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Title : Utilization of vermitechnology for rapid degradation of Lignocellulosic wastes: A quest for useful microorganisms.

ABSTRACT

Nearly 50% of the solid waste generated in the world is biogenic and contains lignocellulosic substances. According to a recent report, the annual global generation of lignocellulosic biomass is more than 200 billion tons, with paddy straw and food waste as the dominant components. The food waste generated worldwide has a similar predominance of lignocellulosic substances, which are integral components of plant cell walls, complex in structure, and inherently hydrophobic. Complex networks of these polymeric compounds not only resist microbial intervention but also deactivate some vital enzymes. The recalcitrance of lignocellulosic materials thus limits their efficient utilization, and appropriate treatment is required to successfully recover nutrients from these substances. Composting and vermicomposting are key technologies for converting numerous types of solid waste into valuable organic fertilizers. Composting is an aerobic biological system that promotes the inherent microorganisms to decompose organic biowastes. Vermicomposting, on the other hand, takes advantage of synergy among earthworm activity, earthworm gut microorganisms, and microbial communities inherent in feedstocks. In this context, epigeic earthworms like *Eisenia fetida* are most effective due to their wide adaptability, unique defense mechanisms, and voracious feeding habit.

Nevertheless, the true value of earthworm-mediated lignocellulosic waste transformation can only be assessed by studying the microbial community structure during the biocomposting process. This can only be achieved through high-level next generation sequencing approaches. As such, little is known about the functional and taxonomic diversity of *E. fetida* mediated lignocellulosic waste-based vermicomposting systems. So far, microbial metagenomic analyses are used to interpret microbial diversity and community shifts in response to change in the immediate environment. Such knowledge is rarely applied to generate microbial resources.

Previous 16S rRNA gene-based studies of bacterial and fungal communities provided only partial knowledge because numerous eukaryotic and prokaryotic organisms can arise during bio-composting. A next-generation sequencing (NGS)-based whole metagenomic approach can

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by Ratan Chowdhury

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