OP-069 [Bee Biology]
Microbial Community Profiling of Tetragonula biroi (Friese) Hives: Insights from Pollen-Microbiome Interactions

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Pollinators play a crucial role in global biodiversity and agricultural sustainability, yet bee populations are declining due to habitat loss and environmental stressors. The microbiome is increasingly recognized as a key factor in bee health, influencing digestion, immunity, and overall colony fitness. However, the effects of temporal environmental changes on bee microbiomes remain poorly understood.

Here we show that bacterial communities in the hive of the native stingless bee Tetragonula biroi (Friese) exhibit positive correlations with pollen sources over time. Using a longitudinal approach, we sampled beehive propolis and bee bread bimonthly over three months from a meliponary in Laguna, Philippines. 16S rRNA amplicon sequencing revealed 41 bacterial genera across six major phyla, with lactic acid bacteria (Lactobacillus, Oenococcus, and Tetragenococcus) dominating the propolis microbiome. Pollen spectra analysis identified 26 plant species, with Veitchia merrillii (Becc.) H.E.Moore, Crotalaria L., and Mangifera indica L. among the most abundant, likely due to their blooming periods, hive proximity, and floral traits that enhanced bee attraction. Notably, lactic acid bacteria exhibited strong positive correlations with pollen sources, particularly resinous plants or those producing exudates used in propolis production, highlighting the intricate link between bee foraging behavior, pollen selection, and microbial community dynamics.

Overall, these findings improve our understanding of microbial-pollen interactions within stingless bee colonies and highlight the potential for strategic floral enrichment to enhance bee health and conservation efforts.

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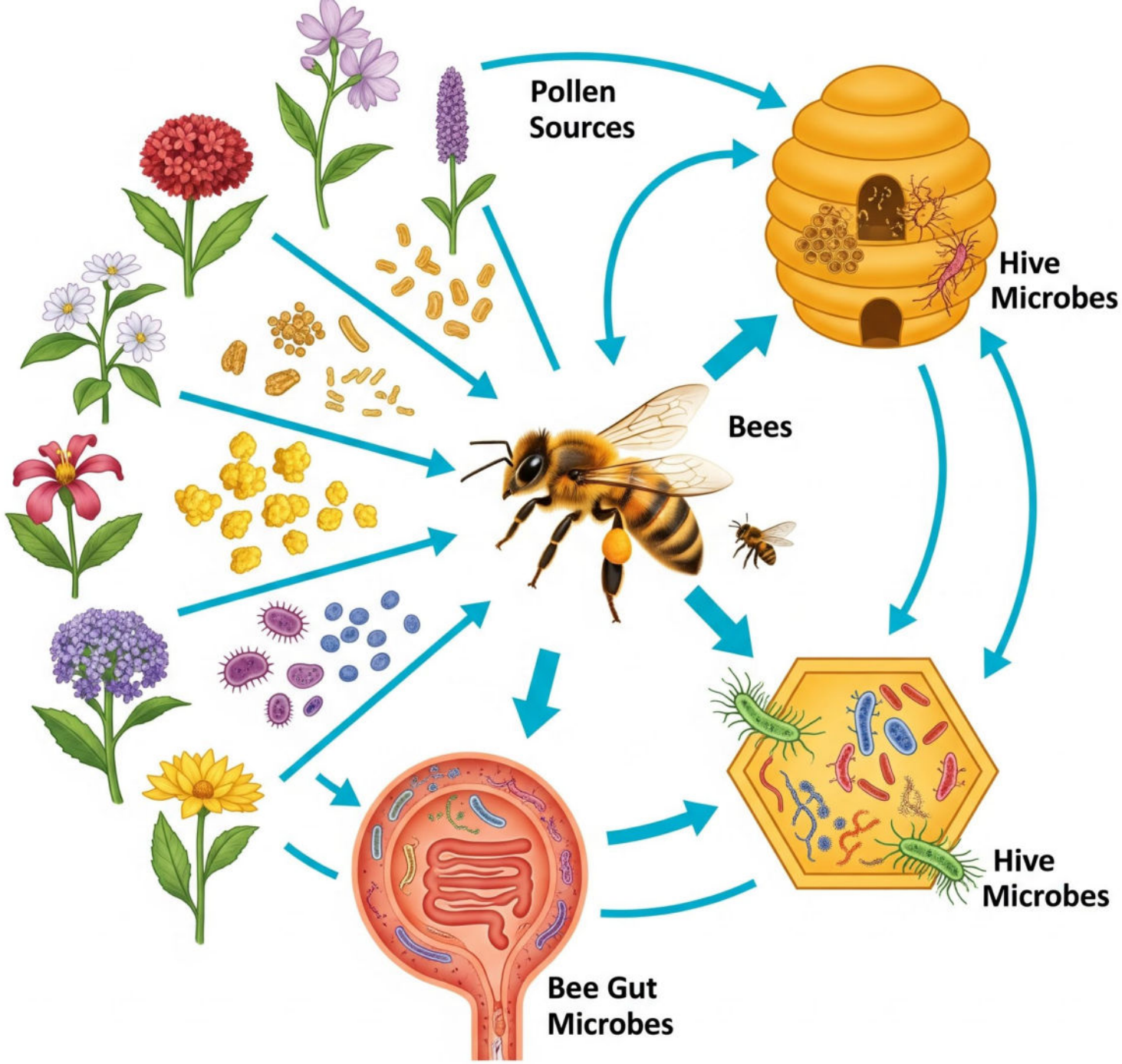


The interconnected system of bees, pollens, and microorganisms

Microbes as hidden players in bee health

Aid in food digestion

Detoxify harmful molecules

Provide essential nutrients

Protect against invading pathogens and parasites

Modulates development and immunity

Microbiome of beehives are shaped by the environment and the behavior of bees

Microorganisms are obtained whilst bees are foraging on flowers

Microorganisms are acquired via social transmission

Microorganisms from the nesting materials used by bees

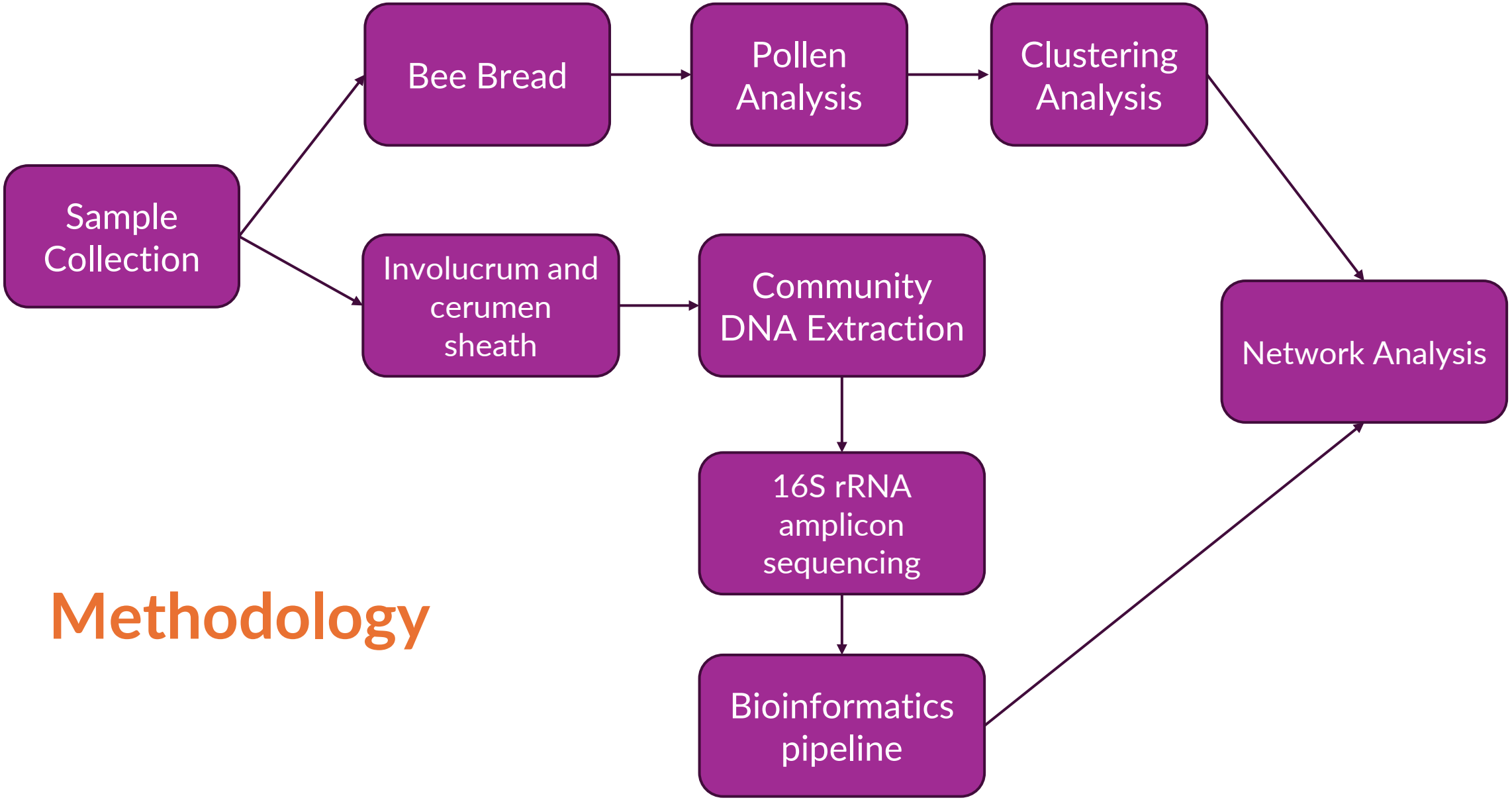
🐝 Our Goal

To understand how the food sources of stingless bees (*Tetragonula biroi*) , especially the pollen they collect, are connected to the tiny microbes living in their hives.

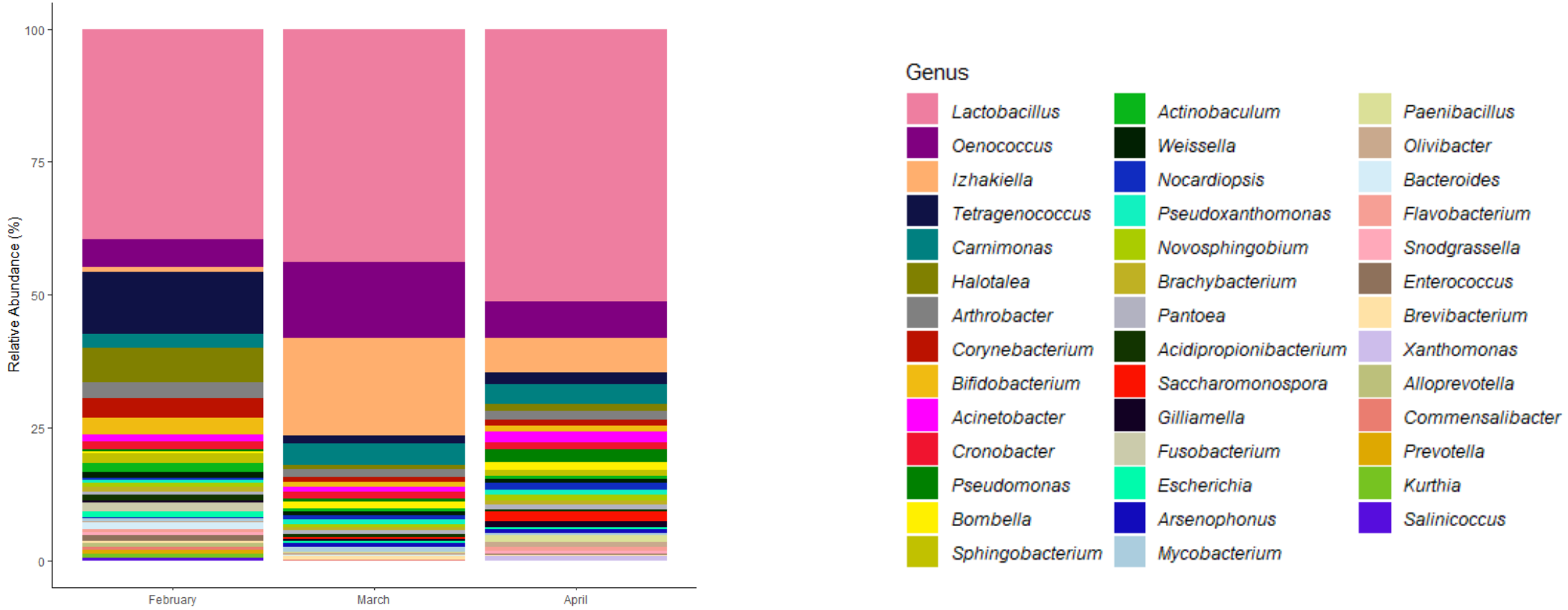
🌿 Why This Matters

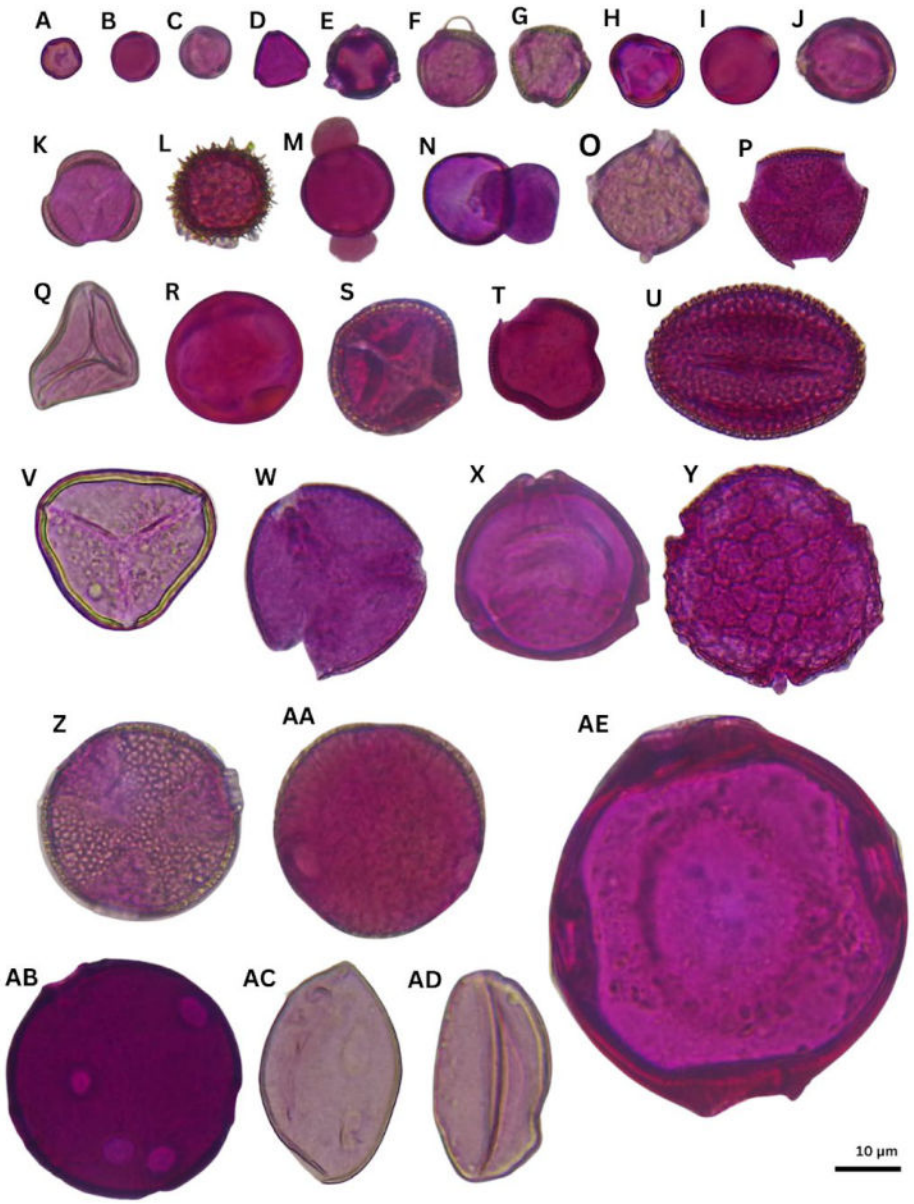
- Bees rely on pollen for nutrition and hive building.
- Microbes help bees digest food and protect them from diseases.
- Linking pollen and microbes can show how bees stay healthy and adapt to changes in their environment.

Methodology



Lactobacillus dominate the microbiome of the hive material during the honey-harvesting season.

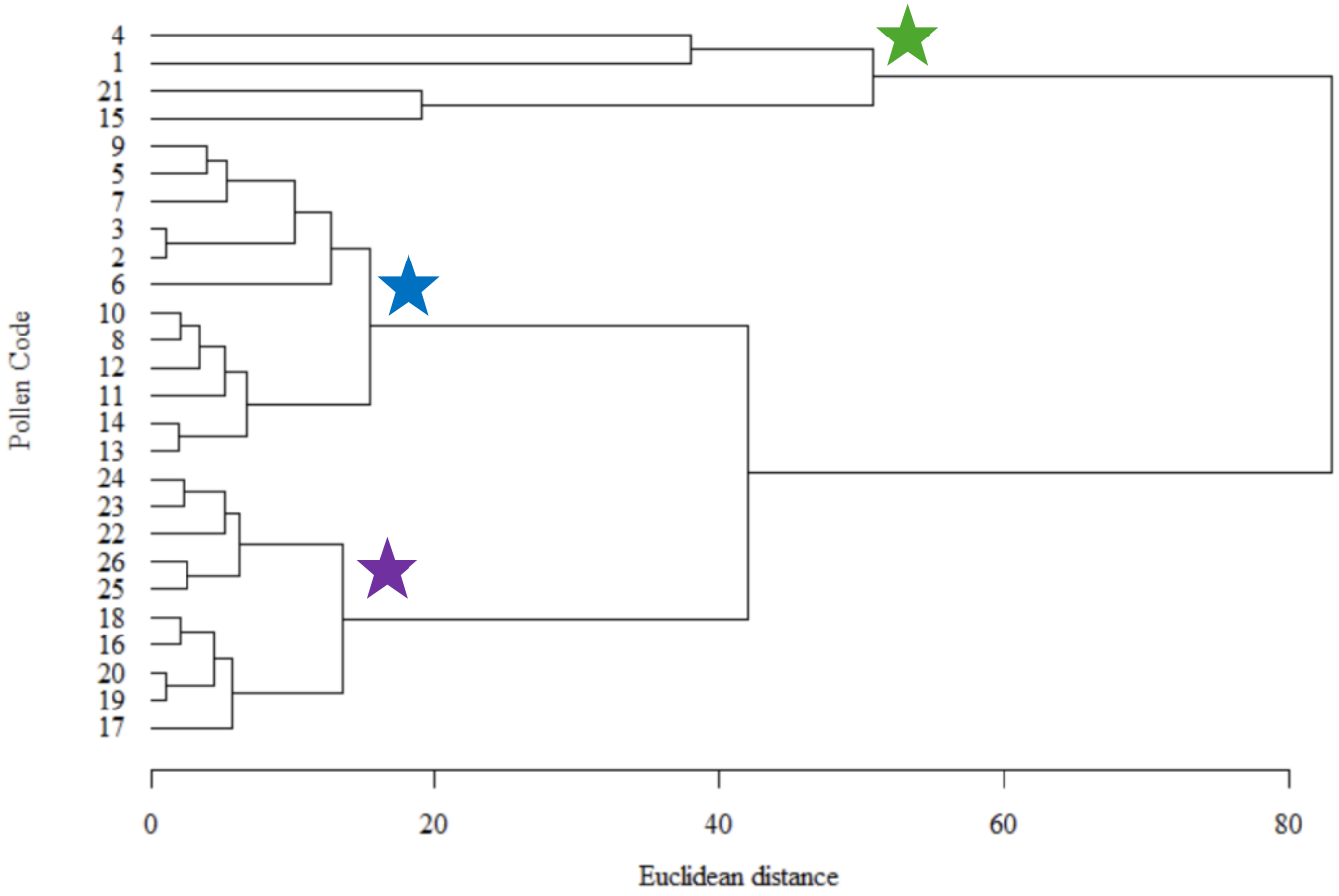




26 pollen types from 18 botanical families were identified

A. Mango/"Mangga"
B. Goosefoot
C. Evening primrose (type)
D. Bottlebrush
E. Knotwood (type)
F-G. Jamaica cherry/"Aratiles"
H. Papaya (type)
I. Grasses (1)
J. Crape Myrtle/"Melendres"
K. Mugworts
L. Sweet potato/"Kamote"
M. Spurges (type)
N. Sedges
O. Silverberry
P. Rattlepod
Q. Coconut/"Niyog"
R. Grasses (2)
S. Kamala
T-U. Spurges
V. Guava/"Bayabas"
W-X. Tick clover
Y. Royal poinciana/"Fire tree"
Z-AA. Peacock flower/"Caballero"
AB. Dogbanes
AC-AD. Manila palm
AE. River tamarind/"Ipil-ipil"

Cluster analysis reveals stable core pollen types and season-specific foraging



Pollen Code

1	*M. indica*	10	*Elaeagnus* sp.	19	*L. indica*
2	Apocynaceae	11	*Euphorbia* sp.	20	*M. calabura*
3	*C. nucifera*	12	*Mallotus* sp.	21	*Callistemon* sp.
4	*V. merrillii*	13	Euphorbiaceae type	22	*P. guajava*
5	*Artemisia* sp.	14	*C. pulcherrima*	23	Oenotheraceae type
6	Carica type	15	*Crotalaria* sp.	24	Poaceae 1
7	Chenopodiaceae	16	*D. regia*	25	Poaceae 2
8	*I. batatas*	17	*Desmodium* sp.	26	Polygonaceae type
9	Cyperaceae	18	*L. leucocephala*		

- **Cluster A** - Core pollen sources consistently used across months.
- **Cluster B** - Secondary pollen types with moderate seasonal overlap.
- **Cluster C** - Opportunistic/seasonal pollen sources unique to certain months.

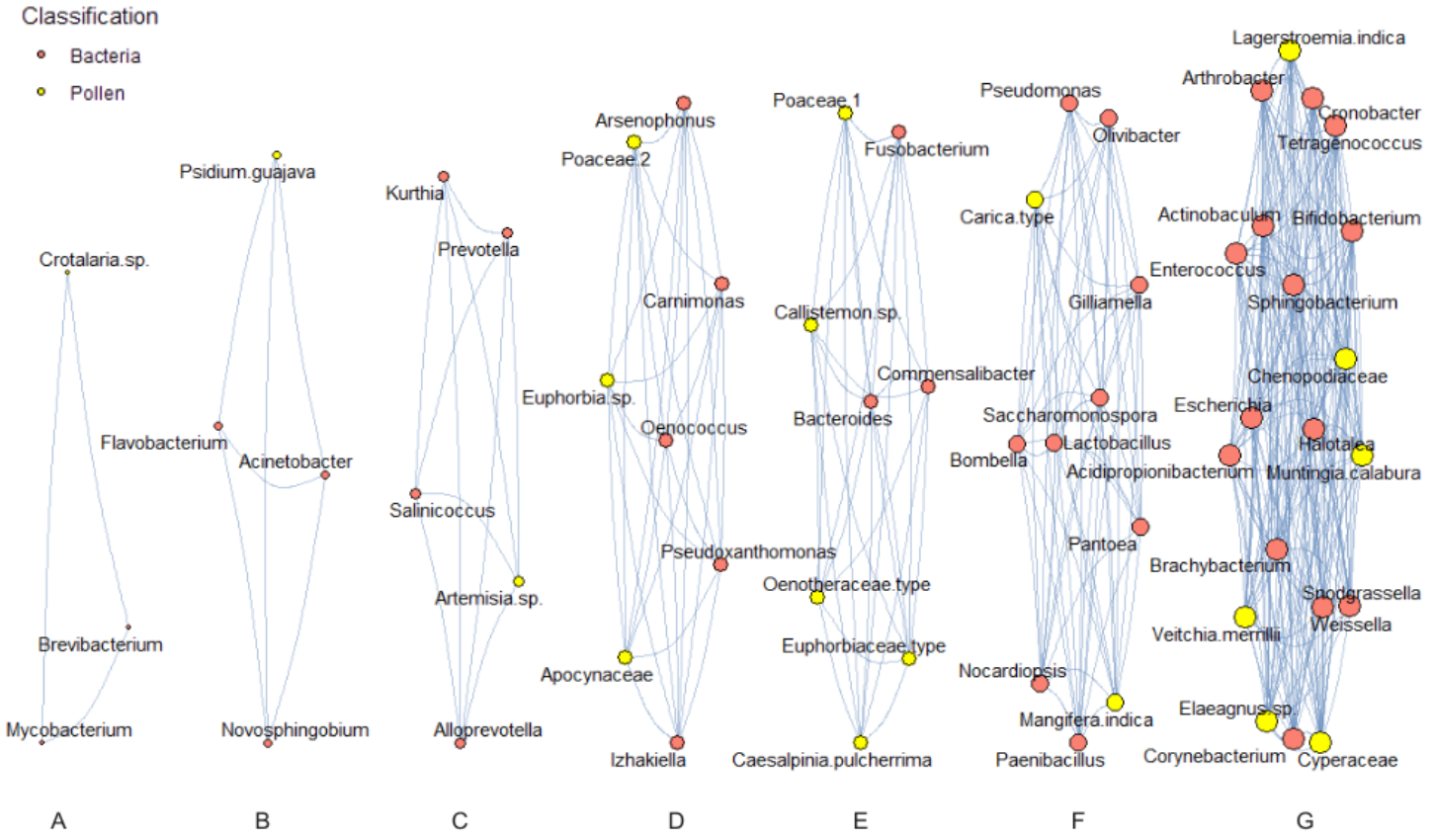
Network analysis reveals functional microbial–pollen modules in *T. biroi* hives

Cluster A – C : minor or opportunistic pollen sources

Cluster D – E : Mid-sized clusters linking genera like *Oenococcus*, *Izhakiella*, and *Commensalibacter* with pollen from *Poaceae*, *Euphorbia*, and *Caesalpinia*. Suggests microbial fermentation or transformation of diverse pollen types.

Cluster F – Seasonal foraging signature (*Lactobacillus*, *Bombella*, *Gilliamella* linked with *Mangifera indica*)

Cluster G – Core metabolic hub supporting hive stability (*Tetragenococcus*, *Weissella*, *Enterococcus* linked to *Veitchia merrillii*, *Chenopodiaceae*)



Key Findings: Microbiome and Pollen Associations in *T. biroi* Colonies

🧬 Bacterial Communities (Propolis Microbiome)

- Dominated by **Bacillota**, with **Lactic Acid Bacteria (LAB)** >60%
- LAB (e.g., *Lactobacillus, Weissella, Tetragenococcus*) linked to digestion, food preservation, pathogen defense

Key Findings: Microbiome and Pollen Associations in *T. biroi* Colonies

🌸 Pollen Analysis

- Wide range of pollen sources, confirming **generalist foraging**
- No single dominant pollen; frequent taxa include *Mangifera indica*, *Veitchia merrillii*, *Callistemon sp.*
- Seasonal shifts noted, reflecting **availability of floral resources**

Key Findings: Microbiome and Pollen Associations in *T. biroi* Colonies

🌿 Cluster Analysis of Pollen (Ward's Method)

- **Cluster A:** Stable core pollen sources (consistent across months)
- **Cluster B:** Secondary sources with moderate overlap
- **Cluster C:** Opportunistic/season-specific pollen

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Key Findings: Microbiome and Pollen Associations in *T. biroi* Colonies

Network Analysis (Bacteria–Pollen Correlations)

- Seven distinct **modules (A–G)** reveal microbial–pollen associations
- **Cluster F:** Seasonal mango module (*Lactobacillus, Bombella* ↔ *Mangifera indica*)
- **Cluster G:** Core LAB hub (*Tetragenococcus, Weissella* ↔ *Veitchia merrillii*, *Chenopodiaceae*)

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🐝 Take-Home Message

The microbiome of T. biroi hives is shaped by a combination of stable core LAB communities and seasonal pollen foraging patterns, forming functional modules that support hive health and resilience.

Thank you for listening!

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