Relationship between soil nitrification activity and population dynamics

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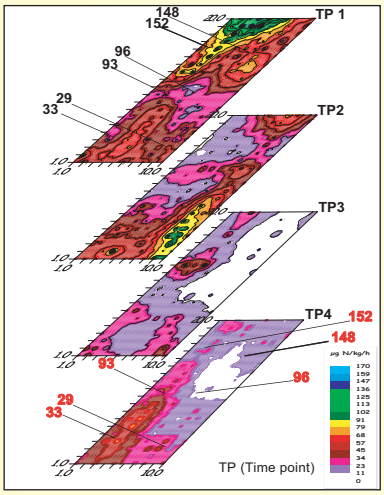
Introduction

Previous work at SCRI showed potential nitrification rates in 3 neighbouring fields, 200m apart, to be significantly different, with distinct temporal patterns in each.
Competitive PCR suggested nitrifying population sizes were different between, but did not change with time within, each field.
There was no relationship between population size and PNR.
Molecular analysis, using phylogenetic PCR, placed the nitrifiers in the *Nitrosospira* spp. cluster (Wheatley *et al*, EJSS,54 707-714).
We have analysed spatial patterns of nitrification, denitrification and other soil characters in one field at SCRI.
We present results of a preliminary molecular analysis of nitrifying populations (using an *amo* A gene fragment) from samples selected to give a range of activities.



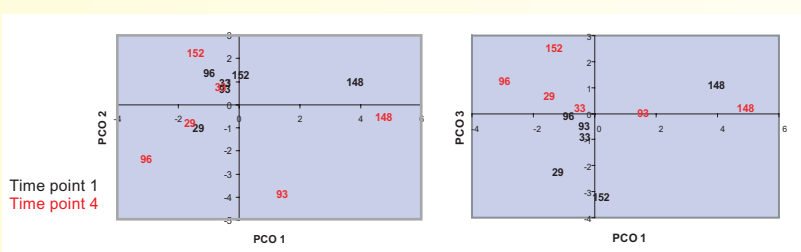
Method

Potential nitrification was estimated and *amo* A gene fragments amplified, by PCR, from selected samples. Products were cloned and high-throughput sequencing, phylogenetics and multi-variant statistics applied to assess nitrifying population complexity.

Potential nitrification is spatially and temporally variable. Inverse distance weighted plots represent the distribution of activity across the field site. Sampling locations for molecular analysis are indicated.

	Sample	Sequence Group 1	2	3	4	5	6	7	8	9	10	11	12	13	14	single clones	clone number
Time Point 1 March	29	61.8	14.5	3.9	1.3	1.3	1.3	1.3	2.6	1.3		1.3	1.3		1.3	6.6	76
	33	65.2	8.7	8.7	4.3	2.2	6.5			2.2						2.2	46
	93	64.4	4.4	8.9	11.1		2.2	4.4	2.2	2.2							45
	96	57.4	14.9	6.4	12.8		4.3		2.1							2.1	47
	148	25.0	12.5		12.5	25.0				12.5	12.5						8
	152	70.0	12.0	2.0	6.0	4.0									2.0	4.0	50
Time Point 4 June	29	35.7	20.2	13.1	7.1	7.1	4.8	3.6			1.2	1.2				6.0	84
	33	49.5	19.8	13.2	5.5		1.1	1.1	1.1	2.2	2.2					4.4	91
	93	21.2	6.1	3.0	6.1	33.3	3.0	6.1		3.0	3.0		3.0	3.0		9.1	33
	96	30.9	17.3	19.8	4.9	2.5	3.7	6.2	4.9			1.2	1.2			7.4	81
	148	25.0	8.3			41.7				8.3	8.3			8.3			12
	152	25.0	23.9	15.9	30.7		2.3		2.3								88
Total		45.7	15.7	10.4	9.4	4.5	2.7	2.1	1.7	1.2	0.9	0.5	0.5	0.3	0.3	4.1	661

Summary of the distribution of sequence groups, expressed by percentage, and the total clone number. 27 single clone groups were found. Colour indicates sequence group position on phylogenetic tree.



Principal component analysis was performed to assess sequence group distribution.
PCO 1 separates sample 148 from other samples (loadings suggest this is mainly due to changes in sequence group 3, 5, 9, 10 and 13; note low sample size).
PCO 2 separates respective time points for samples 93 and 96 but clusters time points of other samples (loadings suggest this is mainly due to changes in sequence groups 4, 7, 12 and single clones).
PCO 3 separates samples on the basis of time (loadings suggest this is mainly due to changes in sequence groups 1-4 and 14).

A neighbor-joining tree (F84 model with gamma rates). Bootstrap analysis was performed (1000 repetitions) and shown where support exceeds 69%. All sequences detected fall in *Nitrosospira* spp. group confirming initial findings with phylogenetic primers, the *amo* A fragment utilised gave greater resolution.

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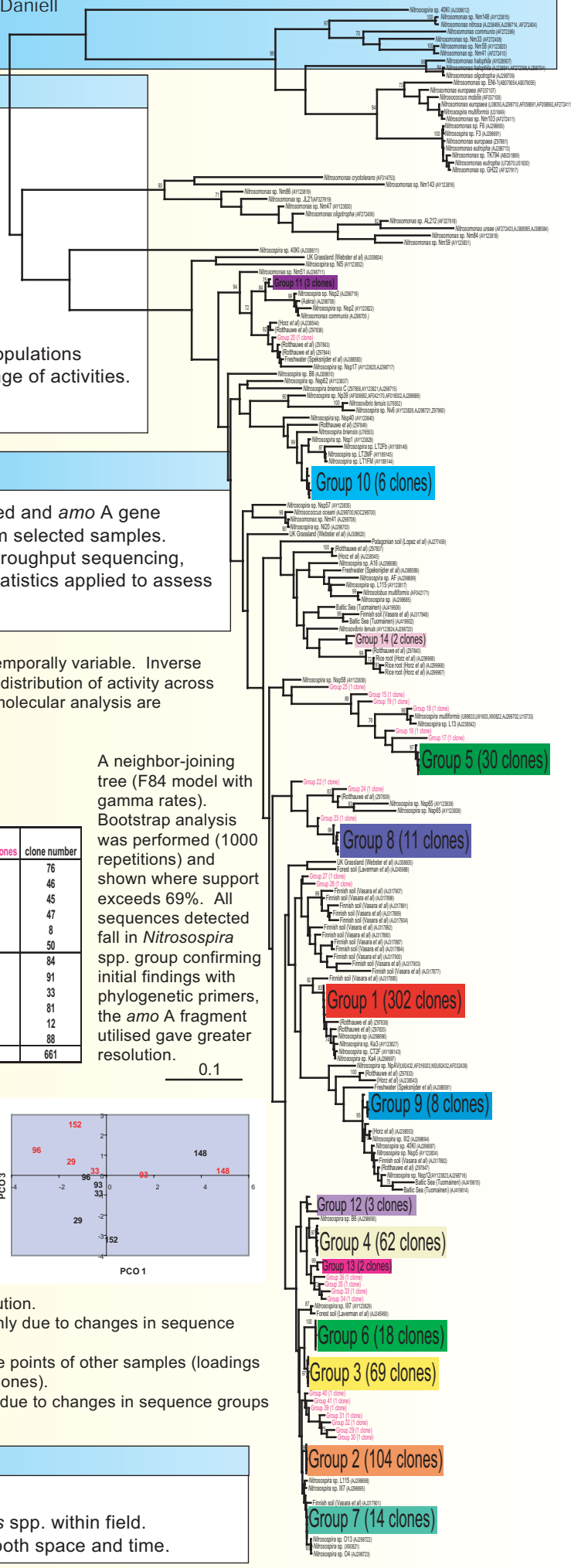

Summary

Nitrification rates show temporal and spatial variation.
Sequence analysis confirms no detectable presence of *Nitrosomanas* spp. within field.
Preliminary analysis suggests variation in nitrifier population across both space and time.