

S07-A Genomic characteristics and comparative genomics analyses of non-rhizobial endophytic bacteria isolated from legumes

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In addition to typical nitrogen-fixing endosymbionts, legumes harbour other endophytic bacteria within their tissues that may also contribute to plant growth and health (Hardoim *et al.* 2015). Our previous works revealed that endophytic bacteria isolated from legumes not only have plant growth-promoting traits but are also well adapted to common constraints present in soils of the Mediterranean region (Brígido *et al.* 2019ab). In this work, we intend to further characterize these endophytic bacteria through genomic and comparative genomic analyses to potentiate their applications in agriculture, providing opportunities for sustainable plant health and food security. Twelve endophytic bacterial isolates were selected based on their potential for plant growth promotion and/or biocontrol of phytopathogens. Based on the 16S rRNA gene sequence analysis, the isolates were assigned to the genera *Pseudomonas*, *Kosakonia*, *Stenotrophomonas*, *Serratia*, *Bacillus* and *Agrobacterium*. Nevertheless, *in silico* DNA-DNA hybridization analyses revealed that 3 strains represent novel species distinct from their closest relatives. Their genome sizes ranged from 4.4 M to 7.1 M with a GC content varying from 35.41 to 66.4%. Orthologous gene clusters analysis revealed 9346 clusters and 345 single-copy gene clusters, albeit only 499 gene clusters (comprising 6110 proteins) were shared among all strains. Whole genome sequence analysis revealed genes potentially associated with attachment and plant colonization, growth promotion and stress protection as well as antifungal activity. In detail, sets of genes for twitching motility, chemotaxis, flagella biosynthesis, and ability to form biofilms (which are related with host plant colonization) were found in their genomes. Presence of genes associated to nitrogen fixation, auxin biosynthesis, siderophore production or phosphorous assimilation reveals their potential as plant growth promoters. Furthermore, genes required for biosynthesis of pyoluteorin, 2,4-diacetylphloroglucinol and pyrrolnitrin underline bacterial biocontrol potential against phytopathogens. Genes related to the production of different molecules and enzymes mediating stress tolerance suggest their ability to rapidly adapt to stressful conditions. Overall, our data provide a better understanding of these endophytic bacteria abilities and further comparative genomic analysis provided insight into the genomic basis of their endophytic lifestyle, plant growth promotion and antifungal activity.

References

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Funding

This work is funded by National Funds through FCT - Foundation for Science and Technology under the Project UIDB/05183/2020.

Acknowledgements

CB acknowledges a CEECIND2018 contract (CEECIND/00093/2018). EM acknowledges a CEECIND2017 contract (CEECIND/00270/2017)