

Genome Sequences of *Burkholderia* sp. Strains CCGE1002 and H160, Isolated from Legume Nodules in Mexico and Brazil

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The genome sequences of *Burkholderia* sp. strains CCGE1002 from Mexico and H160 from Brazil, isolated from legume nodules, are reported. Their gene contents in relation to plant-microbe interactions and xenobiotic degradation are discussed.

Members of the *Burkholderia* genus fulfill important ecological roles, with potential biotechnological applications including symbiotic nitrogen fixation, plant-growth promotion, and degradation of xenobiotics (6). Reported herein are the genome sequences of two *Burkholderia* sp. strains belonging to the phylogenetic clade of *Burkholderia tuberum*. Strain CCGE1002 was isolated from a *Mimosa occidentalis* nodule collected in Tepic, Nayarit, Mexico. Strain H160, isolated from a bean (*Phaseolus vulgaris*) nodule, is indigenous to the Brazilian Cerrado, from an area of Planaltina, Distrito Federal, Brazil.

Genome sequencing, gene prediction, and annotation were performed at the Joint Genome Institute. The RAST Server (2) was also used for functional analyses. The 7,884,858 bp (63.3% GC) genome sequence of CCGE1002 is composed of three chromosomes (3.52, 2.59, and 1.28 Mbp) and one plasmid (489 kbp). The draft genome sequence of H160 was distributed in 310 contigs ($N_{50} = 45$ kb) with a total size of 7,893,354 bp (62.9% GC). Chromosome 1 and a high proportion of chromosome 2 of CCGE1002 were well conserved in H160 but not the remaining replicons. An average nucleotide identity (ANI) of 91.2% evidenced the close relatedness between the two strains but indicated that they belong to different species (5). About 80% of the 7,354 and 7,513 coding sequences (CDS) predicted for CCGE1002 and H160, respectively, could be assigned to Clusters of Orthologous Groups (COG) functional categories. Both strains had similar numbers of CDS in each category, except in the lipid transport and metabolism class, where H160 surpassed CCGE1002.

Many burkholderias are known for their capacity to degrade xenobiotics (6). CCGE1002 and H160 share about 190 CDS related to aromatic compound metabolism but lack genes for *p*-cymene and biphenyl degradation. Only CCGE1002 possessed CDS of the toluene-4-monooxygenase pathway. Additionally, they shared about 150 CDS for resistance to antibiotics and toxic compounds.

Known traits related to plant colonization, such as type IV pilus, widespread colonization island, and type VI secretion systems, were found in both strains. Only H160 possessed genes for sigma-fimbriae, a flavohemoglobin for nitric oxide resistance, and capsular polysaccharide biosynthesis. Genes for utilization of a wide array of plant-exuded compounds were identified in both genomes. H160 harbored genes for opine utilization, which may confer on it a competitive advantage (4).

The symbiotic plasmid (pSym) of CCGE1002 carried a 62-kbp cassette containing *nodDBC1JHASUQ*, *nifAENX-fixB-nifX-fdxB-nifQ*, *fixXCBA-nifWVB-fdxN-nifZ*, and *nifHDK* gene clusters, similar to the cassette reported in the *Cupriavidus taiwanensis*

LMG19424 pSym (1), although the maximum gene sequence identity between the cassettes was 76.7%. There was no conservation between the remaining genes of both pSyms. Nodulation and nitrogen fixation genes were not detected in H160. Although this strain is able to nodulate and fixes nitrogen with beans, its pSym is unstable, being easily lost, as has been reported for another *Burkholderia* strain (3). It is conceivable that some burkholderias acquire the pSym as a strategy to survive under poor nitrogen conditions, like those of the Cerrado's soils, but lose these plasmids when grown in enriched synthetic media.

Nucleotide sequence accession numbers. Genome sequences are available under GenBank accession numbers CP002013, CP002014, CP002015, and CP002016 for CCGE1002 and ABYL0000000 for H160.

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