













the same time, the fact that the *Chryseobacterium* strains were able to grow on a wide range of carbon sources, including organic acids, amino acids, and sugars, suggests that they may be able to utilize a variety of carbon sources in their natural environment. This is consistent with the idea that these bacteria are members of the soil microbiota, which are known to be highly diverse and metabolically versatile.

The phylogenetic analysis of the 16S rDNA sequences of the *Chryseobacterium* strains revealed that they belong to the *Chryseobacterium* genus, which is a member of the *Chryseobacterium* family. This family is part of the *Chryseobacterium* order, which is a member of the *Chryseobacterium* class. The *Chryseobacterium* class is a member of the *Chryseobacterium* phylum, which is a member of the *Chryseobacterium* kingdom. The phylogenetic analysis also revealed that the *Chryseobacterium* strains are closely related to other members of the *Chryseobacterium* genus, including *Chryseobacterium* sp. 1, *Chryseobacterium* sp. 2, and *Chryseobacterium* sp. 3.

The results of this study suggest that the *Chryseobacterium* strains are members of the soil microbiota, which are known to be highly diverse and metabolically versatile. The fact that these bacteria were able to grow on a wide range of carbon sources, including organic acids, amino acids, and sugars, suggests that they may be able to utilize a variety of carbon sources in their natural environment. This is consistent with the idea that these bacteria are members of the soil microbiota, which are known to be highly diverse and metabolically versatile.

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