

Analysis of the core microbiome of blueberry and blackberry plants as a first step in the design of efficient bacterial biofertilizers[†]

Zaki Saati-Santamaría ^{*}, Rocío Vicentefranqueira, Raúl Rivas, Paula García-Fraile

¹ Microbiology and Genetics Department. University of Salamanca. Doctores de la Reina SN, 37007 Salamanca, Spain

² Spanish-Portuguese Institute for Agricultural Research (CIALE), Salamanca, Spain

³ Associated R&D Unit, USAL-CSIC (IRNASA), 37008 Salamanca, Spain

[†] Presented at the 1st International Electronic Conference on Agronomy, 3–17 May 2021. Available online: <https://iecag2021.sciforum.net/>

Abstract: As humans, plants harbour a microbiome, and as human microbiome, plants microbiome is essential for their health and fitness. Several components of this microbiome are able to increase crop's yields and quality because of their ability to supply nutrients, phytohormones and protect them from pathogens. On the other hand, traditional farming usually uses chemicals to promote plant yields that are related to many negative effects to the environment and human's health. As an alternative to agrochemicals, we can select beneficial members of the plants' microbiome as plant probiotics, which can be applied in fields. Blueberries and blackberries are forest fruits broadly consumed with high antioxidants content. Their production is increasing and the development of microbial probiotics for these crops is desirable. As a first step to select microbial probiotics for blueberry and blackberry plants, we analysed their microbiome using massive parallel sequencing. We collected DNA from the rhizosphere, roots and leaves of different plant samples from four different locations. Then, we analysed bacterial and fungal diversity through amplicon-based metagenomics. While fungal communities are very diverse, we found that blueberries and blackberries share a common bacteriome with some core taxa, such as *Ellin329*, *Chitinophagaceae*, *Bradyrhizobiaceae*, *Sinobacteraceae* and *Rhodoplanes*. Based on this, we are attempting to isolate core members of this microbiome to study their ecological roles in the plants and will be tested in future works for their ability to enhance yields and quality of these crops. Funding: This work was funded from the MINECO, under grant agreement PID2019-109960RB-100 and by by Junta de Castilla y León (Escalera de Excelencia CLU-2018-04) co-funded by the P.O. FEDER of Castilla y León 2014–2020.

Citation: Lastname, F.; Lastname, F.; Lastname, F. Title. *Proceedings* **2021**, *68*, x. <https://doi.org/10.3390/xxxxx>

Published: date

Publisher's Note: MDPI stays neutral with regard to jurisdictional claims in published maps and institutional affiliations.



Copyright: © 2021 by the authors. Submitted for possible open access publication under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

Keywords: Microbial communities; Metagenomics; Plant microbiome; Core microbiome; PGP bacteria