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A PRELIMINARY STUDY ON THE DIVERSITY OF BACTERIAL COMMUNITY IN THE GUT OF SPIDER *Gasteracantha geminata* Fabricius1798

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Abstract

Spiders represents one of the most important components of global biodiversity, they are diversified which are ubiquitous expect for few niches. They are good indicators of environmental health. *Gasteracantha germinate* Fabricius1798 *an* orb weber described in southern part of India was studied for the microhabitat present within the gut. The specimen was collected and the 16S rRNA was isolated from the V3 and V4 hyper variable region and sequenced using Illumina sequencing and the microbiome was studied which revealed it consists of 4 phyla and 6 Species.

Key Words: Spiders, Microbiome, Environment, 16S rRNA, *Gasteracantha germinate*

Introduction

Spiders are diversified group of Invertebrate under phylum Arthropod belonging to Araneae. Spiders represent one of the most important components of global biodiversity. They are abundant and widespread in almost all ecosystems and play a significant role in ecology by being exclusively predatory thereby maintaining the ecological equilibrium (Sebastein and Peter, 2009; Riechert and Bishop, 1990). Spiders are also good indicators of environmental health. They play important roles in the dynamics of a specific habitat and are sensitive to habitat loss, climatic change, and environmental upheavals (Chetia et *al*., 2012). The ubiquity, diversity and ecological role of spiders make them a promising focal group (Hore, 2009). The origin of spiders can be dated back nearly 400 million years to the Devonian period. The abundance and resemblance of the spiders to their modern descendants can be dated back to the early tertiary period (almost 70 million years ago) Rainer Foelix, 1996. Recordings of spider diversity was done more than a century ago, from various parts of the world (Blackwall, 1864;Bonnet,1945,1955,1961; Simon; 1897a, 1897b; Pocock, 1899, 1900a,1900b,1901; Sheriffs, 1919,1927,1928,1929; Horell, 1877) .

Gasteracantha germinata Fabricius 1798 belongs to the sub family Araenomorphae Family Araneiae. It is known as spiny orb-webs, it is an oriental species initially it was described from Ramnad in Tamilnadu state of southern India and distributed in India and Sri Lanka. (Pradeep *et al*., 2015; Pocock, 1900; Tikarder, 1982; Patel, 2003). They prefer undisturbed space, webs are seen among the bushes above 1.5 feet to 6.5 feet above the ground level. They exhibit sexual dimorphism ,in male prosoma is black and the opisthosoma are creamy white with black patches the marginal and ventral have numerous tubercles, opisthosoma consist of legs ,in female the prosoma are brown and the opisthosoma is hexagonal, white posteriorly and laterally with paired thick spins laterally the spins are closed on the posterior side it is separated but they have brown with yellowish brown patches on their legs in common

(Siliwala et al ., 2005; Sivaperuman and Thiyakesan, 1991). To unravel the microbiome, present the following study was carried out.

Materials and Method

Gasteracantha germinata Fabricius 1798 was collected from Auxilium College (Autonomous) Gandhi Nagar, Katpadi Vellore Tamilnadu. The specimen was collected from the campus by handpicking method and kept in containers taken to the laboratory. The specimen was transferred to 70% Ethanol and stored at 4^{o}C.The specimen used in the study are non-endangered and non-protected species.

The DNA from the gut was isolated sample using the standardized protocol. The extracted DNA from the samples were subjected to Nano drop and GEL before taken for PCR amplification and amplified using Primer sets of V3-V4 hypervariable regions of 16s rRNA .40ng of extracted DNA is used to amplification along with 10 pM of each primer. the PCR cycle involved denaturation for 5 secs at 95^{o}C followed by annealing at 60^{o} C for 15 Sec followed by elongation at 72^{o}C for 2 minutes and Final Extension at 72^{o}C for 10 mins and hold at 4^{o}C. The PCR products were visualized using agarose gels for high throughput sequencing of microbial diversity. The sequence of targeted gene of 16S rRNA metagenome was carried out by illumine sequencing and the microbiome was characterized.

Result

The sequence of targeted gene of 16S rRNA metagenome was carried out by illumine sequencing the V3- V4 region was amplified the number of reads were taken in millions about 0.2 M and the GC content was about 52.5% was calculated using FastQC. The Phylum level taxonomy plot analyse Phylum Firmicutes which was present in abundant then the proteobacteria and the least presence of Bacteroidetes (Fig 1.0) and the top enriched genus revealed the presence of 49% of Bacillus, 32% of Lactobacillus and 18 % of Actinobactor and 1% of Herbaspirillium, Pseudomonas and Ocanobacillus (Fig 2.0). The data was processed, filtered and normalized.

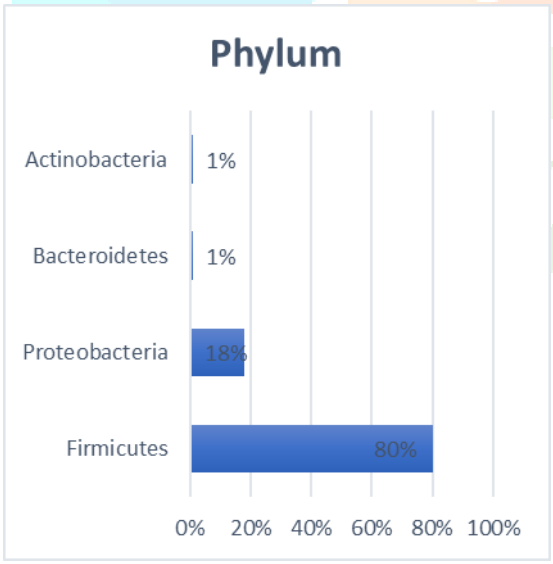

Fig1.0 Phylum level taxonomy plot analyse

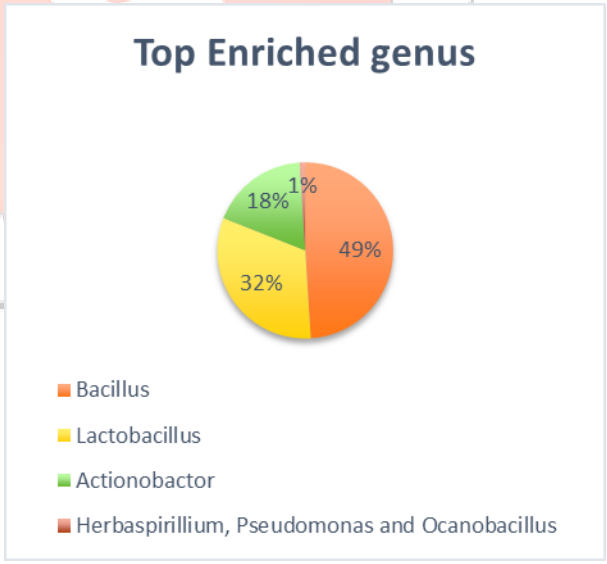

Fig 2.0 Top Enriched Genus

Discussion

In the present study effort made to understand the microbiome present in the gut. Targeted 16S RRNA amplicon revels the presence of 4 phyla and 6 Species. The dominant phyla were Firmicutes and Proteobacteria and less abundance of Bacteroides and Actinobacteria moreover the dominant phyla Firmicutes consists of 49% of Bacillus and 32% of Lactobacillus 18% of Actinobacteria other 1% consists of Bacteroides and Proteobacteria. Various other work has done on the gut of spiders and reveled that the phyla proteobacteria and Firmicutes dominate the gut of the spiders (Rivera *et al.*,2017; Hu *et al*., 2019; Sheffer *et al* ., 2020) and the presence of phylum proteobacteria is dominated in the phylum arthropods like scorpions, prawns, shrimps, ticks, honeybee, fruit fly cockroaches ants, lion ants fleas, beetles and worms (Hu *et al*.,2019; *Chen et al*., 2016; Hammer *et al.*, 2017; Esposti and Romero 2017; Bolanos *et al*., 2016; Degli Esposti and Martinez Romero, 2017; Brune and Dietrich, 2015; Briones-roblero *et al.*, 2017) .The Actinobacteria are known to produce enzyme for synthesizing of

nutrients and food processing and metabolic activities of invasive pathogenic bacteria, Pseudomonas may help in the metabolism of vitamins in the gut , degradation of organophosphates and show active antagonism towards entoptic fungi and Bacillus helps in degradation of polysaccharides and aromatic compounds (Douglas 2015,Delalibera *et al*., 2005, Van Dexter and Boopathy 2019, Engel and Morgan 2013,Itoh *et al.*, 2018 and Kaltenpoth 2019,).The Prescence of functional groups with the metabolic capacity in the arthropod microbiome can imply on the effect if micro habitat in framing the bacterial community. The microbial community shows variation in the distribution of the taxa which is unlikely to be the basic driving of arthropod.

Conclusion

The microbiota in the host may impact on development, metabolism, nutrient acquisition, sex ratio, health, behaviours which leads to selection of habitat and evolution of the host. The interaction between the host microbiota and the microbiome present in the surrounding may have effect on the organisms. The host microbiome study helps to understand the microbial relationships to gain the insights into the microbial community and the potential functions of the diversity in spiders. The microbial community which recedes in the spiders are still in its infancy state and the microorganisms which are present within the spiders microbiota which remains unclear whether the bacterial taxa present will represent the other insect bacterial taxa and what are the potential functions of them.

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