Enhancing composting efficiency by promoting indigenous cellulose decomposing microorganisms

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Cellulose metabolism is one of the key component of carbon cycle on the planet (Beguin and Aubert, 1994), and it is also important during composting process. However, given the fact that over 99% of indigenous bacteria in natural environment are still uncultivable (Kaeberlein et al., 2002), the majority of the cellulose decomposing microorganisms remain unknown and their key roles and behaviour in composting process are hidden within the complex microbial community. For the first time, we successfully separated the functional cellulose decomposing microorganisms from composting microbiota by introducing the cutting-edge magnetic-nanoparticle mediated isolation (MMI) technique (Zhang et al., 2015).

A case study was carried out at a farmland composting site in the UK. After functionalizing all the compost microorganisms with cellulose@MNPs nanocomposites (Zhao et al., 2016), the magnetic microbiota was cultivated in original composting environment for 15 days. The cellulose decomposing bacteria eventually consumed the cellulose and lost their magnetism via division. Applying external magnetic field, the magnetic-free cellulose decomposing bacteria were therefore separated from the other inert magnetic microorganisms. Different from the cultivable *Aeromonas veronii*, the isolated cellulose decomposing microbial community was consisted of bacteria belonging to the phylum *Firmicutes*, *Clostridiaceae* and *Ralstonia*, which have been proved with cellulose decomposing capacity (Feng et al., 2011). Though the magnetic-free fraction accounted for less than 0.1% of the total population of the original compost, they contributed to over 80% of cellulase activity and 72% of cellulose decomposing capacities, proving that the isolated microbes play the key roles in cellulose decomposing.

Given the most attractive feature of MMI technique that the isolated cellulose decomposing microbes are still alive, we applied the BIOLOG phenotype microarray for deeper analysis of their ecological functions and environmental factors affecting the composting efficiency. Four carbon (D-alanine, a-D-glucose, tyramine and L-glutamine) and five nitrogen (L-arginine, L-histidine, L-citrulline, L-pyroglutamic acid and δ-Amino-N-valeric acid) sources significantly promoted the microbial respiration and therefore enhance the cellulose decomposing rate. With the extra additive of L-arginine or L-histidine, we successfully increased the cellulase activity by 2.5 times and significantly reduce the composting time from 15 days to 8 days.

Without cultivation and expensive substrate labelling, this novel MMI technique combines magnetic-nanoparticle mediated isolation and phenotype microarray, opening a door as a cost-effective tool to reveal the *in situ* physiological behaviour and ecological functions of uncultivable cellulose decomposing bacteria in composting microbiota. Instead of foreign cellulose decomposing microbes additive to improve composting efficiency, our method for the first time achieves composting efficiency improvement by providing stimulative nitrogen sources and promoting the activities of indigenous cellulose decomposing microorganisms. It reduces both the costs and risks of introducing gene-modified microbes (Davison, 2005).

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