

POSTER ABSTRACTS

Non-symbiotic N₂ fixation in soil, litter and phyllosphere in Dry Chaco forest of Argentina

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It is assumed that N input through non-symbiotic biological fixation is of low significance in terrestrial ecosystems, on the basis of measurements of BNF in soils. However, there is evidence that BNF occurs in other habitats, like in decomposing litter and on leaf surface (phyllosphere), but their magnitude is scarcely known. We evaluated N₂ fixers abundance and activity of the nitrogenase enzyme (N₂-ase) in leaves (of trees, shrubs and grasses), litter (of trees and grasses), and soil (under trees, under shrubs and bare soil) in a dry forest of Argentina. BNF was always lower in soils and higher on leaves and litter. The highest value was detected in leaves of grasses (1.59 nM g⁻¹) and the lowest in the soil under trees (0.12 nM g⁻¹). Abundance of N₂ fixers was similar at all sites, this would be indicating that populations fix N₂ only under favourable conditions for N₂-ase activity. Our results show that probably, BNF in arid environments has been underestimated, because non-symbiotic fixers in litter and phyllosphere were not considered.

Unique root-nodule bacteria isolated from Southern African legumes

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Lotononis and *Lessertia* are two genera of southern African legumes. Species are mostly herbaceous perennials or annuals and several have shown potential as pasture plants in southern Australian agricultural systems. Root-nodule bacteria (RNB) isolated from *Lotononis* and *Lessertia* species are being characterised and have been found to possess some unique properties. Data from this study suggest that *Lotononis* is nodulated by phylogenetically diverse RNB and that different specificity groups exist within *Lotononis*. Species of plants from the *Listia* section of *Lotononis* were all collar-nodulated by pink-pigmented RNB. Isolates from South African *Listia* species were medium-slow growing, selective in their carbon substrate utilisation and formed dry, dark-pink colonies. Although sequencing of the 16S rRNA gene indicated that these isolates were related to *Methylobacterium*, none of the strains tested were able to utilise methanol as a sole carbon source. Isolates from *L. angolensis* (also in the *Listia* section, but collected in Zambia), in contrast were fast growing, mucilaginous, pale-pink and closely related to bacterial genera belonging to the family *Beijerinckiaceae*. A third group of isolates from other *Lotononis* spp were non-pigmented and heterogeneous in their phylogenetic, morphological and physiological properties. Sequence analysis of the 16S rRNA gene has found one authenticated isolate to be related to *Sinorhizobium*.