

PLoS ONE, 2017, vol.12, N10

# Fungal and bacterial successions in the process of co-composting of organic wastes as revealed by 454 pyrosequencing

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## Abstract

© 2017 Galitskaya et al. This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited. Composting is viewed as one of the primary methods to treat organic wastes. Co-composting may improve the efficiency of this treatment by establishing the most suitable conditions for decomposers than those present in the individual wastes. Given that bacteria and fungi are the driving agents of composting, information about the composition of their communities and dynamics during composting may improve reproducibility, performance and quality of the final compost as well as help to evaluate the potential human health risk and the choice of the most appropriate application procedure. In this study, the co-composting of mixtures containing two similar components (organic fraction of municipal solid waste and sawdust polluted by oil) and one discriminate component (sewage sludges of different origin) were investigated. Bacterial and fungal community successions in the two mixtures were analyzed during the composting process by determining the change in their structural dynamics using qPCR and 454 pyrosequencing methods in a lab experiment for a period of 270 days. During the initial composting stage, the number of 16S bacterial copies was  $(3.0 \pm 0.2) \times 10^6$  and  $(0.4 \pm 0.0) \times 10^7 \text{ g}^{-1}$ , and the Rhodospirales and Lactobaciales orders dominated. Fungal communities had  $(2.9 \pm 0.0) \times 10^5$  and  $(6.1 \pm 0.2) \times 10^5$  ITS copies  $\text{g}^{-1}$ , and the Saccharomycetales order dominated. At the end of the thermophilic stage on the 30<sup>th</sup> day of composting, bacterial and fungal communities underwent significant changes: dominants changed and their relative abundance decreased. Typical compost residents included Flavobacteriales, Chitinophagaceae and Bacteroidetes for bacteria and Microascaceae, Dothideomycetes, Eurotiomycetes, Sordariomycetes, and Agaricomycetes for fungi. During the later composting stages, the dominating taxa of both bacterial and fungal communities remained, while their relative abundance decreased. In accordance with the change in the dominating OTUs, it was concluded that the dynamics of the bacterial and fungal communities were not similar. Analysis by non-metric multidimensional scaling (NMDS) revealed that the bacterial communities of the two composts became progressively more similar; a similar trend was followed by the fungal community.

<http://dx.doi.org/10.1371/journal.pone.0186051>

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