

Fig. S1. Continuous Hill diversity profile across q values from 0 to 2 (steps of 0.1) for harvestmen assemblages in tropical dry forest (TDF, green) and oil palm monoculture (OPM, orange). The persistent separation between habitat types across the full profile indicates robust differences in diversity regardless of the weight assigned to rare or dominant species. Shaded bands represent 95% bootstrap confidence intervals (200 replicates).

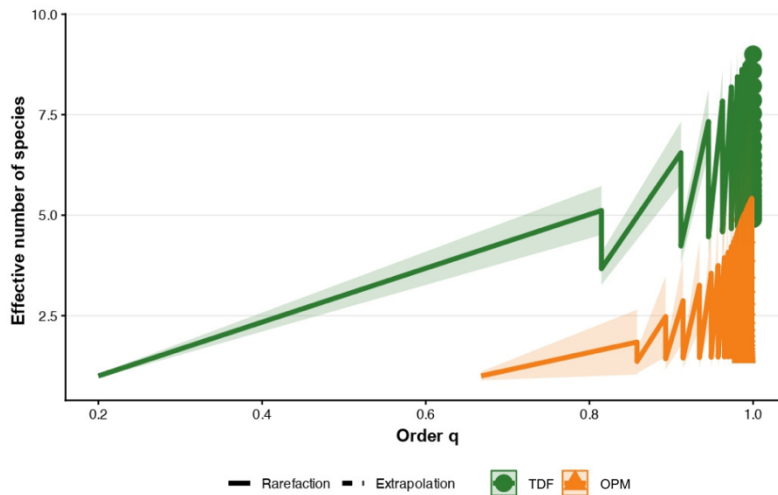


Fig.S2. DHARMA residual diagnostics for all generalized linear mixed models. For each panel, the left plot shows the uniform Q-Q plot and the right plot shows scaled residuals versus fitted values. (A) Negative binomial GLMM of harvestmen species richness. (B) Gamma GLMM of Hill $q = 1$ diversity. (C) Species-level GLMM of *Eucynorta quadripustulata* (EUCQU). (D) Species-level GLMM of *Hevelia crucis* (HEVCR). (E) Species-level GLMM of *Barinas piragua* (BARPI). (F) Species-level GLMM of Samoidae sp. (SAMSP). (G) Species-level GLMM of Gagrellinae sp. (GAGNA). (H) Species-level GLMM of *Stygnomma* sp. (STYSP).

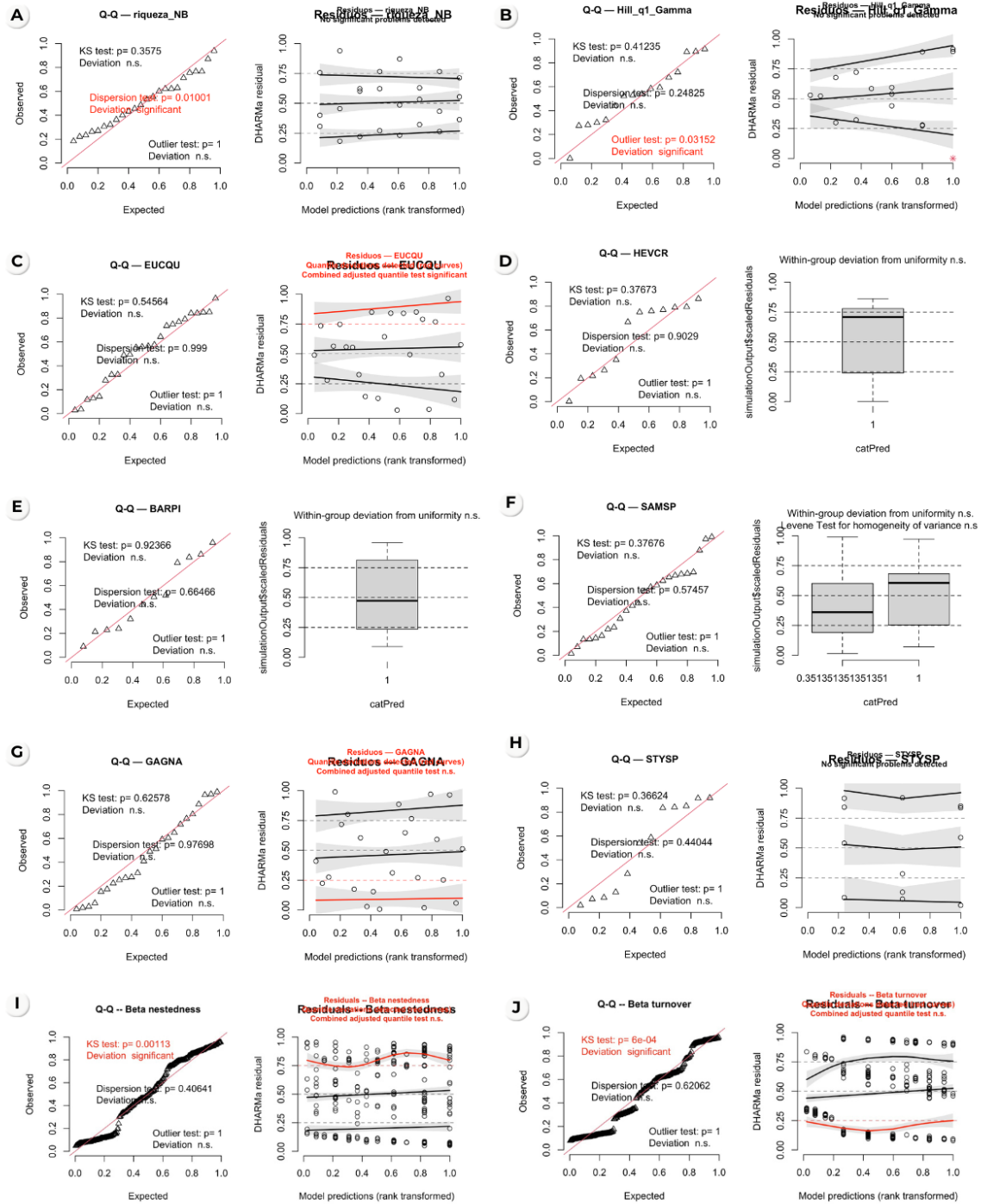


Fig.S3. Multivariate dispersion of harvestmen assemblages by habitat type (PERMDISP, betadisper). Each point represents the distance of a sampling unit to its group centroid in Bray-Curtis space, colored by sampling campaign. The white diamond indicates the mean

distance per habitat. Greater dispersion in TDF reflects higher internal compositional heterogeneity among plots, consistent with the structural complexity of riparian tropical dry forest (pseudo-F = 2.9; $p = 0.111$). TDF = tropical dry forest; OPM = oil palm monoculture.

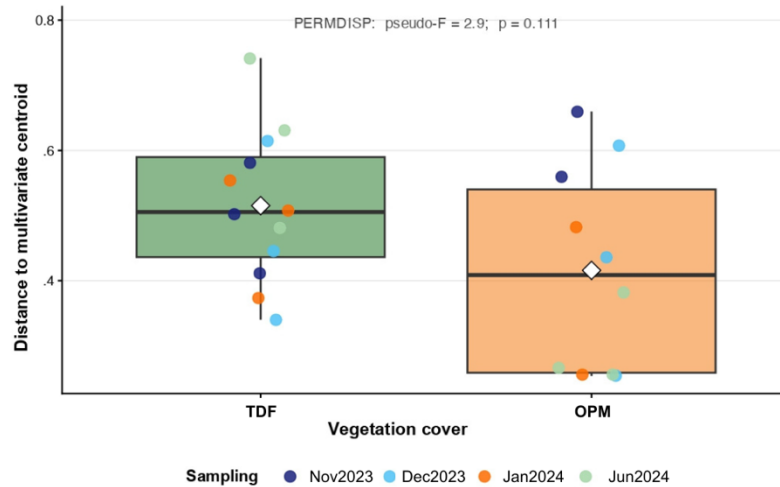


Fig.S4. Observed and predicted abundance of representative harvestmen OTUs by habitat type (BST = TDF, tropical dry forest; PLM = OPM, oil palm monoculture). For OTUs without complete habitat separation, large points and error bars show GLMM-derived marginal means with 95% confidence intervals, overlaid on individual observations (small grey points). For OTUs exclusive to TDF (marked with an asterisk), only observed abundances and their mean are shown, as no model with habitat as a predictor could be fitted. (A) *Barinas piragua* (BARPI)*. (B) *Eucynorta quadripustulata* (EUCQU). (C) *Gagrellinae* sp. (GAGNA). (D) *Hevelia crucis* (HEVCR)*.

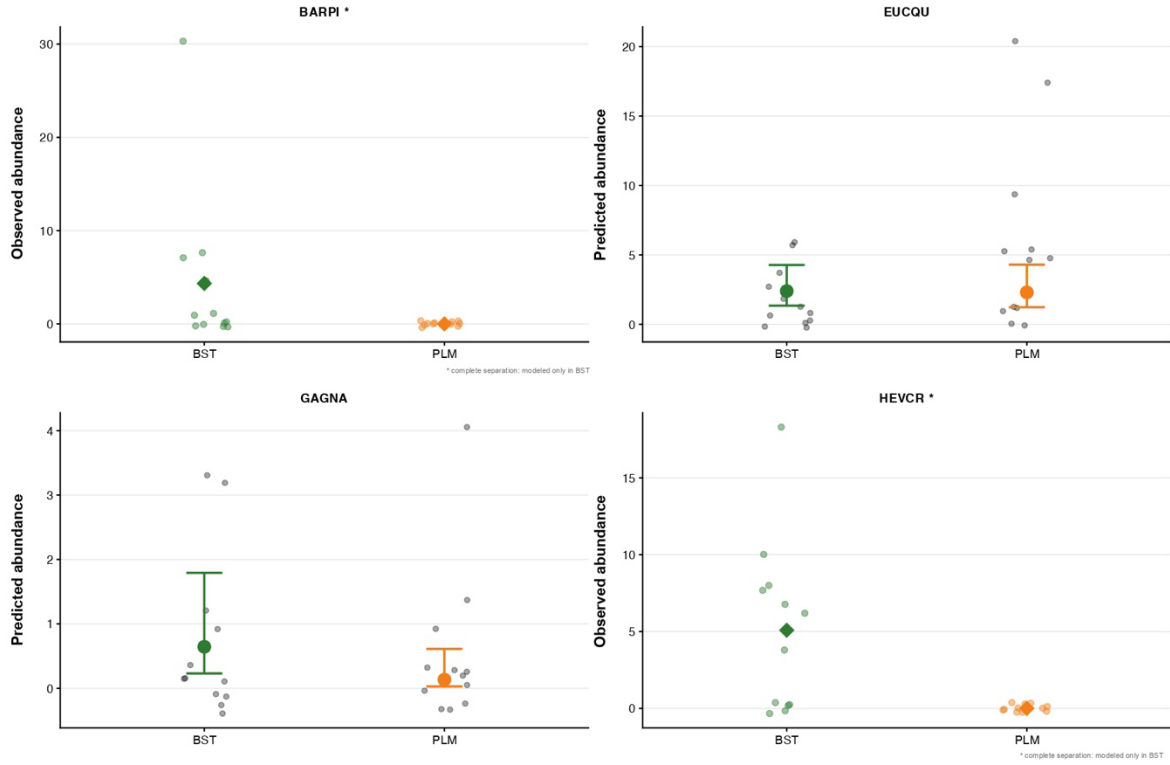


Fig.S5. Estimated marginal means of pairwise nestedness (β_{jne}) and turnover (β_{jtu}) components (response scale) by comparison type, derived from the Beta GLMMs. Error bars indicate 95% confidence intervals. (A) Nestedness. (B) Turnover. Intra-TDF = pairs within tropical dry forest; Intra-OPM = pairs within oil palm monoculture; Inter = pairs between habitat types.

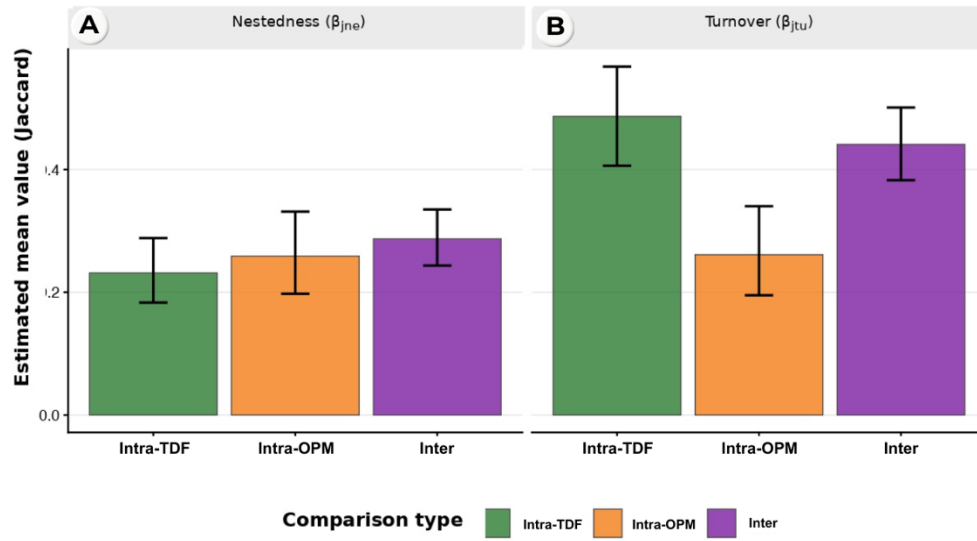


Table S1. GLMM coefficients for harvestmen species richness (negative binomial distribution, log link). IRR = incidence rate ratio = $\exp(\beta)$; 95% confidence intervals. Reference level: TDF, November 2023. $R^2_m = 0.467$; $R^2_c = 0.467$.

Parameter	IRR	95% CI lower	95% CI upper	p
Intercept (TDF, Nov 2023)	4.000	2.272	7.043	< 0.001
Habitat: OPM	0.250	0.071	0.886	0.032
Month: Dec 2023	1.250	0.585	2.670	0.565
Month: Jan 2024	1.083	0.494	2.374	0.842
Month: Jun 2024	0.417	0.147	1.183	0.100
OPM $\times$ Dec 2023	1.333	0.264	6.739	0.728
OPM $\times$ Jan 2024	1.231	0.227	6.671	0.810
OPM $\times$ Jun 2024	4.000	0.680	23.513	0.125

Table S2. Species-level p-values (Holm-adjusted) for the effect of habitat type on individual OTU abundances (mvabund, likelihood ratio test, 999 bootstrap replicates, negative binomial distribution).

OTU	Adjusted p	Significant (p < 0.05)
<i>Hevelia crucis</i> (HEVCR)	0.010	Yes
<i>Barinas piragua</i> (BARPI)	0.038	Yes
<i>Eucynorta quadripustulata</i> (EUCQU)	0.089	No
<i>Stygnomma</i> sp. (STYSP)	0.131	No
<i>Icaleptidae</i> sp. (ICASP)	0.246	No
<i>Cosmetidae</i> sp. (COSSP)	0.614	No
<i>Samoidae</i> sp. (SAMSP)	0.614	No
<i>Zalmoxidae</i> sp. (ZALSP)	0.614	No
<i>Agoristenidae</i> sp. (AGOSP)	0.625	No
<i>Gagrellinae</i> (GAGNA)	0.914	No

Table S3. SIMPER analysis of OTU contributions to mean Bray-Curtis dissimilarity between TDF and OPM (999 permutations). δ = mean percentage contribution; Ratio = δ /SD (consistency of contribution); $\bar{x}$ TDF and $\bar{x}$ OPM = mean abundance per plot in each habitat.

OTU	δ (%)	SD	Ratio	$\bar{x}$ TDF	$\bar{x}$ OPM	Cumul. (%)
EUCQU	27.40	0.247	8.08	2.00	6.90	32.2
HEVCR	18.38	0.195	26.04	5.08	0.00	53.9
SAMSP	14.13	0.193	11.20	2.17	0.70	70.5
BARPI	10.61	0.149	28.99	4.33	0.00	83.0
GAGNA	4.33	0.061	11.01	0.67	0.60	88.0
COSSP	2.98	0.064	5.21	0.33	0.10	91.5
STYSP	2.96	0.046	25.21	1.17	0.00	95.0
ICASP	1.80	0.036	9.28	0.33	0.00	97.1
ZALSP	1.73	0.067	0.00	0.00	0.20	99.2
AGOSP	0.70	0.023	17.89	0.42	0.00	100.0

Table S4. AICc-selected GLMMs for each OTU with ≥ 10 individuals. For OTUs with complete separation (exclusive to TDF), the candidate predictor set was reduced a priori to four ecologically justified variables to avoid overfitting ($n = 12$ observations within TDF). R^2_m = variance explained by fixed effects; R^2_c = total variance explained including random effects.

OTU	N ind.	Habitat(s) modelled	Candidate predictors	Selected predictors
BARPI	52	TDF only (complete separation)	4 (a priori)	None (null model selected)
EUCQU	93	Both	9 (automatic)	HR_media, EVI
GAGNA	14	Both	9 (automatic)	NDVI
HEVCR	61	TDF only (complete separation)	4 (a priori)	None (null model selected)
SAMSP	33	Both	9 (automatic)	None (null model selected)
STYSP	14	TDF only (complete separation)	4 (a priori)	dist_agua_m (uninformative CI)

Table S5. Mean pairwise beta-diversity components (Jaccard family) by comparison type.
 β_{total} = total dissimilarity; β_{turnover} = replacement component; $\beta_{\text{nestedness}}$ = richness-difference component.

Comparison type	N pairs	β_{total}	β_{turnover}	$\beta_{\text{nestedness}}$
Intra-TDF	66	0.712	0.511	0.201
Intra-OPM	45	0.465	0.163	0.302
Inter-habitat	120	0.787	0.460	0.327