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EFFECT OF FEEDING STRATEGY ON FUNCTIONAL MICROBIAL COMMUNITIES DURING INTENSIVE IN-VESSEL COMPOSTING OF URBAN BIOWASTE

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Introduction

Intensive in-vessel composting accelerates urban biowaste stabilization through controlled mixing, moisture and thermophilic operation. Feed composition also affects porosity, oxygen transfer and C/N balance, selecting microorganisms involved in ammonia and nitrite oxidation, denitrification, N_2O reduction and phosphorus accumulation. Tracking these functional groups can reveal how operational feed choices redirect nutrient cycling. This study evaluated how urban biowaste feeding strategies shape the qPCR-derived functional microbial profile associated with nitrogen and phosphorus transformations during intensive in-vessel composting.

Materials and methods

Six modular closed reactors were run in parallel with semi-continuous feeding, mixing and thermophilic operation. After ~30 days of activation, loading increased from 0.5 to 1.0 kg d^{-1} $reactor^{-1}$. Paired reactors received A, cooked restaurant waste; B, cooked restaurant waste plus dry leaves; or C, predominantly raw vegetable kitchen waste. Overall mass reduction was 52–79%. The primary comparison used paired 22.02 samples (A1/A2, B1/B2, C1/C2). MB sample was retained only as a biological reference. DNA was extracted with DNeasy PowerSoil Pro and qPCR performed with PowerUp SYBR Green on QuantStudio 7 for universal bacteria and N/P functional markers. The sequence of forward and reverse of each primer pair used is available at [1]. Ct=40 was treated as ND. Results were normalized descriptively as $\Delta Ct = Ct(target) - Ct(universal\ bacteria)$.

Results and conclusions

Measured universal-bacterial Ct averaged 25.03 (A), 24.78 (B) and 28.05 (C), versus 23.48 in MB, indicating less amplifiable bacterial target DNA in C under comparable conditions. After normalization, B had the lowest mean ΔCt among feeds for *AOB* 16S (5.61), *amoA-1* (−2.04), *amoA-2* (2.25) and *Nitrospira/Nsr* (4.86). However, *nxrB* was lowest in C (5.28), followed by A (5.74) and B (6.68). B therefore favored several ammonia-oxidation markers, but not both nitrification steps uniformly.

C showed the lowest ΔCt among feeds for *nirK* (1.38), *nirS* (−1.96), *cnorB* (−3.20) and *nosZ* (2.02). These values indicate relative occurrence of gene targets, not reaction rates or N_2O emissions. *PAO* was most represented relative to the universal marker in A (mean ΔCt 3.34), although replicate variability was substantial; B and C averaged 8.77 and 6.33. Archaeal ΔCt was lowest in C (4.64), followed by B (5.87); A was based on one quantifiable replicate because A1 returned Ct=40. The lower total bacterial signal in C together with retained functional markers could reflect inhibition or substrate depletion during stabilization; available process data cannot distinguish them. Overall, feeding strategy shaped the functional microbiome, but the hypothesis that B produced a globally more balanced N/P profile was not fully supported. B favored several ammonia-oxidation targets, C retained comparatively strong *nxrB*, denitrification, *nosZ* and archaeal markers, and A showed the strongest normalized *PAO* signal. Functional-gene abundance should be coupled with N-species and gas measurements before inferring process rates.

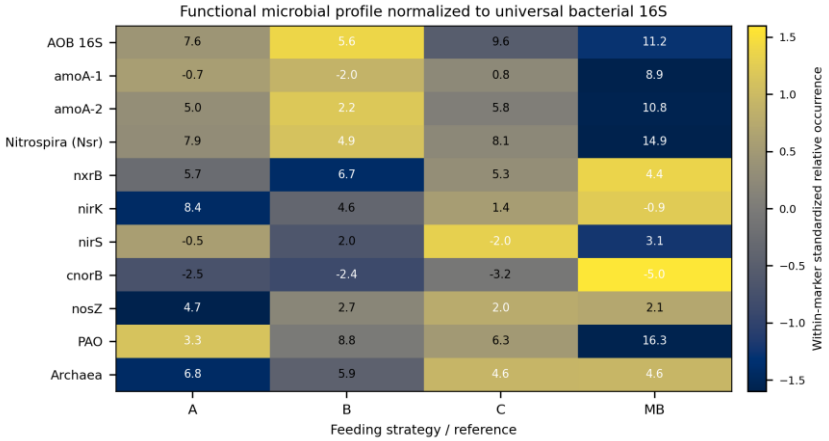


Figure 1 - qPCR functional profile for A, B, C and biological reference MB. Numbers are mean ΔCt; lower values indicate greater target occurrence relative to universal bacterial 16S. Colour encodes within-marker standardized −ΔCt; Ct=40 was treated as ND. MB was not used for ΔCt.

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