The genus *Herbaspirillum* contains diazotrophic species capable to associate endophytically with plants and promote their growth. Currently, 13 species are included in the genus, which were isolated from diverse environments and distinct geographic locations. Isolates from patients with cystic fibrosis were also assigned to *Herbaspirillum*. To better understand the complexity of metabolic diversity, we sequenced the genome of 13 strains from different species and clinical isolates using the new generation sequencing platform SOLiD-ABI. *De novo* assembly allowed to obtain draft genome sequences which were annotated. Genes coding for isocitrate lyase, beta-lactamase, and ACC deaminase were found in all genomes. Also, all strains lack genes for phosphofructokinase-1 and the Entner-Doudoroff pathway for glucose oxidation is a marked characteristic. Only *H. seropedicae* and *H. rubrisubalbicans* have genes for nitrogen fixation. A clinical isolate identified as *H. seropedicae* does not have the nif gene cluster nor the type 3 secretion system (T3SS), which are important traits in the plant associative strains of *Herbaspirillum*. This result indicates that nitrogen fixation is not a main characteristic of the genus, as previously believed. Cellulose synthase, possibly associated to plant pathogenesis, was detected in *H. rubrisubalbicans* and *H. hutteniense* subspp. *putei* and genes for T3SS were found in *H. seropedicae*, *H. hiltneri*, and *H. rubrisubalbicans*; gene coding for RuBiSCO-like protein was found in *H. lusitanum* and *H. hiltneri*. The presence of pathways for IAA biosynthesis and phenolic compounds degradation are present in all strains. Using a set of housekeeping genes we reconstructed a more reliable phylogenetic tree revealing insights in the evolution of the genus.

**Word Keys:** *Herbaspirillum*, comparative genomics, Next-gen

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