

#### **Psylloidea: An Overview of Their Biological Traits**

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#### Abstract: -

Prior to the discovery that a small number of species transmit bacterial plant diseases, psyllids a diverse group of sapfeeding Sternorrhyncha were mostly unknown. However, with over 4,000 identified species displaying a variety of life cycles and host exploitation methods, the superfamily Psylloidea is far richer than the sum of its crop-associated vectors. Interesting new information about the biology, behavior, evolution, and interactions between species of psyllids is being uncovered by an expanding corpus of research. This research has uncovered distinct evolutionary patterns of lineage divergence and host utilization, as well as similarities and contrasts with better-studied Sternorrhyncha. Additionally, we are discovering how life cycle features and psyllid roles in communities are influenced by foraging ecology and psyllid evolution. We are connecting symbiotic and psyllid lineages, unraveling the web of symbionts throughout the psyllid family tree, and uncovering the mechanisms behind the reciprocal exchange between symbiont and host at finer scales. With an emphasis on free-living (nongalling) Psylloidea, we synthesize and evaluate significant developments in these fields in this study.

#### 1. Introduction:

In the order Hemiptera, the suborder Sternorrhyncha contains the ecologically varied and little-studied superfamily Psylloidea (psyllids). More than 4,000 species have been identified and categorized into seven families thus far, albeit this number most likely understates the overall diversity. Psyllids consume plant sap that is high in carbohydrates, much like similar Sternorrhyncha families like aphids,

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E-ISSN: 2583-5173

Volume-3, Issue-12, May, 2025



whiteflies. and coccoids (scales and mealybugs). They do this mainly by gaining access to the phloem sieve tube components of Publications on psyllid biology, plants. behavior, microbial relationships, genetics, and ecology have rapidly increased during the last few decades. A small number of pest species are the subject of much of this research, especially those that have been found to be carriers of bacterial plant diseases that are phloem limited and unculturable in the Candidatus Liberibacter and Ca. Phytoplasma taxa. Although the majority of the study is applied, taken as a whole, this expanding corpus of work is bridging important knowledge gaps on the fundamentals of psyllid behavior, psyllid microbiomes, and host exploitation mechanisms. Psyllids interact with a variety of host assemblages, hold significant but little-understood roles fin Rinoncrop R ecosystems, and occupy vital places in food webs. Psyllids create keystone relationships with other arthropods and birds by producing feces that are high in carbohydrates, which can have a domino effect on entire ecosystems. The wide range of phenotypes that psyllids cause in their hosts through their salivary secretions has also piqued attention in studies. These include complicated gall morphologies, distinct senescence-like conditions, and leaf curling. The genes and proteins that underpin the induction of various host phenotypes are

becoming more clearly thanks to genomic resources released in the last ten years. With an emphasis on free-living psyllids that do not develop galls on host plants, this study summarizes and highlights significant developments in our knowledge of psyllid behavior, host feeding, microbial interactions, and ecological significance.

We also identify important research topics and highlight optimal experimental procedures.

### 2. Overview of Psylloidea Distribution and Lifestyles

# 2.1.Psylloidea Diversity and Global Distribution

Specificity in host plant utilization for feeding and reproduction is a characteristic of the Psylloidea. According to fossil data, the of monophyletic group anatomically contemporary E psyllids' radiations were preceded by those of their (mostly) dicot hosts. Therefore, rather of cospeciation with hosts, psyllid speciation may often involve sympatric host swapping between related species or genera with comparable traits or chemistries. It is evident that psyllid radiations on closely related, endemic host species are the cause of several hotspots of psyllid biodiversity. For instance, 15% of the world's psyllid diversity is found in Australia, where 85% of the species' host plants belong to the same plant family (Myrtaceae). Approximately 90% of



them consume only one genus of plants in this family, eucalyptus. Despite having just about 4,700 species, the Myrtaceae family of plants contains more than 25 psyllid genera. Surprisingly, this trend seems to be very widespread: Plant families with fewer than 4,000 species comprise about half of the psyllid genera, with some having fewer than 1,000 species. With over 19,000 species worldwide, the Fabaceae is the only big plant family that also has a sizable percentage of psyllid variety. It is the third largest plant family.

The origins of psyllids' distinct host specificity lineage-specific and host relationships, as well as how biodiversity levels today were reached, are still unknown. The most recent effort to identify trends and produce theories involves analyzing over 66% of the known psyllid host plant connections listed on the Psyl'list website. Radiation mostly happens at the species level through changes among related host plants, but at higher taxonomic levels, the study made it possible to identify rare apparent host leaps to distant, unknown host taxa. Some psyllids put their eggs somewhat carelessly, and these oviposition errors may be a major factor in the promotion of divergence to both related and unrelated taxa. Psyllids' adult feeding habits include nonhost plant species, according to recent developments in gut content analysis,

which may present chances for off-target oviposition Evidence of niche events. participation was also found in the Psyl'list data set when host association patterns were closely examined across taxonomic levels. Members of the huge families Triozidae and Psyllidae, which contain the majority of known pest species, share multiple host families. However, within certain plant families, Triozidae and Psyllidae members never co-occur on the same plant genus. Notably, psyllids also show relatively strong preferences for particular microhabitats, which could point to niche partitioning amongst related species on the same host. Additionally, there is proof that psyllids and other Sternorrhyncha groups like aphids partition their niches. The evolution and host specificity of other Sternorrhyncha lineages may have been impacted by host mediated competition between psyllids and other lineages. With the release of Psylloidea recent strong phylogenies, these theories can now be investigated more thoroughly, particularly in light of revised regional vascular plant phylogenies.

#### 2.2.Psylloidea Biology and Lifestyles

Geographically speaking, psyllid diversity is higher in tropical areas than in temperate ones.

According to Hodkinson's synthesis of psyllid life history features, the tropics'

#### E-ISSN: 2583-5173



concentration of psyllid diversity is connected to higher latitudes' need for compressed or delayed life cycles, which is related to seasonality. Psyllid voltinism and periodicity have been examined quite well and can vary fluidly based on precipitation and temperature. Psyllids may or may not experience diapause, and the highest elevations are home to the longest life cycle, which lasts two years. The majority of temperate species are univoltine, although depending on the humidity and warmth of their surroundings, some may produce up to six generations annually. However, compared to 15% of psyllid species in temperate regions, 50–60% of tropical psyllid species are gall formers, indicating that gall-forming species are overrepresented in the tropics. Tropical species don't have a diapause period and can have over 15 generations annually. Gall-formation may offer particular benefits to psyllid lifestyles in contrast to the more varied assemblages of parasitoids, predators, and pathogens found in tropical settings. Regardless of location or life history, the phenology of the host plants that the psyllids feed on and develop as immature beings has a significant impact on the timing of psyllid generations. For instance, immatures of certain Cacopsylla species regularly hatch a few days after their hosts' initial bud break, allowing them to enter their favorite microhabitat of tissues from young shoots.

Even while the total timing of these events changes from site to site and year to year depending on ambient conditions, it is remarkable that this synchronicity is maintained. Likewise, the onset of gall development and the creation of new plant tissue are closely correlated, which may optimize the effectiveness of psyllid alterations to plant developmental pathways mediated by salivary effectors. Additionally, phenological synchrony might have a significant role in sustaining and advancing speciation. This was clear for closely related psyllid species that were spreading in the Canary Islands; phenologically, sympatric species that shared a host tended to be distinct from one another. The majority of psyllids are obligatory outbreeders, with roughly 1:1 sexual ratios. Psyllid parthenogenesis is uncommon. compared to aphids, and has only been observed in a small number of species with primarily single-sex populations. Therefore, sexual mating is the primary method used to produce new psyllid generations. According to recent studies on vibratory communication in psyllids, biotremology is widely used in samesex communication as well as mate finding, guarding, and disruption. This could make it possible to use vibrational traps to manage psyllid pests. Only four species have evidence of sex pheromone-mediated mate finding: the Asian citrus psyllid (Diaphorina citri), the



tomato psyllid (sometimes called the potato psyllid) (Bactericera cockerelli), and the two psyllid pests of pears (Cacopsylla bidens and Cacopsylla pyricola). Tradeoffs between vibration versus chemical communication and single versus multimodal techniques are influenced by the interaction between the environment, particularly the plant substrate, and community behavior, including levels of aggregation.

Pseillids are known to be choosy in their host selection for reproduction, but little is known about how they deposit eggs and evaluate their hosts during oviposition. A pedicel is usually used to deposit eggs on the plant surface with attachment, while other species use shallow insertions to deposit eggs into plant tissue. Although closely related species may have extremely varied or mostly invariant egg structures, nothing is known R molecular data. On the other hand, it is thought about the functional or adaptive importance of these traits. Certain species show extremely selective site selection on host organs, especially on the apical tissue of freshly emerging shoots or floral structures. Although they tend to cluster eggs along leaf midribs, species that oviposit on leaf laminae seem to be less discriminating, indicating that they evaluate particular leaf characteristics to choose oviposition their sites. Host characteristics that limit oviposition and/or adult and immature feeding are unknown for

the majority of species. Nonetheless, studies involving a small number of pest species have begun to clarify the complexities of psyllid host evaluation procedures.

### 3. Obligate and Facultative Endosymbiont **Relationships**

#### **3.1.Obligate Nutritional Symbionts**

Essential vitamins and amino acids are lacking in phloem sap. Sternorrhyncha have nutritional symbionts in a specialized bacteriome organ in the abdomen to make up for this. The bacteriome of every psyllid that has been studied to date has uninucleate bacteriocyte cells that contain Ca. Carsonella ruddii (Gammaproteobacteria: Oceanospirillales), also known as Carsonella. The common ancestor of Sternorrhyncha may be the source of the psyllid and whitefly (Aleyrodidae) symbionts, according to

that the symbiont linked to the most recent common ancestor of all Sternorrhyncha was replaced by symbionts of other contemporary Sternorrhyncha lineages, such as coccids and aphids.

Because of its severe genetic decrease and disintegration, Carsonella is positioned halfway between living things and organelles like plastids and mitochondria. It possesses the highest known adenine thymine (AT) bias among symbionts and one of the smallest genomes of any cellular organism; the



genome's guanine cytosine (GC) concentration is just 16.5%. An increase in the rate of DNA substitution causes mutational bias that results in the accumulation of A and T nucleotides and reduces the stability of the secondary structure of 16S ribosomal RNA (rRNA). Additionally, the gene density of Carsonella genomes is incredibly high, with almost all of the genes overlapping. Compared to other bacteria, including other long term symbionts, its genes are noticeably shorter. Interestingly, compared to the genetic complement of the more thoroughly researched Buchnera symbiont in aphids, Carsonella likewise lacks functional genes for around half of the metabolic pathways required in the manufacture of critical amino acids. The distinct characteristics of the Carsonella genome have sparked research into how this organism carries out fundamental biological R incapacity zto supply certain nutrients. A functions related to bacterial existence. Sloan et al. demonstrated that the psyllid host can integrate the metabolic pathways lacking in Carsonella by activating both native genes (16 genes) and horizontally transferred bacterial genes (10 genes), including one encoding argininosuccinate lyase that was probably obtained directly from Carsonella, using a psyllid (Pachypsylla venusta) that does not harbor The any additional symbionts. horizontal gene transfer events are similar to those that occur in other sap-feeding insects,

like the citrus mealy bug, which harbors Tremblaya princeps (139 kb), another obligate symbiont. Genes from the same functional categories, such as riboflavin biosynthesis, rRNA methylation, and amino acid biosynthesis and metabolism, have been acquired by both insects.

#### **3.2.Secondary Long Term and Facultative Symbionts**

In addition to one or more secondary facultative symbionts that may be found in cells of different tissues, the majority of psyllid lineages have at least one extra secondary, long term symbiont (likely in bacteriome syncytial cells). The widespread presence of long-term secondary symbionts in psyllid lineages may be caused by Carsonella's drastic genome reduction: secondary symbionts could make up for Carsonella's symbiont's classification as facultative or longterm is determined by the combination of traits it displays. In addition to signs of closely coevolved relationships with host insects, such vertical transmission and bacteriome as localization, long-term symbionts typically exhibit higher genome reduction and AT bias. On the other hand, facultative symbionts typically possess traits that allow for symbiosis with less significant genome degradation or canalization to a single host lineage. Many facultative symbionts of allied Sternorrhyncha



have been shown to transmit horizontally (for example, by parasitoid vectors or common host plants) and, on occasion, secondary symbiont genera that contain taxa ranging from facultative to long term (e.g., Arsenophonus). The majority of secondary psyllid symbionts lack complete genome sequences, localization analyses, and other biological information that would enable us to determine whether or not they are obligatory, long term partners. We do, however, have sequences of conserved genome regions for symbionts from a large range of psyllid species, including sections of the 16S rRNA gene. We may assess a subset of metrics in using these data. For instance, Hall et al., for looked signs of symbiont host codivergence in 35 psyllid species from seven families. Carsonella phylogeny was quite predictive of host phylogeny, as was to be R predicted. In samples of the 34 species that were positive for Arsenophonus, the species was 100% prevalent, making it the leading secondary symbiont across 34 of 35 taxa. A subset of these species for which this characteristic was studied also had vertical transmission of Arsenophonus. Phylogenetic incongruence, however, suggested that host switching and/or endosymbiont replacement were the causes of Arsenophonus distributions. A study by Kwak et al., which looked at the symbionts of psyllid species from 35 genera

and five families, showed a similar result. Based on GC content analysis of a 429 nucleotide 16S rRNA gene sequence, two clades of operational taxonomic units (OTUs) within the Enterobacteriaceae showed genomic hallmarks of obligate symbiotic status, and each clade was congruent with one family of psyllids. Nevertheless, not every species evaluated within each family had OTUs that fit into that clade. Although techniques other than amplicon sequencing are required to confirm this, it is possible that these species lost their symbionts during a replacement event. According to data from codivergence studies, psyllids usually have at least one long-term secondary symbiont that is at or close to obligatory status; yet, even within lower taxonomic levels, the identification of this symbiont varies greatly.

### 4. **Psyllids in e**cological communities: Roles and importance

Psyllids engage in a wide range of trophic relationships. Through the consumption of sap and the excretion of sugarrich excrement (honeydew), psyllids, like other Sternorrhyncha, provide access to a carbon resource that is typically inaccessible (the phloem contents). Pselids' roles in food webs are thus elevated above the comparatively interchangeable role of soft-bodied, barely mobile prey items because the honeydew resources produced by psyllids and other



honeydew-producing hemipterans have disproportionate effects on the abundance of numerous other interacting species in the ecosystem, they are even regarded as keystone species in certain food webs. Simple sugars and trace amounts of amino acids make up the majority of honeydew, but it can also include proteins, inorganic ions, and secondary metabolites from the host plant. Bacterial, fungal, arthropod, and vertebrate species all eat it. Predation will eliminate this resource by removing honeydew growers. In order to avoid predation and maintain honeydew production, a variety of ostensibly mutualistic interactions have developed between insects that produce. honeydew and those that consume it, The entire especially ants. community structure may be impacted by these keystone interactions, which also enhance arthropod biodiversity by enhancing floral supplies. IR food for Z honeyeater Several species of bumble bees (Bombus spp.) have been seen feeding on honeydew generated by Cacopsylla macleani on Salix alaxensis in boreal and arctic eco-zones, where floral resources are frequently scarce. Vespid wasps, important arthropod predators, also benefited from this honeydew resource. Psyllid honeydew may encourage the diversity of hymenopteran species, according to this study and others on the interactions between Sternorrhyncha and bees. Ant-psyllid mutualisms mediated by honeydew may have

the reverse impact in agricultural settings by decreasing psyllid interactions with parasitoids and predators. In the western United States, for instance, syrphid flies and introduced hymenopteran parasitoids are less effective in controlling D. citri when it is tended by nonnative, invasive Argentine ants (Linepithema humile). In contrast to the majority of their Sternorrhynchan cousins, psyllids have advanced the practice of excreting honeydew. Psyllid honeydew can be formed into several useful shapes or wrapped in wax tubes. Certain psyllid species' nymphs create tiny protective covers called lerps from their quickly drying honeydew secretions. These homes, which are mostly composed of starch, are another fecal product produced by psyllids that mediates keystone connections. The lerps of different Glycaspis psyllid species are a major source of bell miner birds (Manorina spp.) in Australian eucalyptus trees. These birds frequently eat lerps without harming the psyllid nymph underneath them, allowing it to create more lerp material. Due to their extreme aggression, these so called dictatorial birds expel other birds from their territory, eliminating the majority of avian insectivores that regulate psyllid populations on eucalyptus. Co-occurring psyllid outbreaks of Glycaspis and more harmful leaf-feeding psyllids that do not generate lerps, such senescence-inducing Cardiaspina spp., are



common in forests inhabited by lerp consuming bell miners. When these epidemics are severe, several Eucalyptus species die back. Following the experimental removal of bell miners, psyllid outbreaks are reduced and a variety of bird insects return. This is another indirect proof that psyllids constitute a significant source of food for birds in eucalyptus trees, which might not have been apparent in the absence of experiments examining the relationship between psyllids and bell miners. It's unclear who gets to the area first, the psyllids or the bell miners, but this study makes it abundantly evident that psyllids can have a significant impact on processes at the landscape and community levels.

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