Title : Exploring the Potential of *Snodgrassella alvi* as a Host for Genetic Engineering

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ABSTRACT

Snodgrassella alvi is a key bacterium lining in the gut of honey bees. This bacterium plays an essential role immune system stimulation and infection prevention. 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. In the investigation of antibiotic sensitivity, *S. alvi* was cultured in liquid Tryptone Soy Broth (TSB) and subsequently spotted onto solid Trypticase Soy Agar (TSA) using the spot test assay method. The results showed that *S. alvi* exhibited antibiotic susceptibility spectinomycin, kanamycin, erythromycin, chloramphenicol and ampicillin at a concentration of 20 mg/L, except for strain AF_R2A_R3, which displayed susceptibility erythromycin at 50 mg/L. Additionally, *S. alvi* AM_R2A_I4 was cultured in Tryptone Soy Broth (TSB) supplemented with three different sugar types: glucose, fructose, and a combination of glucose and fructose. The bacterial growth was measured by optical density at 660 nm (OD660). 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 *S. alvi* wbK2 2022 (CP091515), *S. alvi* wbK2 2014 (CP007446), and *Escherichia coli* BL21 (DE3) from the NCBI database. The Codon Usage Calculator was used to analyze codon usage within the genomes. 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. This study enhances the understanding of *S. alvi* codon usage bias, providing a foundation for designing synthetic genes with optimized codon selection for target organisms. Such insights can improve protein production efficiency and contribute to advancements in genetic engineering.

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