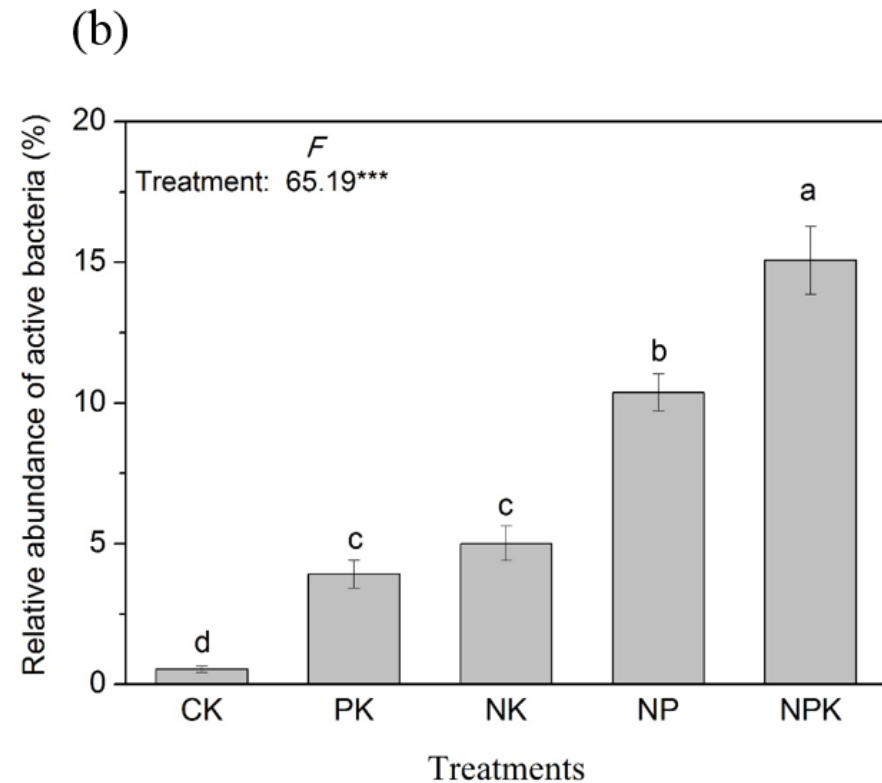
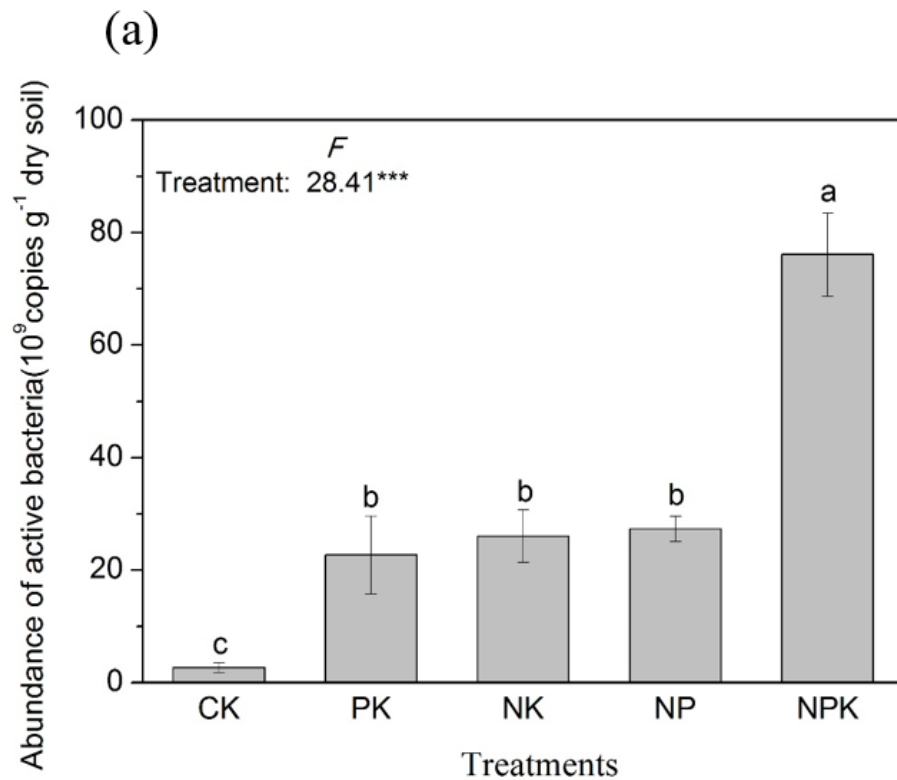
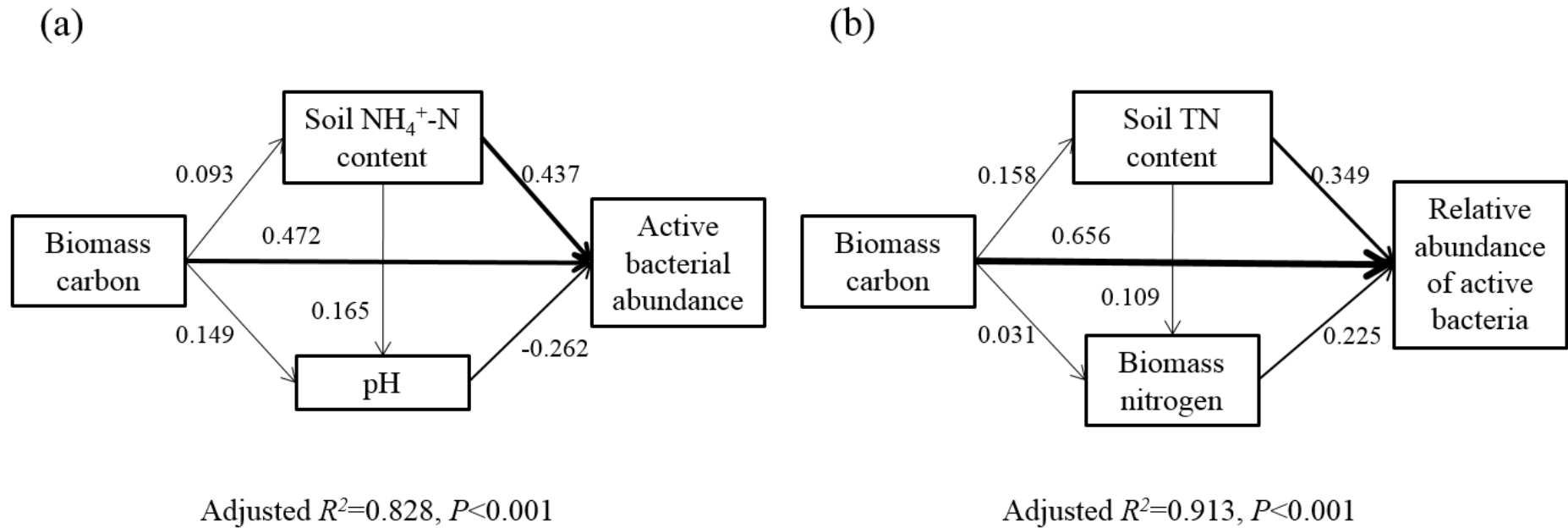


1 **Fig.1** Absolute (a) and relative (b) abundances (mean±SE) of active bacteria in the fertilization treatments. Relative abundance is the ratio of  
2 active to total bacterial abundance. CK, no fertilizer; PK, chemical phosphorus and potassium fertilizer; NK, chemical nitrogen and K fertilizer;  
3 NP, chemical N and P fertilizer; NPK, chemical N, P and K fertilizer. Different letters indicate significant differences.



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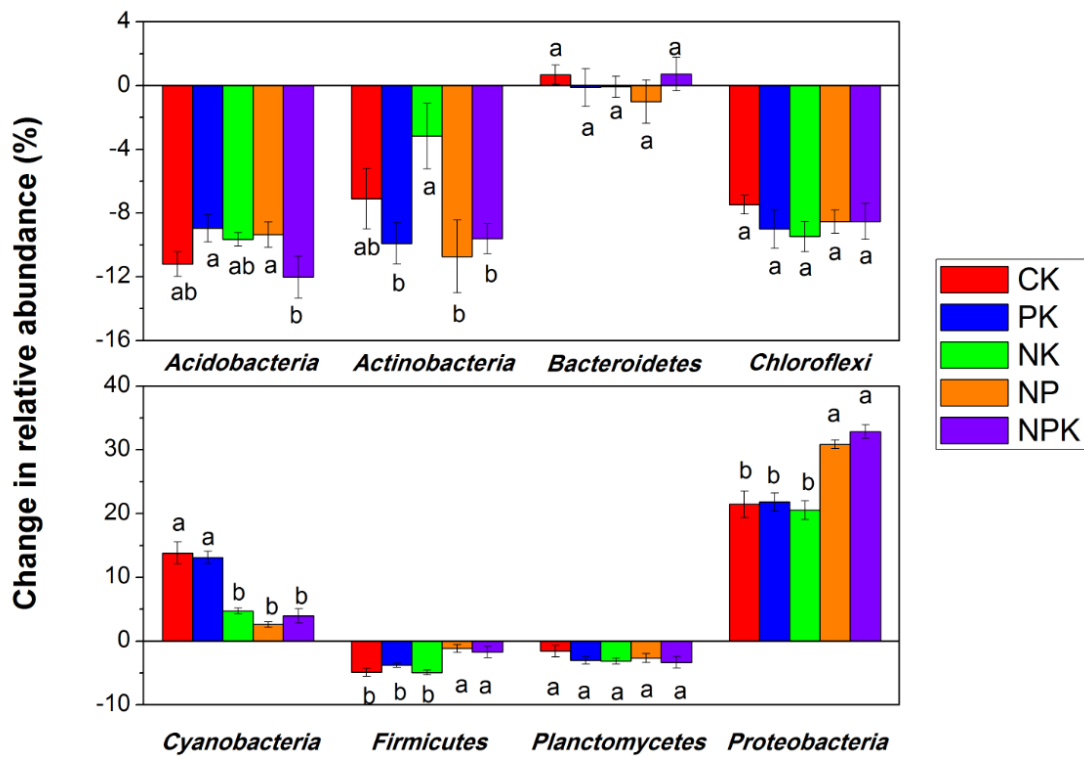
6 **Fig.2** Path analysis based on stepwise regression identifying the relationships among the environmental variables and the absolute (a) and relative  
 7 (b) abundances of active bacteria. TN, total nitrogen content. The arrows between the environmental factors and the active bacteria denote direct  
 8 effects, and the arrows among the environmental factors denote indirect effects. The number above the arrows represents path coefficient.



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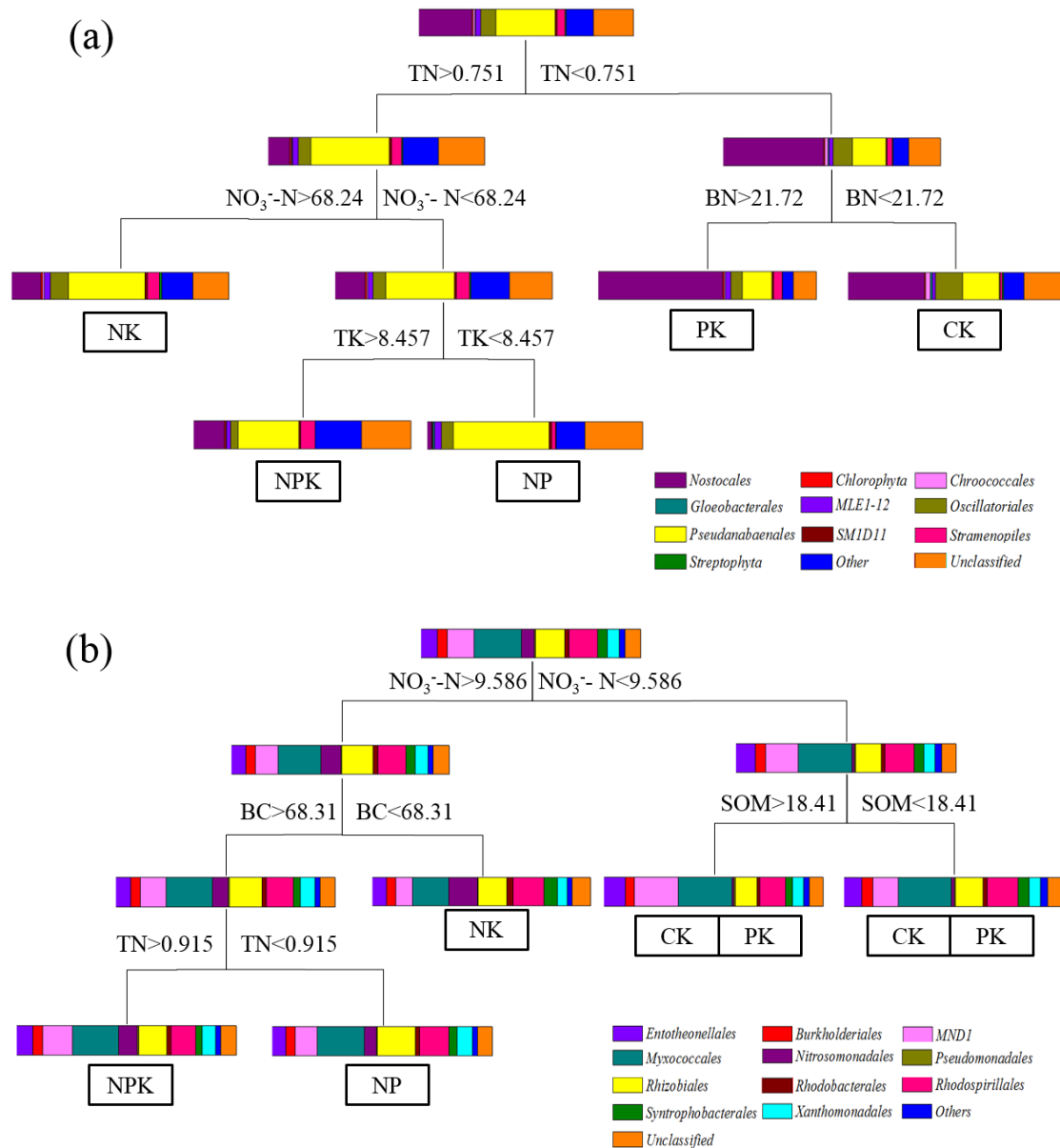
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11 **Fig.3** Changes in the relative abundances (mean±SE) of eight dominant phyla that  
 12 represents the differences between the active and total bacteria in the treatments. The  
 13 values (%) were the differences between relative abundances from RNA-derived and  
 14 DNA-derived community. CK, no fertilizer; PK, chemical phosphorus and potassium  
 15 fertilizer; NK, chemical nitrogen and K fertilizer; NP, chemical N and P fertilizer; NPK,  
 16 chemical N, P and K fertilizer. Different letters indicate significant differences.



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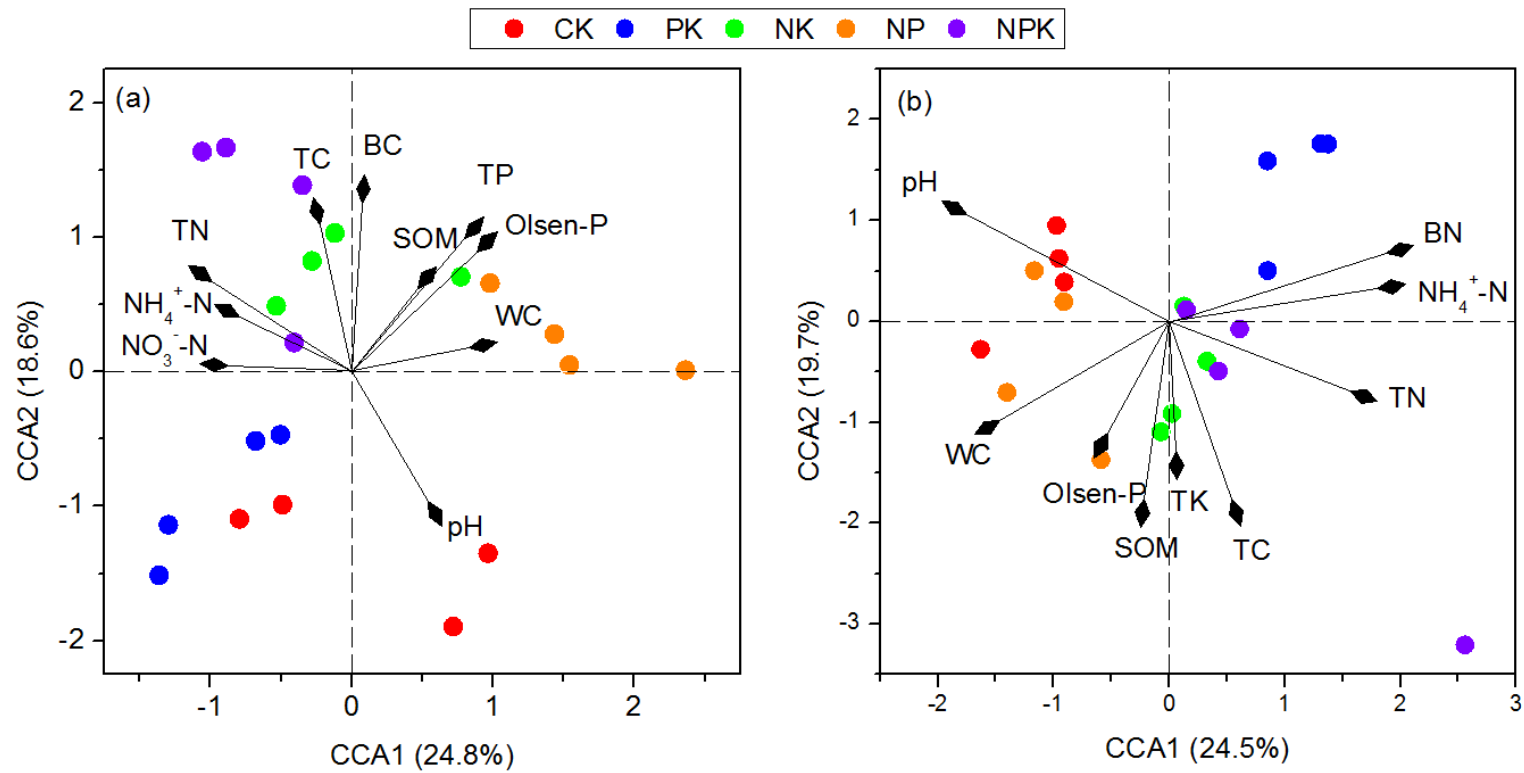
18 **Fig. 4** Multiple regression tree analysis indicating the relationships between the  
 19 environmental variables and the compositions of the active communities of  
 20 *Cyanobacteria* (a) and *Proteobacteria* (b). SOM, soil organic-matter content(g/kg);  
 21 TC, total carbon content(g/kg); TN, total nitrogen content(g/kg); TK, total potassium  
 22 content(g/kg); BC, biomass carbon content(mg/kg); BN, biomass N content(mg/kg).



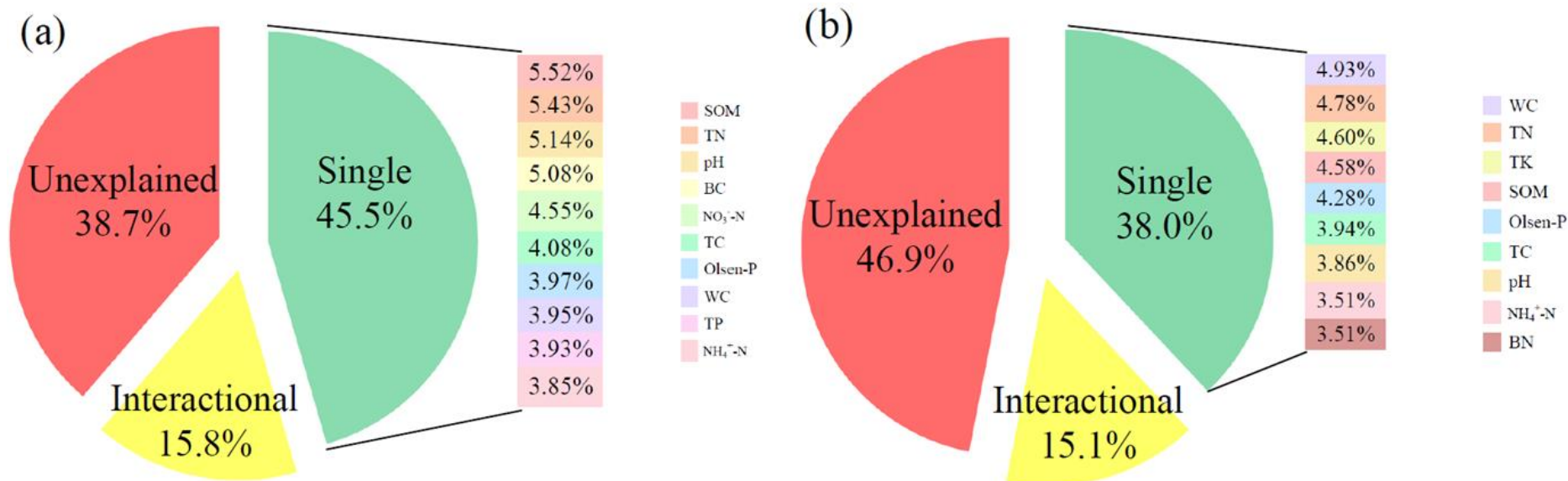
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25 **Fig. 5** Canonical correspondence analysis of the *Cyanobacteria* (a) and *Proteobacteria* (b) communities based on environmental data. The  
 26 environmental factors were selected after testing for variation inflation factors (VIF). WC, water content; SOM, soil organic-matter content; TC,  
 27 total carbon content; TN, total nitrogen content; TP, total phosphorus content; TK, total potassium content; BC, biomass carbon content; BN,  
 28 biomass N content.



30 **Fig.6** Variance partitioning analysis based on a partial canonical correspondence analysis indicating the effect of the environmental factors and  
 31 their interactions on the active communities of *Cyanobacteria* (a) and *Proteobacteria* (b). The columns on the right represent the contributions of  
 32 single factors on the variance of the microbial communities. WC, water content; SOM, soil organic-matter content; TC, total carbon content; TN,  
 33 total nitrogen content; TP, total phosphorus content; TK, total potassium content; BC, biomass C content; BN, biomass N content.



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