Supplementary Material

Table S1. Activities of leucine aminopeptidase and β-1,4-N-acetylglucosaminidase under different nitrogen-addition treatments at two soil depths.

Soil depth (cm)	Treatment	LAP (nmol·g^{-1}·h^{-1})	NAG (nmol·g^{-1}·h^{-1})
0—15	CK	171.04±26.29Aa	50.32±3.74Aa
	N−I	145.48±26.18ABa	43.36±3.83Aa
	N−II	129.43±7.00Bb	32.96±5.85Ba
	N−III	164.34±16.06ABa	18.61±3.62Ca
15—30	CK	189.57±14.39Aa	13.49±3.51ABb
	N−I	149.82±7.38Ba	17.60±0.88Ab
	N−II	170.13±4.47ABa	14.48±2.33ABb
	N−III	152.56±22.63Ba	12.35±2.00Ba

Note: LAP, L-leucine aminopeptidase; NAG, β-1,4-N-acetylglucosaminidase. Values are means ± SD (n = 3 per treatment × soil-depth combination). Within the same soil layer, means with different uppercase letters differ significantly among N-addition treatments according to Duncan's multiple range test ($p < 0.05$). Within the same N-addition treatment, means with different lowercase letters differ significantly between soil depths according to independent-samples Student's t-tests ($p < 0.05$).

Table S2. Out-of-bag predictive performance of random forest models for vector length and vector angle by soil depth.

Soil depth (cm)	Response variable	Number of plots (n)	OOB RMSE	OOB R^2
0—15	Vector length	12	0.073	0.327
	Vector angle	12	1.028°	−0.620
15—30	Vector length	12	0.072	0.644
	Vector angle	12	1.128°	−0.009

Note: OOB, out-of-bag; RMSE, root mean squared error. OOB RMSE and R^2 were calculated from plot-level OOB predictions. RMSE is dimensionless for VL and is expressed in degrees for VA.

Table S3. Permutation importance of soil predictors in random forest models of vector length (VL) and vector angle (VA) by soil depth.

Soil depth (cm)	Response variable	Predictor	Increase in MSE (%)	Unadjusted permutation *p* value	BH-adjusted *p* value
0—15	VL	AP	25.507	0.0020	0.0444
0—15	VL	DOC	9.235	0.0300	0.2086
0—15	VL	C/P	5.085	0.0581	0.2841
0—15	VL	TC	3.214	0.1263	0.4629
0—15	VL	AN	3.018	0.1185	0.4629
0—15	VL	TP	0.878	0.2465	0.7210
0—15	VL	N/P	0.275	0.3120	0.7210
0—15	VL	pH	−0.474	0.4309	0.7210
0—15	VL	TN	−1.122	0.5594	0.7458
0—15	VL	MBC	−1.559	0.6137	0.7682
0—15	VL	C/N	−1.685	0.7183	0.7709
0—15	VA	C/N	0.279	0.3280	0.7210
0—15	VA	AP	−0.177	0.4597	0.7210
0—15	VA	TN	−0.378	0.5060	0.7210
0—15	VA	MBC	−0.392	0.5080	0.7210
0—15	VA	C/P	−0.649	0.6285	0.7682
0—15	VA	TP	−0.849	0.7036	0.7709
0—15	VA	TC	−0.858	0.6700	0.7709
0—15	VA	N/P	−0.859	0.6841	0.7709
0—15	VA	DOC	−1.043	0.7545	0.7905
0—15	VA	AN	−1.460	0.8657	0.8859
0—15	VA	pH	−2.456	0.9539	0.9539

Soil depth (cm)	Response variable	Predictor	Increase in MSE (%)	Unadjusted permutation *p* value	BH-adjusted *p* value
15—30	VL	AP	42.010	0.0020	0.0444
15—30	VL	MBC	22.561	0.0101	0.1239
15—30	VL	AN	19.438	0.0141	0.1239
15—30	VL	TP	3.739	0.1506	0.5097
15—30	VL	TN	0.409	0.3695	0.7210
15—30	VL	C/N	0.365	0.2826	0.7210
15—30	VL	TC	−0.315	0.3576	0.7210
15—30	VL	N/P	−0.416	0.4012	0.7210
15—30	VL	C/P	−0.776	0.4808	0.7210
15—30	VL	DOC	−1.596	0.4829	0.7210
15—30	VL	pH	−1.617	0.5282	0.7263
15—30	VA	C/P	6.117	0.0141	0.1239
15—30	VA	TC	4.991	0.0379	0.2086
15—30	VA	DOC	4.961	0.0364	0.2086
15—30	VA	C/N	2.358	0.1147	0.4629
15—30	VA	TN	0.887	0.3158	0.7210
15—30	VA	N/P	0.524	0.3441	0.7210
15—30	VA	AN	0.378	0.3775	0.7210
15—30	VA	pH	0.062	0.4297	0.7210
15—30	VA	AP	−0.023	0.4648	0.7210
15—30	VA	MBC	−0.449	0.5859	0.7582
15—30	VA	TP	−0.989	0.7048	0.7709

Note. MSE, mean squared error; BH, Benjamini-Hochberg. The *p* values were adjusted across all 44 predictor-by-model tests using the BH procedure. Asterisks in Figure 5 indicate unadjusted permutation *p* values ($p < 0.05$; $p < 0.01$).

Table S4. Sensitivity of predictor importance rankings to leave-one-plot-out refitting of random forest models for vector length (VL) and vector angle (VA).

Soil depth (cm)	Response variable	Predictor	Full-model rank	Valid/ attempted refits	Best – worst rank	Median rank	Rank 1 refits	Top 3 refits
0—15	VL	AP	1	11/12	1—2	1	10	11
0—15	VL	DOC	2	11/12	1—3	2	1	11
0—15	VL	C/P	3	11/12	3—7	4	0	3
0—15	VL	TC	4	11/12	3—8	4	0	4
0—15	VL	AN	5	11/12	2—6	5	0	3
0—15	VL	TP	6	11/12	6—9	7	0	0
0—15	VL	N/P	7	11/12	3—10	7	0	1
0—15	VL	pH	8	11/12	4—11	8	0	0
0—15	VL	TN	9	11/12	7—11	10	0	0
0—15	VL	MBC	10	11/12	6—11	10	0	0
0—15	VL	C/N	11	11/12	4—11	9	0	0
0—15	VA	C/N	1	12/12	1—7	2	5	8
0—15	VA	AP	2	12/12	2—11	6	0	3
0—15	VA	TN	3	12/12	3—11	6.5	0	2
0—15	VA	MBC	4	12/12	1—11	5	2	4
0—15	VA	C/P	5	12/12	2—11	7.5	0	1
0—15	VA	TP	6	12/12	1—9	3.5	2	6
0—15	VA	TC	7	12/12	1—8	4	1	5
0—15	VA	N/P	8	12/12	2—11	7.5	0	2
0—15	VA	DOC	9	12/12	1—10	9	1	2
0—15	VA	AN	10	12/12	1—11	10	1	1
0—15	VA	pH	11	12/12	2—10	7.5	0	2
15—30	VL	AP	1	11/12	1—1	1	11	11
15—30	VL	MBC	2	11/12	2—3	2	0	11
15—30	VL	AN	3	11/12	2—3	3	0	11

Soil depth (cm)	Response variable	Predictor	Full-model rank	Valid/ attempted refits	Best–worst rank	Median rank	Rank 1 refits	Top 3 refits
15—30	VL	TP	4	11/12	4—9	4	0	0
15—30	VL	TN	5	11/12	4—11	7	0	0
15—30	VL	C/N	6	11/12	5—11	8	0	0
15—30	VL	TC	7	11/12	5—10	7	0	0
15—30	VL	N/P	8	11/12	5—11	9	0	0
15—30	VL	C/P	9	11/12	5—11	6	0	0
15—30	VL	DOC	10	11/12	4—11	9	0	0
15—30	VL	pH	11	11/12	7—11	10	0	0
15—30	VA	C/P	1	9/12	1—3	1	7	9
15—30	VA	TC	2	9/12	1—9	3	1	7
15—30	VA	DOC	3	9/12	1—5	2	1	8
15—30	VA	C/N	4	9/12	2—9	4	0	1
15—30	VA	TN	5	9/12	4—11	5	0	0
15—30	VA	N/P	6	9/12	2—10	8	0	1
15—30	VA	AN	7	9/12	5—10	6	0	0
15—30	VA	pH	8	9/12	8—11	10	0	0
15—30	VA	AP	9	9/12	2—8	6	0	1
15—30	VA	MBC	10	9/12	6—9	7	0	0
15—30	VA	TP	11	9/12	7—11	10	0	0

Not: Each leave-one-plot-out refit omitted one plot. A refit was considered valid if all predictor-importance scores were finite. Predictors were ranked by decreasing unscaled permutation importance, with rank 1 indicating the highest importance. The best-worst rank column reports the minimum and maximum ranks across valid refits. Tied predictors were assigned the best rank for that tie. The Rank 1 and Top 3 columns report the number of valid refits in which each predictor ranked first or within the top three, respectively.