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Genome sequencing and annotation of *Bradyrhizobium* sp. strain OHSU_III

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We recently studied previously cryopreserved blood cultures of 3 patients with poorly defined illnesses using fresh SP4 broth media with new supplements and High Throughput Sequencing (HTS). No microbes could be isolated from these blood cultures in former microbiology workups. A novel bacterium *Afipia septicemium* was isolated from the previously cryopreserved blood cultures from two of the patients after a prolonged course of incubation. Further characterization of *A. septicemium* genome revealed the presence of a gene transfer agent cluster that could potentially contribute to its marked genomic plasticity. Using the re-initiated a blood culture of the third patient, our study identified a new microbe *Bradyrhizobium* sp. strain OHSU_III that grew slowly and could not continue to proliferate to high cell density in SP4 broth or form colonies on agar plates. Here, we describe the non-contiguous draft genome of *Bradyrhizobium* sp. OHSU_III, which consists of a 7.9 Mb circular chromosome with no identifiable autonomous plasmids. The functional annotation of the genome was carried out using RAST (Rapid Annotation using Subsystem Technology). Comparative analysis showed that *Bradyrhizobium* sp. OHSU_III and also *B. enterica*, a new *Bradyrhizobium* species recently identified in biopsies of patients with the cord colitis syndrome using HTS; do not carry nitrogen fixation and nodulation genes commonly found in symbiotic *Bradyrhizobium* species of bacteria, such as *B. elkanii* or *B. japonicum*. Both *Bradyrhizobium* sp. OHSU_III and *B. enterica* apparently possess ~100 genes that are not present in the genomes of the symbiotic *Bradyrhizobium* species. It is unclear if these genes play any role in *Bradyrhizobium* sp. OHSU_III and *B. enterica*'s abilities to persist in the human hosts. The genome sequencing and annotation study should facilitate the development of molecular assay for detecting new *Bradyrhizobium* sp. bacteria and understanding the role, if any, they might play in various disease processes.

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Progression of 'OMICS' methodologies for understanding the pathogenicity of *Corynebacterium pseudotuberculosis*: The Brazilian experience

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Since the first successful attempt at sequencing the *Corynebacterium pseudotuberculosis* genome, large amounts of genomic, transcriptomic and proteomic data have been generated. *C. pseudotuberculosis* is an interesting bacterium due to its great zoonotic potential and because it causes considerable economic losses worldwide. Furthermore, different strains of *C. pseudotuberculosis* are capable of causing various diseases in different hosts. Currently, we seek information about the phylogenetic relationships between different strains of *C. pseudotuberculosis* isolates from different hosts across the world and to employ these data to develop tools to diagnose and eradicate the diseases these strains cause. In this review, we present the latest findings on *C. pseudotuberculosis* that have been obtained with the most advanced techniques for sequencing and genomic organization. We also discuss the development of *in silico* tools for processing these data to prompt a better understanding of this pathogen.

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