Seasonal Variation Imparts The Endophytic Bacterial Community Dynamics in Mango Plants and Its Hemiparasites

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Abstract

Assessment of bacterial community dynamics helps to estimate the endophytic community structure and ecological behaviour imposed by them. Such community composition is essential to understand the molecular interplay that lies between them and the host plants. The present study aims to explore the endophytic bacterial communities and their dynamics in the pre-flowering and post-flowering seasons in the horticulturally important Mango (*Mangifera indica* L.) and its hemiparasites *Loranthus* sp., and *Macrosolen* sp. through a metagenomic approach using the sequence of V3 region of 16S rRNA gene. *Bacillus* was found to be the most abundant genera, followed by *Acinetobacter*, and *Corynebacterium*, which belong to the phyla Firmicutes, Proteobacteria, and Actinobacteria. It has been found that during the post-flowering season, twigs and leaves of mango have lower endophytic bacterial loads. Furthermore, the alpha-diversity indices of the representative genera were highest in *Loranthus* sp. during the post-flowering seasons of mango. The ecological, taxonomic, and complex correlation studies unravelled that the hemiparasites act as the potent reservoirs of endophytic community throughout the year, and during favourable conditions, these bacterial communities disseminate to the mango plant.

Introduction

Endophytic bacteria reside in the plant system with a wide community structure without any disease syndrome and benefits the host system by different plant growth-promoting properties, such as the production of phytohormones (indole acetic acid (IAA), cytokines, gibberellins), HCN, enzymes (ACC deaminase), synthesis of nitrogen, nitrates or solubilizes metals (phosphorus, iron, etc.) and also protect from different phytopathogens like fungi, bacteria, nematodes, etc. (Choudhary and Johri 2009; Radhakrishnan et al. 2017; Shafi et al. 2017). Moreover, apart from plant growth promotion or plant protection, bacterial endophytes produce many secondary metabolites that can be used as a source of bioremediation, waste management, pharmaceuticals and so on (Gouda et al. 2016; Sahoo et al. 2017). The culture-dependent endophytic communities were assessed by conventional media-dependent methods. But in this method, only a few community structures were observed due to alteration of growth conditions and nutrient variations (Mashiane et al. 2017). Thus, the total microbial community assessment can be possible in culture-independent metagenomic analysis. However, the significant disadvantages of this method are there are mitochondrial, chloroplast, and ribosomal DNAs also amplified during the PCR amplification process (Lucaci et al. 2019). To overcome this constrain, the locked nucleic acid (LNA) oligonucleotide-PCR clamping technique has been adopted to selective amplification of the endophytic bacterial genes (Ikenaga and Sakai 2014).

The endophytic bacterial community in plants varies according to the host plant's environmental changes and physiological changes (Ding and Melcher 2016). These community variations are also observed when a plant hosts one or more hemiparasitic plants in its system. In this system, the endophytic bacterial community may shift from one plant to another in different seasons due to its favourable environment. In the earlier study, the culture-independent bacterial community structures were observed in several medicinal, horticultural, and crop plants in seasonal and temporal variations (Ou et al. 2019).

However, the endophytic bacterial community variations in the horticultural plant mango (*Mangifera indica* L., family Anacardiaceae) is not reported yet. Mango is an important economic horticultural plant that originated in Sri Lanka and distributed in India, China, Thailand, Pakistan, Bangladesh, Maldives, Myanmar, and the south Asian countries. India is the highest producer of mango (40.5% of the World's total production) and earn ₹67 million during the 2016-17 season (<https://www.arjunfoods.com/Mango>). Additionally, the mango plant also hosts two hemiparasite plants such as *Scurrula parasitica* L. (accepted name; synonym: *Loranthus parasiticus* (L.) Merr.) (Family: Loranthaceae) and *Macrosolen colchinchinensis* (Lour.) Tiegh. (Family: Loranthaceae). The endophytic bacterial communities in these plants were also not assessed to date. In this study, the culture-independent endophytic bacterial communities of mango and its two hemiparasites were observed in the pre-flowering and post-flowering seasons of mango. The possible endophytic bacterial community shift between three plants was also studied in this communication.

Materials And Methods

Sampling

Plant samples such as leaves, stem, and clinging stems of mango (*Mangifera indica* L., Family: Anacardiaceae) and its two hemiparasites *Scurrula parasitica* L. (accepted name; synonym: *Loranthus parasiticus* (L.) Merr.) (Family: Loranthaceae) and *Macrosolen colchinchinensis* (Lour.) Tiegh. (Family: Loranthaceae) were collected from a selected mango plant with hemiparasites from the Malda district's mango orchard, West Bengal, India (24.9624 °N, 88.1823 °E) (Figure 1). Samples were collected during pre-flowering (October 2018) and post-flowering (April 2017) seasons of mango plants of two respective years (2017-2018). The samples were surface sterilized by 4% sodium hypochlorite solution and 80% ethanol solution (v/v, Adhikary et al. 2020) and stored in a sterile falcon tube at 4°C.

DNA isolation and 16SrDNA amplicon-based Illumina library preparation

Metagenomic DNA preparation, 16SrDNA library generation, and Illumina MiSeq sequencing were done by AgriGenome Labs, India. The metagenomic DNA was prepared separately using the DNeasy Power Soil Kit (G1AGEN GmbH, Germany), following the manufacturer's protocol. The concentration and purity of DNA were determined by Nanodrop 2000c spectrophotometer and 1% agarose gel electrophoresis. The V3 region of 16SrRNA was amplified using specific V3 forward primer 5'-CCTACGGGAGGCAGCAG-3' and reverse primer 5'-ATTACCGCGGCTGCTGG-3'. The PCR amplicons were used to construct libraries and then subjected to pair-end sequencing using an Illumina MiSeq sequencing platform.

Data analysis

The quality of the raw metagenomic sequences was then checked according to the base quality, base composition, and GC content. The adapters were trimmed accordingly, and the chimera of the raw sequences was removed by QIIME pipeline v1.9.1 (Caporaso et al. 2010). After that, the V3 regions were

filtered and identified from the paired-end data, and the consensus sequences were constructed from these pair-end data through FLASH or clustelO programs. The trimmed consensus sequence of the V3 region was run through QIIME v1.9.1, and these sequences were simultaneously run through the MG-RAST server at <http://metagenomics.anl.gov> (Meyer et al. 2008). The operational taxonomic units (OTUs) were recorded, filtered (with <5 reads), and similarity of representative sequences searched and analyzed using Uclust (similarity cutoff = 0.97) and QIIME v1.9.1 programs. The taxonomic classifications were performed using the SILVA database (Figure S1). The sharing percentages of OTUs of the three plants and two seasons were observed through the Venn diagram using Venny 2.1.0 (Oliveros 2015). The species richness, evenness, Shannon, and Simpson diversity indices were estimated for each of the samples, and these indices were compared between habitats and seasons using Kruskal–Wallis test. The beta diversity was estimated using the Cody index and Bray–Curtis dissimilarity using Past4.1.0. Then, non-metric multidimensional scaling (NM-MDS) was used to compare dissimilarities of the bacterial community structure between the two seasons with the Bray–Curtis similarity coefficient using Past v4.1.0. The detailed methods are described in schematic approaches (Figure S1). All the plant samples were collected from the same mango plant in a triplicate manner. First, the unweighted pair group method with arithmetic mean (UPGMA) tree was constructed based on endophytic bacterial genera present within mango and its hemiparasites plants during two seasons of consecutive years Past v4.1.0 software. Next, the analysis of variance (ANOVA) studies was performed from the OTUs and ecological data of the two years endophytic community, keeping $p \leq 0.05$ as a significant level through GraphPad Prism 8.0 software. The mean values of the two seasons' data were represented as mean $\pm$ SD (standard deviation).

Characterization of potential pathogens in endophytic communities

According to standard protocol, the potential of pathogenicity in the plant and humans of the identified genera in the endophytic community was determined through a literature survey to determine the agricultural, industrial, and economic threat in the total endophytome of the three plants (Maropola et al. 2015).

Data deposition

Raw reads of six samples were deposited in fastq format to the National Center for Biotechnology Information. Sequences were deposited under Bioproject PRJNA737054. The accession numbers for the submitted sequence of the endophytic community of pre-flowering season present in mango, *Loranthus*, and *Macrosolen* samples are SAMN19460308, SAMN19460304, and SAMN19460306, respectively. In contrast, the accession numbers for the submitted sequence of the endophytic community of post-flowering season present in mango, *Loranthus*, and *Macrosolen* samples are SAMN19460309, SAMN19460305, and SAMN19460307, respectively. (Following links <https://www.ncbi.nlm.nih.gov/bioproject/PRJNA737054>).

Results

Sample description, behaviour, and collection of plant samples

The endophytic bacterial populations and their dynamic nature were studied on mango and its two hemiparasitic plants, *Loranthus parasiticus* (L.) Merr. and *Macrosolen colchinchinensis* (Lour.) Tiegh (Family: Loranthaceae). The primary host plant mango (*Mangifera indica* L., Anacardiaceae) is the national fruit of India, Haiti, Philippines, and the national tree of Bangladesh, a tropical tree with juicy drupe fruit. The plant has flowering seasons starts from the end of the winter in the tropical region, i.e., the end of January to March. The hemiparasite plants *Loranthus* sp., *Macrosolen* sp. are commonly grown on the branches of mature-aged mango plants. In this study, the sampling was done where both the hemiparasites infested the host mango plant, and the sampling time was done during the pre-flowering seasons and post-flowering seasons of mango plants. The leaf and stem samples of mango and its hemiparasites were collected from a selected mango plant with hemiparasites from the mango orchard of the Malda district, West Bengal, India (24.9624 °N, 88.1823 °E; Figure 1) and were carried out DNA extraction and sequence analysis.

Taxonomic composition analysis

The taxonomic diversity of all the sequences of the two seasons and the three hosts were classified from phylum to genus according to the default QIIME v1.9.1 program. More than 340,200 reads with GC% <50% were considered in each host plant during each host and season. There were 11 different phyla, 14 classes, 17 orders, 21 families, and 22 genera (Figure S2). There were a large percentage of OTUs were from unidentified and uncultured populations. The population variations of the endophytic bacterial community were evident with the seasonal variations. On the overall account of the two seasons and three hosts, Actinobacteria, Proteobacteria, Firmicutes, Cyanobacteria, and Bacteroidetes were the five most dominant phyla carrying 99.48% of the total reads while the rest phylum is containing 0.52% reads only. Among the top five phyla, Proteobacteria (38.04%) are the most dominant, followed by Actinobacteria (25.03%), Firmicutes (17.97%), Cyanobacteria (15.56%), and Bacteroidetes (2.88%) (Figure S2a, b). The total unculturable communities possessed total 21 families, and among them, 60.83% belong to the major 5 families, and the other 16 families contain the rest 39.17% reads. These major 5 families were Bacillaceae (27.56%), Moraxellaceae (15.76%), Corynebacteriaceae (6.76%), Propionibacteriaceae (6.08%), Acetobacteraceae (4.65%) (Figure 2a, Figure S2c, d). Among the unculturable genera, the top 5 reads share 69.2% reads which contain *Bacillus* (32.46%), *Acinetobacter* (20.12%), *Corynebacterium* (6.36%), *Actinomycetospora* (5.99%), *Methylobacterium* (4.27%) (Figure 2b, Figure S2e, f). These observations showed that although many reads were left unidentified, diverse numbers of reads were present in each taxon from phylum to genera.

Ecological diversity of the microbial populations in hosts and seasonal variations

The ecological diversity from the represented percentages of bacterial OTUs was assessed by measuring ecological dominance, evenness, alpha, and beta diversity indices (Figure 3). The maximum dominance of families (0.319) and genus (0.4329) were showed in the *Macrosolen* sp. during the pre-flowering

season of mango and lowest in *Loranthus* sp. in both families (0.1528) and genus (0.1879) during the post-flowering season of mango (Figure 3a, e). The ecological evenness was reciprocal to the ecological dominance because ecological dominance and evenness are always inversely proportional (Figure 3b, f). The Simpson index (D) among the family's OTUs was highest in the *Loranthus* sp. (0.8472) at post-flowering seasons of mango and followed by both *Macrosolen* sp. (0.8443), mango (0.8413), respectively at the same season. The lowest family diversity index (D) was *Macrosolen* sp. (0.681) at the pre-flowering season of mango. The Shannon index (H) of alpha diversity was highest in the *Loranthus* sp. (1.931) at pre-flowering seasons of mango and lowest in *Macrosolen* sp. (1.526) at the pre-flowering seasons of mango (Figure 3c). The beta diversity (Cody index) of all three hosts and two seasons were 17.5, and the individual analysis of Bray-Curtis dissimilarities explained that the highest beta diversity was present in the Staphylococcaceae members, resides in the *Loranthus* plant (0.72987) at the pre-flowering season of mango followed by Streptococcaceae in *Macrosolen* plant (0.68117) at the post-flowering season of mango. The lowest Bray-Curtis dissimilarities were observed in the Bacillaceae family in the mango plant (-0.45372) at pre-flowering seasons of mango, followed by Moraxallaceae in the mango plant (-0.42564) at the same season. The majority of the families belong to the dissimilarity indices between 0.41 to -0.31 (Figure 3d). From the genera point of view, the Simpson diversity indices (D) of the representative genera of bacterial endophytes were highest in *Loranthus* sp. (0.8121) during post-flowering seasons of mango followed by *Macrosolen* sp. (0.7755) at the same season. The lowest bacterial genus diversity index (D) was *Macrosolen* sp. (0.5671) at the pre-flowering season of mango. The Shannon index (H) of alpha diversity was highest in the *Loranthus* sp. (1.732) at post-flowering seasons of mango, followed by *Macrosolen* sp. (1.55) of the same season and lowest in *Macrosolen* sp. (1.242) at the pre-flowering season of mango (Figure 3g). The beta diversity (Cody index) of all three hosts and two seasons were 12. The individual analysis of Bray-Curtis dissimilarities explained that the highest beta diversity was present in the *Spirosoma* and *Hymenobacter* members, resides in mango and *Loranthus* sp. (0.56438 and 0.53773, respectively) at post-flowering and pre-flowering seasons of mango, respectively followed by *Sphingomonas* (0.49389) and *Bacillus* (0.48738) in *Macrosolen* plant at pre-flowering and post-flowering seasons of mango. The lowest Bray-Curtis dissimilarities were observed in *Actinomyces* in *Loranthus* sp. (-0.55908) at pre-flowering seasons of mango followed by *Cutibacterium* in the same host (-0.45184) at the same season. The majority of the genera belonging to the dissimilarity indices between 0.45794 to -0.39786 (Figure 3h). The Bray-Curtis dissimilarities indicate a wide range of dissimilarity indices because of the restricted relative abundance of the representative taxa (both families and genera). Additionally, most taxa have positive dissimilarity indices due to their absence or minimum relative abundance in their respective hosts and seasons. The ecological dominance (df=17, p>0.05) was statistically insignificant, whereas the ecological evenness was significant (df=17, p<0.05) differences in different hosts and seasons. The ANOVA studies of alpha diversity showed statistically insignificant differences in both Simpson (df=17, p>0.05) and Shannon diversity indices (df=17, p>0.05). This result indicates that depending on variable diversity indices, the significance may vary. The beta diversity of both family (df=125, p>0.05) and genus (df=89, p>0.05) rank showed insignificant variations. The non-metric multidimensional scaling (NM-MDS) of the bacterial community analysis showed that the family and genera of the two seasons were

intermingled between each other and distributed almost equally throughout the axis (Figure 4a, b). This observation indicates that the bacterial community was dispersed from the entire plot to the mid axis, i.e., the bacterial community is dispersed during the different seasons of mango.

Microbial community distribution

The majority of the phylum were present in both pre-flowering and post-flowering seasons. The microbial community dynamics between the three host plants in the seasonal variation are a significant subject of inquisition. Several endophytic bacterial phylum, families, and genera were present within the plant systems that were shifted between the hosts in the different seasonal variations (Figure S3, S4; Table 1, 2; Table S1, S2). The maximum fold increase found in the case of the relative abundance of Firmicutes (>9.5 folds) followed by Actinobacteria during the pre-flowering season compared to the post-flowering season (Table 1). Furthermore, the abundance of endophytic bacterial phyla were maximum in *Macrosolen* than in mango and *Loranthus* (Table 2). The genera *Bacillus* resides in the mango and *Loranthus* sp. They were multiplied and disseminated in the three hosts (Figure S3, Table S2). In contrast, *Actinomycetospora* resided in the *Macrosolen* plant in the pre-flowering season disseminated in all three hosts during the post-flowering season. Another genus, *Streptococcus* present in the *Loranthus* sp. during the pre-flowering season and is disseminated in *Loranthus* sp. and *Macrosolen* sp. during the post-flowering season. (Table S2). Similarly, the family Bacillaceae resides in all three hosts during the post-flowering season in lesser abundance, increasing several-fold during the pre-flowering season. Propionibacteriaceae, another family in mango as a primary reservoir in post-flowering season, were disseminated in each host during the pre-flowering season. In contrast, Pseudonocardiaceae resided in the *Macrosolen* sp. during the pre-flowering season and were disseminated in *Loranthus* sp. and *Macrosolen* sp. (Table S1). Rest families and genera were found to be the host and season-specific instead of having any shift in abundance between seasonal or host variations (Figure S3, S4). From these observations, it can be stated that specific endophytic populations were shifted between the three plants on seasonal variations from the respective reservoir hosts. *Macrosolen* acted as a reservoir of the endophytic bacterial community and *Loranthus* in both the pre-and post-flowering season of mango. So, most bacterial communities were shifted from hemiparasites to host mango plants during their favourite seasons. The Venn diagram also showed that the endophytic bacterial community was disseminated throughout the three hosts during the pre-flowering season of mango because maximum (45.5% families or 57.1% genera) endophytic bacterial taxon was present in all the three hosts (Figure 5). The UPGMA showed that the endophytic populations were more similar between these two hemiparasites plants than mango, and that is why mango belongs to a separate clade with 100 bootstrap values (Figure S5). This analysis also reflects the similar postulate that the hemiparasites commonly act as a reservoir of the endophytic community, and when the environment becomes favourable, they disseminate in mango plants.

Characterization of potential pathogens in endophytic communities

The pathogenic potency to develop pathogenicity in the host plants was estimated (Table 3) from the previously published literature. It was observed that many of the endophytic genera present predominantly in the hemiparasite plants as the reservoir system (Figure S5). However, when the favourable condition occurs, such as summer and rainy season, they (*Bacillus*, *Corynebacterium*, *Staphylococcus*) were disseminated to the mango plant and potentially caused diseases such as wilt and rotting of fruits, roots, etc. (Agrios 2005; Vidaver 1982; Prithiviraj et al. 2005).

Discussion

Plants harbour diverse populations of endophytes, most of which help the host for growth and metabolism and protect from different phytopathogens (Ou et al. 2019). Exploration of the endophytic populations may help to understand the functional aspect of the host plants. For the exploration of entire endophytic populations, DNA extraction, library preparation, and identification of microbial community diversity are the most critical components in any culture-independent study (Demeke and Jenkins 2010). The present study was undertaken to explore the movement of the endophytic bacterial community in mango and its two hemiparasites *Loranthus* sp. and *Macrosolen* sp. in different seasonal variations. The bacterial populations were variable in different seasonal and temporal bases in the plants and open environment (Ou et al. 2019; Lou et al. 2020). We observed the noticeable difference and higher relative abundance of bacterial community compositions in bacterial OTUs in mango and the hemiparasite plants with seasonal variation. As far we know, this is the first report emphasizing the endophytic bacterial community dynamics between the three interconnected plants on a seasonal basis. In this study, Proteobacteria, Actinobacteria, Firmicutes, Cyanobacteria, and Bacteroidetes were found to be the most abundant phyla present in all the hosts in both seasons. Previously Akinsanya et al. (2015) reported that Proteobacteria, Firmicutes, Actinobacteria, Bacteroidetes are the major endophytic bacterial phyla present in *Aloe vera*. The endophytic communities of peony plants also possessed Proteobacteria, Firmicutes, Bacteroidetes, Acidobacteria, and Actinobacteria as the most dominant phyla with 86% relative abundance (Yang et al. 2017), whereas, in our study, 99.48% reads possessed major five phyla (Figure S2a, b). Most of the previous metagenomic analysis possesses many uncultured bacterial reads similar to our studies (Hong et al. 2019; Castañeda and Barbosa 2017). At genus-level, *Bacillus* was found to be the most abundant (32.46%) genus in all the three plants, followed by *Acinetobacter* (20.12%) and *Corynebacterium* (6.36%) (Fig. 2c). The earlier study also showed that the phyllospheric region of tomato also possessed *Bacillus* as an abundant genus (Romero et al. 2014). Despite this, *Acinetobacter* and *Corynebacterium* had higher relative abundance (next to *Bacillus*), but it was restricted during the pre-flowering season of mango within each host (Fig. 2; Table S2).

Plant-associated habitats are undulating due to the involvement of many factors in the dynamic environments that affect the species compositions in the microbial communities. Shen and Fulthorpe (2015) and Ou et al. (2019) reported that the endophytic bacterial community becomes flourished during the summer and rainy seasons. Similarly, in our study, the pre-flowering season of mango (summer and rainy seasons) showed the highest beta diversity and dissemination of endophytic bacterial communities between the three plants, and the alpha diversity denotes the diversity of bacteria were shown higher in

the post-flowering season of mango plants (late winter). These observations of the endophytic community are highly variable, and the bacteria community act as a source in the hemiparasites, and when the favourable condition comes, these though out the three plants. In the account of core genera assessment, Ding and Melcher (2016) reported that *Sphingomonas*, *Methylobacterium*, and *Pseudomonas* were the most abundant endophytic genera in the non-cultivated plants; such as *Ambrosia psilostachya* DC., *Asclepias viridis* Walt., *Panicum virgatum* L., *Sorghastrum nutans* (L.) Nash and *Ruellia humilis* Nutt. during all the seasons. However, in the present study, the genera *Spirosoma*, *Hymenobacter*, *Sphingomonas*, and *Bacillus* were the most dominant genera in all the hosts throughout the year. Among these two genera, *Bacillus* spp. found the most abundant microbiota, and *Bacillus* sp. was the only genera present in the culturable part present in these three hosts in different seasons (data not shown). The majority of the *Bacillus* spp., present in the host plants, play an important role as a potent plant growth promoter, biocontrol agent and protect the host plant from phytopathogens (Radhakrishnan et al. 2017; Shafi et al. 2017). However, the specific role and the biology of *Bacillus* and other genera on the plant system need to be explored further, preferably through a culture-dependent approach (Shen and Fulthorpe 2015).

The pathogenicity development in the mango plants may cause production loss and leads to financial disaster. In the post-flowering season, the mango plants possess a lower number of endophytes due to developing a better immune system. However, in the summer and rainy seasons, i.e., pre-flowering season, a higher abundance of endophytic community was observed in the mango plants, and these endophytic populations may develop pathogenicity and leads to crop loss. In this concern, it can be suggested that removal of these two hemiparasites from the mango plants before the summer may reduce the probability of disease induction during fruit setting and ripening of fruit by the potential quiescent pathogens that reside in the hemiparasite plants. A detailed study needs to elaborate on the interactions between mango, hemiparasite plants, and endophytic bacterial communities to improve the yield and quality of the economically important mango plants.

Conclusions

The endophytic communities in the mango (*Mangifera indica* L.) and its two hemiparasites, i.e., *Loranthus* sp. and *Macrosolen* sp. were shifted between the plant systems with the seasonal and physiological variations. However, this study was based on the three sample sets of a single mango plant containing hemiparasitic plants in two different seasons. To better assess the microbiome shift between the three plants, it will be essential to assess the microbiome community more frequently, and this work is going on. In this study, we were aware of knowing the dominant genera present within these plants as endophytic bacteria and can conceptualize the beneficial functions they belong to. This study reveals the overall interactions of endophytic bacterial community dynamics between plant and bacteria. To the best of our knowledge, this is the first report to study the dynamics of endophytic populations between a host, and its hemiparasites.

Declarations

Conflict of interest

The authors declare that they have no conflict of interest.

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Authors' Contributions

RA collected samples, procure and analyzed the data, and wrote the draft. SM and VM conceptualize the idea, designed experiments, wrote and edited the manuscript.

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Tables

Tables are not available with this version.

Figures

Figure 1

Location map of the sampling site. The '*' mark indicates the specific sampling site.

Figure 2

Heatmap of relative abundance of families and genera present within the host plants in different seasons. Here 'a' representing the relative abundance of families, and 'b' representing the relative abundance of genera. 'Man', 'Lor', and 'Mac' indicate mango, Loranthus and Macrosolen. All the data were represented as considering relative abundance $\geq 0.75\%$ OTUs.

Figure 3

Ecological diversity of families and genera of endophytic bacteria. Here, (a), (b), (c) and (d) represents ecological dominance, ecological evenness, alpha-diversities, and Bray-Curtis beta-diversities of families, respectively; whereas (e), (f), (g), and (h) represents ecological dominance, ecological evenness, alpha-diversities, and Bray-Curtis beta-diversities of genera, respectively. Here, in (c) and (g), the black bars represent Simpson indices and hollow bars represent Shannon indices. In (d) and (h) represents the diversity of endophytes in mango (cross), Loranthus (square) and Macrosolen (triangle) in post-flowering season, and in mango (circle), Loranthus (rhombus) and Macrosolen (star) in pre-flowering season. Here all the data were represented as considering the abundance $\geq 0.75\%$ OTUs.

Figure 4

Non-metric multidimensional scaling (NM-MDS) of the bacterial community analysis, in the family (a) and genus-level (b), present within the host plants. Here, 'triangle' and 'circle' represents the taxon present in the pre-flowering and post-flowering season of mango. All the data were represented as considering abundance $\geq 0.75\%$ OTUs.

Figure 5

Venn diagram of the distribution of families and genera between the three hosts in different seasons. The distribution of families during post-flowering (a) and pre-flowering (b) season of mango; whereas the distribution of genera during post-flowering (c) and pre-flowering (d) season of mango present in mango (blue circle) Loranthus sp. (yellow circle) and Macrosolen sp. (green circle) are shown. Here all the data were represented as considering the abundance $\geq 0.75\%$ OTUs.

Supplementary Files

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