

Lineage-specific allometric scaling of the first metacarpal: a quantitative reassessment of the Sima de los Huesos sample

Javier Pérez-Pelayo, Carlos Lorenzo-Merino, Mercedes Conde-Valverde, Ignacio Martínez, José-Miguel Carretero

Full numerical results underlying Figures 1 and 2 of the poster.

Measurements. MB = midshaft breadth (mediolateral); MH = midshaft height (dorsopalmar); DB = distal breadth (epicondylar, measured between the dorsal epicondyles of the head); DH = distal height (dorsopalmar). Size was estimated as the geometric mean (GM) of the four measurements. All regressions were fitted on natural-log-transformed variables. Only individuals preserving all four measurements enter the allometric analysis.

Table S1. OLS regression coefficients

Ordinary least squares regressions of log(measurement) on log(GM), fitted separately within each species. *p* isometry tests the slope against $\beta = 1$.

Species	Var.	n	Slope	Intercept	R ²	σ	<i>p</i> isometry	95% CI	Pattern
<i>H. neanderthalensis</i>	MB	12	1.232	−0.589	0.597	0.0821	0.485	0.519–1.946	Isometric
<i>H. neanderthalensis</i>	MH	12	0.886	−0.037	0.557	0.0641	0.658	0.330–1.443	Isometric
<i>H. neanderthalensis</i>	DB	12	0.849	0.677	0.656	0.0498	0.455	0.416–1.282	Isometric
<i>H. neanderthalensis</i>	DH	12	1.033	−0.051	0.587	0.0702	0.907	0.423–1.643	Isometric
<i>H. sapiens</i>	MB	107	0.965	0.111	0.768	0.0509	0.498	0.862–1.067	Isometric
<i>H. sapiens</i>	MH	107	1.211	−0.858	0.842	0.0504	0.0001	1.109–1.312	Positive allom.
<i>H. sapiens</i>	DB	107	0.978	0.244	0.842	0.0406	0.589	0.896–1.059	Isometric
<i>H. sapiens</i>	DH	107	0.847	0.503	0.738	0.0484	0.0024	0.749–0.944	Negative allom.

Note the width of the Neanderthal confidence intervals. With *n* = 12, slope estimates are imprecise and the isometric result should be read as a lack of resolution rather than as evidence of isometry.

Table S2. ANCOVA

Two-step comparison of the *H. sapiens* and *H. neanderthalensis* regressions. Step 1 tests the interaction term (different slopes); step 2, evaluated only when step 1 is non-significant, tests the species main effect (different intercepts).

Variable	F interaction	<i>p</i> interaction	F species	<i>p</i> species	Case
MB	1.491	0.2245	3.127	0.0796	C — common slope and intercept
MH	2.430	0.1218	0.216	0.6430	C — common slope and intercept
DB	0.591	0.4435	74.994	< 0.0001	B — parallel, different intercepts (HN > HS)
DH	0.829	0.3644	32.064	< 0.0001	B — parallel, different intercepts (HS > HN)

Case A = significantly different slopes (*p* < 0.05). Case B = parallel slopes but different intercepts. Case C = a single line describes both species.

Table S3. Standardized residuals of the Sima de los Huesos specimens

Standardized residuals (z) of each SH individual relative to the *H. sapiens* slope (z_{HS}), the *H. neanderthalensis* slope (z_{HN}), and the pooled slope (z_{pooled}). Values exceeding ± 2 SD are shown in bold red.

Specimen	Var.	Case	z_{HS}	z_{HN}	z_{pooled}	Interpretation
AT-936	MB	C	1.47	1.51	1.42	Within ± 2 SD of both
AT-936	MH	C	0.31	-0.24	0.28	Within ± 2 SD of both
AT-936	DB	B	0.56	-1.95	0.25	Compatible with HS; near HN limit
AT-936	DH	B	-2.34	-0.16	-1.85	Departs from HS; compatible with HN
AT-1340	MB	C	-1.16	-0.21	-1.02	Within ± 2 SD of both
AT-1340	MH	C	0.16	-0.22	0.14	Within ± 2 SD of both
AT-1340	DB	B	3.35	0.39	2.36	Departs from HS; compatible with HN
AT-1340	DH	B	-1.75	0.17	-1.34	Within ± 2 SD of both
AT-1363	MB	C	1.19	1.31	1.15	Within ± 2 SD of both
AT-1363	MH	C	2.21	1.29	2.13	Departs from HS; compatible with HN
AT-1363	DB	B	-0.86	-3.09	-0.85	Compatible with HS; departs from HN
AT-1363	DH	B	-2.82	-0.51	-2.25	Departs from HS; compatible with HN
AT-5565	MB	C	0.60	0.73	0.60	Within ± 2 SD of both
AT-5565	MH	C	0.46	0.24	0.45	Within ± 2 SD of both
AT-5565	DB	B	-0.97	-3.01	-0.99	Compatible with HS; departs from HN
AT-5565	DH	B	-0.29	1.06	-0.07	Within ± 2 SD of both

z_{pooled} is computed against the common regression line and is therefore most meaningful for Case C variables. Note that z_{HS} does not depend on the composition of the Neanderthal sample.

References

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Acknowledgments. J.P.P. thanks the Atapuerca Foundation for the predoctoral grant. We are grateful to the Sima de los Huesos excavation and research team, whose fieldwork and study of the site made this material available. Funding was provided by Project PID2024-156477NB-C33, supported by MCIN/AEI/10.13039/501100011033 and FSE+, Government of Spain.