MicroLife: from prediction to function

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Bacteria have a wide variety of lifestyles ranging from pathogenic, causing diseases in animals, plants or humans, to beneficial. Some of these beneficial bacteria have evolved together with plants and provide specific traits such as plant growth promotion or help to tolerate (a)biotic stresses. *Burkholderia* spp. and *Pseudomonas* spp. are among the most ubiquitous bacterial genera whose species, 60 and 220 respectively, have been isolated worldwide in all kinds of environments. For example, species belonging to *B. cepacia* and *B. pseudomallei* complexes, and *P. aeruginosa* are often human pathogens, while *B. plantarii*, *B. glumae* and *B. gladioli*, and *P. syringae* strains are strictly plant pathogens. On the other hand, *Paraburkholderia* and *P. fluorescens* strains are mainly found in soil and/or in beneficial associations with plants. In this study, we have used MicroLife, a high-throughput computational workflow to explore large-scale genomic datasets and perform a deep comparative genomic analysis between all the *Burkholderia* and *Pseudomonas* genomes publicly available. The comparative genomic analysis has identified more than 709 and 385 genes that were associated with plant pathogenic lifestyle in *Burkholderia* and *Pseudomonas*, respectively. We observed a larger set of genes that are well-known for their roles in the virulence of these bacteria. However, many of the identified genes were of unknown function or unrelated to known virulence processes. Here, we are using targeted mutagenesis to validate the unknown genes predicted by MicroLife. Currently, we are testing the phenotype in plants of 34 independent mutants. In addition, heterologous expression and biochemical analyses are ongoing to determine the roles of these predicted genomic signatures with the lifestyle associated.