Sequencing, Assembly and Annotation of the Genome of *Herbaspirillum lusitanum* P6-12, an Endophyte Isolated from *Phaseolus vulgaris* Root Nodules


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Several species of *Herbaspirillum* such as *H. seropedicae* and *H. rubrisubalbicans* are capable of fixing nitrogen and endophytic colonization of cereals of economical relevance. *Herbaspirillum lusitanum* P6-12 was isolated from root nodules of *Phaseolus vulgaris* showing that *Herbaspirillum* species can also associate with leguminous plant. To better understand the lifestyle of *H. lusitanum* and its potential use in Agriculture, its genome was sequenced on ABI-SOLiD4 sequencer. The draft genome was assembled from over 60 millions mate-paired reads producing 37 scaffolds. The chromosome was estimated to contain 4.8 Mb with a G+C content of ~60%. Annotation using RAST (rast.nmpdr.org) revealed 5,240 ORFs. The GAAT platform (www.genopar.org) was used for manual curation. Overall, a high level of synteny was observed between the *H. lusitanum* genome and that of *H. seropedicae* SmR1. However, structural and metabolic differences were observed, such as the lack of the *nif* gene cluster, indicating that *H. lusitanum* P6-12 is unable to fix nitrogen. On the other hand, the presence of ACC deaminase gene suggests that this bacteria can act as plant growth promoter. The genome sequence also showed a large number of ABC-type transporter genes and the presence of the Type I and Type II Secretion System. Another interesting finding was the presence of a RuBisCO-like protein involved in carbon fixation.

Keywords: genome, *Herbaspirillum lusitanum*, SOLiD, nitrogen fixation.

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