

INTRODUCTION

In coastal peatlands, global climate change is expected to alter precipitation events increasing the flux of CO₂ from soils to the atmosphere. Few studies have explored this phenomenon in coastal peatlands of the tropics, where sea-level rise would be expected to also alter soil C dynamics. With the intent of initiating new, cross-site research of neotropical coastal peatlands to investigate controls on CO₂ fluxes, we characterized bacterial diversity, soil nutrients, enzyme activities and soil CO₂ flux in 9 sites along a soil P/aboveground production gradient in Bocas del Toro, Panama.

The Panama wetland is the focus of a study where the hypothesis that the sequential development of an ombrotrophic peat bog leads to differentiation of limiting nutrients is under investigation. Based on paleoecological work characterizing peat depth and age, a decline in P concentrations has been linked with the development of this ombrotrophic bog in the wetland interior (Phillips *et al.* 1997).



Raphia palm forest at 0.3 km



Interior bog plain at 2.4 km

METHODS

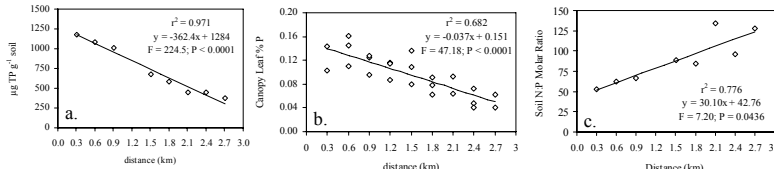
In the province of Bocas del Toro, Panama, the Changuinola mire is a 90 km² wetland area which developed on the western bank of Almirante Bay. A large portion of this wetland, the San San-Pond Sak, is a designated Ramsar site. This region of the Caribbean coast, predominantly from the southern coast of Costa Rica to the Chiriqui Lagoon of Panama encompasses an alluvial floodplain that drains numerous rivers from the Talamanca mountains (Phillips *et al.* 1997). This wetland assemblage type represents less than 0.5%, and the tropical bog therein, only 0.02% or 1300 ha of natural vegetation cover in the country of Panama, and is therefore a geographically unique resource (Correa *et al.* 2004).

Previous research characterizing the N and P status (foliar N, P and ¹⁵N of dominant species, soil N and P concentrations and soil N:P molar ratio) of plant communities every 300 m along a 2.7-km transect demonstrated increasing P limitation with distance into the interior bog plain (Troxler 2007). To link plant community nutrient status and microbial structure and function with soil CO₂ flux, we characterized soil P concentrations, bacterial diversity, enzyme activities, and soil CO₂ flux along the 2.7-km transect. DGGE patterns of two different primer sets for bacteria were characterized. Enzyme activities were measured using 4-methylumbelliferyl (MUF) substrates. Fluorescence was measured using a spectrofluorometer. Soil CO₂ flux rates were measured on replicate slurried soil samples that were incubated for 40 hours in 20 mL gas vials. Headspace gas was measured on a HP gas chromatograph. Soil P concentrations were determined using the Solorzano method.

RESULTS

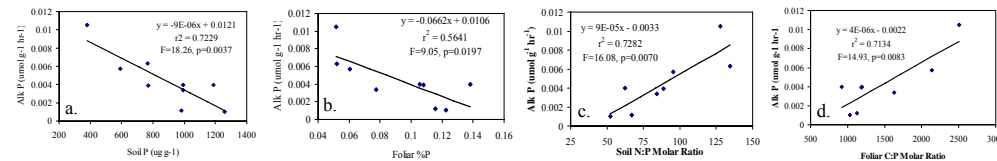
Changes in plant community nutrient status

Distance into the interior bog plain was negatively related to soil P and foliar P concentrations (Figure 2a,b), and positively related to soil N:P molar ratios (Figure 2c).



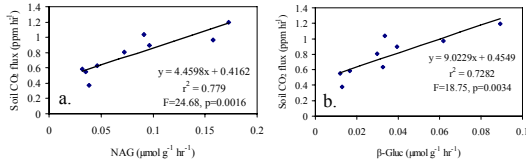
Relationships between alkaline phosphatase activity & nutrient status

Soil P and foliar %P of canopy species were negatively related to alkaline phosphatase activity (AlkP; Figure 3a,b) whereas soil N:P and foliar C:P were positively related to AlkP (Figure 3c,d).



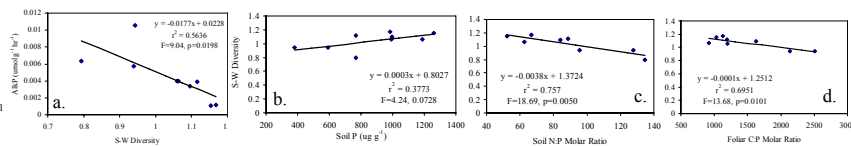
Relationships between C & N enzyme activities and soil CO₂ flux

Of the soil parameters measured, activities of β-N-Acetylglucosaminidase (NAG) and β-D-Glucosidase (β-Glu) were positively related to CO₂ flux rates, explaining 78% and 73% of the variation, respectively (Figure 4a,b).



Relationships between bacterial diversity & nutrient status

We found a negative relationship between bacterial diversity and AlkP (Figure 5a), a positive relationship between bacterial diversity and soil P (Figure 5b) and negative relationships between soil N:P and foliar C:P and bacterial diversity (Figures 5c,d).



DISCUSSION

In contrast to other peatland studies, we found no relationship between bacterial diversity and soil CO₂ flux. In this tropical coastal peatland, bacterial diversity was related to soil P dynamics. It is plausible that these patterns may be driven by species richness as a function of P availability as opposed to species diversity. We are currently sequencing DGGE bands to characterize bacterial functional groups and species where possible. In this coastal peatland, soil P dynamics do not appear to be important drivers of soil CO₂ flux. Here, enzymes important in mineralizing C and N were strongly related to soil CO₂ flux. Activities of these enzymes have been linked to hydrologic factors. Thus, while changes in precipitation with global climate change may alter watershed dynamics related to the position of the ombrotrophic bog, these changes that lead to the altered inundation of peat soils in this wetland are likely to have a large effect on soil CO₂ flux. However, further study is needed to understand the effects of hydrology and nutrient status on soil CO₂ fluxes in low-latitude coastal peatlands.

REFERENCES

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