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

Ernesto Ormeño-Orrillo, Marco A. Rogel, Ligia Maria Oliveira Chueire, James M. Tiedje, Esperanza Martínez-Romero and Mariangela Hungria


Updated information and services can be found at: http://jb.asm.org/content/194/24/6927

**REFERENCES**

This article cites 6 articles, 2 of which can be accessed free at: http://jb.asm.org/content/194/24/6927#ref-list-1

**CONTENT ALERTS**

Receive: RSS Feeds, eTOCs, free email alerts (when new articles cite this article), more»
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 kbp) 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-monoxygenase pathway. Additionally, they shared about 150 CDS for resistance to antibiotics and toxic compounds.

Known traits related to plant colonization, such as type IV pili, 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 \((p\)Sym\) of CCGE1002 carried a 62-kbp cassette containing nodDBCJHASUQ, nifAENX-fxbB-nifX-fdxB-nifQ, fxxCXA-njWVB-fdxN-nifZ, and \(n\)ijHDK gene clusters, similar to the cassette reported in the *Cupriavidus taiwanensis* LMG19424 \((p\)Sym\) (1), although the maximum gene sequence identity between the cassettes was 76.7%. There was no conservation between the remaining genes of both \((p\)Sym\)s. Nodulation and nitrogen fixation genes were not detected in H160. Although this strain is able to nodulate and fix nitrogen with beans, its \((p\)Sym\) is unstable, being easily lost, as has been reported for another *Burkholderia* strain (3). It is conceivable that some burkholderias acquire the \((p\)Sym\) 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 ABYLO00000000 for H160.

**ACKNOWLEDGMENTS**

This work was supported by the U.S. Department of Energy Joint Genome Institute sequencing program and the Mexico-Brazil bilateral collaboration project 490048/2009-9 from the Consejo Nacional de Ciencia y Tecnología-National Council for Scientific and Technological Development (CONACYT-CNPa).

Strain H160 was isolated in an EC-INCO project, and we thank the project leader, M. Megías (Universidad de Sevilla), for preparing and sending the DNA to the Joint Genome Institute.

**REFERENCES**