
1 Tables

Table S1. Description of 104 sites where soil nematode samples were obtained.

Sample Site	Longitude (E)	Latitude (N)	Elevation(m)	Vegetation type
M-15-1	101.2014	35.2915	3528	Meadow
M-15-2	100.8318	35.0091	3836	Meadow
M-15-3	100.1538	34.4896	3857	Meadow
M-15-4	99.9401	34.5652	3756	Meadow
M-15-5	100.2708	34.2512	4179	Meadow
M-15-6	99.8313	33.8764	4212	Meadow
M-15-7	97.4615	33.1271	4407	Meadow
M-15-8	97.4014	33.1126	3998	Meadow
M-15-9	96.1128	33.1128	4428	Meadow
M-15-10	96.3188	33.2934	4331	Meadow
M-15-11	95.8525	32.9429	4629	Meadow
M-15-12	96.1478	32.9617	4267	Meadow
M-15-13	96.8923	32.8644	4003	Meadow
M-15-14	96.5565	32.6296	3906	Meadow
M-15-15	96.4544	31.5417	4425	Meadow
M-15-16	96.4014	31.4689	4105	Meadow
M-15-17	96.4763	31.1532	4162	Meadow
M-15-18	96.571	31.2378	3887	Meadow
M-15-19	95.613	31.475	4069	Meadow
M-15-20	94.2724	31.8964	4479	Meadow
M-15-21	93.5679	31.8232	4870	Meadow
M-15-22	93.3366	31.9156	4827	Meadow
M-15-23	91.3147	30.5152	4389	Meadow
M-15-24	89.7148	29.6577	4431	Meadow
M-15-25	92.0202	31.4353	4483	Meadow
M-15-26	92.0125	31.4206	4479	Meadow
S-15-1	100.1082	35.3874	3284	Steppe
S-15-2	100.5006	35.2462	3029	Steppe
S-15-3	96.45	32.3168	3699	Steppe
S-15-4	90.7124	30.2694	4474	Steppe
S-15-5	91.0839	30.4916	4285	Steppe
S-15-6	91.2745	29.9607	4598	Steppe
S-15-7	90.3735	29.9951	4430	Steppe
S-15-8	89.5055	29.3326	3872	Steppe

S-15-9	88.8023	29.2064	3912	Steppe
S-15-10	88.4205	29.185	3947	Steppe
S-15-11	88.1535	29.1432	4097	Steppe
S-15-12	89.813	29.3073	3970	Steppe
S-15-14	98.1247	36.0569	3388	Steppe
M-16-1	98.9905	35.282	4236	Meadow
M-16-2	99.3905	35.432	3971	Meadow
M-16-3	98.6238	35.032	4336	Meadow
M-16-4	98.1238	34.7987	4273	Meadow
M-16-5	97.6071	35.0154	4257	Meadow
M-16-6	97.3238	35.032	4254	Meadow
M-16-7	97.4238	33.332	4181	Meadow
M-16-8	96.9738	33.782	4673	Meadow
M-16-9	96.6238	33.982	4488	Meadow
M-16-10	95.7071	34.3154	4310	Meadow
M-16-11	95.8738	34.1487	4405	Meadow
M-16-12	94.1738	35.082	4408	Meadow
M-16-13	95.3738	33.7987	4328	Meadow
M-16-14	95.2738	33.6487	4656	Meadow
M-16-15	92.8905	34.7654	4680	Meadow
M-16-16	92.3405	34.032	4651	Meadow
M-16-17	91.6905	31.8654	4755	Meadow
M-16-18	91.5738	31.582	4571	Meadow
M-16-19	92.6071	31.782	4595	Meadow
M-16-20	91.9071	32.882	5217	Meadow
M-16-21	91.8571	33.232	4839	Meadow
M-16-22	98.0238	33.0154	4329	Meadow
M-16-23	98.3405	32.982	3956	Meadow
M-16-24	98.5905	32.382	4007	Meadow
M-16-25	99.0738	31.9987	4016	Meadow
M-16-26	100.1904	31.6154	3965	Meadow
M-16-27	100.7071	31.6654	3526	Meadow
M-16-28	99.1071	31.882	4040	Meadow
M-16-29	99.4238	31.8154	3654	Meadow
M-16-30	99.7571	31.1487	4238	Meadow
M-16-31	99.6071	31.032	3977	Meadow
M-16-32	99.3571	31.1154	3830	Meadow
M-16-33	100.5571	31.982	3555	Meadow
M-16-34	100.7071	32.9987	3549	Meadow
M-16-35	100.9738	33.4654	3891	Meadow
M-16-36	101.5071	37.532	3208	Meadow

M-16-37	100.9904	37.7154	3524	Meadow
M-16-38	101.3238	37.6154	3180	Meadow
M-16-39	100.8404	37.982	3237	Meadow
M-16-40	100.3571	38.0987	2930	Meadow
M-16-41	98.9238	38.8487	3736	Meadow
M-16-42	99.3405	38.6487	3440	Meadow
M-16-43	99.6071	38.4154	3245	Meadow
M-16-44	100.4738	37.8154	3484	Meadow
M-16-45	100.5071	37.3654	3377	Meadow
M-16-46	100.9238	36.982	3086	Meadow
S-16-1	98.1238	34.9654	4209	Steppe
S-16-2	95.4071	34.5654	4182	Steppe
S-16-3	95.0238	34.7987	4302	Steppe
S-16-4	94.4071	35.032	4346	Steppe
S-16-5	93.9071	35.2654	4399	Steppe
S-16-6	93.7405	35.5154	4527	Steppe
S-16-7	93.1238	35.2654	4589	Steppe
S-16-8	92.7238	34.4654	4536	Steppe
S-16-9	91.7071	32.132	4733	Steppe
S-16-10	90.5905	31.382	4552	Steppe
S-16-11	91.0571	31.4987	4557	Steppe
S-16-12	90.0905	31.432	4641	Steppe
S-16-13	90.0905	31.432	4586	Steppe
S-16-14	92.1905	33.7654	4615	Steppe
S-16-15	92.7071	34.282	4482	Steppe
S-16-16	100.0571	38.232	2793	Steppe
S-16-17	100.1738	37.2987	3237	Steppe
S-16-18	99.4071	37.1487	3238	Steppe
S-16-19	99.8571	37.2654	3185	Steppe

Table S2. Soil nematode genera identified in the grassland on the Tibetan Plateau.

	Taxonomic rank	c-p class¹	p-p class	Feeding type	Prevalence (%) ²
<i>Axonchium</i>	Genera	-	5	Herbivores - ectoparasites	0.01
<i>Belondira</i>	Genera	-	5	Herbivores - ectoparasites	0.04
<i>Bitylenchus</i>	Genera	-	3	Herbivores - ectoparasites	0.14
<i>Criconemoides</i>	Genera	-	3	Herbivores - ectoparasites	0.45
<i>Helicotylenchus</i>	Genera	-	3	Herbivores - semi-endoparasites	3.01
<i>Longidorus</i>	Genera	-	5	Herbivores - ectoparasites	0.05
<i>Merlinius</i>	Genera	-	3	Herbivores - ectoparasites	2.09
<i>Pratylenchus</i>	Genera	-	3	Herbivores - migratory endoparasites	1.63
<i>Rotylenchus</i>	Genera	-	3	Herbivores - semi-endoparasites	5.37
<i>Tylenchorhynchus</i>	Genera	-	3	Herbivores - ectoparasites	0.93
<i>Tylenchus</i>	Genera	-	2	Herbivores - epidermal/root hair feeders	7.61
<i>Xiphinema</i>	Genera	-	5	Herbivores - ectoparasites	0.56
<i>Aphelenchoides</i>	Genera	2	-	Fungivores	2.71
<i>Aphelenchus</i>	Genera	2	-	Fungivores	5.47
<i>Filenchus</i>	Genera	2	-	Fungivores	7.77
<i>Tylencholaimus</i>	Genera	4	-	Fungivores	1.02
<i>Acrobeles</i>	Genera	2	-	Bacterivores	3.75
<i>Acrobeloides</i>	Genera	2	-	Bacterivores	11.45
<i>Anaplectus</i>	Genera	2	-	Bacterivores	0.73
<i>Cephalobus</i>	Genera	2	-	Bacterivores	7.70
<i>Cervidellus</i>	Genera	2	-	Bacterivores	0.35
<i>Chiloplacus</i>	Genera	2	-	Bacterivores	0.40

<i>Diploscapter</i>	Genera	1	-	Bacterivores	0.12
<i>Eucephalobus</i>	Genera	2	-	Bacterivores	1.34
<i>Heterocephalobus</i>	Genera	2	-	Bacterivores	1.34
<i>Mesorhabditis</i>	Genera	1	-	Bacterivores	1.03
<i>Monhystera</i>	Genera	2	-	Bacterivores	0.01
<i>Panagrobelus</i>	Genera	1	-	Bacterivores	0.01
<i>Panagrolaimus</i>	Genera	1	-	Bacterivores	2.45
<i>Pelodera</i>	Genera	1	-	Bacterivores	0.01
<i>Plectus</i>	Genera	2	-	Bacterivores	2.76
<i>Prismatolaimus</i>	Genera	3	-	Bacterivores	0.23
<i>Protorhabditis</i>	Genera	1	-	Bacterivores	2.47
<i>Teratocephalus</i>	Genera	3	-	Bacterivores	1.26
<i>Tylocephalus</i>	Genera	2	-	Bacterivores	1.01
<i>Clarkus</i>	Genera	4	-	Predators	0.30
<i>Coomansus</i>	Genera	4	-	Predators	0.07
<i>Enchodelus</i>	Genera	4	-	Predators	2.72
<i>Ironus</i>	Genera	4	-	Predators	0.52
<i>Mononchulus</i>	Genera	4	-	Predators	0.02
<i>Mononchus</i>	Genera	4	-	Predators	1.50
<i>Tripyla</i>	Genera	3	-	Predators	0.10
<i>Allodorylaimus</i>	Genera	4	-	Omnivores	0.98
<i>Aporcelaimus</i>	Genera	5	-	Omnivores	0.23
<i>Discolaimus</i>	Genera	4	-	Omnivores	0.20
<i>Dorylaimus</i>	Genera	4	-	Omnivores	1.44
<i>Drepanodorylaimus</i>	Genera	4	-	Omnivores	0.01

<i>Ecumenicus</i>	Genera	4	-	Omnivores	0.01
<i>Epidorylaimus</i>	Genera	4	-	Omnivores	1.50
<i>Eudorylaimus</i>	Genera	4	-	Omnivores	1.81
<i>Labronema</i>	Genera	4	-	Omnivores	2.89
<i>Laimydorus</i>	Genera	4	-	Omnivores	1.66
<i>Mesodorylaimus</i>	Genera	4	-	Omnivores	1.08
<i>Myiodiscus</i>	Genera	4	-	Omnivores	0.02
Dolichodoridae	Family	-	3	Herbivores - ectoparasites	0.01
Hemicycliophoridae	Family	-	3	Herbivores - ectoparasites	0.01
Cephalobidae	Family	2	-	Bacterivores	0.01
Rhabditidae	Family	1	-	Bacterivores	0.23
Dorylaimidae	Family	4	-	Omnivores	3.08
Mydonomidae	Family	4	-	Omnivores	0.04
Qudsianematidae	Family	4	-	Omnivores	2.34

¹ Coloniser-persister classification is based on life cycle properties. Nematodes of c-p-1 are regarded as enrichment opportunists; they have short life cycles and are often found in disturbed environments. In contrast, nematodes of c-p-5 have long life cycles and tend to inhabit stable, mature ecosystems. c-p of herbivores are called p-p (Bongers 1990; Bongers et al. 1995).

² Prevalence was calculated as the percentage of samples in which a nematode genus was diagnosed with respect to total number of samples. Prevalence which was lower than 0.01% was recorded as 0.01%.

Table S3. Differences in the taxonomic diversity, trophic groups, and soil food web characteristics of soil nematode communities (median (interquartile range, IQR)) between alpine meadows (n=360) and alpine steppes (n=160). Bold type indicates significant differences (Wilcoxon rank-sum test). Different letters in each column of trophic groups indicate significant differences between trophic groups within the ecosystem (Dwass–Steel–Critchlow–Fligner test, $p < 0.001$).

	Meadows	Steppes	p-value
<i>Taxonomic diversity</i>			
Abundance (individuals/100 g of dried soil)	52.6 (80.2)	31.2 (40.4)	0.001
Genus richness (genus)	16.0 (13.0)	13.0 (9.3)	0.001
<i>Trophic groups</i>			
Plant parasites (%)	20.0 (20.3) ^a	17.3 (17.0) ^a	0.019
Fungivores (%)	15.8 (11.6) ^b	16.1 (14.5) ^a	0.695
Bacterivores (%)	37.2 (21.9) ^c	40.6 (20.8) ^b	0.082
Predators (%)	0.3 (4.3) ^d	0 (0.3) ^c	0.001
Omnivores (%)	17.9 (13.7) ^e	19.6 (14.8) ^{bd}	0.397
<i>Soil food web characteristics</i>			
Structure Index	33.2 (22.3)	30.3 (20.2)	0.270
Enrichment Index	31.9 (15.2)	32.4 (16.5)	0.544
Channel Index	49.5 (69.1)	45.5 (59.2)	0.104

Table S4. Partial redundancy analysis of the relationships between the genus composition of nematode community and environmental variables in the alpine meadows and alpine steppes. pH: soil pH, MOI: soil moisture (%), TN: total nitrogen (mg/g), NH₄: ammonium (mg/kg), NO₃: nitrate (mg/kg), PSR: plant species richness, PBM: plant biomass (g/m²), PCV: plant coverage (%).

Variable	Alpine Meadow			Alpine Steppe		
	F	p	Significance	F	p	Significance
pH	0.723	0.610		1.141	0.279	
MOI	11.216	0.001	***			
TN	4.485	0.005	**			
NH ₄	0.723	0.014	*			
NO ₃				2.597	0.0363	*
PCV	0.723	0.532				
PSR				0.592	0.8255	
PBM				1.937	0.0683	

Table S5. Partial redundancy analysis of the relationships between the trophic composition of nematode community and environmental variables in the alpine meadows and alpine steppes. pH: soil pH, MOI: soil moisture (%), TN: total nitrogen (mg/g), TP: total phosphorus (mg/g), NH₄: ammonium (mg/kg), PBM: plant biomass (g/m²), PCV: plant coverage (%).

Variable	Alpine Meadow			Alpine Steppe		
	F	p	Significance	F	p	Significance
MOI	6.176	0.010	*	1.573	0.191	
TN	2.834	0.060				
TP	2.686	0.068				
NH ₄				3.915	0.028	*
PCV	0.287	0.826		4.416	0.016	*
PBM				3.318	0.043	*

Table S6. Multiple regression of the effects of environmental variables on soil nematodes in the alpine meadows. Nematode's abundance is calculated as individuals/100 g of dried soil. Richness is the genus richness of nematodes. Trophic groups, such as plant parasites, fungivores, bacterivores, predators and omnivores, are represented as relative abundances (%). Each individual predictor's contribution was calculated by lmg in the relaimpo package in R, which is the r^2 contribution averaged over orderings among regressors. The +/- symbols indicate positive/negative correlations. pH: soil pH, MOI: soil moisture (%), TN: total nitrogen (mg/g), TP: total phosphorus (mg/g), NH4: ammonium (mg/kg), PCV: plant coverage (%).

	Contribution of the predictor (%)							
	r^2	p	pH	MOI	TN	TP	NH4	PCV
Abundance	0.21	0.001		81.34 (+)	18.66 (-)			
Richness	0.12	0.001	42.66 (+)	11.08 (+)	17.52 (-)	11.77 (+)	16.97 (-)	
Plant parasites	0.09	0.001	56.37 (-)	13.66 (-)			29.96 (+)	
Fungivores	0.01	0.148		100.00 (-)				
Bacterivores	0.04	0.007	51.64 (+)					48.36 (+)
Predators	0.11	0.001		58.32 (+)	13.88 (-)	4.23 (+)	18.75 (-)	4.83 (-)
Omnivores	0.10	0.001	16.53 (+)	43.66 (+)	8.08 (-)	4.02 (+)		27.70 (-)
EI	0.07	0.001	12.09 (+)	31.93 (+)		49.45 (+)		6.53 (-)
SI	0.10	0.001		54.86 (+)	12.11 (-)	5.42 (+)	4.12 (-)	23.49 (-)
CI	0.09	0.001	29.59 (-)	9.70 (-)		60.70 (-)		

Table S7. Multiple regression of the effects of environmental variables on soil nematodes in the alpine steppes. Nematode's abundance is calculated as individuals/100 g of dried soil. Richness is the genus richness of nematodes. Trophic groups, such as plant parasites, fungivores, bacterivores, predators and omnivores, are represented as relative abundances (%). The individual predictor's contribution was calculated by lmg in the relaimpo package in R, which is the r^2 contribution averaged over orderings among regressors. The +/- symbols indicate positive/negative correlations. pH: soil pH, MOI: soil moisture (%), NH4: ammonium (mg/kg), NO3: nitrate (mg/kg), PBM: plant biomass (g/m²), PCV: plant coverage (%), PSR: plant species richness.

	Contribution of the predictor (%)								
	r^2	p	pH	MOI	NH4	NO3	PBM	PCV	PSR
Abundance	0.3	0.001	11.33 (-)	65.60 (+)	14.99 (+)		3.91 (-)		4.18 (+)
Richness	0.23	0.001	6.57 (-)	37.01 (+)			36.24 (-)	20.19 (+)	
Plant parasites	0.07	0.015						53.67 (+)	46.33 (+)
Fungivores	0.14	0.002	29.39 (-)	14.02 (-)			20.85 (+)		35.74 (+)
Bacterivores	0.09	0.029	8.49 (-)		24.68 (+)		41.72 (-)		25.11 (-)
Predators	0.02	0.127						100.00 (+)	
Omnivores	0.23	0.001	13.82 (+)	15.62 (+)	20.97 (-)	10.06 (-)	7.67 (+)	31.85 (-)	
EI	0.1	0.003	56.10 (-)		43.90 (-)				
SI	0.19	0.002	2.83 (+)	13.74 (+)	20.14 (-)	12.70 (-)	8.44 (+)	22.84 (-)	19.32 (-)
CI	0.1	0.007	40.25 (+)	28.08 (-)					31.66 (+)

Figure S1. biplots of partial redundancy analysis of the relationships between the genus composition of nematode community and environmental variables in the alpine meadows (a) and alpine steppes (b), and the relationships between the trophic composition of nematode community and environmental variables in the alpine meadows (c) and alpine steppes (d). pH: soil pH, MOI: soil moisture (%), TN: total nitrogen (mg/g), NH4: ammonium (mg/kg), NO3: nitrate (mg/kg), PSR: plant species richness, PBM: plant biomass (g/m²), PCV: plant coverage (%).

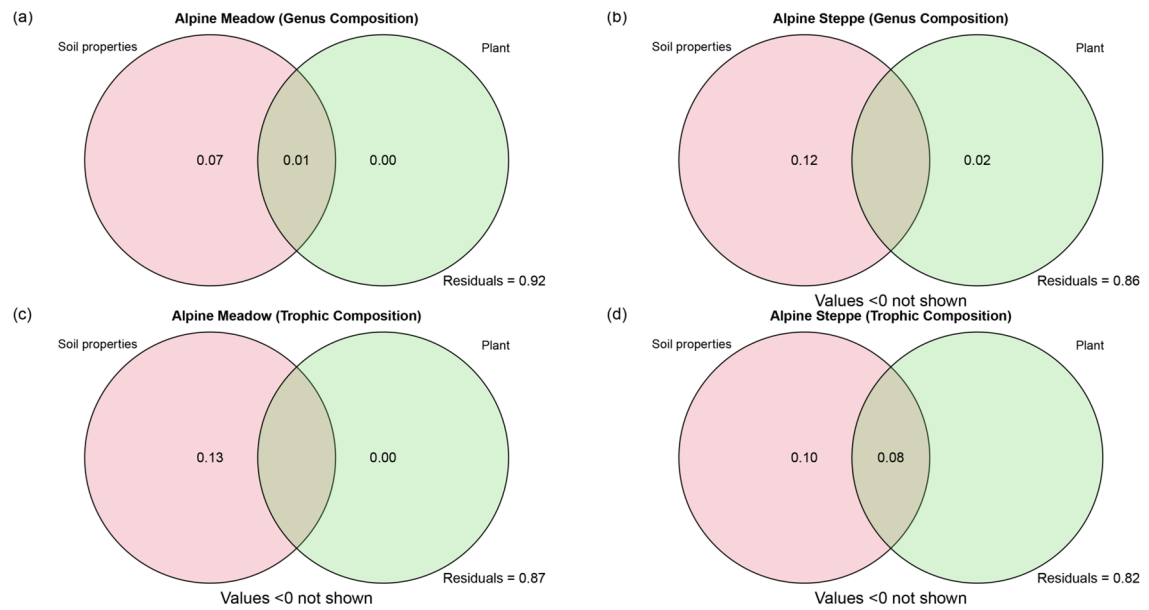


Figure S2. Variation partitioning analyses explained by variable sets of soil properties, aboveground plants and climate for nematode genus and trophic compositions between alpine meadow and alpine steppe. Unique fractions of each explanatory set were evaluated by 9999 permutations.

3 Nematode analyses

Species richness, which represented the number of nematode genera, and abundance were used as measures of diversity for the soil nematode community. For each trophic group, the abundance proportion was used to perform analyses.

As suggested by Ferris et al. (2001), the enrichment index (EI) and structure index (SI) were used to assess the food web response to the availability of resources in the soil and to determine whether the soil community was basal (typical of disturbed systems) or structured (typical of stable systems).

$$EI = 100 \times \frac{e}{e + b}$$

$$SI = 100 \times \frac{s}{s + b}$$

where e is the abundance of nematodes in the enrichment component weighted by k_e values; b is the abundance of nematodes in the basal component weighted by k_b values; s is the abundance of nematodes in the structural component weighted by k_s values; k_e is the weighting assigned to the guilds Ba_1 and Fu_2 (enrichment component); k_b is the weighting assigned to the guilds Ba_2 and Fu_2 (basal component); and k_s is the weighting assigned to the guilds Ba_{3-5} , Fu_{3-5} , Om_{4-5} and Pr_{2-5} (structural component).

Channel Index (CI) is a powerful index for assessing the soil decomposition process and analyzing nematode assemblages, as described by Ferris et al (2001). The CI ranges from 0 (totally bacterially mediated) to 100 (totally fungally mediated). In the following equation, Fu_2 and Ba_2 are the numbers of fungivores with c-p 2 and bacterivores with c-p 2, respectively.

$$CI = 100 \times \frac{0.8 \times Fu_2}{3.2 \times Ba_1 + 0.8 \times Fu_2}$$

Rényi diversity is the generalized case of species number, shannon diversity, inverse simpson and etc. (Rényi 1961; Tóthmérész 1995). It improved the measurement of diversity by methods of diversity ordering, and it was sensitive to the rare and abundant species as the scale parameter changes (Tóthmérész 1995).

$$H_{\alpha}(X) = \frac{1}{1 - \alpha} \log \left(\sum_{i=1}^n p_i^{\alpha} \right)$$

When the sensitivity parameter $\alpha=0$, the value is the species number, $\alpha=1$ is the exponential Shannon, $\alpha=2$ is the inverse Simpson, and $\alpha=\infty$ is the inverse relative dominance (Tóthmérész 1995; Oksanen et al. 2007). According to the theory of diversity ordering, one community can be regarded as more diverse than another only if its Rényi diversities are all higher (Tóthmérész 1995).

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