

Genotype-phenotype correlations with the Geodermatophilaceae

María del Carmen¹, Adnan Yaramis², Dr Jan P Meier-Kolthoff³, Dr Manfred Rohde⁴, Dr Markus Göker³

¹Andalusian Institute of Agriculture and Fisheries Research and Training (IFAPA), ²School of Natural and Environmental Sciences, Newcastle University, , ³Leibniz Institute DSMZ – German Collection of Microorganisms and Cell Cultures, ,

⁴Central Facility for Microscopy, HZI – Helmholtz Centre for Infection

The integration of genomic information into microbial systematics along with physiological and chemotaxonomic parameters provides for a reliable classification of prokaryotes. The use of in silico analysis Laboratory-based DNA-DNA hybridisation methods have routinely been replaced by ANI and in silico DNA-DNA analysis. In silico analysis for phenotypic traits are now being introduced to replace characteristics traditionally determined in the laboratory with the dual goal of increasing the speed of the description of taxa and the accuracy and consistency of taxonomic reports. In conjunction with the taxonomic characterisation of four strains phylogenetically located within the Geodermatophilaceae, we conducted a phylogenetic analysis of the whole proteomes of the sequenced type strains and established genotype–phenotype correlations for traits related to chemotaxonomy, cell morphology and metabolism. Results indicated that the four isolates under study represent four novel species within the genus *Blastococcus*. In silico chemotaxonomic results were overall consistent with wet-lab results. Even though in silico discriminatory levels varied depending on the respective chemotaxonomic trait, this approach is promising for effectively replacing and/or complementing chemotaxonomic analyses at taxonomic ranks above the species level. Finally, interesting but previously overlooked insights regarding morphology and ecology were revealed by the presence of a repertoire of genes related to flagellum synthesis, chemotaxis, spore production and pilus assembly in all representatives of the family. A rich carbon metabolism including four different CO₂ fixation pathways and a battery of enzymes able to degrade complex carbohydrates were also identified in *Blastococcus* genomes.

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