Variation in Bacteriohopanepolyol content of soils and sediments

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Background

Bacteriohopanepolyols (BHPs) are pentacyclic triterpenoids biosynthesised by many prokaryotes to perform a regulating and rigidifying function in membranes analogous to that of some sterols in eukaryotes. BHPs have been detected in a wide range of prokaryotes. Many BHP structures are known, differing in the number, position and nature of the functional groups on the side chain (see handout). In some cases these BHPs are unique to specific bacterial sources and these relationships can be used to identify the presence of bacterial processes in the soil (Table 1).

Table 1. Relationship between BHPs and Source Bacteria

Abbreviated name	Structure Number	Known Source organisms[a]
BHT	**1a'**	Various
Aminotriol	**1f'**	Various
BHT ce	**1d'**	Various
BHT glu	**1g'**	Various
BHpentol ce	**1l'**	various
Unsat. aminotriol	**5f', 6f'**	*Rhodopseudomonas palustris*[47]
Adenosylhopane	**1e'**	Purple non-sulfur bactéria1[4,22,26,36,47] *Nitrosomonas europaea*[39,47] *Bradyrhizobium japonicum*[46]
2-me adenosylhopane	**2e'**	*Bradyrhizobium japonicum*[46]
'Adenosylhopane type- 1'[a]	**1u'**	Purple non-sulphur bacteria[47]
$\Delta^{6 \text{ or } 11}$-BHT	**5a', 6a'**	Acetic acid bacteria[27,48]
3-me BHT	**3a'**	Acetic Acid Bacteria,[48]
3-me BHT ce	**3d'**	*Gluconacetobacter xylinus*[48]
3-me BHpentol ce	**3l'**	*Gluconacetobacter xylinus*[48]
2-me BHT	**2a'**	Cyanobacteria[3,13,40,44,50,55] *Rhodopseudomonas palustris*[32] *Methylobacterium organophilum*[34]
2-me aminotriol	**2f'**	Cyanobacteria[56] *Rhodopseudomonas palustris*[32]
Unsat. BHT pentose	**5n', 6n'**	Cyanobacteria[50]
BHT pentose	**1n'**	Cyanobacteria[36,50]
2-me BHT pentose	**2n'**	Cyanobacteria[50]
2-me BHT ce	**2d'**	Cyanobacteria[50]
2-me BHpentol cyclitol ether	**2l'**	Unknown, potentially cyanobacteria as 2-Methyl
3-me aminotriol	**3f'**	Methanotrophs[57]
Aminotetrol	**1h'**	Methanotrophs[23,24,36,42,43,56] *Desulfovibrio* sp.[4]
2-me Aminotetrol	**2h'**	Methanotrophs
Aminopentol	**1c'**	Methanotrophs[11,23,36,42,43,56]
Guanidine sub. BHT ce	**1s'**	Methylotrophic bacteria[47]
Hopane lactone	**1t'**	Ammonia oxidising bacteria[39,47] PNSB[47]
Unsat. BHpentol ce	**5l', 6l'**	*Gluconacetobacter xylinus*[48]
'2-me adenosylhopane type-1'	**2u'**	Unknown
BHpentol pentose	**1o'**	Unknown
Unsat. 2-me BHT ce	**7d'**	Unknown
BHpentol glu	**1q'**	Unknown
BHhexol ce	**1k'**	Unknown
2-me BHhexol ce	**2k'**	Unknown
3-me BHhexol ce	**3k'**	Unknown

[a] see Talbot et al., 2008 and subsequent references;

This Study

The Palace Leas pasture plots, Cockle Park Farm, Hebron, Northumberland, have undergone a consistent fertiliser treatment regime of over 100 years. The BHP signature of these plots was investigated using HPLC analysis to identify any differences due to the differing fertiliser treatments.
Plot 2 – manure treatment, Plot 6 – No applied fertiliser
Plot 7 – Nitrogen fertiliser only Plot 8 – Phosphate treatment only
Plot 9 – Potassium fertiliser only.
The results are shown in Figs 1 and 2

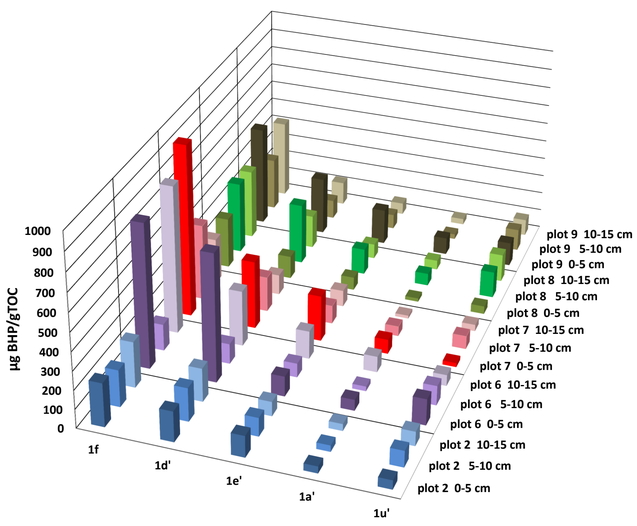

Fig. 1 Average Concentration of Major BHPs in Palace Leas Plots

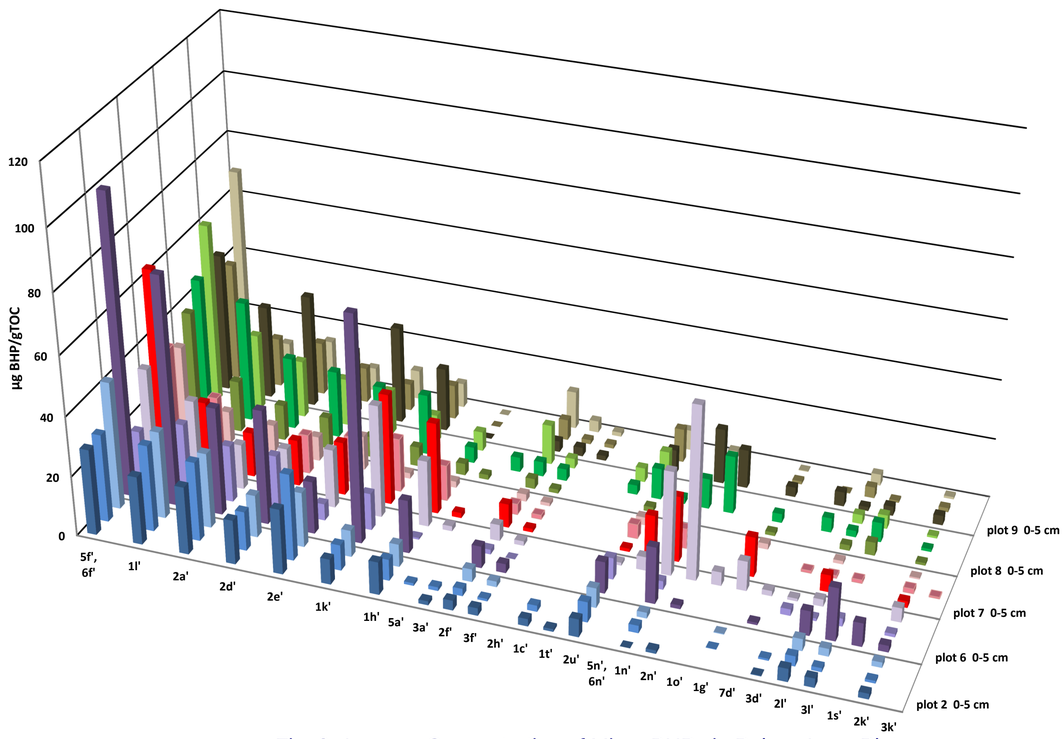

Fig. 2 Average Concentration of Minor BHPs in Palace Leas Plots

Results and Discussion

Up to 32 different BHPs were identified in the soil samples (Table 1).The BHPs can be split into major and minor components. The major components are 5 BHPs that dominate the total BHP concentration. Aminotriol (**1f'**), BHT cyclitol ether (**1d'**) and BHT (**1a'**) are commonly found in all environments tested and adenosylhopane (**1e'**) and adenosylhopane type-1 (**1u'**) have been identified as soil marker BHPs, being unique to soils (Cooke et al, 2008).
Potentially far more instructive are the minor BHPs that comprise the remaining BHP concentration. These BHPs indicate subtle differences between the various plots that may have arisen due to the various fertiliser regimes. For example plot 2 contains significant quantities of aminopentol (**1c'**), a methanotroph marker (Table 1) whereas this BHP is absent from all other plots. This observation is in agreement with the expected increased presence of methanotrophs in manured plots (Seghers et al., 2003). Each plot displays significant differences in the presence / absence of specific minor BHPs or significant concentration differences indicating differences in the bacterial population.
The differences can, however be hard to visualise so an alternative approach must be taken to highlight the impact of the BHP signatures. As previously stated many BHPs are strongly linked to specific bacteria and bacterial types (Table 1). Grouping the BHPs into bacterially related clusters enables PCA analysis of the results.
Fig 3 shows the loadings plot for the analysis of the Palace Leas plots and clearly demonstrates that different bacterial groups have different influences on the plots. The scores plot (Fig 4) shows that the different plots are separated by the their BHP content. Again it is clear that for the case of plot 2 it is the presence of a methanotroph signature that distinguishes this plot. For plot 7 it is the diversity of the BHP signature that is important, indicating either a diverse bacterial population or conditions that require the production of a wide range of BHPs.

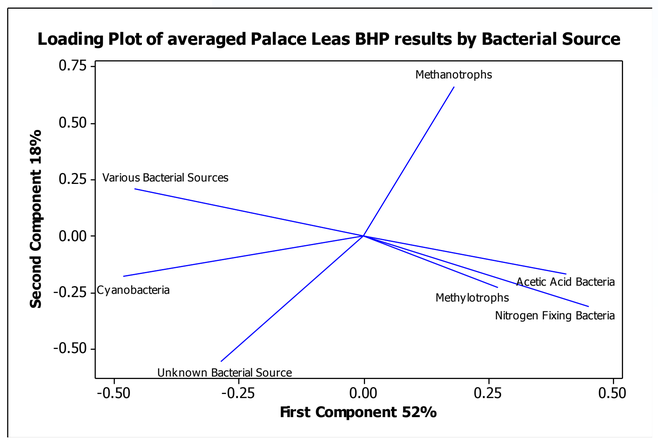

Fig. 3 Loading Plot of averaged Palace Leas BHP results by Bacterial Source

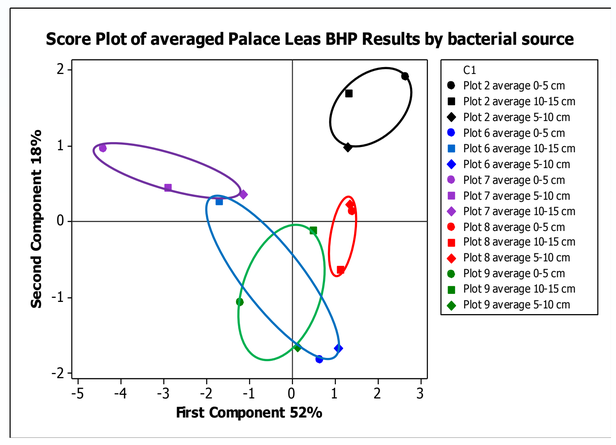

Fig. 4 Scores Plot of averaged Palace Leas BHP results by Bacterial Source

Global Relationships

An identical analysis was conducted on a suite of global soil and river fan sediments (Cooke 2010; Cooke et al., 2008a, 2008b, 2009; Redshaw et al., 2008; Xu et al., 2009), to assess the potential of this approach to separate soils and sediements. The loading plot (Fig. 5) indicates that again the presence of methanotrophs and the ability to identify a wide range of BHPs are significant factors in the separation of the soils and sediments (Fig. 6). There is a clear distinction between many of the locations . The majority of the soils are separated by the relationship between the common known sources and the dominant variously sourced BHPs. The presence of methanotrophs and the lack of soil markers separates the sediments from the soils.
The most unusual result was the location of the Palace Leas plot soils and a set of soils from a NE woodland soil. These are distinct from the other soils and it is believed that the diverse BHP signature from these soils influences their position on the plot.

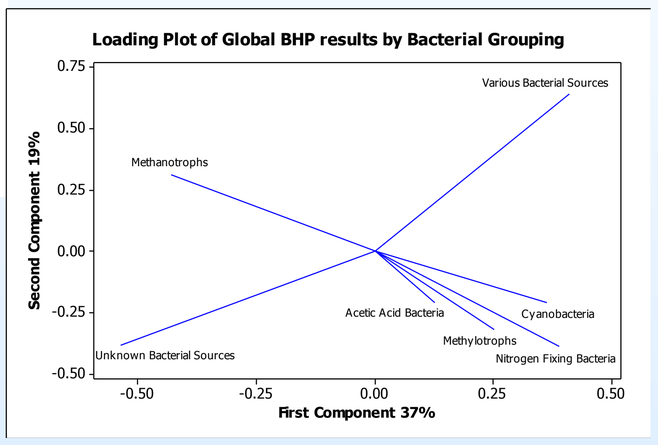

Fig. 5 Loading Plot of Global BHP results by Bacterial Grouping

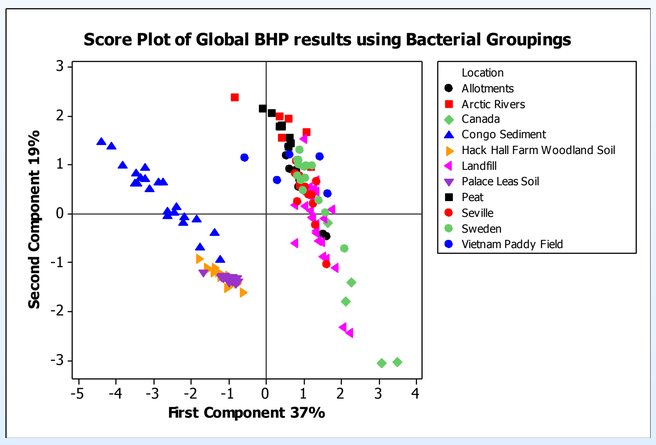

Fig. 6 Scores Plot of Global BHP results by Bacterial Grouping

Conclusions

It is clear from these results that there is great potential in the use of BHPs to identify soil bacterial processes and distinguish between different soils. However much work is needed to be conducted on a much greater suite of soils and on improving the relationship between the BHPs and the source bacteria, especially in those BHPs that are currently of unknown origin.

References

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