

Impact of the spreading of urban waste on agricultural soil bacterial communities in the periphery of Ouagadougou, Burkina Faso

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Abstract

Recycling organic wastes is of interest in agriculture and horticulture for improving soil quality, favoring plant development [1].

Recently, usual farmers' practices in Burkina Faso involved the use of untreated domestic and urban wastes. However raw organic wastes may contain undesirable constituents, e.g. heavy metals, toxic organics, pathogens, with adverse impacts on soil and environmental quality, and possible hazards to human health [2,3].

The objective of this study was to evaluate the influence of anthropogenic activities such as the application of urban waste on agricultural land which can promote the emergence and / or spread of pathogens. Assessing the influence of the spreading of raw municipal waste on soil bacterial communities and the abundance of opportunistic pathogens of man was realized.

Soils amended or unamended (control) with waste has been sampled at three sites in the suburban area of Ouagadougou (Burkina Faso). The impact on the total indigenous bacterial community and the risk of spread of pathogens has been assessed by counts of culturable bacteria (heterotrophic cultivable microflora, faecal indicator bacteria and pathogenic species of humans), as well as an analysis of the genetic structure of bacterial community in a culture independent approach (ARISA Method for Automated Ribosomal intergenic Spacer Analysis).

The results showed a total cultivable bacteria enrichment and modification of the genetic structure of bacterial communities in the amended plots. The lack of detection of pathogens such as enterococci and fecal coliform, *Staphylococcus aureus* and opportunistic human pathogens (*Pseudomonas aeruginosa*) suggested that the amendments are not sources of these pathogens and do not select the communities. However, monitoring populations of the species *Stenotrophomonas maltophilia*, an opportunistic pathogen of man frequently found in soils, showed the enrichment of these populations in amended plots.

This work showed that human activities spreading of waste on agricultural land may pose health and environmental risks.

Keywords: municipal waste, soil, bacterial community, opportunistic pathogens of humans.

Introduction

Usual farmers' practices in Burkina Faso involved the use of untreated domestic and urban wastes on agricultural fields for improving soil fertility. However raw organic wastes may contain undesirable constituents, e.g. heavy metals, toxic organics, pathogens, with adverse impacts on soil and environmental quality, and possible hazards to human health. More research is then required to ensure that land application of wastes is safe. The objective of this study was to evaluate the influence of the application of raw municipal wastes on agricultural lands on soil bacterial communities and the abundance of human pathogens.

Material and Methods

Soils amended or non-amended (control) with wastes has been sampled at three sites in the suburban area of Ouagadougou (Burkina Faso) in 2008. All sampled fields were cropped with sorghum. In each

plot 10 samples were taken at 5 cm depth every 2 meters along a 20 m transect. Three transects per plot were done and samples from one transect were mixed together to make the composite sample. The impact on the total indigenous bacterial community and the risk of spread of pathogens has been assessed by counts of culturable bacteria (total heterotrophic culturable bacteria, faecal indicators and human opportunistic pathogens), as well as an analysis of the genetic structure of bacterial community in a culture independent approach (ARISA Method for Automated Ribosomal intergenic Spacer Analysis). Selective media combine to species identification were used to evaluate the abundance of faecal indicators and pathogens.

Results

The results showed a total culturable bacteria enrichment (Fig. 1) and modification of the genetic structure of bacterial communities in the amended plots at each site.

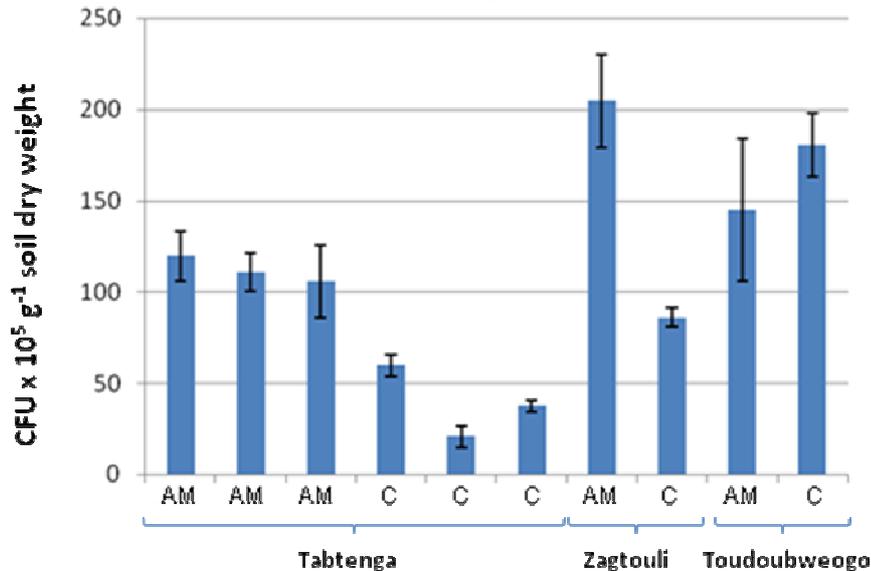


Figure 1: Total heterotrophic bacterial counts of soils in the amended (AM) and control (C) plots of the Tabtenga, Toubwéogo and Zagtouli sites in Burkina Faso. Data are mean of three replicates. CFU : colony forming unit.

Results from pathogen investigation showed the absence of enterococci and fecal coliform, *Staphylococcus aureus* and *Pseudomonas aeruginosa* in all plots at each site. On the opposite we showed the presence of *S. maltophilia* in the amended plots at each site whereas it was not detected in the control plots of Tabtenga and Zagtouli (Fig.2). *S. maltophilia* was detected in the control plot of Toudoubwéogo but at a lower level than in the amended plot.

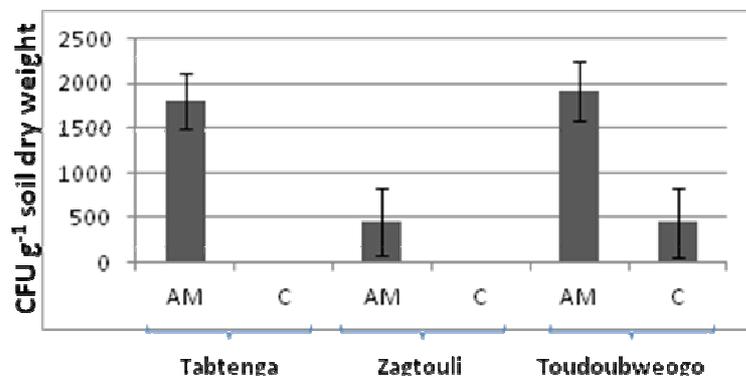


Figure 2: Abundance of *S. maltophilia* in the amended (AM) and control (C) plots of the Tabtenga, Toudoubwéogo and Zagtouli sites in Burkina Faso.

Conclusion

In conclusion the lack of detection of pathogens suggested that the amendments are not sources of these pathogens and do not select for these species. However, monitoring populations of the species *Stenotrophomonas maltophilia*, an opportunistic pathogen of man frequently found in soils, showed the enrichment of these populations in amended plots probably due to enrichment of indigenous populations. Preliminary work aiming at comparing the antimicrobial susceptibilities of the environmental isolates to those of clinical strains evidenced a high resistance to antibiotic and multidrug resistance phenotypes among soil isolates from Burkina Faso. This work showed that human activities such as spreading of wastes on agricultural land may pose health and environmental risks.

References

- [1] García-Gil JC, Plaza C, Soler-Rovira P, Polo A. 2000. Long-term effects of municipal solid waste compost application on soil enzyme activities and microbial biomass. *Soil Biol. Biochem.*, 32(13): 1907-1913.
- [2] Lejon DP, Sebastia J, Lamy I, Chaussod R, Ranjard L. 2007. Relationships between soil organic status and microbial community density and genetic structure in two agricultural soils submitted to various types of organic management. *Microb. Ecol.*, 53(4): 650-663.
- [3] Lejon DP., Martins JM, Lévêque J, Spadini L, Pascault N, Landry D, Milloux MJ, Nowak V, Chaussod R, Ranjard L. 2008. Copper dynamics and impact on microbial communities in soils of variable organic status. *Environ. Sci. Technol.*, 42(8): 2819-2825.