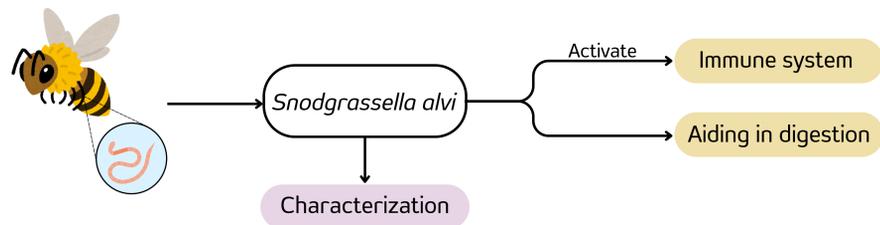


## Introduction



## Abstract

*Snodgrassella alvi*, a key bacterium living in the gut of honey bees, plays an essential role in immune system stimulation, infection prevention and digestion in bees. This study focuses on investigating the antibiotic sensitivity and growth of *S. alvi* isolated from bee guts, as well as conducting genomic analysis to examine codon usage for further in-depth studies. Spot test assay using Tryptone Soy Agar (TSA) was used to investigate the antibiotic resistance of five *S. alvi* strains. The results showed that *S. alvi* exhibited antibiotic susceptibility to all antibiotics tested at a concentration of 20 mg/L, except for AF\_R2A\_R3, which displayed susceptibility to erythromycin at 50 mg/L. Additionally, *S. alvi* AM\_R2A\_I4 was cultured in TSB supplemented with different sugars: glucose, fructose, and a combination of glucose and fructose. The findings indicated that *S. alvi* exhibited different growth patterns depending on the type of sugar provided. For codon usage analysis, the genome of *S. alvi* AM\_R2A\_I4 was compared with the genomes of type strains of *S. alvi*, and *Escherichia coli* BL21 (DE3) from the NCBI database. The results revealed that the codon usage of *S. alvi* AM\_R2A\_I4 and the type strains was similar. However, when compared to *E. coli* BL21 (DE3), differences in codon usage were observed.

## Results

### 1.1 Characterization of *Snodgrassella alvi*

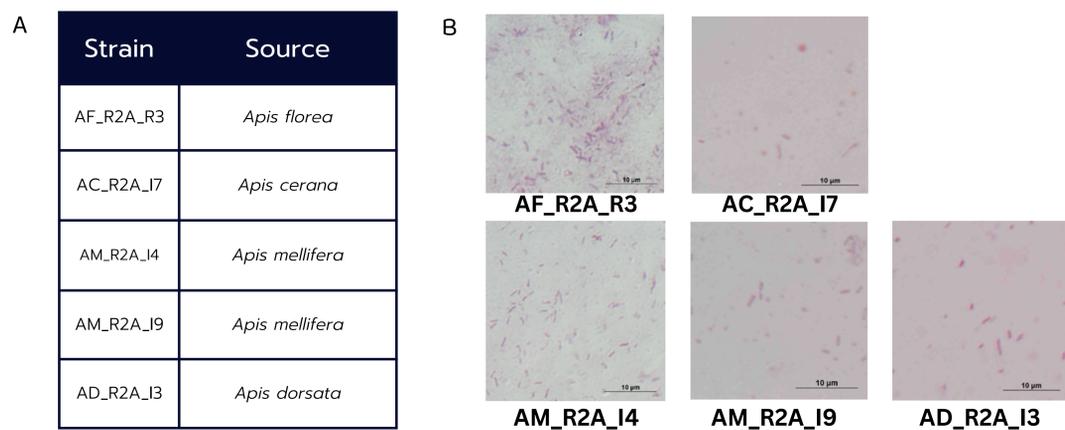


Figure 1: Characterization of the isolated strains. The sources of the strains (A) and the cell morphology (B) are presented.

### 1.3 Culturing *S. alvi* AM\_R2A\_I4 in TSB with modified sugar types.

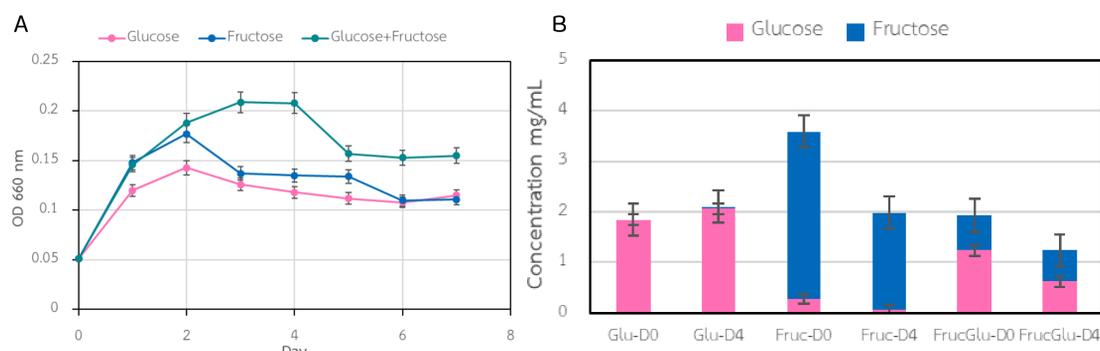


Figure 3: Growth curve of *Snodgrassella alvi* in liquid media with media supplemented with glucose, fructose, and glucose + fructose. The growth curve (A) and Sugar consumption (B) were monitored.

## Reference

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- Kwong, W.K. and Moran, N.A. (2013). Cultivation and characterization of the gut symbionts of honey bees and bumble bees: description of *Snodgrassella alvi* gen. nov., sp. nov., a member of the family Neisseriaceae of the Betaproteobacteria, and *Gilliamella apicola* gen. nov., sp. nov., a member of Orbaceae fam. nov., Orbales ord. nov., a sister taxon to the order 'Enterobacteriales' of the Gammaproteobacteria. *International Journal of Systematic and Evolutionary Microbiology*, 63, 2008-2018. doi:10.1099/ijs.0.044875-0.

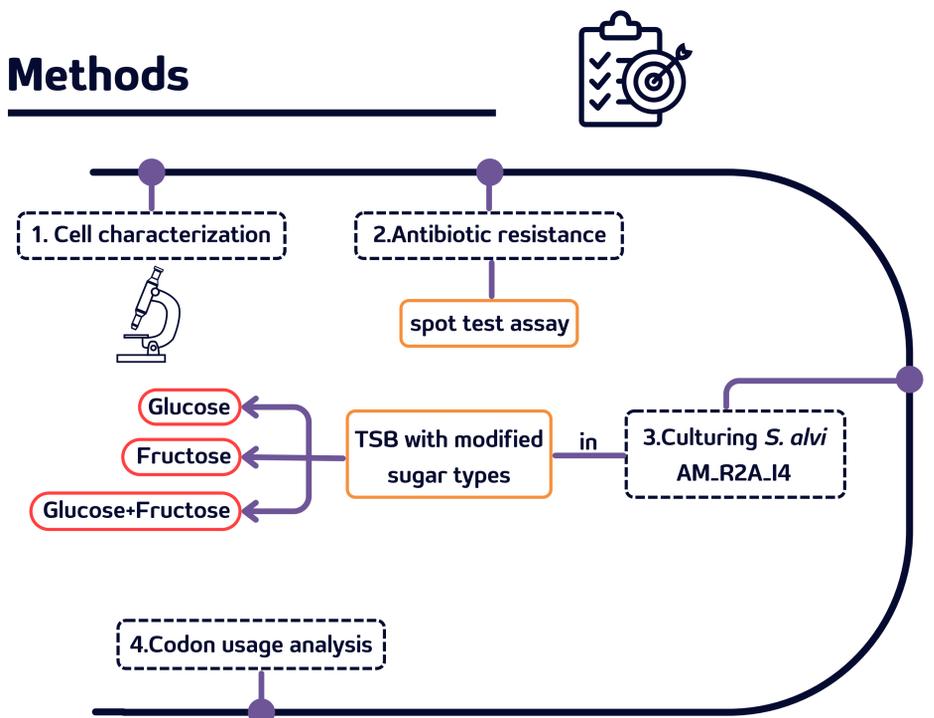
## Acknowledgement

- Asst. Prof. Dr. Pachara Sattayawat, Project's advisor
- Bee Protection Laboratory, Department of Microbiology, Faculty of Science, Chiang Mai University

## Objectives

- To investigate antibiotic resistance of newly isolated *S. alvi*
- To investigate the genomic characteristics of *S. alvi*
- To study the growth of *S. alvi* AM\_R2A\_I4 in liquid media (Tryptone Soy Broth, TSB) with different types of sugars to analyze variations in sugar utilization

## Methods



### 1.2 Antibiotic resistance

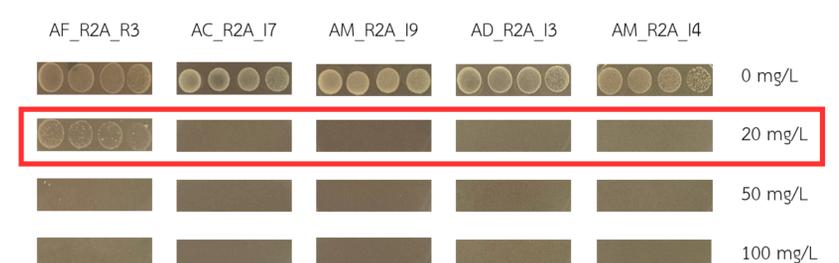


Figure 2: Growth of *Snodgrassella alvi* on culture media with different concentrations of erythromycin.

### 1.4 Codon usage analysis

The results revealed that the codon usage of *S. alvi* AM\_R2A\_I4, *S. alvi* wbK2 2022 (CP091515) and *S. alvi* wbK2 2014 (CP007446) was similar. However, when compared to *E. coli* BL21 (DE3), differences in codon usage were observed.

## Conclusions

- Antibiotic susceptibility testing of five *Snodgrassella alvi* strains revealed that all strains were sensitive to five antibiotics at a concentration of 20 mg/L. However, variations in sensitivity were observed for erythromycin, with one strain, AF\_R2A\_R3, exhibiting susceptibility at 50 mg/L.
- The cultivation experiment of *S. alvi* strain AM\_R2A\_I4, isolated from the gut of *Apis mellifera*, in liquid medium (Tryptone Soy Broth, TSB) with different sugar modifications showed varying growth patterns depending on the sugar type. However, growth eventually declined and stabilized. Additionally, *S. alvi* was able to utilize fructose but not glucose.
- Codon usage analysis using genome data from *S. alvi* strain AM\_R2A\_I4, *S. alvi* wbK2 2014 (CP007446), and *S. alvi* wbK2 2022 (CP091515) revealed specific codon preferences. This finding indicates conserved codon usage within the same species when compared to *Escherichia coli* BL21 (DE3).