

# Genomic analysis of opportunistic bacteria from *Herbaspirillum* genus isolated from immunocompromised patients

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*Herbaspirillum* is a genus of the beta class of the Proteobacteria phylum. Some species of this genus are of biotechnological interest as growth promoters of crops like maize, rice and sugarcane. They are capable to establish endophytic association with these plants and to convert the atmospheric nitrogen (N<sub>2</sub>) in a form that could be used by the plants (NH<sub>4</sub>), besides to secrete phytohormones. However, strains of *Herbaspirillum* spp. have been isolated from immunocompromised patients, sometimes leading the patient to develop a bacteremia and death. To understand how environmental organisms evolve into a clinical variant and the molecular mechanisms involved in this process we sequenced, assembled and annotated the genome of two clinical strains of the *Herbaspirillum* genus: *Herbaspirillum frisingense* AU14559 and *Herbaspirillum* lineage 2 AU13964. Both strains were isolated from sputum of patients with cystic fibrosis and classified as *Herbaspirillum* based on the 16S rRNA gene sequence comparison. The *Herbaspirillum* lineage 2 was assembled in 10 contigs, with total size of 5.35 Mb, the largest contig has 1.87 Mb, GC % 63.21, N50 of 539.6 kb, L50 of 3 contigs, 3 rRNA operons, 4,880 annotated genes and 65 predicted tRNAs. The Average Nucleotide Identity (ANI) comparison of *Herbaspirillum* lineage 2 showed the higher level of identity to *Herbaspirillum seropedicae* SmR1 (97.59%), indicating that this strain can be included within the *Herbaspirillum seropedicae* species. The *H. frisingense* AU14559 was assembled in 15 contigs, with a total size of 5.44 Mb, the largest contig has 2.38 Mb, GC% 63.11, N50 557.3 kb, L50 of 2 contigs, 3 rRNAs operons, 5,213 predicted genes and 56 predicted tRNAs. The ANI comparison to the genome of the environmental strain, *Herbaspirillum frisingense* GSF30, was 97.39%. Searches made through the BLAST algorithm revealed the absence of the *nifHDK* genes that codes the structural proteins of the nitrogenase complex, indicating that these two organisms are incapable to fix nitrogen. Additional genome comparison studies will provide insights about the evolution of these strains from the environmental to clinical lifestyle.

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