Are the physicochemical properties and bacteriological composition of composts linked?

Compost is the product of composting, which is a biological process to valorize and recycle a variety of organic wastes. Given the benefits of composting numerous industrial units have been commercializing this type of product. The parameters for the assessment of compost quality are usually established in terms of electrical conductivity, nutrient content, humified and stabilized organic matter, maturity degree, hygienisation and presence of certain toxic compounds such as heavy metals, soluble salts and xenobiotics.

Because composting is a biological process, the microorganisms play an important role. Although several studies revealed the composition and dynamics of microorganisms during the composting, little is known about the correlation between the microbial composition and the compost quality.

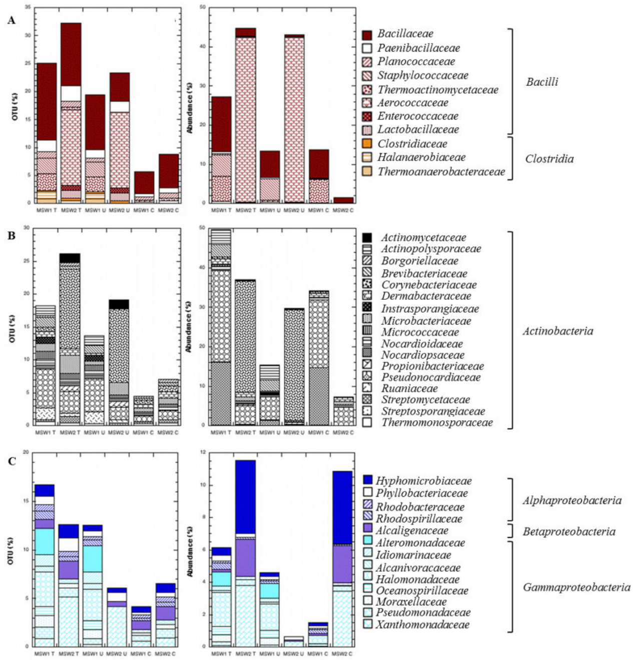

Fig. 1. Percentage (No OTUs/Total OTUs) and relative abundance (number of sequences/6350) of OTUs identified at the family level, in each compost (MSW1 and MSW2), belonging to Firmicutes (A), Actinobacteria (B) and Proteobacteria (C). T-Total, U – Unique, C- common; OTU – Operational Taxonomic Unit (Silva et al., 2016).

Composts are inhabited by complex bacterial communities, with members of different bacterial groups. Because cells are influenced by the environmental conditions, and in turn, are able to change the properties of the surrounding environment, it was important to know if composts with different degrees of quality share, or not, similar bacterial populations.

To answer to this question two commercial composts (MSW1 and MSW2) produced from municipal solid waste but differing on most of their physicochemical, stability and maturity properties were studied.

It was shown that the bacterial communities of composts MSW1 and MSW2 were also different. Overall, the compost with higher degree of maturity and stability (MSW1) had a more diverse bacterial community than the compost with lower quality (MSW2) (Fig. 1).

Aerococcaceae, a bacterial group not commonly found in composts, and *Corynebacteriaceae* dominated the bacterial community of MSW2. Some members of this last group are known to be lipophilic, i.e., they grow better when lipids are included in the culture medium, which may indicate the presence of fats in the MSW2 raw material.

The higher abundance of *Pseudonocardiaceae*, *Streptomycetaceae*, *Bacillaceae* and *Brevibacteriaceae* in MSW1 than in MSW2 may have contributed to the higher degree of humification and lower toxicity of the first compost than the later. Nevertheless, the high electrical conductivity and high Cu content of MSW1 may have contributed to the high abundance of halophilic bacteria (*Halomonadaceae)* and heavy metal tolerant bacteria *(Brevibacteriaceae* and *Bacillaceae*) in this compost*.*

Maria Elisabete F. Silva[1,2,3], Ana R. Lopes[2], Ana Cristina Cunha-Queda[3] and Olga C. Nunes[2]
[1]CI&DEST, Escola Superior de Tecnologia e Gestão de Viseu, Instituto Politécnico de Viseu, Portugal
[2]EPABE, Laboratório de Engenharia de Processos, Ambiente, Biotecnologia e Energia, Faculdade de Engenharia, Universidade do Porto, Porto, Portugal
[3]LEAF, Centro de Investigação em Agronomia, Alimentos, Ambiente e Paisagem, Instituto Superior de Agronomia, Universidade de Lisboa, Tapada da Ajuda, Lisboa, Portugal

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