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The Responses of Microbial Communities to Drought in Bog, Fen, and Riparian Wetlands

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Climate change models suggest that environmental pressures on ecosystems will increase as global warming intensifies (Manabe and Wetherald, 1986; Houghton *et al.,* 2001). In particular, drought is likely to exert a major influence on wetlands which function as a substantial global sink for CO_2. However, information on the response of soil microbial communities to drought is sparse. To explore the abundance, genetic diversity and composition of eubacterial, methanogen and denitrifier communities and their responses to drought, Real-time PCR and Terminal restriction fragment length polymorphism (T-RFLP) analysis were applied using bacterial 16S rRNA, methyl coenzyme M reductase (*mcrA)*, and nitrite reductase (*nirS*) genes in 3 types of wetlands, namely bog, fen and riparian wetland.

The abundance of all microbial communities inhabiting the bog and fen decreased following drought with the exception of methanogens in the fen. Interestingly, the abundance of all microbial communities inhabiting the riparian wetland did not differ by drought (Table 1). The diversity of bacterial 16S rDNAs significantly decreased by drought in the riparian wetland ($p < 0.05$), whereas drought led to an increase in diversity in the bog ($p < 0.1$). There was no difference in the diversity of eubacterial communities in the fen following drought. The diversity of denitrifiers increased with drought in the riparian ($p < 0.1$).

Table 1. Gene copy numbers per dry soil of gram of amplified bacterial 16S rRNA, *mcrA* and *nirS* genes following the drought treatment in riparian, fen, and bog soils. Data were analyzed by t-test at $p < 0.001$***, $p < 0.01$**, and $p < 0.05$* n = 6 (2-tails)

		Gene copy numbers g^{-1} dry soil (Mean SEM)		
		Riparian	Fen	Bog
Bacterial 16S rDNAs	Control	$5.6\times10^{8} \pm 1.9\times10^{8}$	$7.7\times10^{9} \pm 2.1\times10^{9}$	$1.7\times10^{10} \pm 3.2\times10^{9}$
	Drought	$2.0\times10^{8} \pm 5.3\times10^{7}$	$1.1\times10^{9} \pm 2.0\times10^{8}$*	$2.3\times10^{9} \pm 2.0\times10^{8}$**
mcrA	Control	$1.8\times10^{7} \pm 6.3\times10^{6}$	$3.3\times10^{8} \pm 2.7\times10^{8}$	$1.4\times10^{8} \pm 2.0\times10^{7}$
	Drought	$7.2\times10^{6} \pm 2.2\times10^{6}$	$5.8\times10^{8} \pm 5.6\times10^{8}$	$1.7\times10^{7} \pm 3.4\times10^{6}$***
nirS	Control	$1.4\times10^{7} \pm 2.7\times10^{6}$	$1.9\times10^{8} \pm 1.5\times10^{7}$	$1.4\times10^{8} \pm 3.0\times10^{7}$
	Drought	$9.7\times10^{6} \pm 1.5\times10^{6}$	$4.5\times10^{7} \pm 6.9\times10^{6}$***	$2.1\times10^{7} \pm 2.7\times10^{6}$**

Table 2. Shannon's indexes of T-RFLP fingerprints of amplified bacterial 16S rDNA, *mcrA* and *nirS* genes in control or drought treatments in riparian, fen and bog soils. Data were analyzed by t-test at $p < 0.01^{**}$, $p < 0.05^{*}$ and $p < 0.1(^{*})$ n = 6 (2-tails)

	Mean ± SEM		
Treatments	Riparian	Fen	Bog
Control	3.9 ± 0.09	3.6 ± 0.11	3.2 ± 0.07
Drought	3.3 ± 0.11*	3.7 ± 0.05	3.5 ± 0.13(*)
Control	0.8 ± 0.49	1.0 ± 0.13	1.3 ± 0.12
Drought	0.9 ± 0.27	1.0 ± 0.38	1.3 ± 0.38
Control	1.9 ± 0.39	1.8 ± 0.38	1.8 ± 0.22
Drought	2.3 ± 0.18(*)	2.1 ± 0.37	2.2 ± 0.29

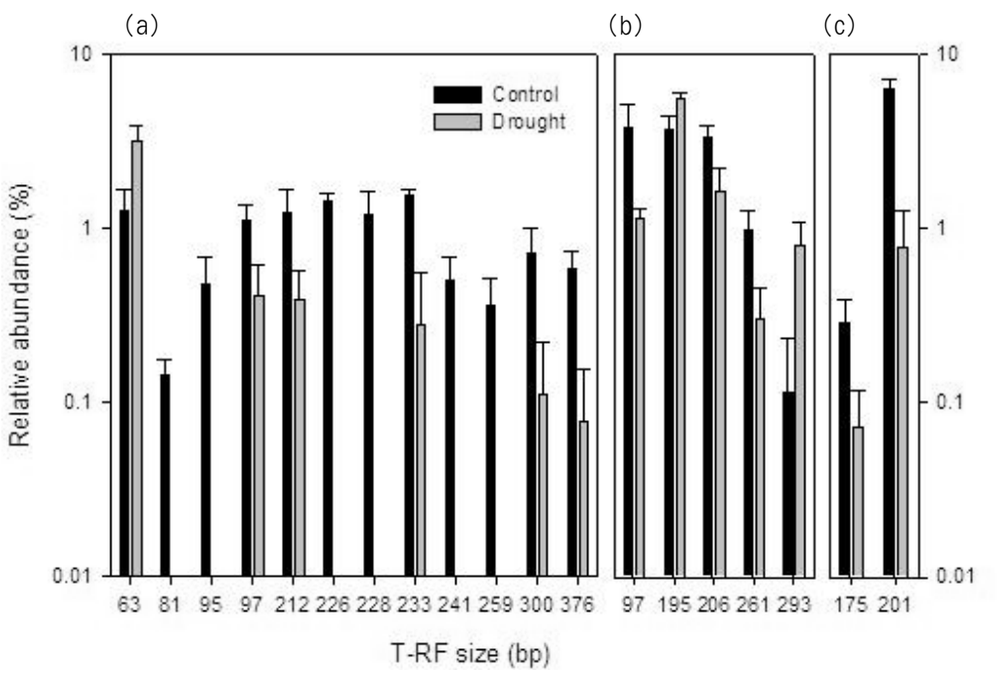

Fig. 1. Eubacterial 16s rDNA T-RFs that differed significantly between control and drought treatments in the riparian (a), fen (b), and (c) bog wetlands, based on indicator species analysis ($p < 0.05$, n = 6, 2-tails).

Drought had no influences on the diversity of methanogens in any of the wetlands examined (Table 2).

As a result of MRPP testing, drought slightly altered the composition of eubacterial communities in the riparian wetland following drought ($A = 0.04$, $p < 0.05$), but not those in the fen and bog sites. The composition of methanogens and denitrifiers did not differ with drought in any of the wetlands examined (Table 3). Indicator Species Analysis for bacterial 16S rDNA profiles yielded a total of 12 T-RF indicators for drought treatments in the riparian wetland ($p < 0.05$). The bog and fen have just 2 (i.e. 175, 201 bp) and 5 (i.e. 97, 195, 206, 261, 293 bp) indicator species, respectively (Fig. 1). For methanogens, T-RF of 26 bp was an indicator species for drought treatments in both fen and riparian samples and T-RF of 45 bp in the bog. For denitrifiers, T-RFs of 102 bp was an indicator species for drought conditions in the riparian wetland ($p < 0.05$), whereas there were no indicator species in the

bog and fen (Fig. 2).

Table 3. Results of MRPP testing for significant differences between different groups determined on the basis of 16S rDNAs, *mcrA*, and *nirS* T-RFLP profiles. Significant results are shown ($p < 0.05$, 2-tails).

Drought effect	Difference in proportional abundance		
	Bacterial 16S rDNAs	*mcrA*	*nirS*
Fen	-	-	-
Riparian	0.04 ($p < 0.05$)	-	-
Bog	-	-	-

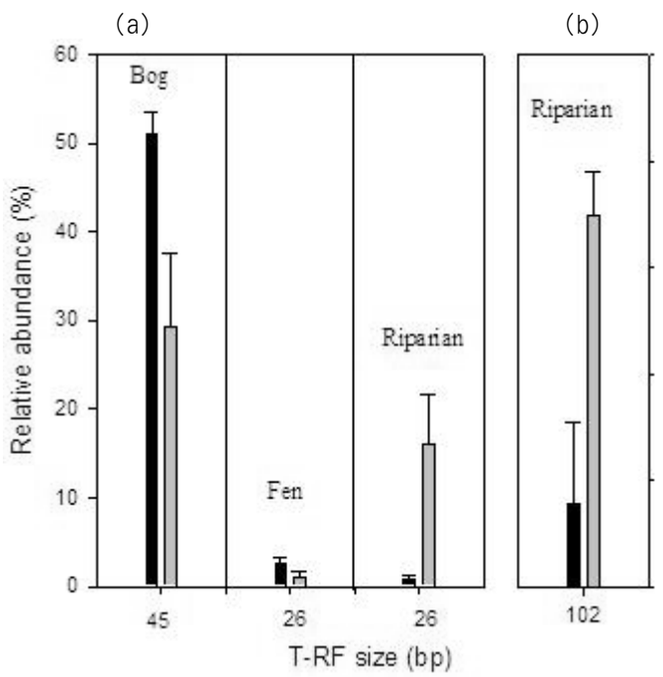

Fig. 2. *McrA* (a) and *nirS* (b) T-RFs that differed significantly between control and drought treatments in the riparian. The black and gray bars represent control and drought respectively.

References

1. Manabe, S., and Wetherald, R.T. (1986) Reduction in summer soil wetness induced by an increase in atmospheric carbon dioxide. *Science* **232:** 626-628.
2. Houghton, J.T., Ding , Y., Griggs, D.J., Noguer, M., van der Linden, P.J., and Xiaosu, D. (2001) Climate Change 2001: The Scientific Basis: Contributions of Working Group I to the Third Assessment Report of the Intergovernmental Panel on Climate Change. USA, New York: Cambridge University Press.