44.44 per cent at Banikhet (Chamba).
- In the present study, 17 species of tephritid fruit flies from 5 genera were recorded, amongst them 14 species were already present in Himachal Pradesh. They have been recognized in 4 tribes of 2 subfamilies (Dacinae and Tephritinae).
- Six fruit flies species were recorded for the first time from Himachal Pradesh. They are *Bactrocera latifrons* (Hendel), *Bactrocera nigrofemoralis* White & Tsuruta, *Dacus longicornis* Wiedemann, *Dacus* sp., *Cyrtostola limbata* (Hendel) from subfamily Dacinae and *Pliomelaena udhampurensis* Agarwal & Kapoor from subfamily Tephritinae.
- *Bactrocera latifrons* (Hendel) has been recognized as insect pest of solanaceous crops in south India. Therefore the pest status and distribution of the species need to be investigated in the Himachal Pradesh, also.
- Eight species of fruit flies (61 isolates) were molecularly characterized with *mtCOI* gene and were submitted to GenBank, NCBI (USA) with accession number HQ378195-HQ378245 and HQ446513-HQ446522.

- *mtCOI* gene/s of *B. nigrofemoralis*, *D. longicornis* and *Dacus sphaeroidalis* are totally new to GenBank, NCBI (USA).
- The population structure of five geographically isolated populations of *B. cucurbitae* from Indian subcontinent (four from India and one from Nepal) were studied/ compared with gene sequences of *B. cucurbitae* from GenBank, NCBI using a 611 bp fragment of *mitochondrial cytochrome oxidase I* (COI). The genetic diversity was too low amongst *B. cucurbitae* populations studied, considering the geographic scale of the sampling.
- One single haplotype (H1) of *B. cucurbitae* was found to be predominant in Indian subcontinent.
- On the basis of *mtCOI* gene (611bp) sequence analysis of 16 *B. tau* isolates from Himachal Pradesh, the observed genetic diversity is exceedingly low and is quite similar to *B. tau* sp A (Thailand). This reveals that cucurbit infestation in H.P. is by *B. tau* sp A of *B. tau* species complex.
- The presence of other species of *B. tau* in H.P. as well as in India may not be ignored as 7 species have been reported in *B. tau* species complex. This needs further detailed investigations.
- Eight species of fruit flies were clearly differentiated on the basis of 611bp *mtCOI* gene sequences which were grouped together as per earlier classification. This validates the utility of *mtCOI* gene as a tool for fruit fly detection and species characterization.
- Out of 63 bacteria isolated from the gut of 9 populations of *B. tau* on two culture media viz. BHIA and PYEA, 30 bacteria were screened as attractant for fruit flies.
- Five most attractive bacterial isolates were characterized on the basis of morphological, biochemical and 16S *rRNA* gene sequence characteristics. These were *Delftia acidovorans* (P1B), *Pseudomonas putida* (P3A), *Flavobacterium* sp. (P10A), *Defluviobacter* sp. (B4A) and

Ochrobactrum sp. (B10B). Their 16S rRNA gene sequences were submitted to GenBank, NCBI and accession numbers HQ446523 to HQ446527 was awarded to them.

- Attractancy of different bacterial isolates was in the range of 6.17 to 11.17 and 5.67 to 8.17 adults/30min for female and male, respectively. *Pseudomonas putida* was found to be the most attractive bacteria to fruit flies followed by *Deftia acidovorans*. All bacterial isolates were, however, found statistically superior over sugar (negative control) and inferior to protein hydrolyzate (positive control).
- To characterize the chemicals responsible for gut bacteria attractancy to fruit flies, GCMS analysis of five bacterial isolates was done. Twenty two volatile chemicals were identified of which only three chemicals viz. Z-(9)-tricosene (House fly), cedrol (*Cryptomeria* bark borer) and chryophllene oxide (*Compoletis sonorensis*) are known to be associated with insect chemical communication behaviour. This, however, needs further in-depth investigation to understand this tritrophic interaction in host-fruit flies-microbes.