Changes in soil microbial metabolic activity during long-term forest restoration on the central Loess Plateau, China

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March 11, 2022

Abstract

Secondary forest restoration can alter terrestrial ecosystem processes and potentially impact subsurface carbon dynamics. However, the effects of long-term forest restoration on the soil microbial metabolic activity remain unclear. So, the aim of this study was to explore the response of soil microbial metabolism to forest restoration. Among them, the soil basal respiration (BR), microbial quotient (qMB), and metabolic quotient (qCO_2) were studied. This study investigated a natural vegetation restoration sequence approximately ~160 years after farmland abandonment on the central Loess Plateau, China, corresponding to five vegetation restoration stages including farmland, grassland, shrubland, pioneer forests, and climax forests. The results showed that BR and qCO_2 were increased following forest restoration, whereas qMB showed the opposite trend. Forest restoration also increased the activities of β -1,4-glucosidase and β -D-cellobiosidase. Restoration age, litter traits such as nitrogen, cellulose and lignin decomposition rates, dissolved organic carbon contents, fungi and bacteria composition were also important indicators affecting microbial metabolic activities. Long-term forest restoration can change soil microbial community structure, reduce carbon mineralization efficiency, improve soil microbial carbon utilization efficiency, and promote soil organic carbon accumulation.

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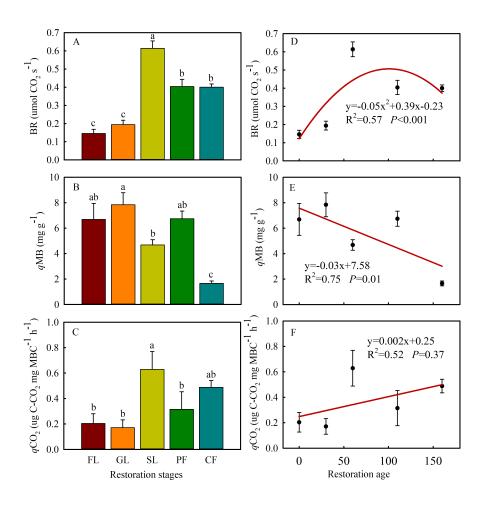
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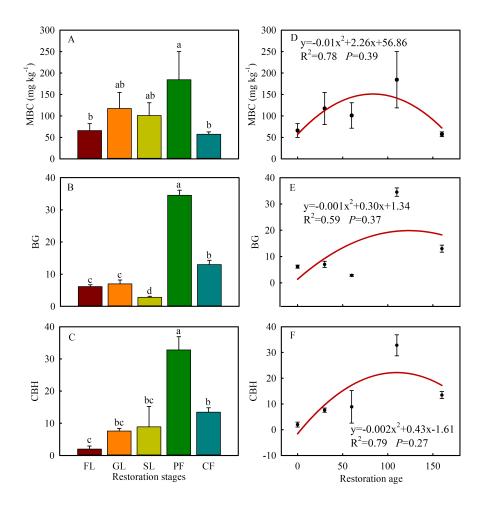
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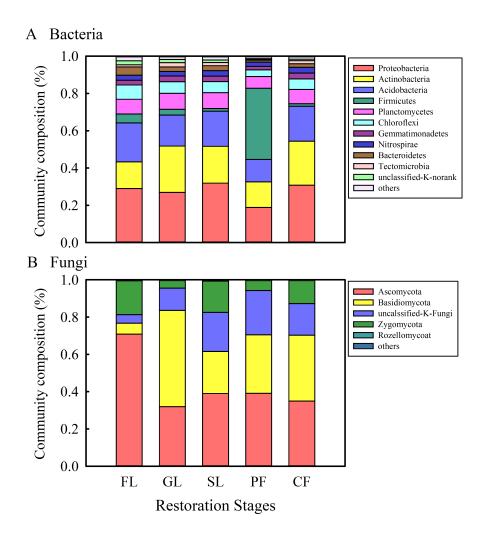
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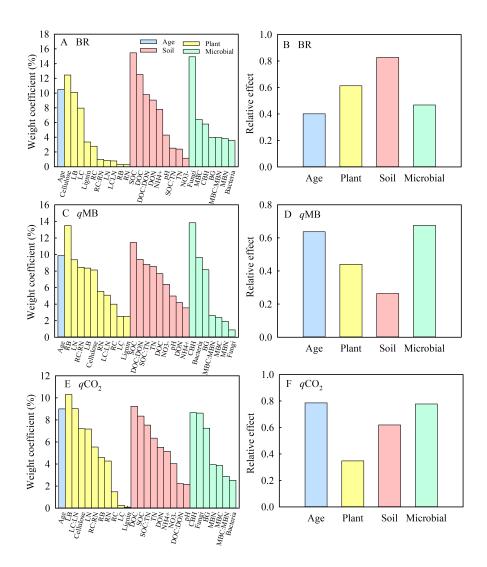
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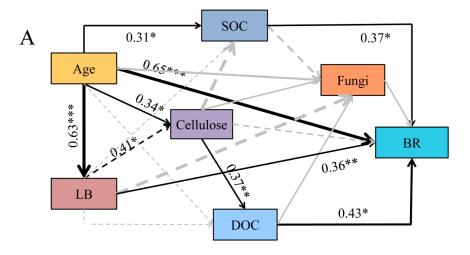




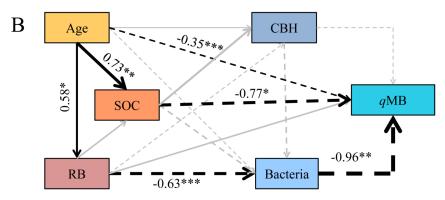


Age	0.49*	-0.67**	0.17	1.0
LB	0.08	-0.32	0.23	
LC	-0.05	0.58*	-0.18	
LN	0.81**	-0.57	0.76**	0.0
LC:LN	-0.77**	0.81**	-0.62**	
Cellulose	0.11	0.01	0.02	
Lignin	0.15	-0.19	0.36	
RB	0.70**	-0.54*	0.56**	-1
RC	0.21	0.42	0.04	
RN	-0.01	-0.67**	0.15	
RC:RN	-0.15	0.60*	-0.28	
SOC	0.41*	-0.77**	0.28	
TN	0.65**	-0.57*	0.29	
SOC:TN	0.09	-0.66**	0.16	
DOC	0.52**	-0.19	0.16	
DON	0.34	-0.25	0.04	
DOC:DON	0.67**	-0.10	0.40	
$\mathrm{NH_4}^+$	0.06	-0.11	0.13	
NO_3	0.20	-0.70**	0.14	
рĤ	0.28	-0.27	0.38	
MBC	0.10	0.56*	-0.51*	
MBN	0.20	0.31	-0.46*	
MBC:MBN	-0.12	-0.31	0.04	
Bacteria	-0.65**	-0.19	0.13	
Fungi	0.21	0.46	-0.64**	
BG	0.34	-0.40	-0.01	
CBH	0.38	-0.34	-0.02	
	BR	$q\mathrm{MB}$	$q\mathrm{CO}_2$	ı

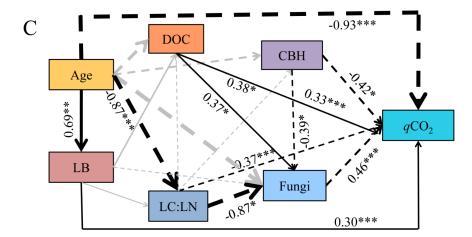




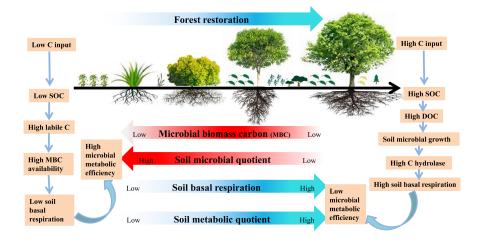
 χ^2 =0.83, df=1, P=0.36, CFI=1, RMSE=0.00



 χ^2 =0.70, *df*=2, P=0.013, CFI=0.96, RMSE=0.01



 χ^2 =0.355, *df*=3, *P*=0.84, CFI=1, RMSE=0.00



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