

Forensic characterisation of soil microbial communities in response to cadaver decomposition

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Introduction

- An accurate estimation of time since death is an important aim of every medico-legal investigation and its determination can direct an entire forensic case.
- The potential for using biochemical and molecular methods to characterise the dynamics of soil microbial communities during the process of cadaver decomposition has been investigated.

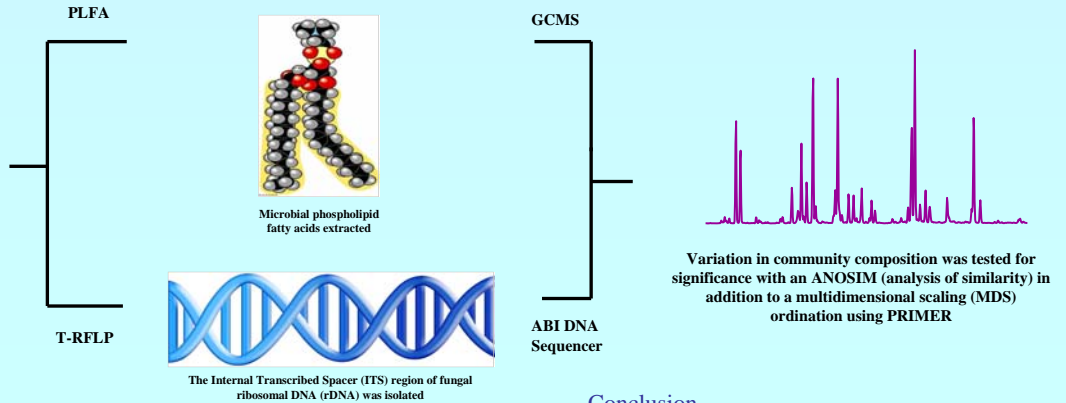
Experiment

- Analyses were performed on soil that was sampled periodically from under two human cadavers at the Forensic Anthropology Centre at the University of Tennessee.
- Phospholipid fatty analysis (PLFA) and terminal restriction fragment length polymorphism (T-RFLP) community profiling of the internal transcribed spacer (ITS) region of fungal ribosomal DNA (rDNA), provided a qualitative and quantitative analysis of these transformations in the microbial populations.

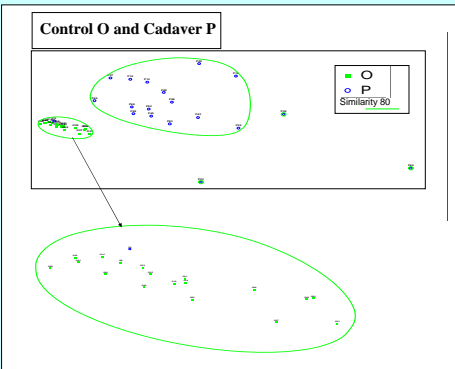
Methods



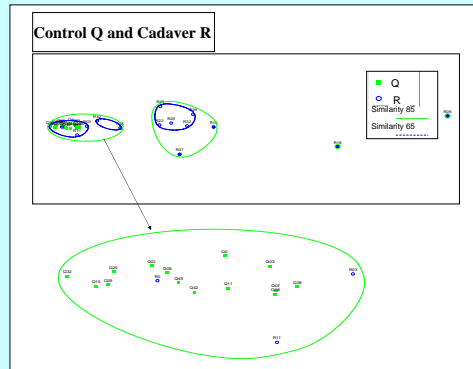
Soil collected from around decomposing Cadaver P and R at the Forensic Anthropology Centre, University of Tennessee



PLFA Results



The control microbial population O is significantly ($p = 0.001$) different from the cadaver microbial population P. Numbers refer to sampling day.

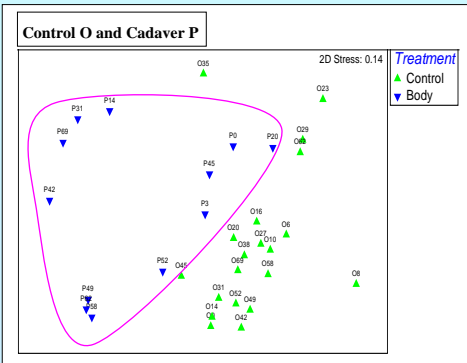


The control microbial population Q is significantly ($p = 0.001$) different from the cadaver microbial population R.

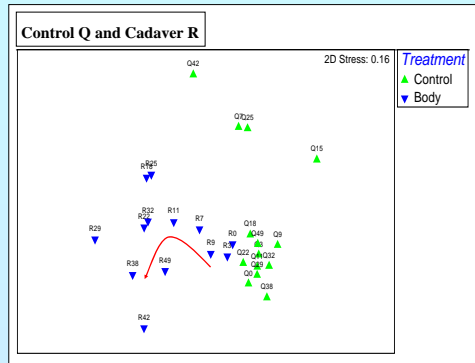
Conclusion

- PLFA analysis demonstrated that the presence of a cadaver undergoing decomposition, resulted in a significant change in the structure and composition of the soil microbial community
- T-RFLP analysis:
 - showed an observable difference in control and cadaver soil fungal populations
 - suggested the possibility of a succession of fungal species at different decomposition phases
 - indicated that fungal species may be able to be grouped into early and late phase fungi

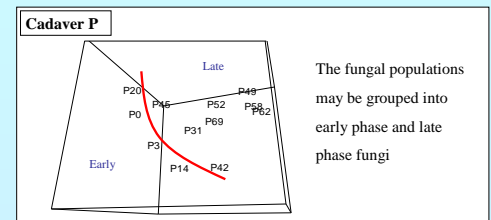
T-RFLP Results



The separation of control (O) and cadaver (P) soil microbial populations based on the ITS region of fungal rDNA.



The separation of control (Q) and cadaver (R) soil microbial populations based on the ITS region of fungal rDNA.



The fungal populations may be grouped into early phase and late phase fungi

The potential exists for the development of a post mortem interval estimation tool based on soil microbial community succession

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