Current Research in Microbial Sciences 2 (2021) 100055

Contents lists available at ScienceDirect

Current Research in Microbial Sciences

journal homepage: www.sciencedirect.com/journal/current-research-in-microbial-sciences

Draft genome sequence of *Paraburkholderia* sp. strain XV isolated from the rhizosphere of mango (*Mangifera indica L.*)

de los Santos-Villalobos Sergio [a,#,*], Kremer James Michael [b,d,#], Parra-Cota Fannie Isela [c], Valenzuela-Ruiz Valeria [a], Hayano-Kanashiro Corina [e], García-Ortega Luis Fernando [f], Tiedje James Michael [b,d], He Sheng Yang [b,g], Peña-Cabriales Juan Jose [h]

[a] *Instituto Tecnológico de Sonora, Cd. Obregon, Sonora, Mexico*
[b] *Department of Microbiology and Molecular Genetics, Michigan State University, East Lansing, MI 48824, USA*
[c] *Campo Experimental Norman E. Borlaug, Cd. Obregón, Sonora, México*
[d] *Center for Microbial Ecology, Michigan State University, East Lansing, MI 48824, USA*
[e] *Departamento de Investigaciones Científicas y Tecnológicas. Universidad de Sonora. Hermosillo, Sonora, México*
[f] *Departamento de Ingeniería Genética, Centro de Investigación de Estudios Avanzados del IPN (CINVESTAV), Irapuato, Guanajuato, México*
[g] *Howard Hughes Medical Institute-Gordon and Betty Moore Foundation, Michigan State University, East Lansing, MI 48824, USA.*
[h] *Centro de Investigación y de Estudios Avanzados-IPN, Irapuato, Guanajuato, México.*

ARTICLE INFO

Keywords:
Whole-genome sequencing
Paraburkholderia
plant growth promotion

ABSTRACT

Here, we report the draft genome of *Paraburkholderia* sp. XV. This strain was isolated from the rhizosphere of mango (*Mangifera indica* L.). Its genome consists of 9,189 coding DNA sequences, 60 tRNAs, a single copy of the 16S rRNA, 5S rRNA, and 23S rRNA gene, and 1 tmRNA. The GC content is 62.6%.

Mango (*Mangifera indica* L.), native to South and Southeast Asia, has been described as one of the most economically important tropical fruits globally. Its annual production is approximately 42 million tons, making it the second most cultivated fruit. The largest mango-producing countries are India, China, Thailand, Indonesia, Pakistan, and Mexico (Kumar et al., 2021; Mirza et al., 2020). Sustainable agricultural practices to maintain or increase mango productivity, such as the use of plant growth-promoting microorganisms, are determinants for its global competitiveness (de los Santos Villalobos et al., 2015; Kuo et al., 2001).

The genus *Paraburkholderia* was recently recognized as a distinct taxon in the broader *Burkholderia* sensu lato group and contains a range of diverse species. The majority of *Paraburkholderia* is composed of plant beneficial species with modes of action that include: antibiotic production, biological nitrogen fixation, siderophore secretion, phytohormone biosynthesis, ACC deaminase activity, and phosphorus solubilization, among others (Mavima et al., 2020).

Strain XV was isolated from the rhizosphere of mango (*Mangifera indica* L.) variety Ataulfo in a commercial field located in Chahuites, Oaxaca, México (de los Santos Villalobos et al., 2013). Baz agar medium was used, with the following composition (g L^{-1}): solution 1 (0.4 K_2HPO_4, 0.4 KH_2PO_4, 0.2 $MgSO_4$, 0.02 $CaCl_2$, 0.01 $FeCl_3$, 0.002 Na_2MoO_4, 0.075 bromothymol blue, and 15 agar) and solution 2 (5.0 arabinose, succinate, or sucrose). Both solutions were adjusted to pH 5.7 and autoclaved separately at 121 °C and 1 atm for 15 min, and then the two solutions were combined. A 10 g root sample was agitated for 1 h at 100 rpm (using a rotary shaker) in 90 ml of sterile 10 mM $MgSO_47H_2O$. The material liberated from the root surface was diluted in series, spread onto the surface of Petri dishes containing Baz agar medium, and incubated at 28 °C for 7 days (de los Santos Villalobos et al., 2012). Bacterial colonies were purified by sequential streaking on Petri dishes containing Baz agar medium, and a macroscopic and microscopic examination was carried out, in triplicate, to ensure axenicity. All obtained isolates were cryopreserved at -80 °C using Baz broth medium and 30% glycerol.

Strain XV was previously reported by Parra-Cota et al., (2014) to promote *Amaranthus cruentus* growth, where an increased grain yield and harvest index occurred when used in combination with chemical fertilization. Also, *A. cruentus* plants inoculated with strain XV showed a tissue-specific induction of several genes involved in photosynthesis, sugar- and N- metabolism, and transport. Additionally, de los Santos

* Corresponding author.
E-mail address: sergio.delossantos@itson.edu.mx (S.-V. Sergio).
# Authors contributed equally to the research James Michael Kremer, current address: Joyn Bio, Boston, MA 02210, USA

https://doi.org/10.1016/j.crmicr.2021.100055
Received 9 June 2021; Received in revised form 27 July 2021; Accepted 31 July 2021
Available online 3 August 2021

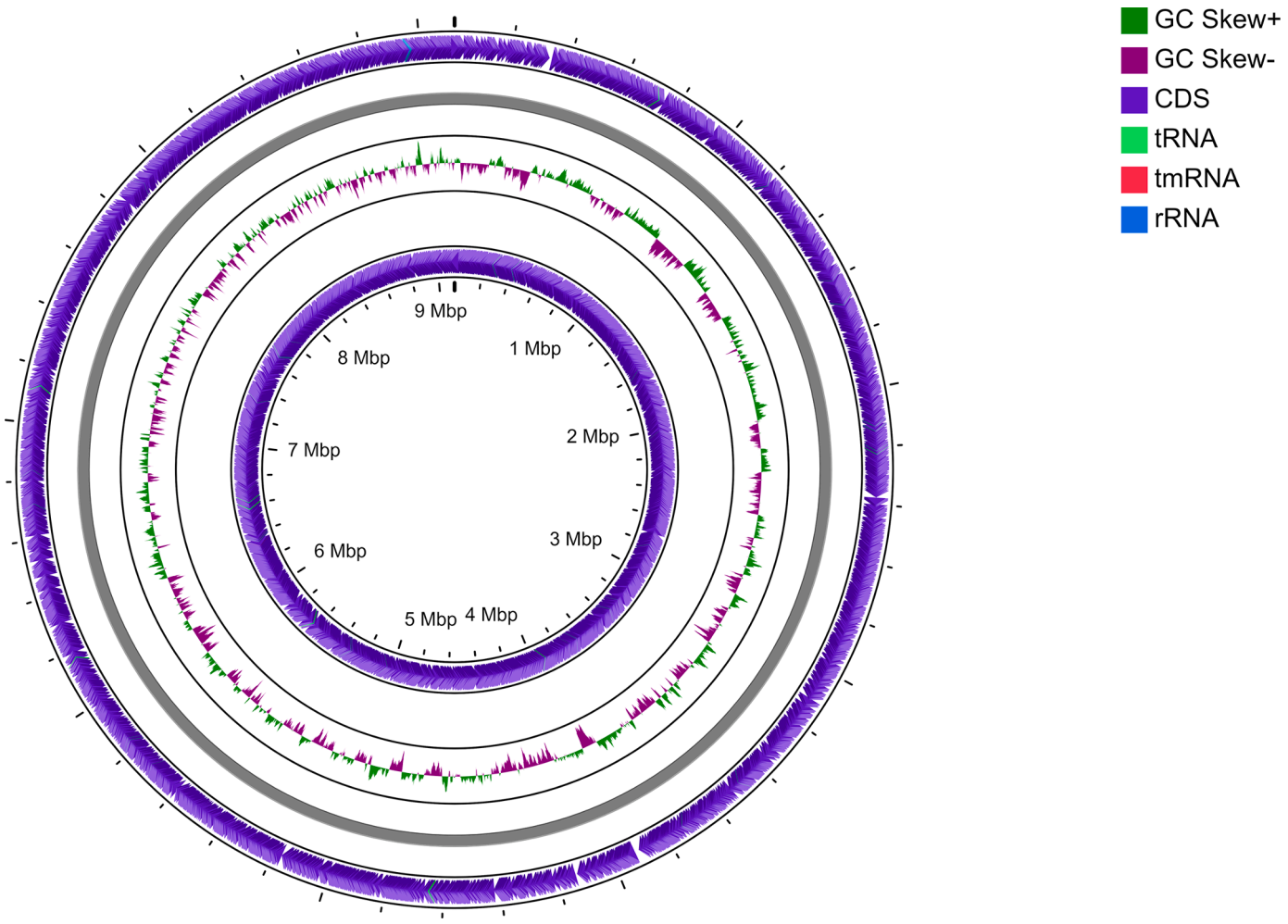

Fig. 1. Circular chromosome map of *Paraburkholderia* sp. strain XV showing the distribution of coding sequences (CDS), tRNAs, rRNAs, and GC content skew (50% of the total base-pair window). The map was generated using the CGView Server beta online tool.

Villalobos et al., (2013) reported a mango growth-promoting effect by co-inoculation of strain XV and *Rhizobium* sp. strain XXV in mango, resulting in increased dry biomass, increased root, stem, and foliar areas, and an increased number of flowers.

Thus, high-quality genomic DNA was extracted from a fresh culture strain of XV grown in Baz Broth medium [24 h at 32 °C, using an orbital shaker at 121 rpm, obtaining 1×10^6 Colony Forming Units (CFU)/mL], following the protocol described by Valenzuela-Aragon et al., (2018). Bacterial DNA ($OD_{260/280}$ = 1.8–2.0, total amount of DNA ≥ 1 μg, concentration ≥ 25 ng/μL) was sequenced on an Illumina MiSeq platform, yielding a total of 1,801,920 reads [2 × 300 base pairs (bp)]. The quality of the obtained raw reads was analyzed by FastQC version 0.11.5 Andrews (2010). Trimmomatic version 0.32 (Bolger et al., 2014) was used to remove adapter sequences and low-quality bases, which represents only 1.89% of the total reads. Subsequently, a *de novo* assembly was generated by SPAdes version 3.10.1 (Bankevich et al., 2012), using the parameter –careful for error correction in reads and -cov-cutoff auto (in which SPAdes automatically computes the coverage threshold using a conservative strategy). The draft genome of strain XV contained 9,120,057 bp and an average GC content of 62.6%, N50: 60,799 bp, and L50: 44. The assembled contigs were ordered by Mauve Contig Mover version 2.4.0 (Rissman et al., 2009), using the reference genome *Paraburkholderia caribensis* MWAP64T (GenBank accession no. CP013102), due to the greatest 16S rRNA gene homology (99.93%). A circular chromosome map was generated using the CGView Server (Fig. 1) (Grant and Stothard, 2008).

Genome annotation was performed by Prokka v 1.11.0 Seeman (2014). The GC content of the genome was calculated as 62.6% (Fig. 1). Plasmid detection was carried out by PlasmidFinder 2.0 (Carattoli et al., 2014), and no plasmids were detected. Subsequently, genome annotation was also carried out through Rapid Annotation Using Subsystem Technology (RAST) server version 2.0 (http://rast.nmpdr.org) (Overbeek et al., 2013), by the default RASTtk pipeline (Fig. 2). Default parameters were used for all software unless otherwise noted.

The genome is predicted to contain 60 tRNAs, a single copy of the 16S rRNA, 5S rRNA, and 23S rRNA genes, 1 tmRNA, and 9,189 coding DNA sequences (CDS). The most abundant subsystem was Carbohydrates (499 CDS); followed by Amino acids and derivatives (490 CDS); Cofactors, Vitamins, Prosthetic Groups, Pigments (222 CDS); protein metabolism (219 CDS); and Respiration (202 genes). Besides, genes of agricultural importance include 43 CDS related to the resistance to antibiotics and toxic compounds and the tolerance to colicin E2, and 5 CDS related to secondary metabolism such as plant hormones (auxin biosynthesis), and plant alkaloid segregation (alkaloid biosynthesis from L-lysine). In addition, strain XV presented 140 CDS associated with stress response, including osmotic stress (16 CDS) and oxidative stress (86 CDS). Finally, the genome of this strain contains CDS involved in iron (8), potassium (14), nitrogen (20), sulfur (43), and phosphorus (35) acquisition and metabolism (Fig 2, and Table S1).

In this manner, the genome of *Paraburkholderia* sp. strain XV includes genes associated with plant growth promotion. Currently, scientific evidence has shown this effect in mango and amaranth crops (de los

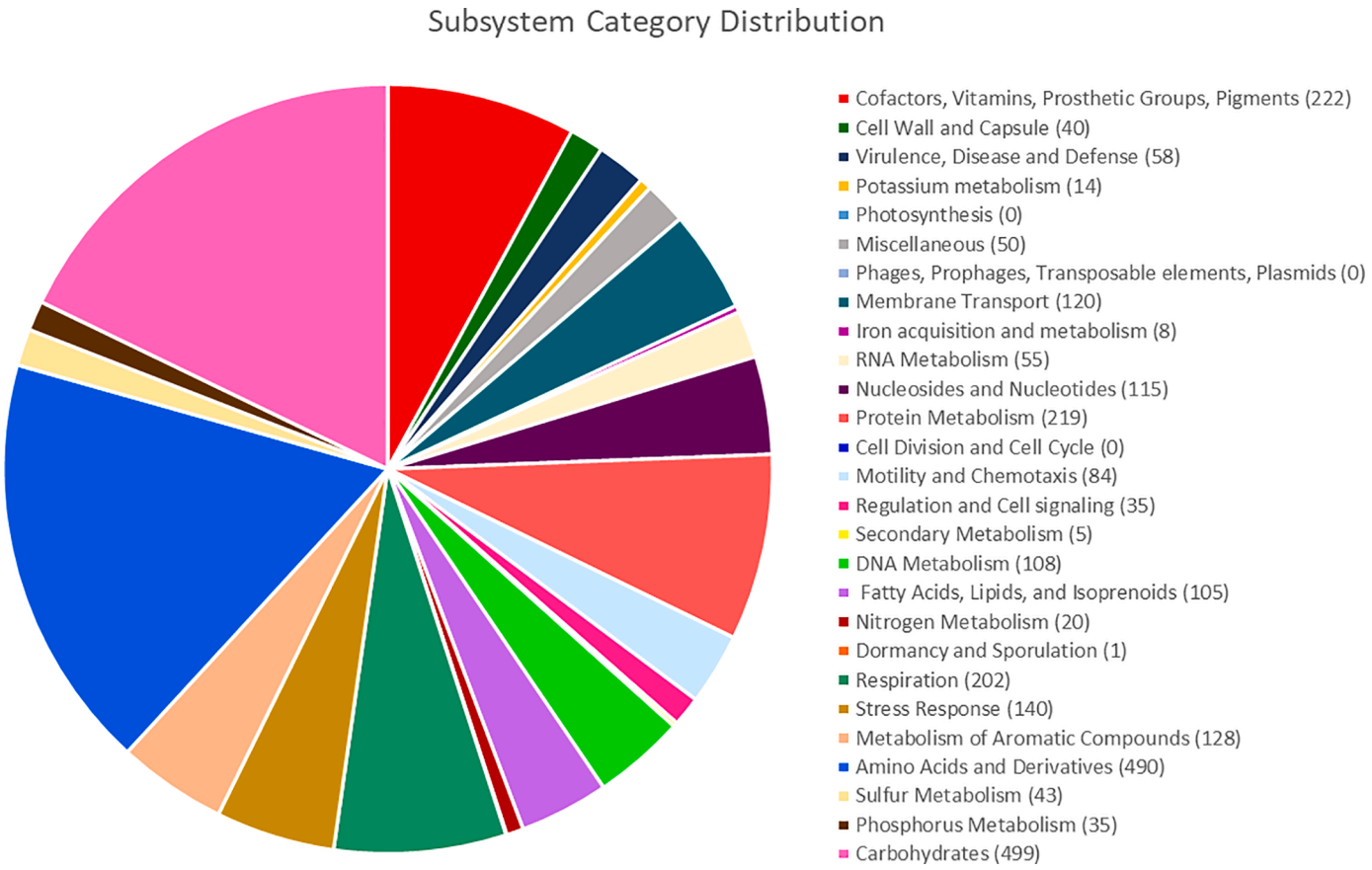

Fig. 2. Subsystem category distribution of coding DNA sequences (CDS) from strain XV, generated through RASTtk pipeline. CDS: 9,189; CDS in subsystems: 1,975; and subsystems: 373.

Santos Villalobos et al., 2013; Parra-Cota *et al.*, 2014). Therefore, due to the genomic and functional features, this strain is a promising active ingredient for biofertilizers formulations for contributing to food security.

Data availability

This draft genome sequence has been deposited in DDBJ/ENA/GenBank under accession number JAGUUD000000000. The version described in this paper is the first version, JAGUUD010000000, under BioProject number PRJNA725878 and BioSample number SAMN18912763. Raw data have been deposited in the NCBI SRA under accession number SRR14372668.

Author contributions

Conceptualization, S.d.l.S.-V., and J.M.K.; writing—original draft preparation and visualization, all authors; writing—review and editing were developed by all authors; supervision, project administration, funding acquisition, S.d.l.S.-V., J.M.T., S.Y.H., and J.J.P.C. All authors have read and agreed to the published version of the manuscript.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Given their role as Guest Editors, Sergio de los Santos-Villalobos and Fannie Isela Parra Cota had no involvement in the peer-review of this article and has no access to information regarding its peer-review. Full responsibility for the editorial process for this article was delegated to Editor-in-Chief David Ojcius.

Acknowledgments

Illumina sequencing was performed at the Research Technology Support Facility at Michigan State University, East Lansing, Michigan. We acknowledge funding from the DOE Great Lakes Bioenergy Research Center (DOE Office of Science BER DE-FC02-07ER64494) to James Tiedje; the Gordon and Betty Moore Foundation (GBMF3037) to Sheng-Yang He; the Instituto Tecnológico de Sonora (PROFAPI_2021_0006) and PRODEP (NPTC 511-6/2020-8594) to Sergio de los Santos Villalobos, and the computing time granted by the IPICYT Supercomputing National Center for Education & Research (CNS-IPICYT), grant TKII-R2020-LFGO.

Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.crmicr.2021.100055.

References

Andrews, S. 2010. FastQC: a quality control tool for high throughput sequence data. https://www.bioinformatics.babraham.ac.uk/projects/fastqc.

Bankevich, A., Nurk, S., Antipov, D., Gurevich, A.A., Dvorkin, M., Kulikov, A.S., Lesin, V. M., Nikolenko, S.I., Pham, S., Prjibelski, A.D., Pyshkin, A.V., Sirotkin, A.V., Vyahhi, N., Tesler, G., Alekseyev, M.A., Pevzner, P.A., 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J. Comput. Biol. 19, 455–477. https://doi.org/10.1089/cmb.2012.0021.

Bolger, A.M., Lohse, M., Usadel, B., 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. J. Bioinform. 30, 2114–2120. https://doi.org/10.1093/bioinformatics/btu170.

Carattoli, A., Zankari, E., Garcia-Fernandez, A., Voldby Larsen, M., Lund, O., Villa, L., Aarestrup, F.M., Hasman, H., 2014. PlasmidFinder and pMLST: in silico detection and typing of plasmids. Antimicrob. Agents Chemother 58 (7), 3895–3903. https://doi.org/10.1128/AAC.02412-14.

de Los Santos Villalobos, S., Barrera Galicia, C., Hernández Rodríguez, L.E., Peña Carbiales, J.J., 2015. Potencial uso agro-biotecnológico de cepas del género *Burkholderia* aisladas de huertas de mango (*Mangifera indica* L.) v. Ataulfo en México. Revista Latinoamericana de Recursos Naturales 11 (2), 78–86.

de los Santos-Villalobos, S., Barrera-Galicia, G.C., Miranda-Salcedo, M.A., Peña-Cabriales, J.J., 2012. *Burkholderia cepacia* XXVI siderophore with biocontrol capacity against Colletotrichum gloeosporioides. World J. Microbiol. Biotechnol. 28, 2615–2623. https://doi.org/10.1007/s11274-012-1071-9.

de los Santos-Villalobos, S., de Folter, S., Délano-Frier, J.P., Gómez-Lim, M.A., Guzmán-Ortiz, D.A., Peña-Cabriales, J.J., 2013. *Growth* promotion and flowering induction in Mango (*Mangifera indica* L. cv "Ataulfo") trees by *burkholderia* and *rhizobium* inoculation: morphometric, biochemical, and molecular events. J. Plant Growth Regul. 32 (3), 615–627. https://doi.org/10.1007/s00344-013-9329-5.

Grant, J.R., Stothard, P., 2008. The CGView server: a comparative genomics tool for circular genomes. Nucleic Acids Res 36, W181–W184. https://doi.org/10.1093/nar/gkn179.

Kumar, M., Saurabh, V., Tomar, M., Hasan, M., Changan, S., Sasi, M., Maheshwari, C., Prajapati, U., Singh, S., Prajapat, R.K., et al., 2021. Mango (*Mangifera indica* L.) leaves: nutritional composition, phytochemical profile, and health-promoting bioactivities. Antioxidants 10, 299. https://doi.org/10.3390/antiox10020299.

Kuo, K.C., 2001. Sensitivity of mango anthracnose pathogen, *Colletotrichum gloeosporioides*, to the fungicide prochloraz in Taiwan. Proc. Natl. Sci. Council, Republic of China. Part B 25, 174–179.

Mavima, L., Beukes, C.W., Palmer, M., De Meyer, S.E., James, E.K., Maluk, M., Gross, E., Junior, F.B.dR., Avontuur, J.R., Chan, W.Y., Venter, S.N., Steenkamp, E.T., 2020. *Paraburkholderia youngii sp. nov*. and '*Paraburkholderia atlantica*' – Brazilian and Mexican Mimosa-associated rhizobia that were previously known as *Paraburkholderia tuberum* sv. *Mimosa*. Syst. Appl. Microbiol. 44 (1) https://doi.org/10.1016/j.syapm.2020.126152.

Mirza, B., Croley, C.R., Ahmad, M., Pumarol, J., Das, N., Sethi, G., Bishayee, A., 2020. Mango (*Mangifera indica* L.): a magnificent plant with cancer preventive and anticancer therapeutic potential. Crit. Rev. Food Sci. Nutr. 1–27. https://doi.org/10.1080/10408398.2020.1771678.

Overbeek, R., Olson, R., Pusch, G.D., Olsen, G.J., Davis, J.J., Disz, T., et al., 2013. The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). Nucleic. Acids. Res. 42, D206–D214. https://doi.org/10.1093/nar/gkt1226.

Parra-Cota, F.I., Peña-Cabriales, J.J., de los Santos-Villalobos, S., Martínez-Gallardo, N. A., Délano-Frier, J.P., 2014. *Burkholderia ambifaria* and *B. caribensis* Promote Growth and Increase Yield in Grain Amaranth (*Amaranthus cruentus* and *A. hypochondriacus*) by Improving Plant Nitrogen Uptake. PLoS ONE 9 (2), e88094. https://doi.org/10.1371/journal.pone.0088094.

Rissman, A.I., Mau, B., Biehl, B.S., Darling, A.E., Glasner, J.D., Perna, N.T., 2009. Reordering contigs of draft genomes using the Mauve aligner. J. Bioinform. 25, 2071–2073. https://doi.org/10.1093/bioinformatics/btp356.

Seemann, T., 2014. Prokka: rapid prokaryotic genome annotation. J. Bioinform. 30, 2068–2069. https://doi.org/10.1093/bioinformatics/btu153.

Valenzuela-Aragon, B., Parra-Cota, F., Santoyo, G., Arellano, G., de los Santos-Villalobos, S., 2018. Plant-assisted selection: a promising alternative for *in vivo* identification of wheat (*Triticum turgidum L. subsp. Durum*) growth promoting bacteria. Plant Soil 435, 367–384. https://doi.org/10.1007/s11104-018-03901-1.