

Diversity and Distribution of Ammonia Oxidizing Bacteria Associated with Plants Roots in Soils of Fynbos Ecosystem

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Molecular methods were used to investigate the microbial diversity and community structure of ammonia oxidizing bacteria (AOB) associated with the roots of the Proteaceae plant family. The identification of ammonia oxidizing bacteria in this ecosystem is of particular interest since Proteaceae are adapted to nutrient-poor acidic soils. The ammonia monooxygenase operon was used as a molecular marker to identify AOB genes in microbial populations associated with the proteoid roots of the three Proteaceae members, and compared to non-plant associated soil. PCR amplification primers sets targeting ammonia monooxygenase gene (*amoA*) and the internal transcribed spacer region (ITS) of *amoC-amoA* subunits were used to construct clone libraries. Sequence diversity was determined by ARDRA analysis, DNA sequencing and phylogenetic analysis. AOB genotypic diversity was greater for the plant-associated samples compared to non-plant associated soil. All AOB phylotypes belonged only to *Nitrosomonas* and *Nitrospira* genera with *Nitrosomonas* phylotypes dominating clone libraries. Specific *Nitrospira* phylotypes were detected only in plant associated soils, suggesting the existence of plant-specific microbial associations. This investigation provides new insights into the relationships between plants and ammonia oxidizing bacteria in natural Fynbos ecosystems.