Supplement Materials

Structural equation models can not only synthesize existing linear analytical methods but also validate and analyze the relationship among variables while maintaining a strict statistical hypothesis testing method and accommodating measurement errors for the variables. Therefore, structural equations perform general linear analyses, while providing the chance to analyze the structural relationships among variables (hidden variables) that cannot be directly measured. Various nutrient and physical indicators can be directly measured in a soil ecosystem, and the overall soil environment can be evaluated by analyzing them. This is the foundation of a structural equation model. These models are divided into measurement and structural models. The former can measure the relationships among hidden and explicit variables as follows:

$$\vec{X} = \Lambda x \xi + \delta \quad (1)$$

$$\vec{Y} = \Lambda y \eta + \varepsilon, \quad (2)$$

where $\vec{X}$ is an exogenous explicit variable vector; $\vec{Y}$ is an endogenous explicit variable vector, x and y are factor loadings of index variables $(\vec{X}, \vec{Y})$; δ and ε are the measurement errors of the exogenous and endogenous dominant variables, respectively; ξ is the exogenous latent variable; and η is the endogenous latent variable. The structural model reflects the relationship among latent variables as follows:

$$\eta = \mathbf{B}\eta + \mathbf{\Gamma}\xi + \xi, \quad (3)$$

where $\mathbf{B}$ is the structural coefficient matrix of the relationship between endogenous latent variables, $\mathbf{\Gamma}$ is the matrix of the relationship between endogenous latent and exogenous latent variables, and ξ is the interference factor in the structural model or the residual value. A path diagram can be established according to this model and maximum likelihood methods.

Supplement Tables

Table S1 Significance of two-way analysis of variance in the vertical direction

Variation	*F*	*P*
ST	**3.751**	**0.026**
SM	**6.192**	**0.003**
UGB	0.819	0.443
BG	**36.92**	**<0.001**
AP	**3.246**	**0.042**
S-LAP	**20.06**	**<0.001**
CBH	0.592	0.555
S-NAG	**16.263**	**<0.001**
XYL	**3.23**	**0.042**
TC	1.641	0.197
TN	2.744	0.068
TP	0.25	0.779
SOM	**3.945**	**0.022**
TAS	1.629	0.200
GlcN	**4.884**	**0.009**
GlcN	0.025	0.976
MurA	2.178	0.117

Table S2 Significance of two-way analysis of variance in the horizontal direction

Variation	Precipitation		Warming		Precipitation & Warming	
	F	*P*	*F*	*P*	*F*	*P*
ST	0.037	0.849	**16.317**	**<0.001**	**8.992**	**0.004**
SM	**39.797**	**<0.001**	0.347	0.558	**19.651**	**<0.001**
AGB	**36.382**	**<0.001**	**7.341**	**0.008**	**6.325**	**0.014**
UGB	**27.121**	**<0.001**	0.925	0.339	2.396	0.126
BG	**5.334**	**0.024**	0.717	0.400	2.024	0.159
AP	**5.253**	**0.025**	0.446	0.506	0.539	0.465
S-LAP	**9.937**	**0.002**	0.691	0.409	0.216	0.643
CBH	**21.828**	**<0.001**	**7.188**	**0.009**	**20.755**	**<0.001**
S-NAG	0.284	0.596	0.257	0.614	0.764	0.385
XYL	**19.781**	**<0.001**	0.564	0.455	**11.337**	**0.001**
TC	**5.729**	**0.004**	**4.032**	**0.047**	1.323	0.271
TN	**8.193**	**0.006**	3.786	0.056	0.249	0.619
TP	3.202	0.078	2.983	0.089	**9.073**	**0.004**
SOM	**10.56**	**0.002**	**8.233**	**0.005**	1.545	0.218
TAS	**22.678**	**<0.001**	1.711	0.195	3.593	0.062
GlcN	**34.629**	**<0.001**	1.769	0.188	**15.743**	**<0.001**
GlcN	3.516	0.065	0.411	0.523	0.581	0.449
MurA	**19.333**	**<0.001**	**7.908**	**0.006**	1.935	0.169

Table S3 Significance of two-way analysis of variance in the horizontal direction

Abbreviation	Full name
ACP	Acid Phosphatase
AGFI	Adjusted Goodness of Fit Index
AGB	Aboveground Biomass
BG	β-Glucosidase
CB	β-D-cellobiosidase
CFI	Comparative Fit Index
CMIN/DF	Chi-square Degree of Freedom Ratio
Dep	Different Depth
GalN	Galactosamine
GFI	Goodness of Fit Index
GluN	Glucosamine
LAP	Leucine Aminopeptidase
MurA	Muramic Acid
NAG	β-N-acetylglucosaminidase
P	Soil Sampling Point Increased Precipitation Treatment
RMSEA	Root Mean Square Error of Approximation
SOM	Soil Organic Matter
SM	Soil Moisture
ST	Soil Temperature
TAS	Total Amino Sugar
TC	Total Carbon
TN	Total Nitrogen
TP	Total Phosphorus
UGB	Underground biomass
W	Soil Sampling Point Warming Treatment
XYL	β-xylosidase

Supplement Figure Legends

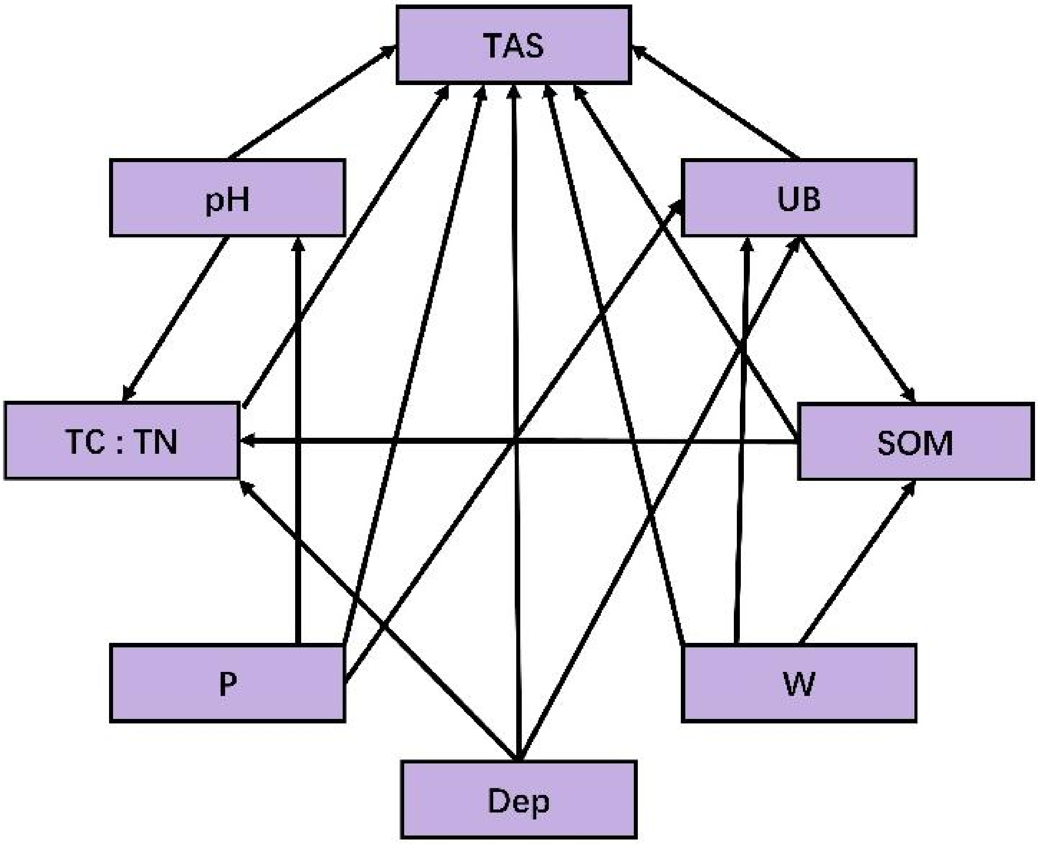
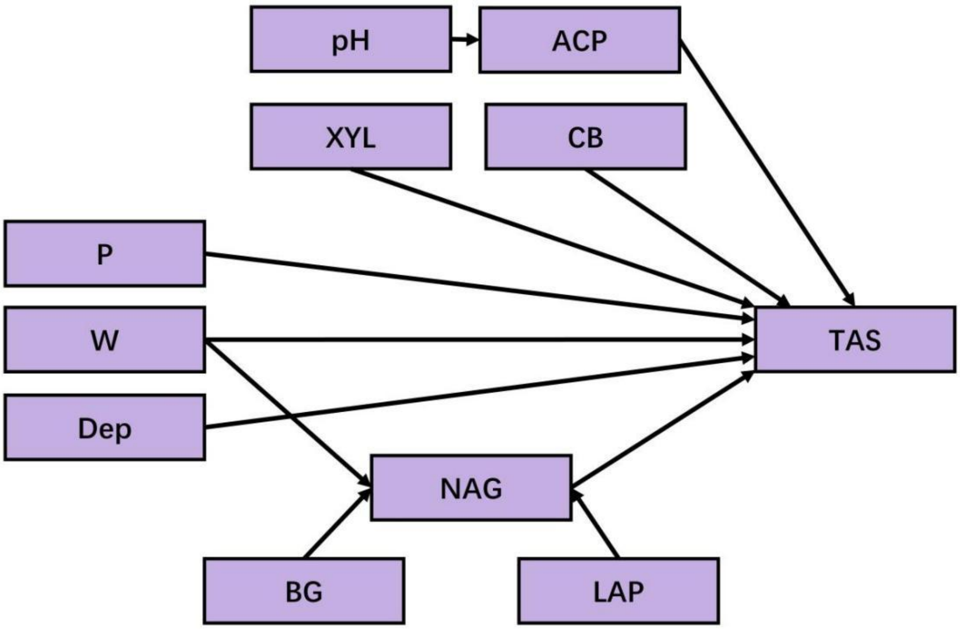


Figure S1: A priori model of physicochemical properties controlling amino sugar turnover in the soil in different scenarios. Boxes represent variables. Single arrows indicate causality. (The residuals are not plotted)



560 **Figure S2:** A priori model for controlling amino sugar turnover in soil by soil extracellular enzyme activities in different scenarios. Boxes represent variables. Single arrows indicate causality. (The residuals are not plotted)

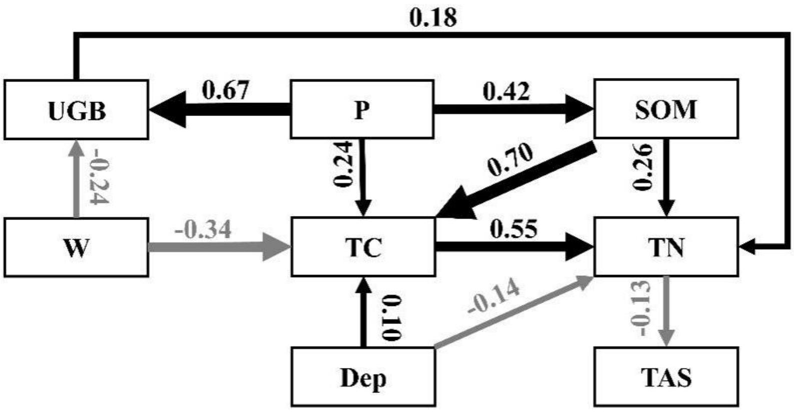


Figure S3: Structural equation model of total amino sugars turnover rate and soil physicochemical properties in different scenarios. An arrow represents a causal relationship ($p < 0.1$). Arrow direction indicates the direction of effect. Arrow width indicates effect size. A black arrow denotes a positive relationship, and a grey arrow a negative relationship. Numbers beside arrows are standardized path coefficients. CMIN/DF = 0.780, CFI = 1.000, GFI = 0.924, AGFI = 0.830, RMSEA = 0.000, PCLOSE = 0.780.

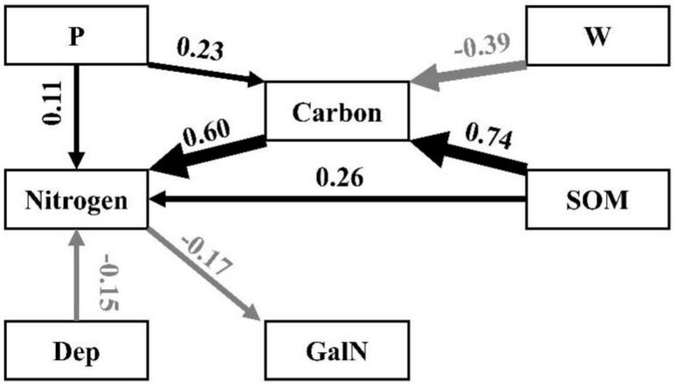


Figure S4: Structural equation model of the turnover rate of GalN and soil physicochemical properties in different scenarios. An arrow represents a causal relationship ($p < 0.1$). Arrow direction indicates the direction of effect. Arrow width indicates effect size. A black arrow denotes a positive relationship, and a grey arrow a negative relationship. Numbers beside arrows are standardized path coefficients. CMIN/DF = 0.100, CFI = 1.000, GFI = 0.917, AGFI = 0.806, RMSEA = 0.006, PCLOSE = 0.526.

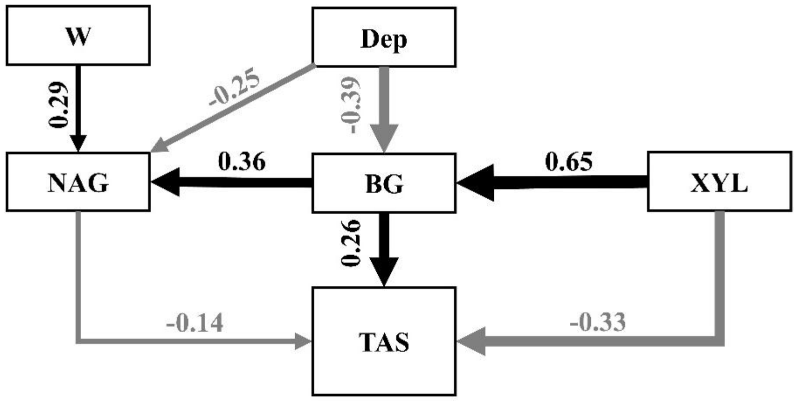


Figure S5: Structural equation model of total amino sugar turnover rate and soil extracellular enzyme activities in different scenarios. An arrow represents a causal relationship ($p < 0.1$). Arrow direction indicates the direction of effect. Arrow width indicates effect size. A black arrow denotes a positive relationship, and a grey arrow a negative relationship. Numbers beside arrows are standardized path coefficients. CMIN/DF = 0.469, CFI = 1.000, GFI = 0.971, AGFI = 0.913, RMSEA = 0.000, PCLOSE = 0.884.

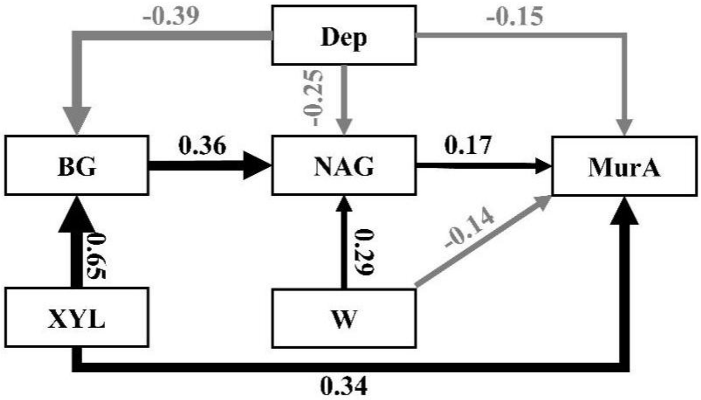


Figure S6: Structural equation model of MurA turnover rate and soil extracellular enzyme activities in different scenarios. An arrow represents a causal relationship ($p < 0.1$). Arrow direction indicates the direction of effect. Arrow width indicates effect size. A black arrow denotes a positive relationship, and a grey arrow a negative relationship. Numbers beside arrows are standardized path coefficients. CMIN/DF = 0.412, CFI = 1.000, GFI = 0.977, AGFI = 0.920, RMSEA = 0.000, PCLOSE = 0.893.