Metagenomic survey of the bacterial communities in the rhizosphere of three Andean tuber crops



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Abstract

Microbes colonizing the rhizosphere are important drivers of plant health, supplying nutrients and antagonizing pathogens, among other beneficial activities. Tubers are important staple crops in the Andean highlands, produced by thousands of small-farmers and consumed by millions. Here we report the composition of the bacterial communities colonizing the rhizospheres of three Andean tuber crops (ATCs), namely oca (*Oxalis tuberosa*), ullucu (*Ullucus tuberosus*) and mashua (*Tropaeolum tuberosum*). We used high throughput sequence analysis of 16S rRNA genes to describe the bacterial diversity of rhizospheric soils associated to thee crops. Between 4862 and 5080 OTUs were exclusively detected in each one of the ATCs' rhizospheres; the majority of the 100 most abundant OTUs belonged to the Bacteroidetes and Proteobacteria phyla. Beta diversity indices revealed a low similarity between the three communities, suggesting differences in their specific composition. Only 566 bacterial OTUs were shared by all three tuber's rhizospheres and absent from the surrounding bulk soil. Apart from studies in potato, this is the first report concerning the diversity and abundance of bacterial taxa associated with the rhizosphere of other important and traditional ATCs.

Keywords Andean tuber crops · Rhizobacteria · 16S rDNA · Rhizosphere microbiome · Taxonomic survey

1 Introduction

According to the Food and Agriculture Organization of the United Nations (FAO), agricultural production must have to be increased by at least 60% (relative to 2005–2007 levels) in 2050 in order to sustain the needs of the world human population (Alexandratos and Bruinsma 2012). Reaching this goal will demand a greater intensification of current agriculture within the constraint of being unable to expand the

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agricultural frontier while also reducing and mitigating past impacts of agriculture on the environment (Doran and Zeiss 2000). Unfortunately, in many densely populated mountainous regions of the world —such as the Himalayas or the Andes Mountains—, agriculture intensification is subject to even more challenges, due to the competing uses of agricultural land, growth-limiting constant low temperatures, unpredictable changes in weather, severe erosion of soils, low nutrient availability, low organic matter content, and lack of irrigation among others (Poulenard and Podwojewski 2006; FAO 2015). All this is further complexed by the greatly fragmented organization of farmers, mostly small family farmers, often impoverished, but who are still key contributors to the food security of their countries.

In the past, advances in agricultural intensification relied on the development of improved plant varieties, and the use of synthetic pesticides and chemical fertilizers, giving rise to the so-called Green Revolution (Pingali 2012). Among the current paradigms, intensification of agriculture can be achieved in a sustainable way by making rational use of an often-neglected resource: the microbes that naturally colonize the rhizosphere of crop plants. Many of these microbes exhibit plant-growth promoting traits and are called thus Plant Growth Promoting Microorganisms or PGPM (Fuentes-Ramirez and Caballero-Mellado 2005;

