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INTRODUCTION

- Soil microbes perform key steps in global biogeochemical cycles and primary productivity, *e.g.* greenhouse gas (GHG) emissions.
- Ecological theories from macroorganisms describe the different relationships between ecosystem processes and biodiversity : ‘complementarity hypothesis’ explains the positive biodiversity-ecosystem relationship whereas ‘selection hypothesis’ suggests that the magnitude of a process results from the activity of few (key) species.

OBJECTIVE

Understand how microbes (*e.g.* methanotrophs) regulate biogeochemical cycles (*e.g.* methane (CH_4) oxidation) to improve precision of predictive models to apply for prediction of future global changes.

HYPOTHESIS

Ecological theories can be applied to microbial processes (methanotrophy) to explain/predict the regulation of GHG cycles (CH_4 fluxes) during land-use change (afforestation).

SITES & LAND USES

Seasonal sampling of soil cores (n=12) repeated across Scotland.



Site	Land use	Age of the forest
Bad à Cheo	Bog	-
	Young Pine	20 years
	Old Pine	40 years
Glensaugh	Grassland	-
	Young Pine	20 years
Craggan	Moorland	-
	Young Birch	62 years
	Old Birch	88 years
Tulchan	Moorland	-
	Young Birch	55 years
	Old Birch	65 years

RESULTS

- Soil function (CH_4 oxidation) and functional microflora (methanotrophic community structure) were affected by afforestation but not by temporal or spatial variations (Figure 1).
- *pmoA*-based T-RFLP and *pmoA* microarray analyses identified an increase in the relative abundance of USC α and Cluster 5 (CL5) methanotrophs in afforested soils (data not shown).
- PLFA-SIP experiments confirmed that active oxidation of atmospheric CH_4 was performed by a group of methanotrophs distantly related to *Methylosinus sporium* and *Beijerinckiaceae* family (not shown).
- Enhanced CH_4 sinks triggered by afforestation were associated with a decrease in the methanotroph species richness (Figure 2A) in favour for an increase in the dominance of members of USC α and CL5 (Figure 2B).

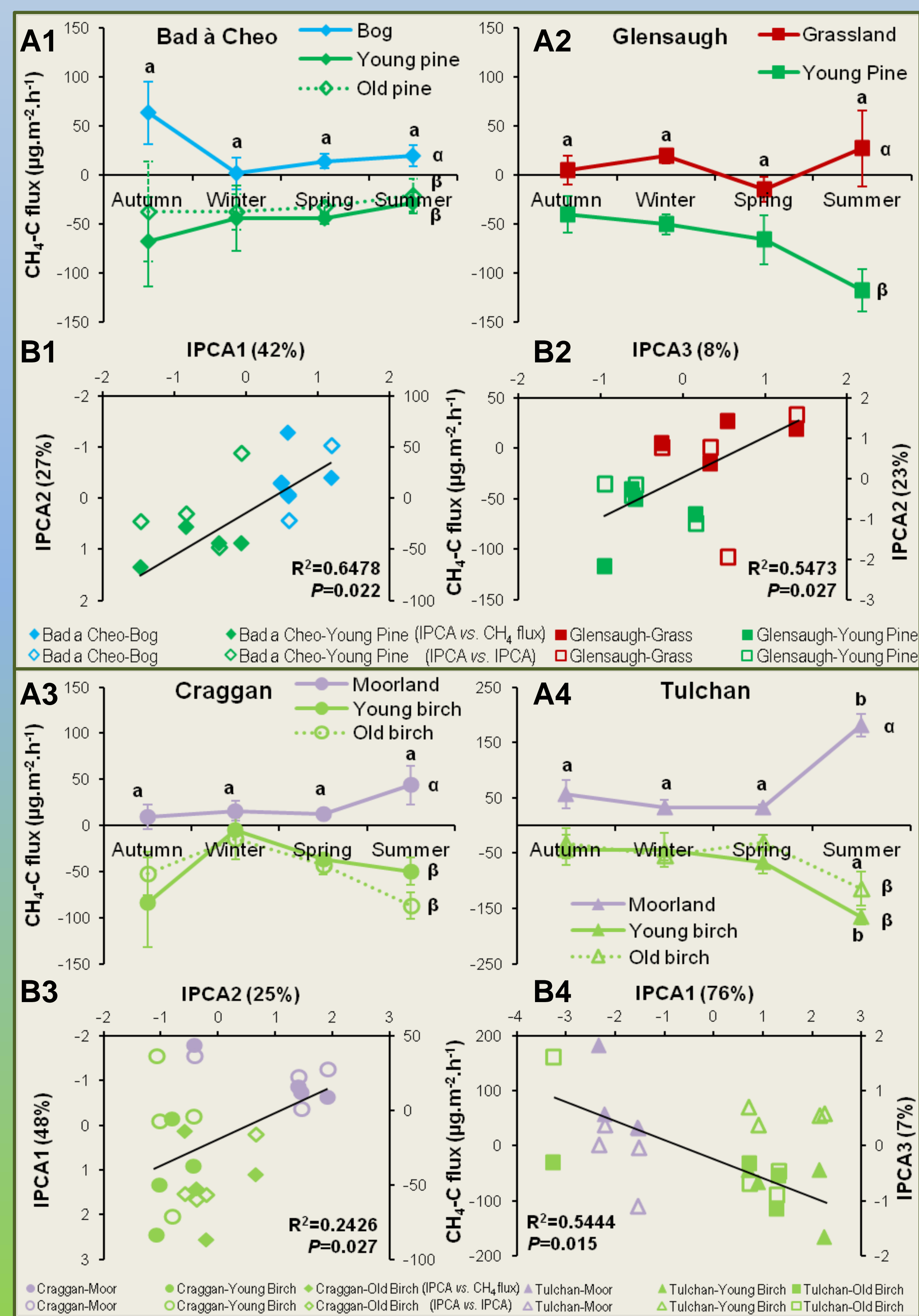


Figure 1: Seasonal net CH_4 fluxes (A1-A4); and relationship between net CH_4 flux and methanotrophic community structure (B1-B4). CH_4 flux measurements were obtained from a closed-chamber experiment (n=4). Seasonal IPCA scores were calculated from T-RFLP data based on the analysis of *pmoA* genes (n=4). For each site, statistical differences between seasons within each habitat are indicated by different Roman letters (a, b), while Greek letters (α , β) indicate statistical differences between land uses, according to multiple pairwise comparison ($\alpha=0.05$).

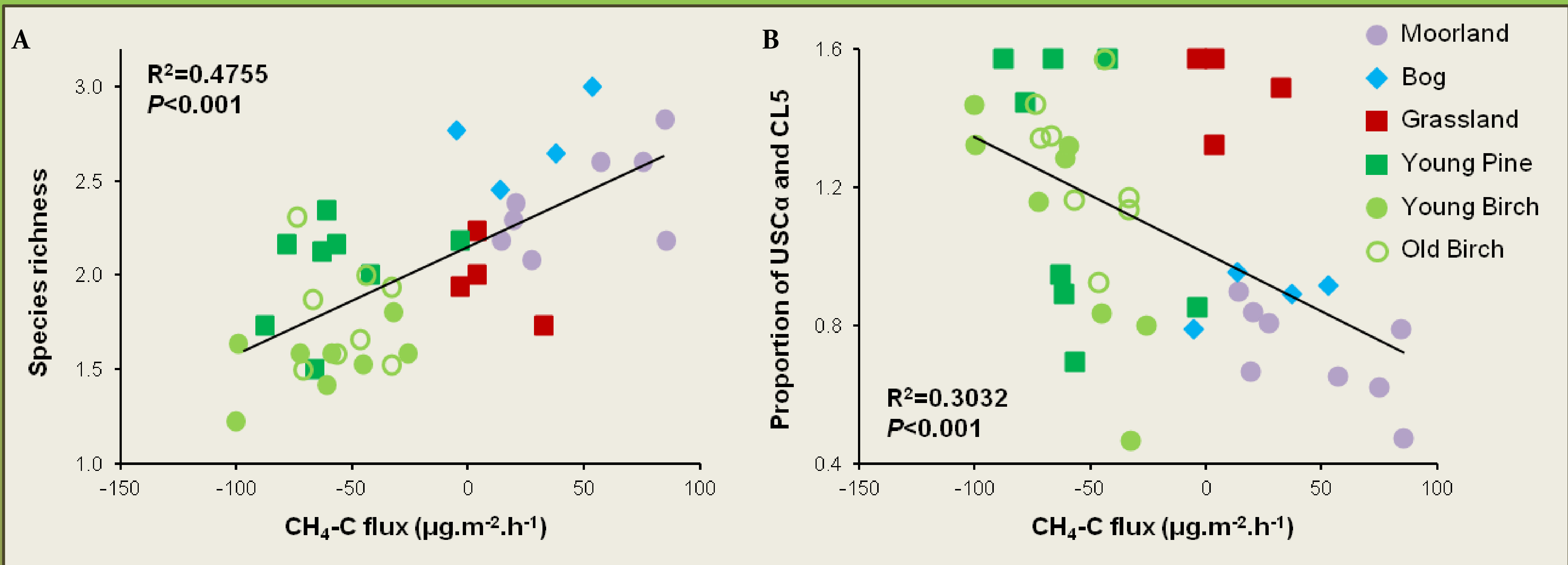


Figure 2: Relationships between methanotroph diversity and changes in net CH_4 fluxes associated with afforestation (n=40). (A) Species richness was calculated from the 15 most abundant T-RFs of the T-RFLP profiles (>94% coverage). (B) USC α /CL5 proportion was arcsine-transformed.

CONCLUSIONS

- Biogeochemical cycles (net CH_4 fluxes) can be explained by the selection theory due to the unique function of methanotrophs.
- Afforestation was characterised by enhanced CH_4 sinks in correlation to increased abundance of USC α in soils.
- Inclusion of microbial control of biogeochemical cycles in predictive models can improve the precision of prediction of future climate changes.