



# Phylogenetic Relationships and Potential Functional Attributes of the Genus *Parapedobacter*: A Member of Family *Sphingobacteriaceae*

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The genus *Parapedobacter* was established to describe a novel genus within the family *Sphingobacteriaceae* and derives its name from *Pedobacter*, with which it is shown to be evolutionarily related. Despite this, *Parapedobacter* and *Pedobacter* do not share very high 16S rRNA gene sequence similarities. Therefore, we hypothesized whether these substantial differences at the 16S rRNA gene level depict the true phylogeny or that these genomes have actually diverged. Thus, we performed genomic analysis of the four available genomes of *Parapedobacter* to better understand their phylogenomic position within family *Sphingobacteriaceae*. Our results demonstrated that *Parapedobacter* is more closely related to species of *Olivibacter*, as opposed to the genus *Pedobacter*. Further, we identified a significant class of enzymes called pectinases with potential industrial applications within the genomes of *Parapedobacter luteus* DSM 22899<sup>T</sup> and *Parapedobacter composti* DSM 22900<sup>T</sup>. These enzymes, specifically pectinesterases and pectate lyases, are presumed to have largely different catalytic activities based on very low sequence similarities to already known enzymes and thus may be exploited for industrial applications. We also determined the complete *Bacteroides aerotolerance* (Bat) operon (*batA*, *batB*, *batC*, *batD*, *batE*, hypothetical protein, *moxR*, and *pa3071*) within the genome of *Parapedobacter indicus* RK1<sup>T</sup>. This expands the definition of genus *Parapedobacter* to containing members that are able to tolerate oxygen stress using encoded oxidative stress responsive systems. By conducting a signal propagation network analysis, we determined that BatD, BatE, and hypothetical proteins are the major controlling hubs that drive the expression of Bat operon. As a key metabolic difference, we also annotated the complete *iol* operon within the *P. indicus* RK1<sup>T</sup> genome for utilization of all three stereoisomers of inositol, namely myo-inositol, scyllo-inositol, and 1D-chiro-inositol, which are abundant sources of organic phosphate found in soils. The results suggest that the genus *Parapedobacter* holds promising applications owing to its environmentally relevant genomic adaptations, which may be exploited in the future.

**Keywords:** *Parapedobacter*, Bat operon, pectinases, inositol, ortholog analysis