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Review on microbiota in fruit piercing moths specifically from erebidea (Noctuoidea: Lepidoptera)

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Abstract

Insects belong to order Lepidoptera include moths, comprising approximately 1,60,000 species acts as a major crop pest of the world. Many insects play as host to different microbes by forming close mutualistic relationships. The study on this topic reveals bacterial symbiont play important role on host's biology, it may impact on host's digestion, immunity, anti-pathogenic responses, nutrient absorption of host food etc.; Fruit piercing moths are common agricultural pest which damages the commercially important fruit crops such as moth of genus *Othreis* as a harmful pest on pomegranate, citrus and orange mostly found in Maharashtra state. Most of the moth vertically transmit the endosymbiotic microorganisms, which can affect the host in different parameters like fitness, reproduction, genetic diversity etc. according to study of genome sequencing of *Erebidae* moths focusing on bacterium *Wolbachia*. Different life stages like egg, larva, pupa, adult, varies in their gut microbiota. This review reveals the work done on the diversity and richness of gut microbiota, their role on host fruit piercing moth, in Maharashtra, India and different countries of world.

Keywords: Family- Erebidae, fruit piercing moth, microbiota, diversity

Introduction

Fruit piercing moths are economically important, as they are serious pest on commercially important fruit crops through the sub-tropical and tropical countries (Waterhouse and Norris, 1987) (Banziger, 1982) ^[55], and microorganisms play key role in insects/hosts physiology as well as nutrition (Dillon and Charnley, 1995; Nardi et al., 2002) ^[18, 56] like production of antifungal and antibacterial phenol in locust gut by P. agglomerance bacteria (Dillon and Charnley, 1995) ^[18], which is most abundantly found in gut of locust S. gregaia (J. Hunt and Charnley, 1981) ^[32]. Insects and their symbiotic bacteria's has evolved diversely and in their diverse interactions, which play role in insect nutrition (Wicker, 1983; Douglas, 1988; Douglas and prosser, 1992; Lal et al., 1994; Bracho et al., 1995; Bernays and Klein, 2002) [57, 21, 22, 34, 5, ^{4]}. Bacteria's play role in the defense mechanism of host insect (Kellner and Dettner, 1996; Piel, 2002; Oliver et al., 1999) ^[33, 58]. Insect gut has diversity of bacteria as gut of insects provide suitable habitat for bacterial association (Bignell, et al., 1984)^[59]. Symbiotic bacteria of host insect plays role in the reproductive fitness and development of host (Caspari and Watson, 1959; Gherna et al., 1991; Hurst et al., 1999) [11, 26, 31]. In many species of insects bacterial presence varies in species to species and even every life stages of insect shows different bacterial composition that is bacteria's are transient do not remain in gut in each life stage. However in some cases, nutrient supplying bacteria's to their host insect remain permanent in gut of host throughout the life and some possess obligate microbial endosymbionts that benefits the insects (Bridges, 1981)^[7]. This bacteria's distinguished it in to two categories as intracellular and extracellular based on their location of habitat in the insect body as whether they live within cell or in gut lumen or body surface and lining of insect cavities (Dillon and Dillon, 2004; Engel and Moron, 2013; Hansen and Moron, 2014) ^[17, 23, 28]. Symbiotic bacteria's are considered primary or secondary depending on their role for the host insect whether they are benefited to host or provide non-essential benefit for hosts survival (Douglas, 2015)^[20].

The bacterial species associated with a host can vary in their diversity across different life stages, that is bacterial communities can be stable or dynamic, symbiotic association can be temporarily persistence of microbes in host insect in different life stages and across generations (Zilber-Rosenberg, 2008; Engel P, Moron, 2013; Salem H. et al., 2015) [54, 23, 48]. In agricultural and forest habitat of particular pest insects, variability in associated microbe community is found in relation to host diet, to enhance the dietary range of phytophagous insects (Dillon R, Dillon V, 2004; Hosokawa et al., 2007; Douglas AE, 2009; Engel, Moon, 2013; Chu C, et al., 2013) ^[17, 30, 19, 23, 15]. Depending on the diet bacterial associated communities varies in several insects (Broderic N.A. et al., 2004; Belda E, et al., 2011; Chandler J. A. et al., 2011; Gayatri P.N. et al., 2012) [8, 3, 12, 25]. But in some insects bacterial community may also be stable across diets (Sudakaran S et al., 2012) ^[50]. Other factors that are responsible for bacterial variation are rearing history of host insect and geographic habitat of host insect population (Xiang H. et al. 2006; Adams A.S. et al., 2010) ^[53, 1]. In Lepidoptera order wide variety of agricultural and forest pest which are most damaging worldwide, which have developed resistance against existing control measures like insecticides, genetically modified plants, genetic host plant resistance (Roush RT,1987; Stoyenoff JL et al., 1994)^[47, 49]. The knowledge of gut microbiota composition and their roles they play in insect's life cycle and their different stages could lead to new approaches for pest management. The Gypsy moth (Erebidae) is most damaging, invasive defoliator of deciduous trees (Montgomery ME, W E Wallner, 1989)^[39]. The Gypsy moth can causes economic losses to agriculture and forest industry, it can alters natural ecosystems, can be pathogenic for humans and enumerate 300 host species which shows highly polyphagous nature of it (Liebhold et al., 1995) [35]. Gut microbiota associated with Lepidoptera are responsible for their host insects nutritional and physiological and other functions (Brand et al. 1975; Buchner P., 1965; Campbell B.C, 1989; Dasch et al., 1984; Mittler T.E, 1988) [6, 9, 10, 16, 38].

Microbiota of Various moth pests

The initial studies on lepidopteron gut microorganisms, then little was known about gut bacterial association suggested the possibility that gut microbiota provided assistance to important biochemical function related to host food ingestion and digestion or provide essential nutrients. In Gypsy moth: Lymantria disper L. (Lepidptera: Erebidae), the effect of diet on bacterial composition has been examined the found study stated that some species shown similar bacterial composition among insects fed on similar diet and variations were found in microbial composition in insect those who fed on different diets like sterilized artificial diet these bacterial analysis has been done by 16s rRNA sequencing as well as culture based analysis, study has provide influence of host plant on gut microbial composition of lepidopteron insects (Broderick et al., 2004)^[8]. Insects provide environmental reservoirs for bacteria's which are resistant to antibiotic. To know the antibiotic resistance of bacterial community in larval mid-gut of Gypsy moth (Lepidoptera: Erebidae) by using Metagenomics for identification of bacterial community and their genotypes which are responsible for resistance (Heather K. Allen et al., 2009) [29]. The association of bacterial community of insects are mostly depend on the subsequent structuring by extreme conditions within hosts gut, environmental acquisition and maternal transmission, to study

this in gypsy moth: Lymantria disper L. (Lepidptera: Erebidae), comparative analysis of interaction between egg mass and larval midgut microbiome and effect of diet and internal host gut environment on their bacterial community by using 16s rRNA gene pyro-sequencing, found midgut bacterial community which reflects its diet weather its foliar diet of wild or laboratory maintained diet, the environmental acquisition can lead to similar bacterial community assemblance (C.J. Mason, K.F. Raffa, 2014)^[13]. Behavior of insect can affect the associated bacterial community composition by direct transmission between insects within colonies and gregarious species (Minkley et al. 2006; Moran et al., 2012; Woodbury et al., 2013) ^[37, 40, 52]. The various insect proportionately carries pathogenic bacteria's, like soft rot Enterobacteriaceae (SRE) which can infect vegetables like potato and fruit plants, insects like Delia florais, Plutella xylostella, Chrysoperla carnea carries this pathogenic bacteria which are harmful to crops (S. Rossmann et al., 2018) [46].

Comparative study of gut microbiome of two fruit piercing moths peach fruit moth and oriental fruit moth which have different habitat and host plant showed common bacterial genera but had difference in their richness despite having different fruit habits and common genera in both the fruit piercing moths, the abundance of bacteria is depend on the functional parameters like their role in metabolism, translation and membrane transport etc. (Q. Gong, J. Cao, et al. 2020) ^[60]. The fall webworm, *Hyphantria cunea* Drury (Erebidae: Hyphantria), is a phytophagous pest species of forest and agricultural ecosystems; where its larvae feed on Deciduous tree leaves (Schowalter T. et al., 2017)^[61], the responsible genes for aggregating behavior, chemosensory, nutrientrelated and silk-web-related genes of H.cunea has been studied and found by metagenomics and this genes can be responsible for host H. cunea environmental adaptations and its cause of rapid invasion at genetic level (Chen et al., 2020) [14]

The fruits piercings moth Othreis: Eudocima (Erebidae family) is polyphagous pests. This serious pest was firstly recorded in India by Lefroy and Hawletl, 1909. At Chennai, Isolation and the characterization of roles of bacteria from gut of different instars of Bombyx mori, these bacteria's help in degradation of polysaccharides by producing digestive enzymes (A. Anand et al., 2009)^[62]. In Maharashtra among the population density of fruit piercing moth in harvesting season of citrus fruits moths belong to Eudocima: Erebidae found the most (Mohite and Deshmukh, 2014) [63]. At Bangalore, the identification of gut bacteria has been done to compare gut microbial flora of Tomato fruit borer Helicoverpa armigera of the wild and laboratory habitat from fourth and fifth instars by 16s rRNA gene sequencing, concluded that habitat impacts on gut microbial flora, founded variation in the bacterial species (S. Madhusudan, S. K. Jalali, et al. 2011)^[36]. At New Delhi the polyphagous Eri silk moth, Samia ricini has been subjected to isolation of gut bacteria's by different methods like 'Culture-dependent 16s rRNA' that reveals diversity in number of species of gut bacteria, the 'Metagenomics' analysis found diversity in culturable as well un-culturable bacterial community and their inhibition in three parts of gut, and by the 'Enzymatic assays' found role of aerobic and un-aerobic bacteria's in digestion and nutrition of host S.ricini (K. MsangoSoko et al., 2020) [41]. The recent study at Delhi, on gut bacteria of cotton bollworm Pectinophora gossypiella by targeting Metagenomics of 16s

rRNA of V3-V4 region, to find out the influence of sex of pink bollworm if exists in diversity of gut microbiota and their functions. According to alpha and beta diversity male and female gut bacterial community varies as well as unique in their bacterial diversity in both larval group, these variations in microbiota may help in pesticide resistance and even Bt-cotton gene resistance (H.S. Chaitra *et al.*, 2022) ^[27].

Conclusion

The all above study reveals that the wide role of bacteria in host life cycle at all life stages, from hosts nutrition, physiology, digestion, resistance against any unfavorable conditions to even reproduction. The pest moth are important economic factor in agriculture as well as forest, the phytophagous nature of these pest moth is because of the symbiotic gut bacteria and different studies has done to find out diversity and role of gut microbiota of different pest moths all over world. Most of the study of microbiota of pest moth belong to order Lepidoptera has done internationally to find out diversity of bacteria on basis of habitat weather wild or cultured, the effect of diet on composition gut bacteria of host, even some researchers reveals the genetic composition of bacteria is responsible for particular behavior of host moth. Most of the analysis has been done by using Metagenomics of 16s rRNA sequencing. The moth belong to Erebidae family are most common agricultural pest of vegetable as well as fruit crops. Microbial analysis of moths belong to family Erebidae can be helpful economically and agriculturally the most of the study has been done internationally, in India very few researches has been done on microbiota of pest moth, so there is huge scope for the new approaches in this field.

Table 1: Some International. National Researches on Microbiota of insects/moths	Table 1	1: Some	International.	National Researches on Microbiota of insects/moth	s
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Sr. No.	Researcher's Name	Gut Microbe	Insect/Moth species	Purpose of Research
1.	J. Robert Bridges (1981) ^[7] (USA)	Entobacter agglomerans and Entobacter spp.	Bark beetles- D. terbrans D. frontalis IPS avulsus	Atmospheric nitrogen fixation in host plant.
2.	Hunt and Charnley (1981) ^[32] ; (United Kingdom)	Pantoea agglomerase (domi.), H. alveii, S. marcescens, S. liquefacies	S. gregaria Desert locust	To find out gut bacterial flora.
3.	Dillon and Charnley (1995) ^[18] ; (UK)	Pantoea (Entobacter) (domi.)	<i>S. gregaria</i> Desert locust	To prove Synthesis of fungitoxic Phenol by gut bacteria
4.	A. A. Prem Anand <i>et al.</i> (2009); ^[62] (Chennai, India)	G+:B. circulans G-: P. vulgaris, K. Pneumonie, E. coli, C. freundii and 7 more	Bombex mori L.	Degradation of cellulose, xylan, pectin and starch and their impact on digestion.
5.	C. J. Mason, <i>et al</i> . (2014) ^[13]	Similar bacterial community in diet associated bacteria, Different in egg mass.	<i>Lymantria dispar</i> L. Gypsy moth (Lepidoptera: Eribidae)	To investigate egg mass bacteria and environmental source (diet) of bacteria on larval mid-gut bacteria.
6.	H. Staudcher <i>et al.</i> (2016) ^[64] ; (Germany)	Laboratory Larvae- Enterococuus (domi) Field larvae-Methylobacterium Eggs- Entobacter Adult- Entobacter	Heliothis virescens	Bacterial community varies in relation to stages, diet and population.
7.	Luis R. Paniagua Voirol, <i>et</i> al. (2018) ^[65] (Netherland)	Gut dominant bacteria families– Enterobacteriaceae, Bacillaceae, Pseudomonadaceae	Lepidoptera species (Almost 30 diff species)	 To review composition of microbial flora across order Lepidoptera Overview on drivers of the variability Routes f transfer Role of bacteria.
8.	Y. Zheng <i>et al.</i> (2020) ^[66] (China)	Escherchia Shigella and Entobacter (domi. Genera)	Phthorimaea operculella (Zellar) Potato tuber Moth	Richnes of bacterial communities was different depending on nutrient level of tissues consumed by moth.

References

- 1. Adams AS, Adams SM, Currie CR, Gillette NE, Raffa KF. Geographic variation in bacterial communities associated with the red turpentine beetle (Coleoptera: Curculionidae). Environ Entomol. 2010;39:406-414. DOI: 10.1603/EN09221 PMID: 20388269
- 2. Atachi P, Desmidts M, Durnex C. Fruit-piercing moths (*Lepidoptera: Noctuidae*) as citrus pests in Benin: A description of their damage and morphology, Plant Protection Bulletin. 1989;37:111-120.
- 3. Belda E, Pedrola L, Peretó J, Martínez-Blanch JF, Montagud A, Navarro E, *et al.* Microbial diversity in the midguts of field and lab-reared populations of the European corn borer Ostrinia nubilalis. PLoS ONE. 2011;6:e21751.

DOI: 10.1371/journal.pone.0021751 PMID: 21738787

- 4. Bernays EA, Klein BA. Quantifying the symbiont contribution to essential amino acids in aphids: The importance of tryptophan for Uroleucon ambrosiae. Physiol. Entomol. 2002;27:275-284.
- Bracho AM, Martinez-Torres D, Moya A, Latorre A. Discovery and molecular characterization of a plasmid localized in, *Buchnera* sp. bacterial endosymbiont of the aphid Rhopalosiphum; padi. J Mol. Evol. 1995;41:67-73.
- Brand JM, Bracke JW, Markovetz AJ, Wood DL, Browne LE. Production of verbenol pheromone by a bacterium isolated from bark beetles. Nature. 1975;254:136-137.
- 7. Bridges. Nitrogen fixing bacteria associated with bark beetles. Microbial Ecol. 1981;7:131-137.

- Broderick NA, Raffa KF, Goodman RM, Handelsman J. Census of the Bacterial Community of the Gypsy Moth Larval Midgut by Using Culturing and Culture-Independent Methods. Applied and Environmental Microbiology. 2004;70:293-300.
- Buchner P. Endosymbionts of animals with plant microorganisms. John Wiley & Sons, Inc., New York, N.Y.; c1965.
- 10. Campbell BC. On the role of microbial symbiotes in herbivorous insects. In E. Bernays (ed.), Insect-plant interactions. CRC Press, Boca Raton, Fla.; c1989.
- 11. Caspari E, Watson GS. On the evolutionary importance of cytoplasmic sterility in mosquitos. Evolution. 1959;13:568-570.
- 12. Chandler JA, Lang JM, Bhatnagar S, Eisen JA, Kopp A. Bacterial communities of diverse Drosophila species: Ecological context of a host-microbe model system. PLoS Genet. 2011;7:e1002272.
 - DOI: 10.1371/journal.pgen.1002272 PMID: 21
- Charles J Mason, kenneth F Raffa. Acquisition and Structuring of Midgut Bacterial Communities in Gypsy Moth (Lepidoptera: Erebidae) Larvae, Environ. Entomol. 2014;43(3):595D604.

DOI: http://dx.doi.org/10.1603/EN14031

- 14. Chen Qi, Zhao Hanbo, Wen Ming, Li Jiaxin, Zhou Haifeng, Wang Jiatong, *et al.* Genome of the webworm Hyphantria cunea unveils genetic adaptations supporting its rapid invasion and spread. BMC Genomics. 2020;21:242. 10.1186/s12864-020-6629-6.
- Chu CC, Spencer JL, Curzi MJ, Zavala JA, Seufferheld MJ. Gut bacteria facilitate adaptation to crop rotation in the western corn rootworm. Proc Natl Acad Sci. USA. 2013;110:11917-11922. DOI: 10.1073/ pnas.1301886110 PMID: 23798396
- Dasch GA, Weiss E, Chang KP. Endosymbionts of insects, In N. R. Krieg and J. G. Holt (ed.), Bergey's manual of systematic bacteriology. Williams & Wilkins, Baltimore, Md.; c1984. p. 811-833.
- Dillon RJ, Dillon VM. The gut bacteria of insects: nonpathogenic interactions. Annu. Rev. Entomol. 2004;49:71-92. DOI: 10.1146/annurev.ento.49. 061802.123416
- 18. Dillon RJ, Charnley AK. Chemical barriers to gut infection in the desert locust: *In vitro* production of antimicrobial phenols associated with the bacterium Pantoea agglomerans. J Invertbr, Pathol. 1995;66:72-7.
- 19. Douglas AE. The microbial dimension in insect nutritional ecology. Funct Ecol. 2009;23:38–47.
- Douglas AE. Multi-organismal insects: Diversity and function of resident microorganisms. Annu. Rev. Entomol. 2015;60:17-34. DOI: 10.1146/annurev-ento-010814-020822
- 21. Douglas AE. Sulfate utilization in an aphid symbiosis. Insect Biochem. 1988;18:599-605.
- 22. Douglas AE, Prosser WA. Synthesis of the essential amino acid tryptophan in the pea aphid (Acyrthosiphon pisum) symbiosis. J Insect. Physiol. 1992;38:565-568.
- Engel P, Moran NA. The gut microbiota of insects diversity in structure and function. FEMS Microbiol. Rev. 2013;37:699-735. DOI: 10.1111/1574- 6976.12025
- 24. Ferrari J, Darby AC, Daniell TJ, Godfray HCJ, Douglas AE. Linking the bacterial community in pea aphids with host plant use and natural enemy resistance. Ecol. Entomol. 2004;29:60-65.

- 25. Gayatri Priya N, Ojha A, Kajla MK, Raj A, Rajagopal R. Host plant induced variation in gut bacteria of *Helicoverpa armigera*. PLoS ONE. 2012;7:e30768. DOI: 10.1371/journal.pone.0030768 PMID: 22292034
- 26. Gherna RL, Werren JH, Weisburg W, Cote R, Woese CR, Mandelco L, *et al.* Arsenophonus nasoniae gen. nov., sp. nov., the causative agent of the son-killer trait in the parasitic wasp Nasonia vitripennis. Intl. J Syst. Bacteriol. 1991;41:563–565
- 27. Chaitra HS, Singh Arjun, Pandiyan Kuppusamy, Kalia Vinay. Sex Biased Variance in the Structural and Functional Diversity of the Midgut Bacterial Community of Last Instar Larvae of Pectinophora gossypiella (Lepidoptera: Gelechiidae). Microbial Ecology, 2022, 83. 10.1007/s00248-021-01829-1.
- Hansen AK, Moran NA. The impact of microbial symbionts on host plant utilization by herbivorous insects. Mol. Ecol. 2014;23:1473–1496. DOI: 10.1111/mec.12421
- 29. Heather K Allen, Karen A Cloud-Hansen, Joseph M Wolinski, Changhui Guan, Serena Greene, Shyue Lu, Mallory Boeyink, *et al.* Resident microbiota of the gypsy moth midgut harbors antibiotic resistance determinants. DNA Cell Biol. 2009 Mar;28(3):109-17. DOI: 10.1089/dna.2008.0812.
- Hosokawa T, Kikuchi Y, Shimada M, Fukatsu T. Obligate symbiont involved in pest status of host insect. Proc R Soc Lond B Biol Sci. 2007;274:1979– 1984.966276
- Hurst GDD, Jiggins FM, Von Der Schulenburg JHG, Bertrand D, West SA, Goriacheva II, *et al.* Male-killing Wolbachia in two species of insect. Proc. R. Soc. Lond. Ser. B. 1999;266:735–740.
- 32. Hunt J, Charnley AK. Abundance and distribution of the gut flora of the desert locust, *Schistocerca gregaria* J Invert. Pathol; c1981.
- Kellner RII, Dettner K. Differential efficacy of toxic pederin in dettering potential arthropod predators of Paelenus (Coleoptera: Staphylinidae) offspring. Oerologica. 1996;107:293-300.
- Lal CY, Baumann L, Baumann P. Amplification of trpEG; adaptation of *Buchnera aphidicola* to an endosymbiotic association with aphids. Proc. Natl. Acad. Sci. USA. 1994;91:3819–3823.
- 35. Liebhold AM, Gottschalk KW, Muzika RM, Montgomery ME, Young R, O'Day K, *et al.* Suitability of North American tree species to the gypsy moth: A summary of field and laboratory tests. U.S. Department of Agriculture Forest Service NE Forest Experimental Station General Technical Bulletin NE-211. U.S. Department of Agriculture, Washington, D.C.; c1995.
- 36. Madhusudan S, Jalali Sushil, Venkatesan, Thiruvengadam, Lalitha, Yadavalli, Srinivas RP. 16S rRNA gene based identification of gut bacteria from laboratory and wild larvae of *Helicoverpa armigera* (Lepidoptera: Noctuidae). 2011;175-183:6.
- Minkley N, Fujita A, Brune A, Kirchner WH. Nest speciPcity of the bacterial community in termite guts (*Hodotermes mossambicus*). Insectes Soc. 2006;53:339Đ 344.
- Mittler TE. Applications of artificial feeding techniques for aphids, p. 145-170. In A. K. Minks and P. Harrewijn (ed.), Aphids: their biology, natural enemies, and control. Elsevier Biomedical Press, Amsterdam, The Netherlands.; c1988.

- 39. Montgomery ME, Wallner WE. The gypsy moth: A westward migrant, p. 353-373. In A. A. Berryman (ed.), Dynamics of forest insect populations: Patterns, causes, implications. Plenum Press, New York, N.Y.; c1989.
- 40. Moran NA, Hansen AK, Powell JE, Sabree ZL. Distinctive gut microbiota of honey bees assessed using deep sampling from individual worker bees. PLoS ONE. 2012;7:e36393
- 41. Msangosoko Kondwani, Gandotra Sakshi, Chandel Rahu, Sharma Kirti, Ramakrishinan Balasubramanian, Sabtharishi Subramanian, *et al.* Composition and Diversity of Gut Bacteria Associated with the Eri Silk Moth, Samia ricini, (Lepidoptera: Saturniidae) as Revealed by Culture-Dependent and Metagenomics Analysis. Journal of Microbiology and Biotechnology. 2020;30:1-12. 10.4014/jmb.2002.02055.
- 42. Msangosoko Kondwani, Gandotra Sakshi, Chandel Rahu, Sharma Kirti, Ramakrishinan Balasubramanian, Sabtharishi Subramanian, *et al.* Composition and Diversity of Gut Bacteria Associated with the Eri Silk Moth, Samia ricini, (Lepidoptera: Saturniidae) as Revealed by Culture-Dependent and Metagenomics Analysis. Journal of Microbiology and Biotechnology. 2020;30:1-12. 10.4014/jmb.2002.02055.
- 43. Oliver KM, Russell JA, Moran NA, Hunter MS. Fcultative bacteria in aphids confer resistance to parasitic wasps. Proc. Natl. Acad. Sci. USA. 2003;100:1803-1807.
- 44. Piel J. A polyketide synthase-peptide synthetase gene cluster from an uncultured bacterial symbiont of Paederus beetles. Proc. Natl. Acad. Sci. USA. 2002;99:14002-14007.
- Robinson C, Schloss P, Ramos Y, Raffa K, Handelsman J. Robustness of the bacterial community in the cabbage white butterfly larval mid-gut. Microb Ecol. 2010;59:199-211. DOI: 10.1007/s00248-009- 9595-8 PMID: 19924467
- 46. Rossmann S, Dees MW, Perminow J, Meadow R, Brurberg MB. Soft rot *Enterobacteriaceae* are carried by a large range of insect species in potato fields. Appl Environ Microbiol. 2018;84:e00281-18. https://doi.org/10.1128/AEM.00281-18.
- Roush RT. Ecological genetics of insecticide and acaricide resistance. Annu. Rev. Entomol. 1987;32:361-380.
- 48. Salem H, Florez L, Gerardo N, Kaltenpoth M. An out-ofbody experience: The extracellular dimension for the transmission of mutualistic bacteria in insects. Proc R Soc B Biol Sci. 2015;282:20142957.
- 49. Stoyenoff JL, Witter JA, Montgomery ME. Nutritional indices in the gypsy moth (*Lymantria dispar* (L)) under field conditions and host switching situations. Oecologia. 1994;97:158-170.
- Sudakaran S, Salem H, Kost C, Kaltenpoth M. Geographical and ecological stability of the symbiotic mid-gut microbiota in European firebugs, Pyrrhocoris apterus (Hemiptera, Pyrrhocoridae). Mol Ecol. 2012;21:6134-6151. DOI: 10.1111/mec.12027 PMID: 23017151
- 51. Sullam KE, Essinger SD, Lozupone CA, O'Connor MP, Rosen GL, Knight R, *et al.* Environmental and ecological factors that shape the gut bacterial communities of fish: A meta-analysis. Mol Ecol. 2012;21:3363-3378. DOI: 10.1111/j.1365-294X.2012.05552.x PMID: 22486918
- 52. Woodbury N, Moore M, Gries G. Horizontal transmission of the microbial symbionts *Enterobacter cloacae* and *Mycotypha microspora* to their Prebrat host.

Entomol. Exp. Appl. 2013;147:160Đ166.

- 53. Xiang H, Wei GF, Jia S, Huang J, Miao XX, Zhou Z, *et al.* Microbial communities in the larval midgut of laboratory and field populations of cotton bollworm (*Helicoverpa armigera*). Can J Microbiol. 2006;52:1085–1092. PMID: 17215900
- 54. Zilber-Rosenberg I, Rosenberg E. Role of microorganisms in the evolution of animals and plants: the hologenome theory of evolution. FEMS Microbiol Rev. 2008;32:723–735. DOI: 10.1111/j.1574-6976. 2008.00123.x PMID: 18549407
- 55. Banziger H. Fruit-piercing moths (Lep., Noctuidae) in Thailand: A general survey and some new perspectives. Mitteilungen der Schweizerischen Entomologischen Gesellschaft. 1982;55(3/4):213-40.
- Nardi S, Pizzeghello D, Muscolo A, Vianello A. Physiological effects of humic substances on higher plants. Soil Biology and Biochemistry. 2002 Nov 1;34(11):1527-36.
- 57. Wicker FW, Payne GC, Morgan RD. Participant descriptions of guilt and shame. Motivation and emotion. 1983 Mar;7:25-39.
- 58. Oliver RL. Whence consumer loyalty? Journal of marketing. 1999 Oct;63(4):33-44.
- 59. Bignell V, Fortune J. Understanding systems failure. Manchester University Press; c1984.
- 60. Liu X, Zhao C, Gong Q, Wang Y, Cao J, Li X, *et al.* Characterization of a caffeoyl-CoA O-methyltransferaselike enzyme involved in biosynthesis of polymethoxylated flavones in Citrus reticulata. Journal of Experimental Botany. 2020 May 30;71(10):3066-79.
- 61. Schowalter TD, Ring DR. Biology and management of the fall webworm, Hyphantria cunea (Lepidoptera: Erebidae). Journal of Integrated Pest Management. 2017 Jan;8(1):7.
- Anand A, Li Y, Wang Y, Lowe MJ, Dzemidzic M. Resting state corticolimbic connectivity abnormalities in un-medicated bipolar disorder and unipolar depression. Psychiatry Research: Neuroimaging. 2009 Mar 31;171(3):189-98.
- 63. Khanage SG, Kale DS, Mohite PB, Deshmukh VK. Reversed phase high performance liquid chromatographic method for simultaneous estimation of pregabalin and aceclofenac in tablet formulation (Acenac-N). Journal of Reports in Pharmaceutical Sciences. 2014 Jul 1;3(2):184-92.
- 64. Staudacher HM, Whelan K. Altered gastrointestinal microbiota in irritable bowel syndrome and its modification by diet: Probiotics, prebiotics and the low FODMAP diet. Proceedings of the Nutrition Society. 2016 Aug;75(3):306-18.
- 65. Paniagua Voirol LR, Frago E, Kaltenpoth M, Hilker M, Fatouros NE. Bacterial symbionts in Lepidoptera: Their diversity, transmission, and impact on the host. Frontiers in microbiology. 2018 Mar 27;9:556.
- 66. Yang J, Zheng YA, Gou X, Pu K, Chen Z, Guo Q, *et al.* Prevalence of comorbidities and its effects in patients infected with SARS-CoV-2: A systematic review and meta-analysis. International Journal of infectious diseases. 2020 May 1;94:91-5.
- 67. Gohil B, Thakkar K, Gondaliya G. Moths (Lepidoptera: Heterocera) of Bhavnagar city, Gujarat, India: A preliminary checklist. International Journal of Entomology Research. 2022;7(4):62-71.