Bacterial community dynamics over successional stages of Australian biological soil crusts

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A key aspect for successful ecological rehabilitation is understanding the naturally occurring ecosystem and landscape function which is to be restored. This allows for recovery indicators to be identified and criteria to be developed to assess progress and outcomes. In arid rangelands, environmental stresses result in characteristically heterogeneous landscapes where biological soil crusts (BSCs) cover large expanses of inter-plant areas. Here, BSCs perform crucial roles in nutrient cycling and re-distribution, affect hydrological patterns and stabilise the soil surface. They also serve as a large reservoir of microbial and avascular plant biodiversity. The recognition of these important roles has resulted in increased global arid rehabilitation efforts employing BSCs. Within Australia, research has focused on the macro components of BSCs including lichens and mosses, however, there have been insufficient studies examining the BSC bacterial communities and their dynamics over different successional stages. This project surveyed the bacterial community of crust-free soil and three successional stages of undisturbed BSCs from New South Wales (NSW), Australia, in order to provide reference standards of naturally occurring Australian BSCs. Visual assessments were conducted and BSCs were categorised as Early, Mid or Late stage depending on colour, thickness, topography and presence of lichens and mosses. The crust-free soil and different stages were sampled within three 50 m^2 plots of the same edaphic conditions near the town of Cobar, NSW. High throughput sequencing using the Illumina MiSeq platform was performed targeting the V2 region of the 16S rRNA gene. Preliminary analysis has revealed a clear distinction between the crust-free and crusted soil while Canonical Analysis of Principal Co-ordinates (CAP) suggests the presence of two distinct BSC microbial communities despite three stages being sampled. Across all sample types, the dominant phyla were Actinobacteria, Cyanobacteria and Proteobacteria. Further analysis will determine indicator species which may be used to track the recovery of Australian BSCs in disturbed lands as well as identify pioneer genera as candidate organisms for inoculum based rehabilitation trials. It is important for BSC research to continue in order to adequately direct rehabilitation efforts and for disturbed arid lands to return to self-sustaining ecosystems.