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Study of bacterial community dynamics during coconut leaf vermicompost production and in earthworm gut contents using pyrosequencing

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Background:
Coconut palm (*Cocos nucifera* L) leaf litter, a recalcitrant waste available in large quantities in India, has been successfully recycled to vermicompost using an earthworm, *Eudrilus* sp. Vermicomposting depends greatly on the microorganisms, and studies on microbial diversity of vermicomposts using molecular methods have been reported. However, no information on the microbial community dynamics during the different vermicomposting stages using pyrosequencing is available.

Objective:
To study the bacterial community dynamics during coconut leaf vermicompost production and in the earthworm gut contents.

Method/Findings:
Genomic DNA was extracted from 12 conditions including i) coconut leaves+cow dung at different stages of decomposition ii) vermicompost and iii) gut contents of *Eudrilus* sp. The V1-V3 region of the bacterial 16s rRNA gene in the genomic DNA was amplified using barcoded primers for pyrosequencing (454 Gs-FLX).The ensuing data was analyzed using QIIME and MOTHUR packages and the SILVA database. A total of 142420 unique sequences were obtained from the substrate/ vermicompost and earthworm gut contents. The Bacteroidetes and α-proteobacteria constituted 50% of the major taxonomic groups in the beginning and middle stages of the vermicomposting process, while the vermicompost had Bacteroidetes, Firmicutes, α-proteobacteria and γ-proteobacteria in equal proportions. The number of Firmicutes increased during the progress of vermicomposting. The earthworm gut contents had Actinobacteria, Firmicutes and α-proteobacteria in predominance.

Conclusions :
The 16S rRNA gene-based analyses revealed changes in the bacterial communities during vermicompost production from coconut leaves. Moreover, it showed that the vermicompost community was different than the gut contents of earthworm.