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Metagenomic profiles of soil microbiota under two different cropping systems detected by STRs-based PCR

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ABSTRACT

In this research, soil microbial structures under a wheat triennial monoculture and horse bean-wheat-horse bean succession were evidenced using a metagenomic approach. Polymorphism analysis of DNA extracted from soil samples collected at the end of the third year of the two crop successions, was performed by PCR, carried-out with six different primers designed on simple tandem repeats sequences. Readable profiles were obtained with M13 primer, from which no polymorphisms were detected, and with the primer (GACA)₄, that gave distinctive patterns. Experimental findings suggest that metagenomic analysis performed by (GACA)₄ primer may be an easy and suitable method to discriminate microbial diversity of different crop successions. (GACA)₄ PCR-pattern indicate that soil microbiota changes are well correlated with crop succession.

KEYWORDS

Cover Plants; Hot-Spot Variability; Mini- and Micro-satellite; PCR Fingerprinting; Soil Biodiversity

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