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Ecological Guild of Beneficial Bacteria Associated with Agricultural Soil Polluted by Spent Automobile Engine Oil

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Background/Objectives. The ultimate aim of any bioremediation process is to restore polluted land to a pre-pollution state. Given the fact that contaminated soils are often nutrient poor, bacteria, which are able to simultaneously degrade PAHs and enhance soil fertility, are valuable as bioaugmentation strains in phytoremediation. Such combination of attributes is indispensable for sustainable agricultural production and environmental protection. Our study aimed to evaluate, in vitro, the ecological guild of PAH-degrading bacterial isolates. Bacterial isolates were screened for their abilities to solubilize phosphates, fix atmospheric nitrogen, and produce IAA as indication of their potentials to contribute to soil fertility and restorative bioremediation. Agricultural soil with no recorded history of pollution was collected from a research farm of the Agricultural Research Council, Vegetable and Ornamental Plant Institute, Pretoria, South Africa. The soil is of alluvial origin and classified as an Oakleaf soil form. Sampling was done from the topsoil (0–250 mm).

Approach/Activities. The collected soil was subsequently contaminated with spent automobile engine oil, whose PAH content was previously determined. The contaminated soil was biostimulated with vermicompost obtained from the vermicompost laboratory of the Agricultural Research Council, in Pretoria. Biostimulation of soil with vermicompost was done at 0% (control), 20%, and 40%, thus maintaining and boosting the indigenous soil microbes. Contamination was done prior to biostimulation to reflect the actual occurrence of events on contaminated sites. We isolated PAH-degrading bacteria from enriched cultures of spent automobile engine-oil polluted soil. Isolates' partial 16S rRNA genes were sequenced and taxonomically classified. Isolates were further screened for their soil fertility attributes such as phosphate solubilization, atmospheric nitrogen fixation, and indoleacetic acid (IAA) production.

Results/Lessons Learned. A total of 44 isolates were obtained and belong to the genera *Acinetobacter, Arthrobacter, Bacillus, Flavobacterium, Microbacterium, Ochrobactrum, Pseudomonas, Pseudoxanthomonas, Rhodococcus,* and *Stenotrophomonas*. Data analysed by principal component analysis showed the *Bacillus* and *Ochrobactrum* isolates displayed outstanding IAA production. Generalized linear modelling statistical approaches were applied to evaluate the contribution of the four most represented genera (*Pseudomonas, Acinetobacter, Arthrobacter,* and *Rhodococcus*) to soil fertility. The *Pseudomonas* isolates were the most promising in all three soil fertility enhancement traits evaluated and all isolates showed potential for one or more of the attributes evaluated. These findings demonstrate a clear potential of the isolates to participate in restorative bioremediation of polluted soil, which will enhance sustainable agricultural production and environmental protection.