GESA
GLOCAL ENVIRONMENT & SOCIAL ASSOCIATION

**International Journal of Biological Innovations**
http://ijbi.org.in | http://www.gesa.org.in/journals.php
https://doi.org/10.46505/IJBI.2026.8204
IJBI 8(2): 175-183 **(2026)**
E-ISSN: 2582-1032

# GENETIC VARIABILITY IN THE FEEDING BEHAVIOUR OF *BACTROCERA* SPP. (TEPHRITIDAE : DIPTERA): A REVIEW

**Divya Dwivedi and Shubhra Malviya***

Department of Zoology
S.S. Khanna Girls' Degree College (University of Allahabad),
Prayagraj (U.P.), India

**Corresponding author*: shubhramalviya10382@gmail.com

**Article Info:**
Review Article
Received
**10.04.2026**
Reviewed
**22.06.2026**
Accepted
**31.07.2026**

**Abstract:** Fruit flies are one of the most fascinating and diverse groups of insects, commonly referred to as 'Peacock flies' due to the habit of strutting and vibrating wings, and rank among the world's most dangerous pests of horticulture crops. In India, fruit flies have been identified as one of the ten most serious problems of agriculture because of their polyphagous nature and causing a huge economic loss to fruits and vegetables. Fruit flies exhibit genetic variation influenced by the specific host plants they utilize. This variation arises from the flies adapting to the chemical and physical characteristics of different host plants. This variation can be genetic and developmental with the host plant. Feeding habit significantly impacts the genetic variation in different species of *Bactrocera* with polyphagous habit (generalist) generally exhibiting higher genetic diversity and monophagous species (specialist) showing lower diversity and more distinct genetic structures. Host plant shifts are also a key driver of genetic differentiation. This review highlights the genetic variation in different species of *Bactrocera* on the basis of their feeding habits on different host plants.

**Keywords:** *Bactrocera*, Fruit fly, Genetic variation, Monophagous, Polyphagous, Tephritidae.

**Cite this article as:** Dwivedi D. and Malviya S. (2026). Genetic variability in the feeding behaviour of *Bactrocera* spp. (Tephritidae : Diptera): A Review. *International Journal of Biological Innovations*. 8(2): 175-183. https://doi.org/10.46505/IJBI.2026.8204

## INTRODUCTION

The family Tephritidae of order Diptera consists of over 4,500 species or subspecies of fruit flies, classified in 500 genera of which 932 species belong to Dacinae fruit flies (Doorenweerd *et al.,* 2018). Tephritidae (Fruit flies) is one of the largest families in the Diptera order, with about 4,500 different species. The family Tephritidae is categorized by Korneyev (1999) into roughly 500 genera and six subfamilies: Trypetinae, Phytalmiinae, Tachiniscinae, Tephritinae, Dacinae, and Blepharoneurinae. According to Agarwal and Sueyoshi (2005), there are 243 species of fruit flies in India, which are divided into 79 genera and four subfamilies: Dacinae, Phytalmiinae, Tephritinae, and Trypetinae.

Fruit flies feed on plants, such as vegetables and fruit trees (Verma, 2017). Fruits from the Rutaceae and Rosaceae families are the most affected, whereas vegetables are from the Cucurbitaceae and Solanaceae families (He *et al.,* 2023). Due to the broad host range or polyphagous nature of its species and the invasive potential of certain species, the genus *Bactrocera* is thought to be the most hazardous pest of horticulture

crops (Clarke *et al.,* 2005). Most species destroy a range of plant hosts, including horticulture crops and inclusive vegetable varieties as a result of their polyphagous nature (Rauf *et al*., 2013). One significant element that promotes the expansion of tephritid fruit flies and the emergence of new biotypes is adaptation to novel host plants. *Bactrocera* species feeding patterns and host plant specificity are strongly correlated with genetic variation. Host shifts, or switching from conventional to novel host plants, have been shown to cause substantial genetic difference and even sympatric speciation.

One significant element that promotes the expansion of tephritid fruit flies and the emergence of new biotypes is adaptation to novel host plants. Use of novel hosts allows herbivorous invasive insects to expand their range and potentially diverge genetically from source populations (Masselière *et al.,* 2017). Exploiting new hosts can help herbivorous insects colonize, establish, and sustain stable populations when they penetrate new settings (Cronin and Abrahamson, 2001). Therefore, comprehending the intrinsic mechanisms of biological invasion for many invasive species requires an understanding of how insect invaders employ novel hosts. For example, a major pest, *Bactrocera tau* (Walker) (Diptera: Tephritidae) belongs to the Tephritidae family, which has extended its typical host range beyond Cucurbitaceae to numerous other plant families.

## HOST PLANT RANGE AND FEEDING BEHAVIOUR IN *BACTROCERA*

Some fruit flies are generalist (polyphagous) in nature and infest more than one type of fruit and other is more specialists (monophagous) in nature and infests one type of fruit. Tephritids rely heavily on host plant development to increase their territory. Tephritids must adapt to the chemical and nonchemical features of a new host fruit, such as colour, phenology, and phytochemicals, in order to spread successfully. These plant traits trigger a succession of events in tephritids, each with its own genetic foundation, implying that tephritids regulate host plant proliferation through a variety of genes. The utilization or potential acclimatization to novel hosts encompasses several intricate processes, including the identification of hosts by the dipteran species, physiological and chemical adjustments to the nutritional composition and secondary metabolites of the hosts as well as host-seeking behaviours influenced by neurophysiological mechanisms (Masselière *et al.,* 2017; Tallamy, 2000). Each of these processes contributing to host adaptation is underpinned by a genetic framework.

According to earlier studies, the fruit families are preferred by members of the *Bactrocera* complex include Myrtaceae, Rutaceae, Sapotaceae, Solanaceae, Annonaceae, Clusiaceae, Moraceae, and Anacardiaceae. Three fruit fly species complexes are polyphagous: *Bactroceracarambolae,* which hosts 77 host species from 27 plant families; *Bactrocera dorsalis*, whose larvae are housed by 209 species from 51 plant families; and *Bactrocerapapayae*, which hosts 124 fruit species from 42 plant families (Drew, 1997).

Fruit flies from *B. carambolae* and *B.dorsalis* prefer fleshy fruits such star fruit, mango, guava, *Psidium guajava, Eugenia aquae*, papaya, and citrus (White and Harris, 1992). Fruit flies are ideal hosts for fruit flies andrequire sufficient food to survive and reproduce during their life cycle for various reasons (Chang *et al.,* 2003). Nutritious supplies include high water content for metabolism, carbohydrates from nectar and honey for locomotion and flight, protein for sexual maturity, and lipid-rich protein for egg production (Fletcher, 1987). Apart from physical attributes, chemical features of host plants may also affect the host preference, as well as the biology and subsequent development of insects (Kostal, 1993). An insect's choice for a particular host plant can influence its life cycle, regeneration, and development in addition to influencing its behaviour (Renwick, 1989).

### Role of plants secondary metabolites

Plant-derived compounds exert diverse effects on insect populations. Beyond serving as a nutritional resource, flora also harbours secondary metabolites that may exert both beneficial and detrimental influences on insects. In tephritid species, male individuals exhibit attraction to phenylpropanoids synthesized by plants (such as methyl eugenol or raspberry ketone) which, upon contact, are ingested and sequestered by the males. These compounds, or their metabolic derivatives, typically possessing minimal nutritional significance, are incorporated into pheromonal signals and additionally provide advantages in reproductive contexts: increased attraction of females and enhanced mating success for males.

Due to the significant impact of numerous tephritid species as agricultural pests, investigations into the influence of phytochemicals on male behavioural patterns have been conducted with the aim of integrating these findings into pest management strategies, including the sterile insect technique (SIT).

## IMPORTANCE OF HOST PLANT ASSOCIATION

Host plant association in *Bactrocera* species is a critical factor that determines their fitness, survival, and invasive potential. These fruit flies exhibit complex relationship with their hosts, ranging from high specialization in monophagous species to

extreme flexibility in polyphagous ones like *Bactrocera dorsalis*. The expansion of host plant utilization represents a critical survival mechanism for tephritid insects as they broaden their geographical distribution. The successful incorporation of novel host species necessitates that tephritids acclimate to both the chemical and non-chemical characteristics of the new fruit, encompassing attributes such as colour, phenological stages, and phytochemical composition. These plant characteristics instigate a cascade of physiological processes within tephritids, each of which is governed by a distinct genetic framework, signifying that multiple genes play a role in modulating the host plant expansion dynamics observed in tephritid populations.

The microenvironment associated with host fruits, which fruit flies endeavour to exploit, exerts a significant influence on the survival and adaptive capabilities of fruit flies. Consequently, when tephritids successfully broaden their host spectrum from ancestral host fruits to novel hosts, they must exhibit adequate adaptations to both the chemical and nonchemical characteristics of the microenvironment associated with the new host fruits, encompassing their phytochemicals, colouration, and phenological traits. The colouration of the host fruit serves as a critical cue for numerous fruit-infesting insects during the process of selecting a new host (Piñero *et al.,* 2017). The ability of a tephritid to employ a new host is also influenced by the novel host's phenology, including when it flowers and fruits (Mattsson *et al.,* 2015).

## BEHAVIOURAL ADAPTATIONS TO HOST PLANTS

1. **Nutritional and Defensive Adaptation**: The nutritional composition as well as secondary metabolites (e.g., bitter triterpenoids in family Cucurbitaceae) of host fruits affects larval survival, development time, and pupal weight, creating selective pressure. The fly's gut microbiome also changes in response to the host plant's chemical composition, which in turn influences the fly's ability to detoxify harmful compounds and extract nutrients. The presence of secondary metabolites like phenolic compounds of host plant acts as chemical defense.
2. **Oviposition Preference:** Fruit flies' choices for oviposition are mostly influenced by the kinds of host fruits that support the growth and survival of their progeny (Brandalha and Zucoloto, 2004). Female fruit flies select their hosts based on several important characteristics of fruit plants, including colour, size, shape, and fragrance (Mahfuza *et al.,* 2011).
3. **Ripeness Preference:** The gravid females overwhelmingly prefer ripe or fully-ripe fruit over unripe stages. This behavioural choice ensures that the emerging larvae have a nutrient-rich, carbohydrate-heavy environment for rapid development.
4. **Social Interactions:** Group housing and interactions with other flies can enhance mating frequency and sensitivity to chemical cues, which improves the overall reproductive success of the population in a new host environment.
5. **Learning and Plasticity:** Host preference is not entirely fixed; it can shift toward available hosts when preferred ones become scarce. Experience plays a role, as prior oviposition success on a specific host can strengthen a female's future preference for that plant.
6. **Sensory Adaptations:** Host location is critical, with female flies using vision, olfaction (smell), and gustation (taste) to find suitable oviposition sites. Genetic variation in genes related to these sensor systems (e.g., opsin genes for vision, olfactory receptors) determines their host preference.

## GENES INVOLVED IN DIFFERENT FUNCTIONS

### 1. Expansion of host plants expansion in Tephritids

The expansion of host plants represents a critical survival mechanism for tephritid flies as they broaden their geographical distribution. The successful extension to new host plants necessitates that tephritids undergo adaptations to both the chemical and non-chemical characteristics of unfamiliar fruit, including attributes such as fruit pigmentation, several developmental stages, and phytochemical composition. These plant characteristics instigate a succession of physiological processes within tephritids, each of which possesses a distinct genetic foundation, thereby indicating that a multitude of genes play a role in the regulation of host plant expansion among tephritids. Numerous genes are implicated in the expansion of host plants across various tephritid species, encompassing genes associated with chemoreception (both olfactory and gustatory), vision, excretion, digestion, detoxification, development, ribosomal function, and energy metabolism. Genes pertaining to chemoreception, detoxification, and digestion are activated by volatile and secondary metabolites from diverse host plants, respectively, which play a crucial role in the modulation of neural signal transduction that instigates behavioural, physiological, and chemical reactions to the newly encountered host fruit.

Conversely, genes linked to vision, neural function, developmental processes, and metabolic functions are stimulated by non-chemical cues from various hosts, such as colour and phenological characteristics, thereby facilitating a holistic adaptation of tephritids to the newly available host. The activation of ribosomal and energy-related genes by both chemical and non-chemical signals from hosts culminates in the fundamental regulation of numerous processes pertinent to host expansion, including detoxification and developmental progression. These genes do not operate in isolation to govern the utilization of novel hosts; rather, a multitude of genes coordinate a multilevel adaptive response to new host fruits through various mechanisms (Shi *et al.,* 2017).

**2. Chemoreception**

Volatile organic compounds activate chemosensory (olfactory and gustatory) receptors in tephritid flies during the evaluation of a potential novel host and the endeavor to broaden their host range (Li *et al.,* 2020). Consequently, genes associated with chemosensation play a crucial role in the preliminary stages of host plant expansion for tephritid species.

Genes related to olfaction in tephritids represent a specific category of chemosensory genes encompassing various gene families such as odorant-binding proteins (OBPs), chemosensory proteins (CSPs), odorant receptors (ORs), ionotro.pic receptors (IRs), and sensory neuron membrane proteins (SNMPs), all of which are predominantly engaged in the detection of volatile compounds, including those emitted by host fruits. Upon receiving chemical signals from odors, these olfactory-related genes are activated to initiate signaling cascades that convey information to designated areas within the brain, ultimately culminating in specific behavioural responses (Xu *et al.,* 2019; Ono *et al.,* 2021). OBP and CSP genes constitute the principal types of genes that ensure the tephritid flies to react to various chemosensory compounds, including the volatile substances released by host plants (Xu *et al.,* 2019).

**3. Detoxification and Digestion**

Once a tephritid adult discerns a prospective novel host fruit for oviposition or nutritional intake, it is imperative that the fruit in question is conducive to larval development, which necessitates the capacity to neutralize any secondary toxic compounds present within the novel host fruit (Hafsi *et al.,* 2016). Consequently, detoxification-related and other digestion-associated genes assume pivotal roles in facilitating the host plant expansion observed in tephritids.

Widely recognized detoxification-associated genes in insects encompass gene families such as cytochrome P450s (P450s), GSTs (glutathione S-transferases), UGTs (UDP-glycosyltransferases), CCEs (carboxyl/cholinesterases) and ATP-binding cassettes (ABC transporters) (Roohigohar *et al.,* 2021). The predominant digestive-related gene families consist of cysteine proteases, proteases, lipases, glucosidases, and serine proteases (Zhong *et al.,* 2017). The serine proteases (SPs) belong to a supergene family that incorporates chymotrypsin, trypsin, thrombin, subtilisin, plasmin, and elastase subclasses (Li *et al.,* 2017).

Diverse digestive proteases play critical roles in the nutritional digestion of tephritid flies as they attempt to exploit novel host plants. The proteins derived from host plants constitute a significant nutritional resource for tephritid flies. Nonetheless, protease inhibitors found in host plants represent a pervasive defensive mechanism against herbivorous pests such as tephritids. Hence, genes encoding various proteases respond to protease inhibitors by modulating inhibitor-sensitive proteases or by expressing proteases that are not susceptible to the inhibitors (Mancera *et al.,* 2012).

In the process of expanding to alternative novel hosts, tephritid flies must acclimatize to distinct chemical environments differing from those of their indigenous hosts. Detoxification-related genes govern the host expansion of tephritids through mechanisms of gene family expansion, analogous to those observed in chemosensory-related genes. The principal gene families associated with detoxification, including GSTs, P450s, CCEs, and ABC transporters, are significantly more abundant in polyphagous *B. dorsalis* (39 GSTs, 90 P450s, 38 CCEs, and 47 ABC transporters) (Pavlidi *et al.,* 2013). Detoxification or digestion-related genes let tephritid flies adapt to diverse hosts by changing gene expression levels.

**4. Vision**

Nonchemical stimuli, including colour, are correlated with vision-related genes that facilitate the discernment of various hosts (Wang *et al.,* 2019). The genetic determinants of chromatic discrimination in Diptera are predominantly associated with opsin proteins located within the photoreceptor cells of the ocular structure (Hardie and Raghu, 2001).

Six distinct types of Rh opsin-expressing genes (Rh1 through Rh6) have been recognized as key contributors to colour perception and photoreception in Diptera species (Montell, 2012). The Rh1 and Rh2 opsin genes are linked to motion perception and

directional awareness, respectively (Pollock and Benzer, 1988; Morante and Desplan, 2008). Rh3 and Rh4 are classified as UV-sensitive opsin genes, Rh5 functions as a blue-sensitive gene, while Rh6 is designated as a green opsin gene (Tang and Guo, 2001). These opsin genes enable the photoreceptors of the eyes to absorb a variety of chromophore pigments, subsequently triggering a cascade of visual transduction pathways that initiate specific colour recognition behaviour. In the case of *B. minax,* the role of Rh6, which mediates sensitivity to green wavelengths, has been elucidated through the gene knockdown in female adults of *B. minax,* revealing a substantial decrease in their attraction to green fruit following the ablation of Rh6 (Wang *et al.*, 2019).

**HOST-ASSOCIATED GENETIC DIFFERENTIATION**

Fruit flies demonstrate genetic variability which is influenced by the particular host plants they exploit. Such variability emerges as the flies adapt to the unique chemical and physical properties of various host plants. Feeding behaviours exert a considerable influence on the genetic variation observed among different *Bactrocera* species, where polyphagous species (generalists) typically exhibit greater genetic diversity, whereas monophagous species (specialists) tend to demonstrate reduced diversity and more pronounced genetic structure.

A study conducted by Rasool (2025) regarding the host preferences of *Bactrocera zonata* for an array of fruits (*Prunus armeniaca*, *Prunus domestica*, *Prunus persica*, *Cucumis melo*, *Citrullus lanatus*, *Prunus avium*, *Ziziphus jujuba*) and vegetables (*Momordica charantia*, *Beta vulgaris*, *Daucus carota*, *Solanum lycopersicum*, *Cucumis sativus*, *Solanum melongena*, *Cucurbita pepo*) under both field and laboratory settings revealed that apricot (*Prunus armeniaca*) emerged as the most favoured fruit, whereas jujube (*Ziziphus jujuba*) was determined to be the least preferred. In terms of vegetables, bitter melon (*Momordica charantia*) was preferentially selected by *Bactrocera zonata*, in contrast to pumpkin (*Cucurbita pepo*), which was the least chosen option. The findings of suggest that fruit flies possess the capacity to modify their host preferences in response to the availability of host plants. This adaptive behaviour may exert a considerable influence on the productivity of fruit-bearing crops.

A study was performed by Amur *et al.* (2022) to assess the oviposition behaviours and locomotion of maggots within five widely recognized mango cultivars (Chunsa, Sindhri, Beganpali, Lal Bad Shah, and Sonaro) prevalent in Sindh, Pakistan. These mango cultivars were subjected to scrutiny during a sequence of experiments conducted in a laboratory setting under meticulously regulated conditions. The mangoes afflicted by infestation were procured from agricultural fields and subsequently sectioned. The larvae were extracted from each variety (per fruit) for the purpose of fly rearing and host preference analysis. The fruits were then enclosed within cages to facilitate hatching, while the maggots subsisted on an artificial diet consisting of a 10% sucrose solution in the laboratory environment. The results indicated that the larval counts exhibited statistically significant differences ($df = 2$, $f = 736.9149$, $p<0.05$) across the five mango varieties. *Bactrocera dorsalis* exhibited a pronounced inclination to oviposit on the Chunsa variety (83.5 ± 1.93 larvae, range 81-85), followed by Sindhri (67 ± 4.06 larvae, range 61-64), Beganpali (59.6 ± 3.090 larvae, range 57-61), and Lal Bad Shah (53.9 ± 2.3, range 55-57), with the lowest oviposition observed on the Sonaro variety (41.2 ± 2.04 larvae, range 38-40). The Sindhri and Beganpali cultivars did not demonstrate a significant difference from Lal Bad Shah; however, both exhibited notable differences ($p<0.05$) when compared to Sonaro.

A significant variability among the host varieties was evident ($p=0.02$). The performance of the maggots was found to be significantly different ($p<0.05$), with superior performance observed in the Chunsa cultivar as opposed to the Sonaro variety, attributable to the elevated sweetness and firmness characteristic of Chunsa flesh. A sex ratio of 3:1 was noted across all mango varieties examined. The correlation between host preference and maggot survival demonstrated a robust coefficient of determination of 47.4% ($p<0.05$) for the respective varieties. In the context of pest management, it is imperative to elucidate the dynamics of host-pest interactions grounded in an appropriate understanding of the factors influencing oviposition behaviour and offspring viability.

A study conducted by Shi *et al.* (2017) to track the effects of new host plants on *B. tau* genetic variation. In this study, they examined the genetic variation of *B. tau* by using microsatellite molecular markers for 15 consecutive generations of development on two traditional hosts (cucumber and pumpkin) and one novel host (banana) in a lab condition Analysis of molecular variance revealed that the genetic difference (10.39%) between populations feeding on different hosts was substantial, but not across populations from different generations. Itsuggests that host food, rather than population generations, had a significant impact on *B. tau* genetic variation. The novel host had a bigger effect on *B. tau* genetic variance than usual Cucurbitaceae hosts. The high genetic

variance of banana-feeding populations was reflected in challenges in balancing gene and genotype frequencies, lower genetic diversity, and more divergent genetic difference.

A study carried out by Rattanapun *et al.* (2021) examined the host plant preferences of *Bactrocera latifrons* (Hendel) (Diptera: Tephritidae), a significant pest affecting chili and nightshade crops, utilizing seven species of host plants belonging to the family Solanaceae. The study incorporated two species of nightshade, specifically eggplant, *Solanum melongena L.*, and turkey berry, *Solanum torvum Sw*.; alongside three varieties of pepper and one large chili cultivar of *Capsicum annum L.*, namely banana pepper, cayenne pepper, noom pepper, and duey kai chili; in addition to one small chili cultivar of *Capsicum frutescens L.*, referred to as bird chili, which were assessed as potential host plants for *B. latifrons* through a series of choice and no-choice experiments conducted within a laboratory environment. The findings indicated that *B. latifrons* exhibited a marked preference for ovipositing in *Capsicum* fruits as opposed to those of *Solanum*.

Among the tested host plants, bird chili and banana pepper emerged as the most favoured by *B. latifrons*, yielding the highest pupal counts per gram of fruit in no-choice and choice experiments, respectively. While the larval performance parameters of *B. latifrons* were found to be superior on eggplant compared to other Solanaceous species, fruit characteristics and the total phenolic content within the fruit were determined to be critical factors influencing the host selection by *B. latifrons*. Conversely, turkey berry was identified as the least preferred host by *B. latifrons*, exhibiting the lowest pupal counts per fruit, and it was entirely absent from ovipositional activities by *B. latifrons* females across all ripeness stages in the choice experiment.

A study was conducted by Sarwar *et al.* (2013) to investigate the influence of various host species on their selection preferences and the performance of their progeny. Host selection experiments were conducted for the fruit flies *Bactrocera zonata (*Saunders) and *Bactrocera cucurbitae* (Coquillett) utilizing a diverse array of fruits and vegetables. The preference for oviposition was assessed by exposing fruits and vegetables to natural infestations by *Bactrocera* in an ecological context, with their larvae subsequently reared and adult specimens maintained under controlled laboratory conditions. The comparative host preference of the *B. zonata* fruit fly was evaluated through field experiments involving mango, peach, and apple fruits. The mango was identified as the most favoured host, followed in preference by peach and apple, as evidenced by the highest number of pupae produced (173.17), the pupae weight recorded (6.40 mg), and the emergence rate of adult fruit flies (84.53%). The vegetables bitter gourd, brinjal, muskmelon, and pumpkin were assessed for their relative attractiveness as hosts for the fruit fly *B. cucurbitae*. Bitter gourd emerged as the most preferred host, exhibiting the highest levels of pupae formation (134.08); pupae weight attained (4.91 mg), and the percentage of adult emergence (82.64%) of fruit flies. Brinjal was categorized as a moderately preferred host, while muskmelon and pumpkin were classified as the least preferred hosts. These findings provide empirical evidence that fruit flies exhibit differential responses to hosts encountered in their natural habitat, suggesting that hosts advantageous to the pests are likely to be more adapted. Furthermore, the results indicate that the host preferences of fruit flies can shift toward more suitable hosts, and in instances where optimal breeding environments become limited, alternative hosts may be accepted. These conclusions substantiate the notion that the host selection and preferences of fruit flies significantly impact both pre-harvest and post-harvest management strategies for horticultural crops.

A comprehensive investigation by Ganie *et al.* (2025) assessed the influence of three distinct host plants: bottle gourd (*Lagenaria siceraria*), ridge gourd (*Luffa acutangula*), and cucumber *(Cucumis sativus)* on the morphology and dimensions of the wings of *Bactrocera cucurbitae* and *B. tau* through the application of geometric morphometrics. The wings of female specimens were observed to be significantly larger than those of their male counterparts, while the wings of *B. cucurbitae* exhibited a markedly reduced size in comparison to those of *B. tau*. Individuals that were nourished on varied host plants did not demonstrate significant discrepancies in wing size. Notably, wing shape exhibited significant variations both across sexes and between species. The deviations in wing morphology between males and females were more pronounced than the variations observed between *B. cucurbitae* and *B. tau*. Wing shape can be employed as a reliable criterion for distinguishing between males and females of the two species with complete accuracy. A significant divergence in wing shape was noted between male representatives of the two species that were sustained on cucumber and bottle gourd. Wing shape can serve as an effective means for accurately identifying male specimens of *B. cucurbitae* and *B. tau* that are feeding on these two host plants without errors. The above studies suggest that feeding habits significantly impact the genetic variation of different *Bactrocera* species. Some examples of genetic variation based on feeding habits are given in table 1.

**Table 1. Some examples of genetic variation based on feeding habits.**

| Species of Fruit fly | Feeding habit | Insights into genetic variation |
|---|---|---|
| *Bactrocera dorsalis* | Polyphagous (hundreds of host) | Shows high genetic diversity and has a larger repertoire of detoxification-related genes compared to specialists. Populations can still show genetic differentiation when reared on novel hosts like navel oranges for multiple generations. |
| *Bactrocera minax* | Monophagous (unripe citrus fruits) | Exhibits extreme specialization and has specific genetic adaptations in its visual system (e.g., the Rh6 opsin gene) that confers a colour preference for its specific host. |
| *Bactrocera tau* | Polyphagous (expanded from Cucurbitaceae) | Exhibits extreme specialization and has specific genetic adaptations in its visual system (e.g., the Rh6 opsin gene) that confers a colour preference for its specific host. |
| *Bactrocera zonata* | Polyphagous (various fruits and vegetables) | Exhibits extreme specialization and has specific genetic adaptations in its visual system (e.g., the Rh6 opsin gene) that confers a colour preference for its specific host. |

## CONCLUSIONS

Feeding habits appear to be an important ecological factor influencing the genetic makeup of *Bactrocera* spp. Multiple host exposure may promote gene flow and diversification, while restricted feeding habits may drive specialization and lineage separation. Thus, it can be concluded that:

1. Polyphagous fruit flies exhibit greater genetic diversity, contributing to their invasive potential.
2. Feeding habits significantly shape genetic variability in *Bactrocera* spp.
3. Host-associated genetic differentiation offers insights for developing host-based monitoring and control strategies.

Therefore, the diverse feeding habits within the *Bactrocera* genus act as a powerful selective force, leading to significant genetic variation and playing a crucial role in their ongoing evolution and speciation.

## REFERENCES


1. **Agarwal M.L. and Sueyoshi M.** (2005). Catalogue of Indian fruit flies (Diptera: Tephritidae). *Oriental Insects*. 39(1):371- 433. 10.1080/00305316.2005.10417450
2. **Amur A., Memon N., Sahito R. and Soomro A.** (2022). *Bactrocera dorsalis* Hendel (Diptera: Tephritidae) egg-laying preferences and larval developmental on five mango varieties of Sindh, Pakistan. *International Journal of Applied and Pure Science and Agriculture*. 7(4): 2617-8680.
3. **Brandalha T.M.L. and Zucoloto F.S.** (2004). Selection of oviposition sites by wild *Anastrepha obliqua* (Macquart) (Diptera: Tephritidae) based on nutritional composition. *Neotropical Entomology*. 33:557-562. 10.1590/S1519-566X2004000 500003
4. **Chang H.Y., Tzeng C.C., Tsai W.H., Kao S.S. and Tseng Y.H.** (2003). Phylogenetic study of the Dacinae (Diptera; Tephritidae) using partial sequences of mitochondrial 16S ribosomal DNA. *Plant Protection Bulletin Taipei*. 45: 1-15.
5. **Clarke A.R., Armstrong K.F., Carmichael A.E., Milne J.R., Raghu S. and Roderick G. K.** (2005). Invasive phytophageous pests arising through a recent evolutionary radiation: the *Bactrocera dorsalis* complex of fruit flies. *Annual Review of Entomology*. 50:293-319. 10.1146/annurev.ento.50.071803.130428
6. **Cronin J.T. and Abrahamson W.G.** (2001). Goldenrod stem galler preference and performance effects of multiple herbivores and plant genotypes. *Oecologia*. 127(1): 87-96. 10.1007/s004420000561
7. **Drew R.A.I**. (1997). The economic and social impact of the *Bactrocerapapayae* Drew and Hancock (Asian papaya fruit fly) outbreak in Australia. In Allwood AJ, Drew RAI. (Ed.). Symposium on Management of Fruit Flies in the Pacific. ACIAR Proceedings No. (76): 205-207.
8. **Doorenweerd C., Leblanc L., Norrbom A.L., Jose M.S. and Rubinoff D.** (2018). A global checklist of

the 932 fruit fly species in the tribe Dacini (Diptera, Tephritidae). *Zookeys*. (730):19-56. 10.3897/zookeys.730.21786

9. **Fletcher B.S.** (1987). The biology of dacine fruit flies. *Annual Review of Entomology*. 32:115- 144. 10.1146/annurev.en.32.010187.000555
10. **Ganie S.A., Rehman S.A., Bano P. and Tofilski A.** (2025). Influence of host plant on the wing shape of *Bactrocera cucurbitae* and *Bactrocera tau* (Diptera: Tephritidae). *Oriental Insects*. *59*(1):19-32. 10.1080/00305316.2024.2369095
11. **Hafsi A., Facon B., Ravigné V., Chiroleu F., Quilici S., Chermiti B. and Duyck P.F.** (2016). Host plant range of a fruit fly community (Diptera: Tephritidae): does fruit composition influence larval performance. *BMC Ecology*. 16:40. 10.1186/s12898-016-0094-8
12. **Hardie R.C. and Raghu P.** (2001). Visual transduction in *Drosophila*. *Nature*. 413: 186-193. 10.1038/35093002
13. **He Y., Xu Y. and Chen X.** (2023). Biology, ecology and management of tephritid fruit flies in China: A Review. *Insects*. 14(2):196. https://doi.org/10.3390/insects14020196
14. **Korneyev V.A.** (1999). Phylogenetic relationships among higher groups of Tephritidae. In: Aluja M, Norrbom A, editors. Fruit flies (Tephritidae). CRC Press. 73-112.
15. **Kostal V.** (1993). Physical and chemical factors influencing landing and oviposition by the cabbage root fly on host-plant models. *Entomologia Experimentalis et Applicata* .66:109-118. doi.org/10.1111/j.1570-7458.1993.tb00698.x
16. **Li L., Gao X., Gui H., Lan M., Zhu J., Xie Y., Zhan Y., Wang Z., Li Z. and Ye M**. (2020). Identification and preliminary characterization of chemosensory-related proteins in the gall fly, *Procecidochares utilis* by transcriptomic analysis. *Comparative Biochemistry and. Physiology Part D: Genomics Proteomics*. 36: 100724. https://doi.org/10.1016/j.cbd.2020.100724
17. **Li Y.L., Hou M. Z., Shen G .M., Lu X. P., Wang Z., Jia F., Wang J. J. and Dou W.** (2017). Functional analysis of five trypsin-like protease genes in the oriental fruit fly, *Bactrocera dorsalis* (Diptera: Tephritidae). *Pesticide Biochemistry and Physiology*. 136: 52-57. 10.1016/j.pestbp.2016.08.004
18. **Mahfuza K., Tahira B.R. and Howlader J.** (2011). Comparative host susceptibility, oviposition, and colour preference of two polyphagous Tephritids: *Bactrocera cucurbitae* (Coq.) and *Bactrocera tau* (Walker). *Research Journal of Agriculture and Biological Science*. 7(3): 343- 349.
19. **Mancera C., Heckel D.G. and Vogel H.** (2012). Transcriptional analysis of physiological pathways in a generalist herbivore: responses to different host plants and plant structures by the cotton bollworm, *Helicoverpa armigera*. *Entomologia Experimentalis et Applicata*. 144(1):123-133. 10.1111/j.1570-7458.2012.01249.x
20. **Masselière M., Ravigné V., Facon B., Lefeuvre P., Massol F., Quilici S. and Duyck P.F.** (2017). Changes in phytophagous insect host ranges following the invasion of their community: long-term data for fruit flies. *Ecology and Evolution*. 7(14): 5181-5190. 10.1002/ece3.2968
21. **Mattsson M., Hood G.R., Feder J. L. and Ruedas L. A.** (2015). Rapid and repeatable shifts in life-history timing of *Rhagoletis pomonela* (Tephritidae) following colonization of novel host plants in the Pacific Northwestern United States. *Ecology and Evolution*. 5: 5823-5827.
22. **Montell C.** (2012). *Drosophila* visual transduction. *Trends Neurosci*. 35(6): 356-363. 10.1016/j.tins.2012.03.004
23. **Morante J. and Desplan C.** (2008). The colour-vision circuit in the medulla of *Drosophila*. *Curr Biol*. 18(8): 553-565. 10.1016/j.cub.2008.02.075
24. **Ono H., Hee A.K. and Jiang H.** (2021). Recent advancements in studies on chemosensory mechanisms underlying detection of semiochemicals in Dacini fruit flies of economic importance (Diptera: Tephritidae). *Insects*. 12(2):106. 10.3390/insects12020106
25. **Pavlidi N., Dermauw W., Rombauts S., Chrisargiris A., Van Leeuwen T. and Vontas J.** (2013). Analysis of the Olive Fruit Fly *Bactrocera oleae* Transcriptome and Phylogenetic 588 Classification of the Major Detoxification Gene Families. *PLoS ONE*. 8(6): 10. https://doi.org/10.1371/journal.pone.0066533
26. **Piñero J.C., Souder S.K. and Vargas R. I.** (2017). Vision-mediated exploitation of a novel host plant by a tephritid fruit fly. *PLoS ONE* .12(4): e0174636. https://doi.org/10.1371/journal.pone.0174636
27. **Pollock J.A. and Benzer S.** (1988). Transcript localization of four opsin genes in the three visual organs of *Drosophila*; RH2 is ocellus specific. *Nature*. 333(6175): 779-782. 10.1038/333779a0

28. **Rasool B.** (2025). Diversity of Host Preference of Peach Fruit Fly *Bactrocera zonata* (Saunders, 1842) (Diptera: Tephritidae). *Journal of the Entomological Research Society*. 27(1): 15-30. https://doi.org/10.51963/jers.v27i1.2654

29. **Rattanapun W., Tarasin M., Thitithanakul S. and Sontikun Y.** (2021). Host Preference of *Bactrocera latifrons* (Hendel) (Diptera: Tephritidae) among fruits of Solanaceous Plants. *Insects*. 12(6):482. https://doi.org/10.3390/insects12060482

30. **Rauf I., Ahmad N., Rashdi S.M.S., Ismail M. and Khan M.H.** (2013). Laboratory studies on ovipositional preference of the peach fruit fly *Bactrocera zonata* (Saunders) (Diptera: Tephiritidae) for different host fruits. *African Journal of Agricultural Research*. 8(15):1300-1303. 10.5897/AJAR2013.6744

31. **Renwick J.A.A.** (1989). Chemical ecology of oviposition in phytophagous insects. *Experientia*. 45: 223- 228. https://doi.org/10.1007/BF01951807

32. **Roohigohar S., Clarke A.R. and Prentis P.J.** (2021). Gene selection for studying frugivore-plant interactions: a review and an example using Queensland fruit fly in tomato. *PeerJ.* 9: e11762. 10.7717/peerj.11762

33. **Sarwar M., Hamed M., Rasool B. and Yousaf M.** (2013). Host Preference and Performance of Fruit Flies *Bactrocera zonata* (Saunders) and *Bactrocera cucurbitae* (Coquillett) (Diptera: Tephritidae) for various Fruits and Vegetables. *International Journal of Scientific Research in Environmental Sciences.* 1(8).188-194. 10.12983/ijsres-2013-p188-194

34. **Shi W., Yang T. Y., Ye H. and Cao J.** (2017). Impact of host plants on genetic variation in the *Bactrocera tau* (Diptera: Tephritidae) based on molecular markers. *J*ournal of Entomological Science . 52(4):411-426. 10.18474/JES17-19.1

35. **Tallamy D.W.** (2000). Physiological issues in host range expansion. InEn: Spencer, N y Nowierski, R. (Ed.), International Symposium on Biological Control of Weeds (pp. 11-26); Bozeman- Montana, USA.

36. **Tang S. and Guo A.** (2001). Choice behaviour of *Drosophila* facing contradictory visual cues. *Science.* 294: 1543-1547. 10.1126/science.1058237

37. **Verma A.K.** (2017). A Handbook of Zoology. Shri Balaji Publications, Muzaffarnagar. 1- 648pp.

38. **Wang Y., Andongma A.A., Dong Y., Chen Z., Xu P., Ren X., Krosch M.N., Clarke A.R. and Niu C.** (2019). Rh6 gene modulates the visual mechanism of host utilization in fruit fly *Bactrocera minax*. *Pest Management Science.* 75(6): 1621-1629. 10.1002/ps.5278

39. **White I.M. and Elson-Harris M.M.** (1992). Fruit flies of economic significance: their identification and bionomics (xii+601). CAB International, Wallingford.

40. **Xu P., Wang Y., Akami M. and Niu C.Y.** (2019). Identification of olfactory genes and functional analysis of *BminCSP* and *BminOBP21* in *Bactrocera minax*. *PLoS One*. 14(9): e0222193. 10.1371/journal.pone.0222193

41. **Zhong H., Li F., Chen J., Zhang J. and Li F.** (2017). Comparative transcriptome analysis reveals host-associated differentiation in *Chilo suppressalis* (Lepidoptera: Crambidae). *Scientific Reports*. 7: 13778. https://doi.org/10.1038/s41598-017-14137-x