METABOLIC MODELING OF HONEYBEE GUT MICROBIOME

Author: Peitong Chen 640515506
Supervisor: Dr. Sahutchai Inwongwan

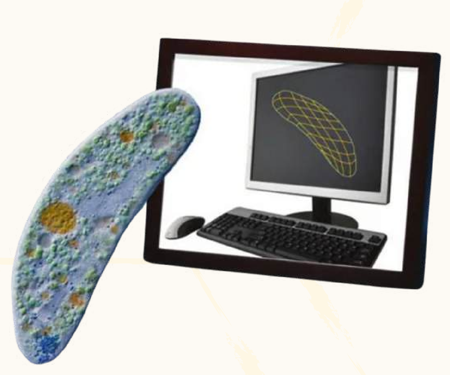
ABSTRACT

The honeybee gut microbiome consists of specialized bacterial species that play crucial roles in digestion, immunity, and overall colony health. This study constructed metabolic models for five key bacteria, analyzing their metabolic interactions. Using genome annotation and pathway mapping, we identified shared and unique metabolic functions, highlighting cooperative nutrient processing and pathogen defense mechanisms. Our findings contribute to understanding the ecological role of the honeybee gut microbiome.

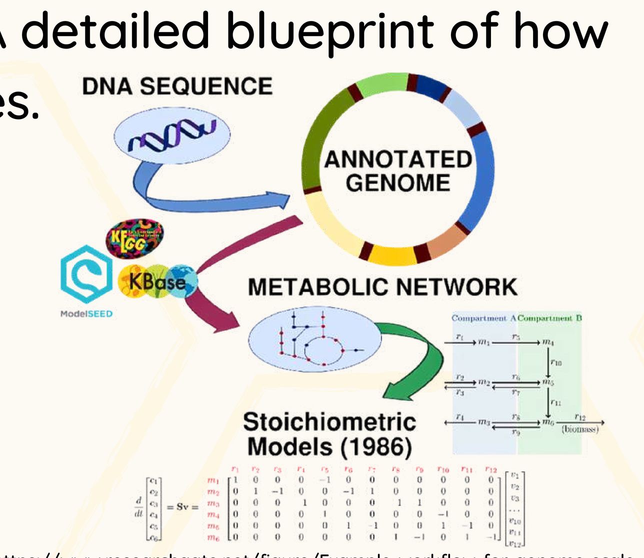
INTRODUCTION

- **Honeybees:** Pollinators, biodiversity, agriculture
- **Decline factors:** Habitat loss, pesticides, climate change
- **Gut microbiome:** Digestion, immunity, metabolic stability
- **Study focus:** Metabolic models, bacterial interactions
- **Five key bacterial species studied:**
  - *Snodgrassella alvi*
  - *Gilliamella apicola*
  - *Bifidobacterium* spp.
  - *Lactobacillus* Firm-4
  - *Lactobacillus* Firm-5
- **Genome-scale metabolic model (GEMs):**

A network-based tool that collect all known metabolic Information of a biological system. A detailed blueprint of how an organism eats, grows, and survives.



https://biox.stanford.edu/highlight/stanford-researchers-produce-first-complete-computer-model-organism



https://www.researchgate.net/figure/Example-workflow-for-genome-scale-metabolic-network-reconstruction-and-analysis-with-FBA_fig3_323759025

METHODOLOGY

Genome data acquiring (Use NCBI) → Analysis of genome data (Use Kbase) → Constructing microbiome model (Use Kbase) → Model characterisation (Use ipath3 & R) → Curation the model (Use ipath3 & R)

TOOLS

National Library of Medicine (National Center for Biotechnology Information); iPATH3; RAST (Rapid Annotation using Subsystem Technology); KBase; RStudio

OBJECTIVES

- **To study the dynamic and functions of honeybee gut microbiome.**
- **Construct metabolic models of honeybee gut microbiome.**

CONCLUSION

- **Achievement:** Successfully constructed metabolic models of five key bacterial species in the honeybee gut microbiome.
- **Key Findings:**
  - Bacteria exhibited unique metabolic traits.
  - Cooperative interactions supported: Nutrient processing, Immunity , and Microbial balance.
- **Significance:** Enhances understanding of the microbiome's role in bee health. Provides a foundation for future research on environmental impacts, such as pesticides and diet.

RESULTS

• Genome annotation and model construction

Table1: Statical information of genomes (NCBI)

Species of bacteria	NCBI RefSeq assembly	Genome size	Sources
Snodgrasslla alvi (*S.alvi*)	GCF_000600005.1	2.5 Mb	Proc Natl Acad Sci U S A 2014 Genomics and host specialization of honey bee and bumble bee gut symbionts WK Kwong, et al. https://pubmed.ncbi.nlm.nih.gov/25053814/
Gilliamela apicola (*G.apicola*)	GCF_000599985.1	3.1 Mb	Proc Natl Acad Sci U S A 2014 Genomics and host specialization of honey bee and bumble bee gut symbionts WK Kwong, et al. https://pubmed.ncbi.nlm.nih.gov/25053814/
Bifidobacterium spp. (*B.spp.*)	GCF_000196555.1	2.4 Mb	Nature 2011 Bifidobacteria can protect from enteropathogenic infection through production of acetate S Fukuda, et al. https://pubmed.ncbi.nlm.nih.gov/21270894/
Lactobacillus Firm-4 (*L.*Firm-4)	GCF_003703885.1	2.2 Mb	Nucleic Acids Res 2013 RefSeq microbial genomes database: new representation and annotation strategy T Tatusova, et al. https://pubmed.ncbi.nlm.nih.gov/24316578/
Lactobacillus Firm-5 (*L.*Firm-5)	GCF_003150935.1	1.7 Mb	Nucleic Acids Res 2013 RefSeq microbial genomes database: new representation and annotation strategy T Tatusova, et al. https://pubmed.ncbi.nlm.nih.gov/24316578/

Table2: Genome annotation (Kbase)

Species of bacteria	Number of features	EC Number
Snodgrasslla alvi (*S.alvi*)	2496	527
Gilliamela apicola (*G.apicola*)	2942	601
Bifidobacterium spp. (*B.spp.*)	1884	426
Lactobacillus Firm-4 (*L.*Firm-4)	1770	383
Lactobacillus Firm-5 (*L.*Firm-5)	2125	358

- The higher the number of features, the higher the EC number.

Table3: Model Construction Results

Model Name	Model type	Number reactions	Number compounds	Number compartments	Number biomass
Snodgrasslla alvi (*S.alvi*)	Test	919	1010	2	1
Gilliamela apicola (*G.apicola*)	Test	1079	1091	2	1
Bifidobacterium spp. (*B.spp.*)	Test	753	830	2	1
Lactobacillus Firm-4 (*L.*Firm-4)	Test	713	843	2	1
Lactobacillus Firm-5 (*L.*Firm-5)	Test	636	743	2	1
Community	Community Model	4100	4166	7	6

- Presents data on various (Individual and Community) metabolic models for different bacterial species.
- The community model is a combination of five individual models.

• Visualization and characterization of models

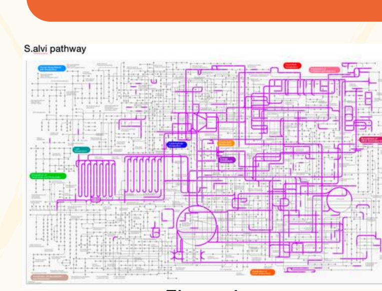


Figure1

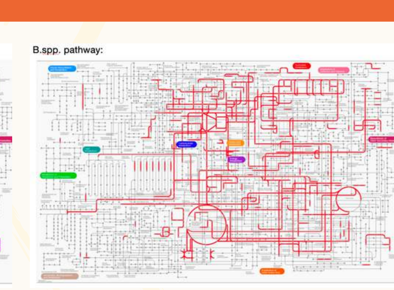


Figure2

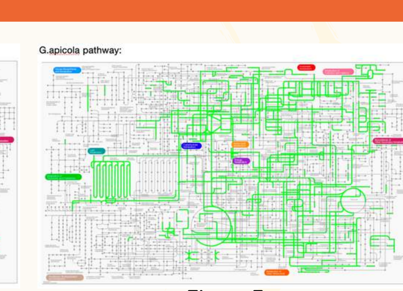


Figure3

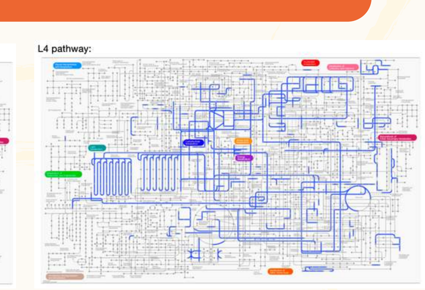


Figure4

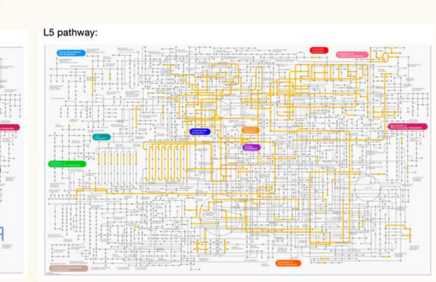
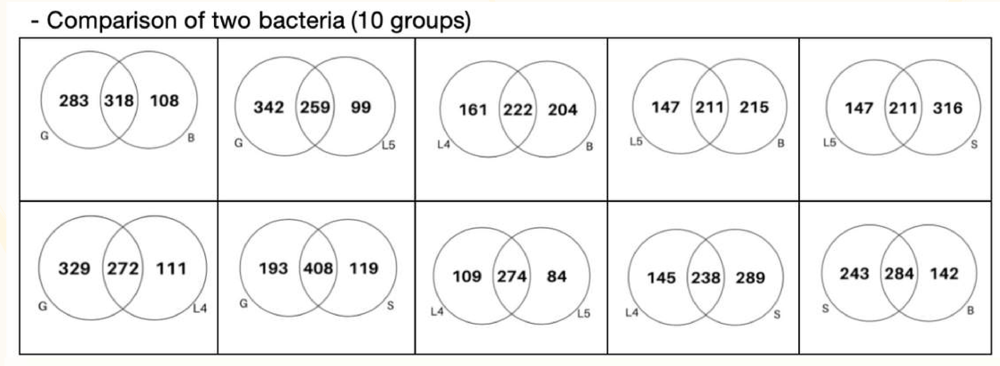


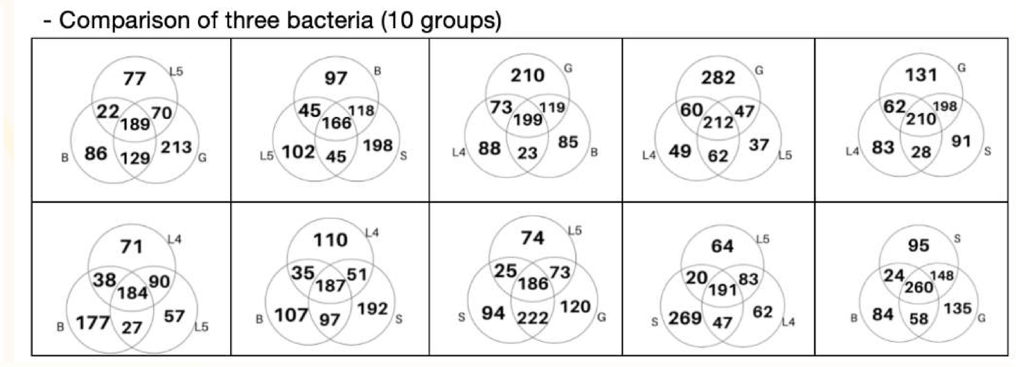
Figure5

Figures 1 to 5 depict the metabolic pathway maps of five key bacterial species in the honeybee gut microbiome. The maps reveal that while these bacteria coexist within the same gut microbial community, their metabolic pathways exhibit significant differences.

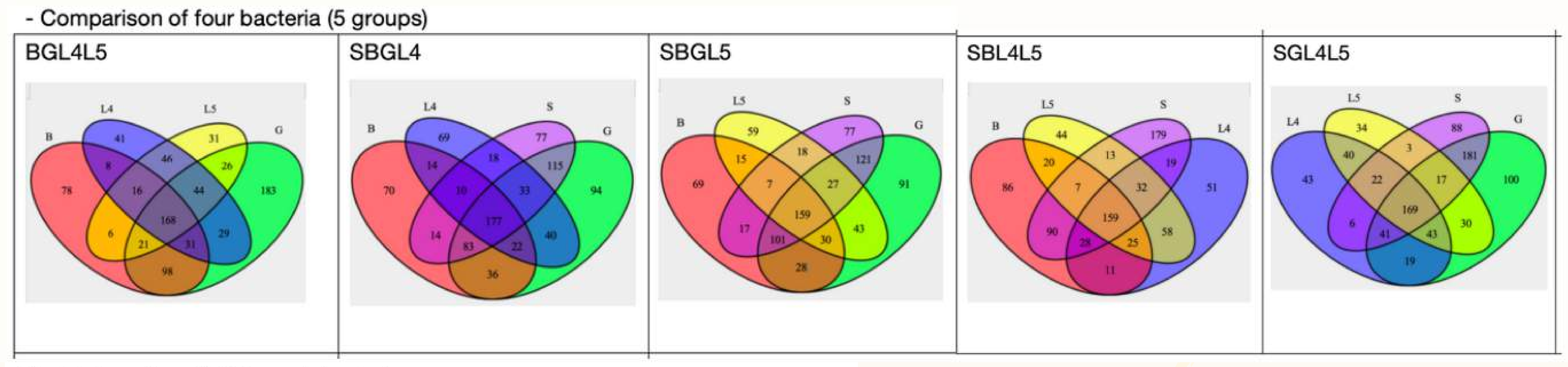
- Comparison of two bacteria (10 groups)



- Comparison of three bacteria (10 groups)

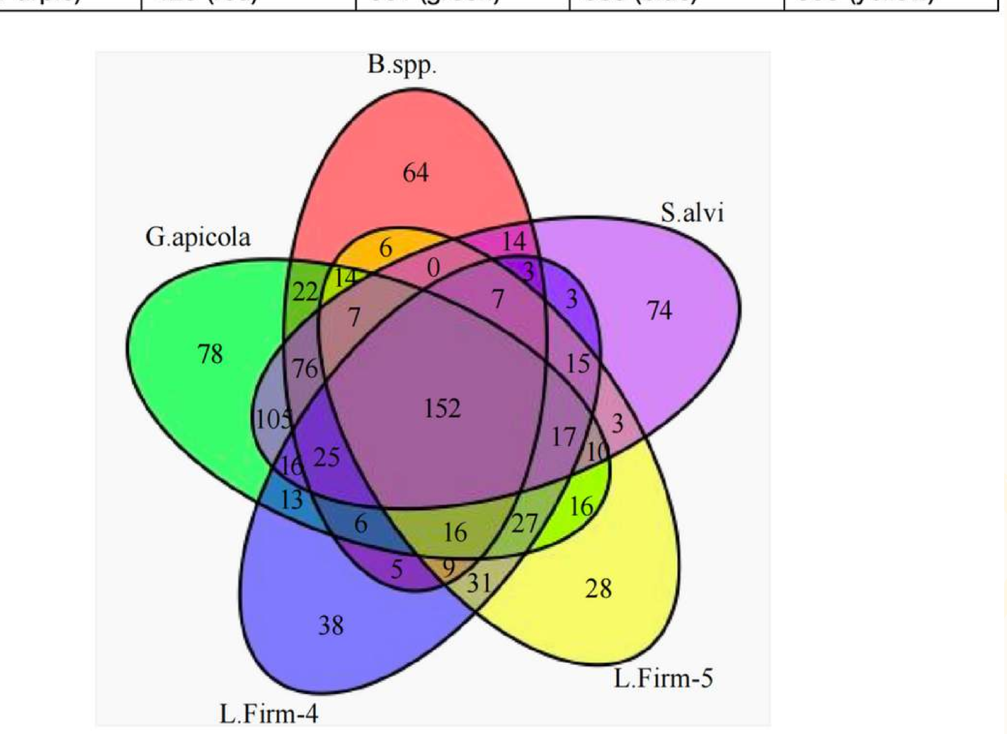


- Comparison of four bacteria (5 groups)



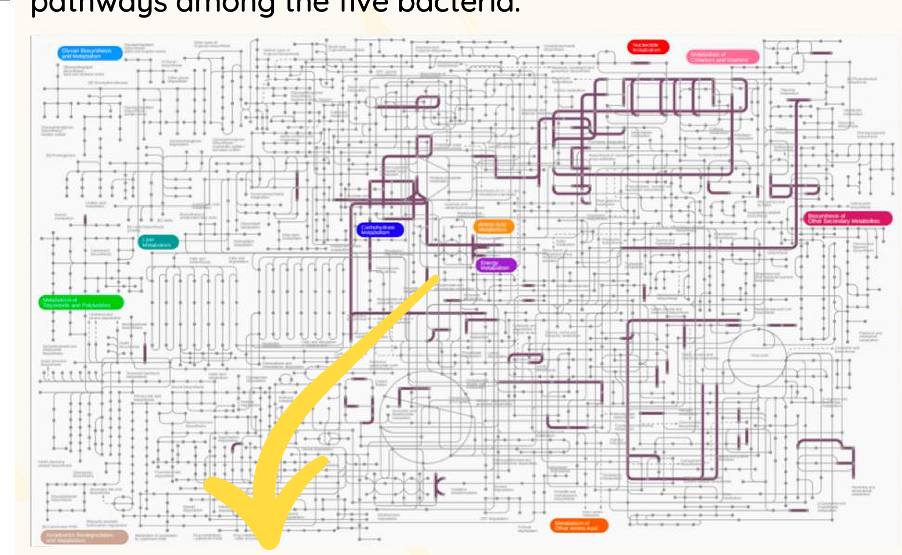
The total number of EC for each bacteria

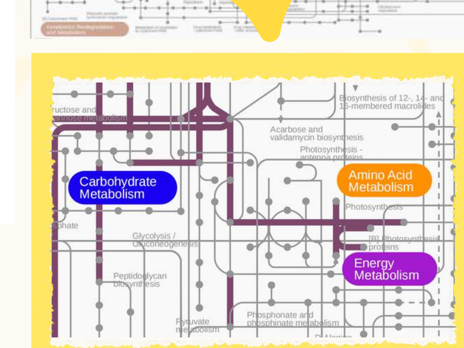
S	B	G	L4	L5
527 (Purple)	426 (red)	601 (green)	383 (blue)	358 (yellow)



The Final Venn diagram clearly distinguishes between the core part (shared metabolic pathways) and the unique parts (species-specific metabolic pathways) of the five key bacterial species in the honeybee. Surprisingly, the five bacteria shared only 152 EC numbers, and each bacterium possessed a distinct set of unique EC numbers, ranging from a minimum of 28 to a maximum of 78.

This is the metabolic pathway map at the core part of the Venn diagram. It represents the shared functional and metabolic pathways among the five bacteria.





- For example, here is a small part of the core metabolic pathway map.
- Including three prominent metabolisms: Carbohydrate, Amino Acid and Energy.
- The dark purple lines highlight the active metabolic routes between these three metabolisms.

REFERENCES