

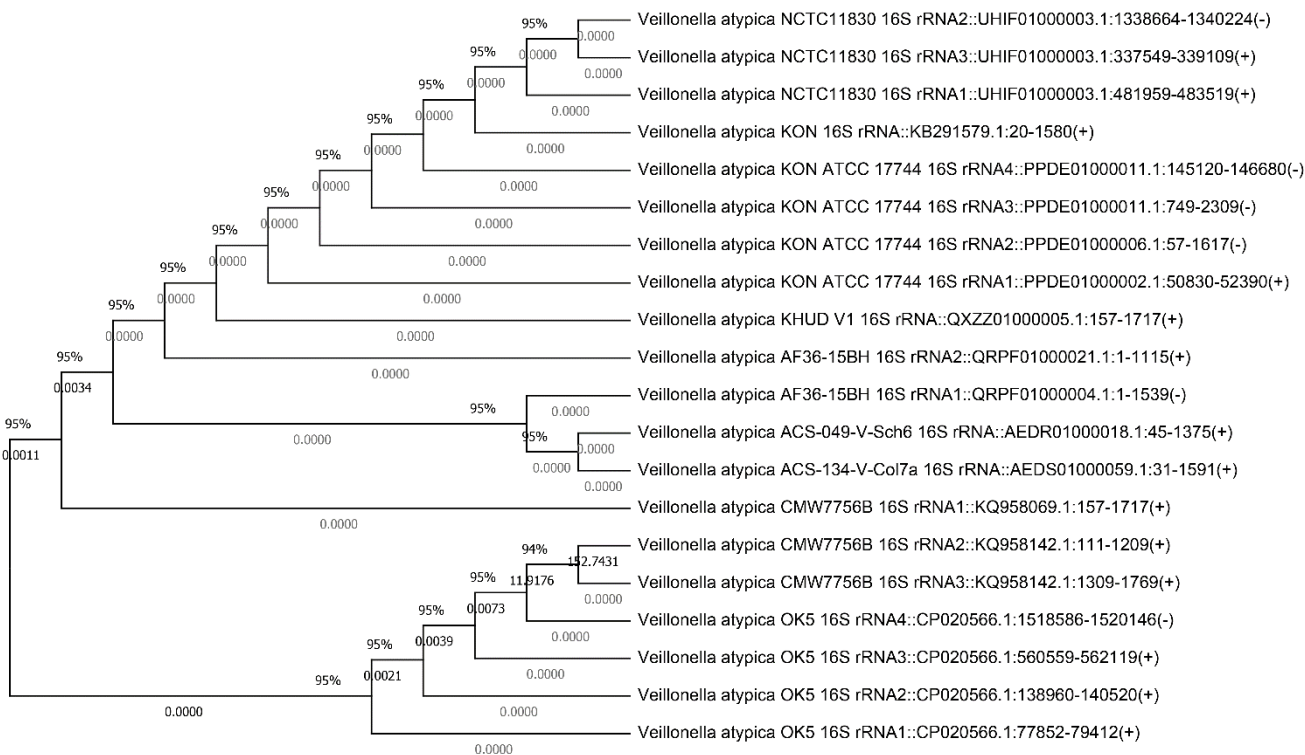
1 **Comparative Genomics Uncovers the Genetic Diversity and Characters of**
2 ***Veillonella atypica* and provides Insights into its Potential Applications**

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13 **Supplementary Figure S1. The phylogenetic tree built based on 16S rRNA sequences of nine *V. atypica***

14 **strains.** The 16S rRNA sequences were extracted from the genomic sequences of nine *V. atypica* strains by using

15 Barrnap (<https://github.com/tseemann/barrnap>) and the phylogenetic tree was built with MEGA software with

16 default parameters. The number of 16S rRNA gene copies ranged from 1 to 4. For example, one 16S rRNA gene

17 copy was presented in *V. atypica* KON, four 16S rRNA gene copies were presented in *V. atypica* KON ATCC 17744,

18 and three 16S rRNA gene copies were presented in *V. atypica* NCTC11830. The result of the phylogenetic tree

19 showed that *V. atypica* KON, *V. atypica* NCTC11830, and *V. atypica* KON ATCC 17744 are in the same cluster and

20 revealed that these strains are same strains. However, the results of similarity analysis among the genomes of *V.*

21 *atypica* KON, *V. atypica* NCTC11830, and *V. atypica* KON ATCC 17744 showed that the symmetric identify

22 between *V. atypica* KON ATCC 17744 and *V. atypica* KON is 98.91%, while the symmetric identify between *V.*

23 *atypica* KON ATCC 17744 and *V. atypica* NCTC11830 is 97.51%. These results suggested that *V. atypica* KON, *V.*

24 *atypica* KON ATCC 17744, and *V. atypica* NCTC11830 are different substrains of *V. atypica* KON.