

## Habitat-Specific Divergences in the Gene Repertoire among the Reference Prevotella Genomes of the Human Microbiome

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**Abstract :** Background-The community composition of the human microbiome is known to vary at distinct anatomical niches. But little is known about the nature of variations if any, at the genome/sub-genome levels of a specific microbial community across different niches. The present report aims to explore, as a case study, the variations in gene repertoire of 28 *Prevotella* reference draft genomes derived from different body-sites of human, as reported earlier by the Human Microbiome Consortium. Results-The analysis reveals the exclusive presence of 11798, 3673, 3348 and 934 gene families and exclusive absence of 17, 221, 115 and 645 gene families in *Prevotella* genomes derived from the human oral cavity, gastro-intestinal tracts (GIT), urogenital tract (UGT) and skin, respectively. The pan-genome for *Prevotella* remains "open". Distribution of various functional COG categories differs appreciably among the habitat-specific genes, within *Prevotella* pan-genome and between the GIT-derived *Bacteroides* and *Prevotella*. The skin and GIT isolates of *Prevotella* are enriched in singletons involved in Signal transduction mechanisms, while the UGT and oral isolates show higher representation of the Defense mechanisms category. No niche-specific variations could be observed in the distribution of KEGG pathways. Conclusion-*Prevotella* may have developed distinct genetic strategies for adaptation to different anatomical habitats through selective, niche-specific acquisition and elimination of suitable gene-families. In addition, individual microorganisms tend to develop their own distinctive adaptive stratagems through large repertoires of singletons. Such in situ, habitat-driven refurbishment of the genetic makeup can impart substantial intra-lineage genome diversity within the microbes without perturbing their general taxonomic heritage.

**Keywords :** body niche adaptation, human microbiome, pangenome, *Prevotella*

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