

Unravelling the microbial involvement in the Namib Desert Fairy Circle enigma using a multi-'omic' approach

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Abstract

Fairy Circles (FCs) are mysterious barren circular patches of soil surrounded by grass which feature in both the gravel plains and dune fields of the Namib Desert. While a substantial number of hypotheses have been presented (e.g., vegetation self-organization, micro-faunal activity, abiotic gas seepage) to explain their origin, none are completely consistent with their properties or distribution. In this study, we proposed the hypothesis that Namib Desert Fairy Circles could result through microbial phytopathogenesis, and for the first time compared Namib Desert dune and gravel plain FCs using a multi-'omic' approach.

16S rRNA gene and ITS region amplicon sequencing analyses demonstrated that FC microbial communities were significantly different from their adjacent vegetated soil communities. Moreover, we identified 9 bacterial, 1 archaeal and 57 fungal phylotypes solely present within dune and gravel plain FCs soils. Of these, a substantial number were assigned to phylogenetic groups harbouring phytopathogenic microorganisms (e.g., *Periconia*, *Culvularia* and *Aspergillus*). Shotgun metagenomes revealed that FC soils present numerous cosmopolitan desert bacteria (Actinobacteria, Proteobacteria, Firmicutes), fungi (Ascomycota) and viruses (Siphoviridae and Myoviridae), and confirmed the presence of FC-specific, and potentially phytopathogenic, microbial taxa (e.g., fungi of the genus *Curvularia*). Preliminary metaproteomics analyses provided evidence that dune and gravel plain FC microbial communities are metabolically active (detection of proteins involved in cellular replication, and energy metabolism) and adapted (detection of chaperones) to the extreme Namib Desert conditions.

The presence of FC-specific microorganisms, and specifically potential phytopathogens, suggests a potential role of microbial taxa in the etiology or maintenance of FCs.