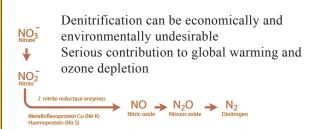
Spatial linkage between *NirK* diversity and denitrification activity in three arable fields. Scottish Crop

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Introduction



Methods

Replicate samples were taken from three arable fields at SCRI. Total DNA was extracted and amplified, by PCR, using *Nir*K primers. Products were cloned and a high throughput sequencing methods ware applied. 96 clones from each sample were sequenced. Sequences were aligned in POA and grouped at a 0.075 substitution per base level in Topal-i. A neighbor joining tree was produced, using a F84 model with gamma rates. Rarefaction analysis was used to estimate saturation of coverage and PCO analysis applied to indicate relationships between samples

Results

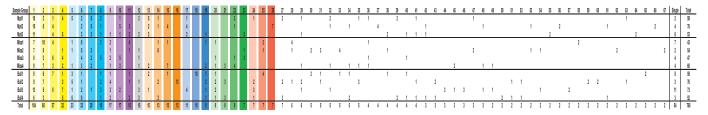
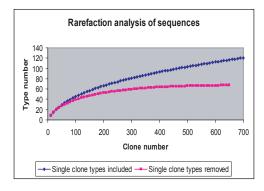
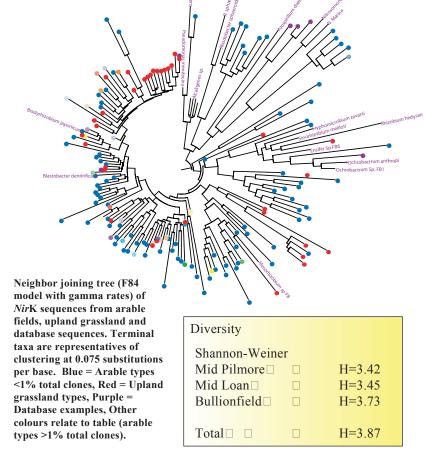
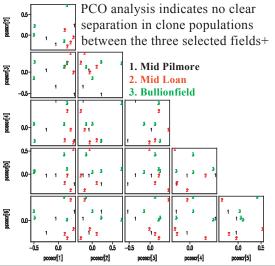


Table of clones grouped at 0.075 substitutions per base coloured backgrounds are shown where groups represent >1% of total clones and correlate with the phylogenetic tree



Rarefaction analysis indicates that, excluding single clone types (each of which represents 0.14% of the total population) sequence diversity has been exhausted.





Conclusions & Acknowledgements

High throughput sequencing has exhausted sequence diversity, excluding single clone types.

There is no clear separation in NirK patterns between sampled fields.

Diversity is high when compared to upland grass rhizoplane samples (Abstract A7-2).

There is little correlation between arable and upland types (Abstract A7-2).