Supplementary materials

From the article ‘Extinction drives recent thermophilization but does not trigger homogenization in forest understory’

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Table S1: *Thermophilization (°C/decades^{-1}) and Δβ-diversity and their component mean value (Value) and standard deviation (s.d) across 80 forest ecoregions. The value from the original dataset (14,167 pairs of plots) and the randomized thermal optimum null model (see methods) are displayed. The P-value were obtained with a Wilcoxon one sample test against 0.*

Variable	***Original dataset***			***Null thermophilization model***		
	Value	**s.d**	**P-value**	**Value**	**s.d**	**P-value**
Thermophilization	0,122	0,11	<0.001	-4,13e-04	0,0054	0.583
Extinction	0,118	0,089	<0.001	-2,05e-04	0,0047	0.31
Colonization	0,00346	0,065	0.664	-2,08e-04	0,0037	0.522
Cold-adapted extinction	0,25	0,14	<0.001	0,185	0,096	<0.001
Cold-adapted colonization	-0,132	0,087	<0.001	-0,186	0,096	<0.001
Warm-adapted extinction	-0,123	0,061	<0.001	-0,122	0,055	<0.001
Warm-adapted colonization	0,126	0,061	<0.001	0,121	0,055	<0.001
Δβ-diversity	0,291	1,4	0.107	0,291	1,4	0.107
Extinction	-0,785	0,91	<0.001	-0,785	0,91	<0.001
Colonization	1,08	0,97	<0.001	1,08	0,97	<0.001
Cold-adapted extinction	-0,744	0,82	<0.001	-0,396	0,48	<0.001
Cold-adapted colonization	-0,0417	0,46	0.397	-0,39	0,44	<0.001
Warm-adapted extinction	0,877	0,72	<0.001	0,542	0,49	<0.001
Warm-adapted colonization	0,199	0,45	0.000159	0,534	0,49	<0.001

Table S2: *Thermophilization (°C/decades^{-1}) and Δβ-diversity and their component mean value (Value) and standard deviation (s.d) across 80 forest ecoregions. The value from the original dataset (14,167 pairs of plots) and the randomized original dataset where occurrences are rarefied so that each time period have an equal number of occurrences. The P-value were obtained with a Wilcoxon one sample test against 0.*

Variable	Original dataset			Rarefaction null model		
	Value	s.d	P-value	Value	s.d	P-value
Thermophilization	0,122	0,11	<0.001	0,121	0,011	<0.001
Extinction	0,118	0,089	<0.001	0,104	0,0071	<0.001
Colonization	0,00346	0,065	0.664	0,0167	0,0072	0.049
Cold-adapted extinction	0,25	0,14	<0.001	0,205	0,0085	<0.001
Cold-adapted colonization	-0,132	0,087	<0.001	-0,101	0,0053	<0.001
Warm-adapted extinction	-0,123	0,061	<0.001	-0,144	0,006	<0.001
Warm-adapted colonization	0,126	0,061	<0.001	0,161	0,007	<0.001
Δβ-diversity	0,291	1,4	0.107	-0,314	1,5	0.0855
Extinction	-0,785	0,91	<0.001	-1,01	0,9	<0.001
Colonization	1,08	0,97	<0.001	0,696	1	<0.001
Cold-adapted extinction	-0,744	0,82	<0.001	-0,825	0,77	<0.001
Cold-adapted colonization	-0,0417	0,46	0.397	-0,185	0,4	0.000141
Warm-adapted extinction	0,877	0,72	<0.001	0,771	0,75	<0.001
Warm-adapted colonization	0,199	0,45	0.000159	-0,0752	0,55	0.253

Table S3: *Thermophilization (°C/decades^{-1}) and Δβ-diversity and their component mean value (Value) and standard deviation (s.d) across 80 forest ecoregions. The analysis was performed with two other thermal optimum value, from the original 2005 and a 2019 analysis of the EcoPlant database[1]. The P-value were obtained with a Wilcoxon one sample test against 0.*

Variable	EcoPlant Thermal optimum 2005			EcoPlant thermal optimum 2019		
	Value	s.d	P-value	Value	s.d	P-value
Thermophilization	0,111	0,15	<0.001	0,061	0,2	0.0038
Extinction	0,0965	0,085	<0.001	0,072	0,12	<0.001
Colonization	0,0147	0,11	0.11	-0,011	0,15	0.212
Cold-adapted extinction	0,273	0,16	<0.001	0,31	0,18	<0.001
Cold-adapted colonization	-0,177	0,12	<0.001	-0,238	0,18	<0.001
Warm-adapted extinction	-0,165	0,09	<0.001	-0,208	0,12	<0.001
Warm-adapted colonization	0,18	0,11	<0.001	0,197	0,16	<0.001
Δβ-diversity	0,0511	1,2	0.941	0,0401	1,1	0.772
Extinction	-0,715	0,74	<0.001	-0,136	0,61	0.012
Colonization	0,766	0,83	<0.001	0,176	0,68	0.0422
Cold-adapted extinction	-0,628	0,68	<0.001	-0,307	0,49	<0.001
Cold-adapted colonization	-0,0868	0,47	0.0709	0,172	0,43	0.00206
Warm-adapted extinction	0,578	0,55	<0.001	0,24	0,48	<0.001
Warm-adapted colonization	0,188	0,48	0.00178	-0,0637	0,37	0.166

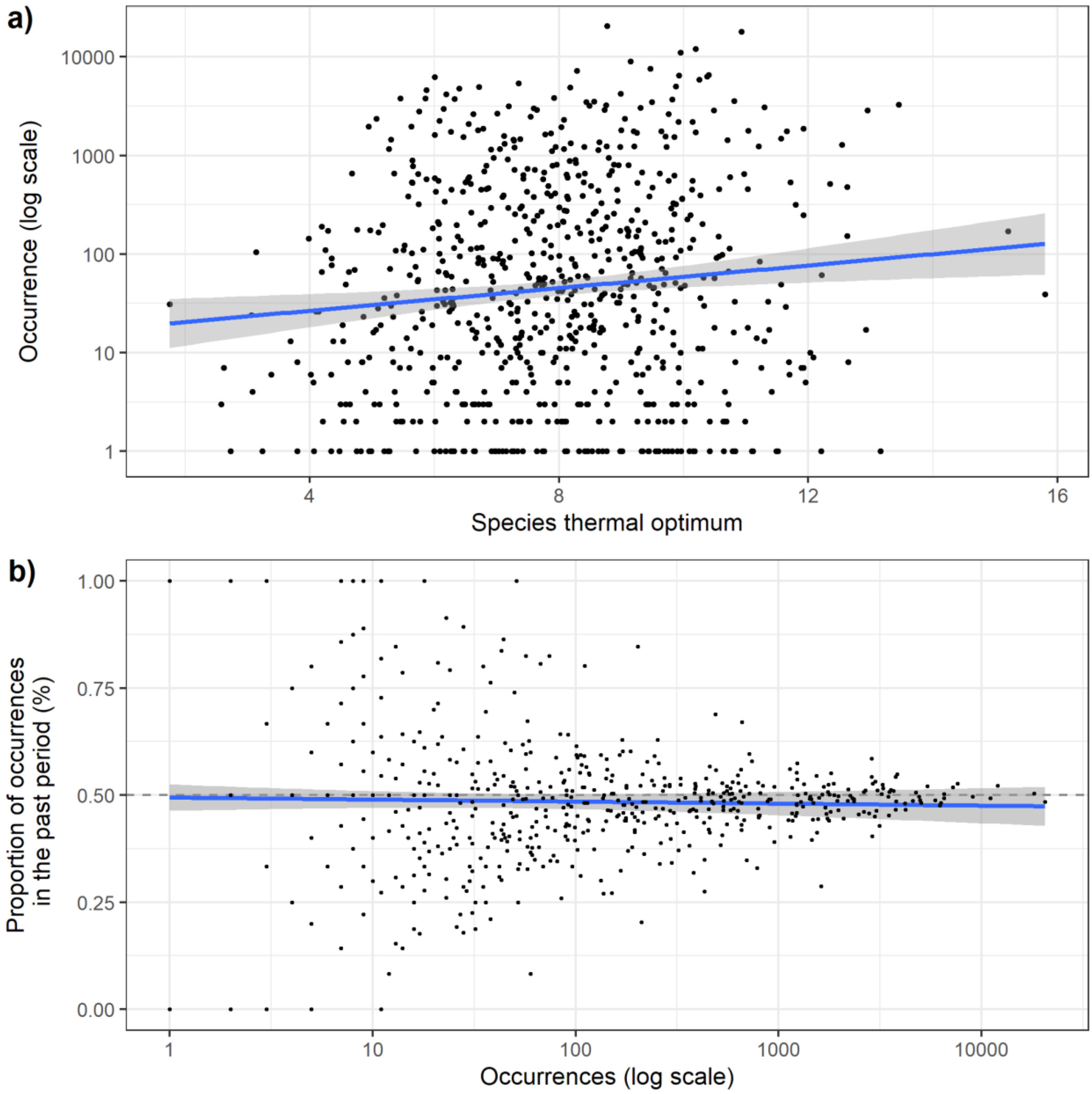

Figure S1: *a) Species occurrences (presence in a plot, log scale) in the entire dataset (n= 25,528 plots) in relation to their thermal optimum. The blue line is a fitted linear model log(occurrences) ~ thermal optimum and its uncertainty. b) Proportion of all the species occurrences recorded in the past period (>50% species gained in occurrences, <50% species lost occurrences) as function of the occurrence (log scale). The blue line is a fitted linear model Prop ~ log(occurrences) and its uncertainty*

Supplementary equations.

We define the weighted thermal optimum of an ecoregion of the past period as follow:

$$Topt_{eco\ past} = \frac{\sum_i topt_i * occ_{i\ past}}{\Sigma occ_{past}} \ (1)$$

Where $Topt_i$ and $occ_{i\ past}$ are the thermal optimum and occurrences in the "past" period of the species i, respectively.

Σocc_{past} is the sum of past occurrences of every species, can also be written $\Sigma_i occ_{i\ past}$.

We define the weighted thermal optimum of an ecoregion of the recent period as follow:

$$Topt_{eco\ recent} = \frac{\sum_i topt_i * occ_{i\ recent}}{\Sigma occ_{recent}} \ (2)$$

Where $occ_{i\ recent}$ is the occurrences of the species I in the "recent" period.

Thus, thermophilization is defined as follow:

$$Thermophilization = Topt_{eco\ recent} - Topt_{eco\ past} \ (3)$$

We defined the species i contribution to thermophilization with the equation:

$$Contrib_i = \frac{(Topt_i - Topt_{eco\ past}) \cdot (occ_{i\ recent} - occ_{i\ past})}{\sum occ_{recent}} \ (4)$$

And we want to demonstrate that

$$\sum_i contrib_i = Thermophilization \ (5)$$

We first develop (4)

$$Contrib_i = \frac{Topt_i * occ_{i\ recent} - Topt_{eco\ past} * occ_{i\ recent} + Topt_{eco\ past} * occ_{i\ past} - topt_i * occ_{i\ past}}{\sum occ_{recent}} \ (6)$$

Then the sum of (6) is written as follow:

$$\sum_i contrib_i = \frac{\sum_i topt_i * occ_{i\ recent} - Topt_{eco\ past} * \sum_i occ_{i\ recent} + Topt_{eco\ past} * \sum_i occ_{i\ past} - \sum_i topt_i * occ_{i\ past}}{\sum occ_{recent}} (7)$$

We can then simply (7) to

$$\sum_i contrib_i = \frac{\sum_i topt_i * occ_{i\ recent}}{\sum occ_{recent}} - \frac{Topt_{eco\ past} * \sum_i occ_{i\ recent}}{\sum occ_{recent}} + \frac{Topt_{eco\ past} * \sum_i occ_{i\ past} - \sum_i topt_i * occ_{i\ past}}{\sum occ_{recent}} \ (8)$$

We can further simplify (8) to

$$\sum_i contrib_i = Topt_{eco\ recent} - Topt_{eco\ past} + \Phi \ (9)$$

With:

$$\Phi = \frac{Topt_{eco\ past} * \sum_i occ_{i\ past} - \sum_i topt_i * occ_{i\ past}}{\sum occ_{recent}} \ (10)$$

We thus need to prove that $\Phi = 0$, however:

$Topt_{eco\ past} * \sum_i occ_{i\ past} = \sum_i topt_i * occ_{i\ past}$ (11)

Thus:

$$\Phi = \frac{\sum_i topt_i * occ_{i\ past} - \sum_i topt_i * occ_{i\ past}}{\sum occ_{recent}} = 0 \quad (12)$$

Which leads to

$$\sum_i contrib_i = Topt_{eco\ recent} - Topt_{eco\ past} = Thermophilization \quad (13)$$

References

1. Gégout, J.-C., Coudun, C., Bailly, G. & Jabiol, B. EcoPlant: A forest site database linking floristic data with soil and climate variables. *J. Veg. Sci.* **16**, 257–260 (2005).