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Bioremediation potential by probable 'nitrogen-fixing' actinobacteria residing in the root nodules of *Casuarina equisetifolia* for cadmium removal under *in vitro* conditions

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Frankia and many of the nitrogen fixers found in the nodules of the Casuarinacaea lineage, belong to actinobacteria, which are largely a group of aerobic, filamentous, gram-positive bacteria which harbor high G+C content in their respective genomes. Actinobacteria have been earmarked for their bioremediation potential and have been identified as strong candidates superior to fungi and gram-negative bacteria in their capacity to remediate polluted environments. It is important to ascertain the contribution of actinobacteria in sites of environmental pollution, namely areas of heavy metal contamination such as agricultural land with strong fertilizer usage, industrial effluents and waste disposal sites. The potential role of *Frankia* and auxiliary actinobacteria colonizing actinorhizal plants, in bioremediation, is largely unknown, with the exception of a few of studies.

A study was carried out, to assess the cadmium tolerance of *Frankia* and co-colonizing actinobacteria inhabiting root nodules of the actinorhizal tree *Casuarina equisetifolia*. The actinobacteria, *Frankia*, *Micromonospora* and *Streptomyces,* were isolated from root nodules of *Casuarina* plants and identified preliminary by colony and mycelial morphology. It is of significance that this is the first reported isolation of *Streptomyces* from *Casuarina equisetifolia*. Furthermore, the actinobacteria were able to grow on N-free media, signifying that all three actinobacteria were likely nitrogen fixers. The isolated actinobacteria were demonstrated to possess cadmium lowering capacities of up to 10 mg/l. It appears that actinobacteria from root nodules of *Casuarina equisetifolia* are diazotrophs with capabilities to lower cadmium from an external medium. A comprehensive molecular characterization of the three diazotrophs using *nif*, 1*6s rDNA* and *glutamine synthetase* gene sequences is being carried out at present.

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