ISBN: 978-93-83083-65-7

Metagenomic Diversity of Bacteria and Archaea in the Rhizosphere of Bioenergy Crop Jatropha Curcas

Garima Dubey, Usha Ahirwar, Sneha Tiwari, Bharati Kollah, S R Mohanty*

Indian Institute of Soil Science Bhopal, India 462038

Abstract Diversity of bacteria and archaea in the rhizosphere of *J curcas* was estimated to define how the bioenergy crop interacts with ecosystem through rhizospheric microbes. Root samples of *J curcas* varying with different cropping attributes were collected. Genomic DNA from the rhizoplane was extracted by bead beating followed by column separation. Purified DNA samples were PCR amplified using the primers targeting 16S rRNA gene of archaea and bacteria. The archaeal primers were 109F and 915R, while that of bacteria were 8F and 535R. Both forward primers were labeled with 6-FAM dyes at the 5' end. PCR products of archaea (105F/915R) were digested with Alu (AG^CT), while that of eubacteria (8F/535R) were digested with RsaI (GT^AC). Selection of restriction enzyme carried out using in-silico digestion of full length representative DNA sequences downloaded from RDP. Fragment analysis carried out in an automated capillary genetic analyzer. Base calling and area of fragments were calculated by applied biosystems PeakScanner software. Data revealed that both archaea and bacteria species associated with bioenergy crop were mostly uncultured type. Terminal restriction fragments comprising 24, 45, 46, 55, 61, 75, 82, 85, 95, 101, 107, 108, 115, 143, 171, 201, 233, 273, 280 and 294 base pairs were predominant in all samples. TRFs representing uncultured archaea, crenoarcheota, and ferroplasma contributed 20-25% of total fluorescence. Bacterial TRFs of 40, 55, 64, 92,179,266,417, 432, 450, 462 base pairs were predominant ribotypes. Diversity indices varied significantly corresponding to plant growth attributes ($p<0.0001$). This study has provided insight into the spatial variability of the microbial community in response to crop attributes and highlighted role of functional groups towards the sustainability of the bioenergy crop *J curcas*.