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Baleka, Sina, Herridge, Victoria L., Catalano, Giulio et al. (7 more authors) (2021)
Estimating the dwarfing rate of an extinct Sicilian elephant. *Current Biology*. 3606-3612.e7.
ISSN 0960-9822

<https://doi.org/10.1016/j.cub.2021.05.037>

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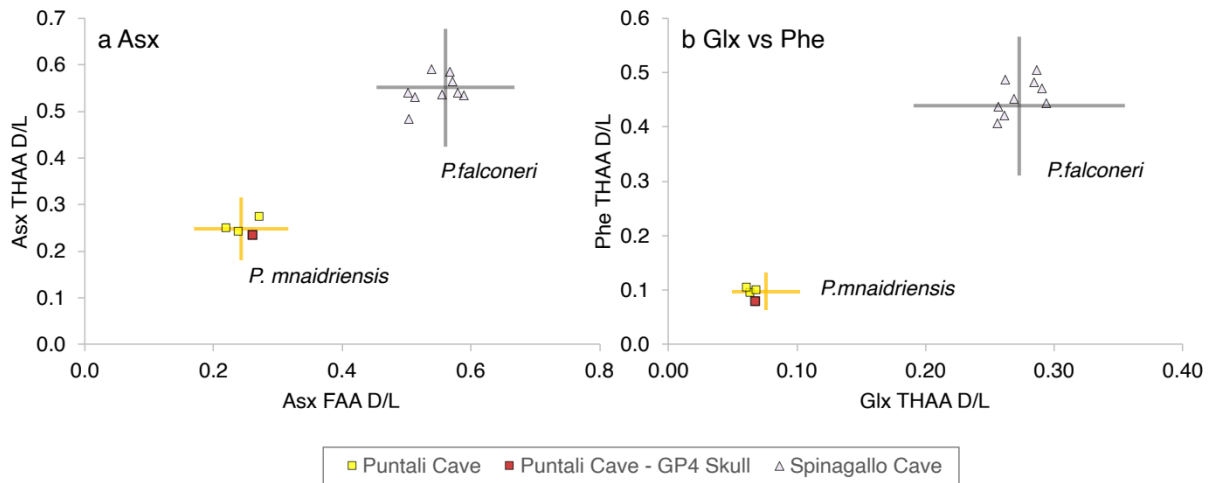


Figure S1: Extent of intra-crystalline protein degradation (IcPD) of tooth enamel samples from Puntali and dwarf elephant samples from other Sicilian sites. Related to STAR methods. Total hydrolysable amino acid (THAA) versus free amino acid (FAA) D- and L-isomer ratio (D/L) of Asx (a) and Phe versus Glx THAA D/L (b). Crosses show the range of enamel IcPD data from *P. cf. mnaidriensis* (lower) and *P. falconeri* (upper) material from Sicily, encompassing unpublished data not included in this publication, as well as the comparative material from Spinagallo (Table S1).

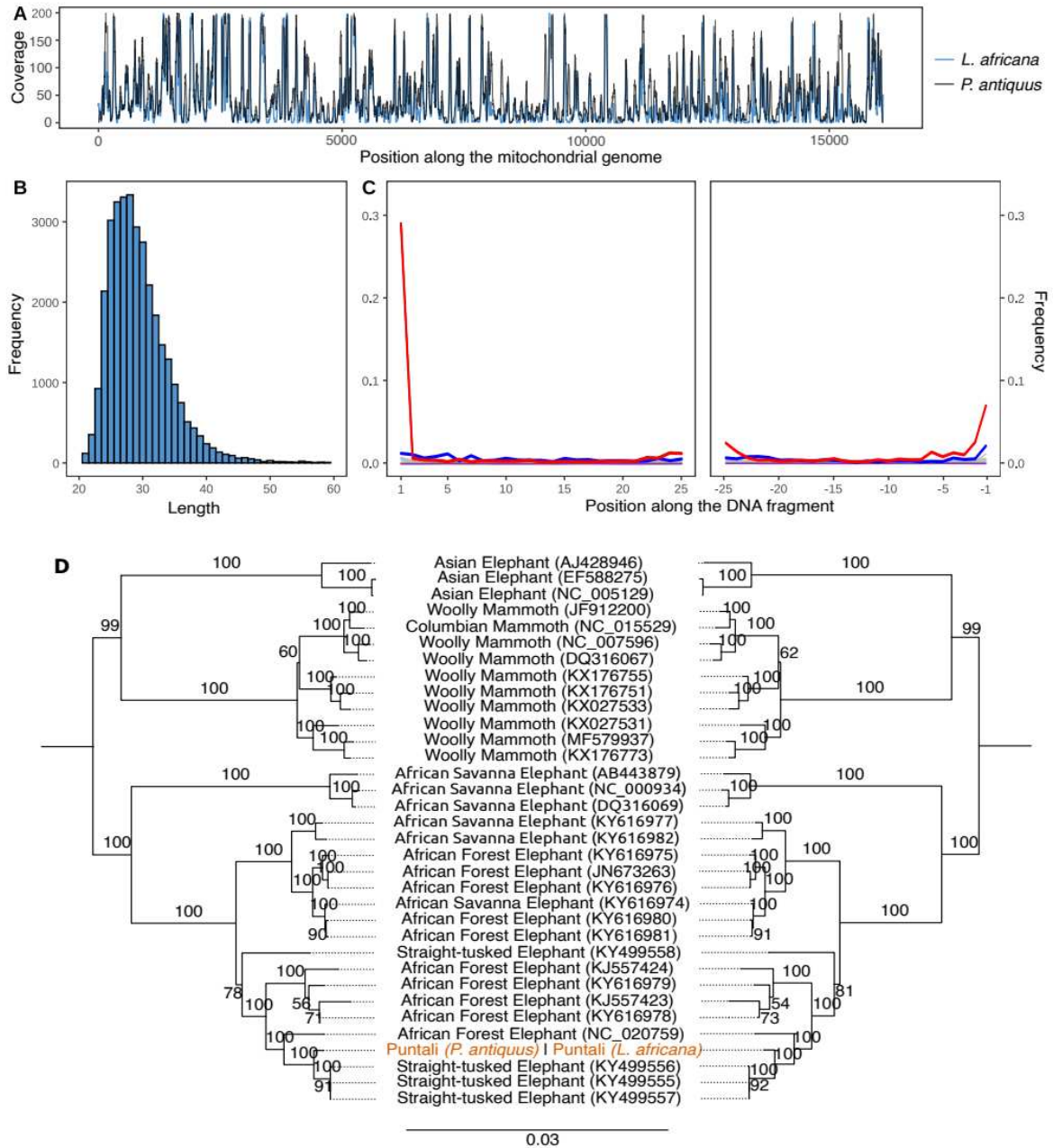


Figure S2: DNA authentication. Related to Figure 2 and STAR Methods. A) Sequence coverage plot of the mitochondrial genome of the Puntali sample according to reference sequence. B) Fragment length distribution of reads mapping to the *P. antiquus* reference. C) Frequency of C to T misincorporations (red) from the 5' (left) and 3' (right) end for reads mapping to *P. antiquus*. D) Maximum-likelihood phylogenetic tree using 100 bootstrap replicates for the two Puntali elephant consensus sequences in relation to 33 other elephantid sequences.

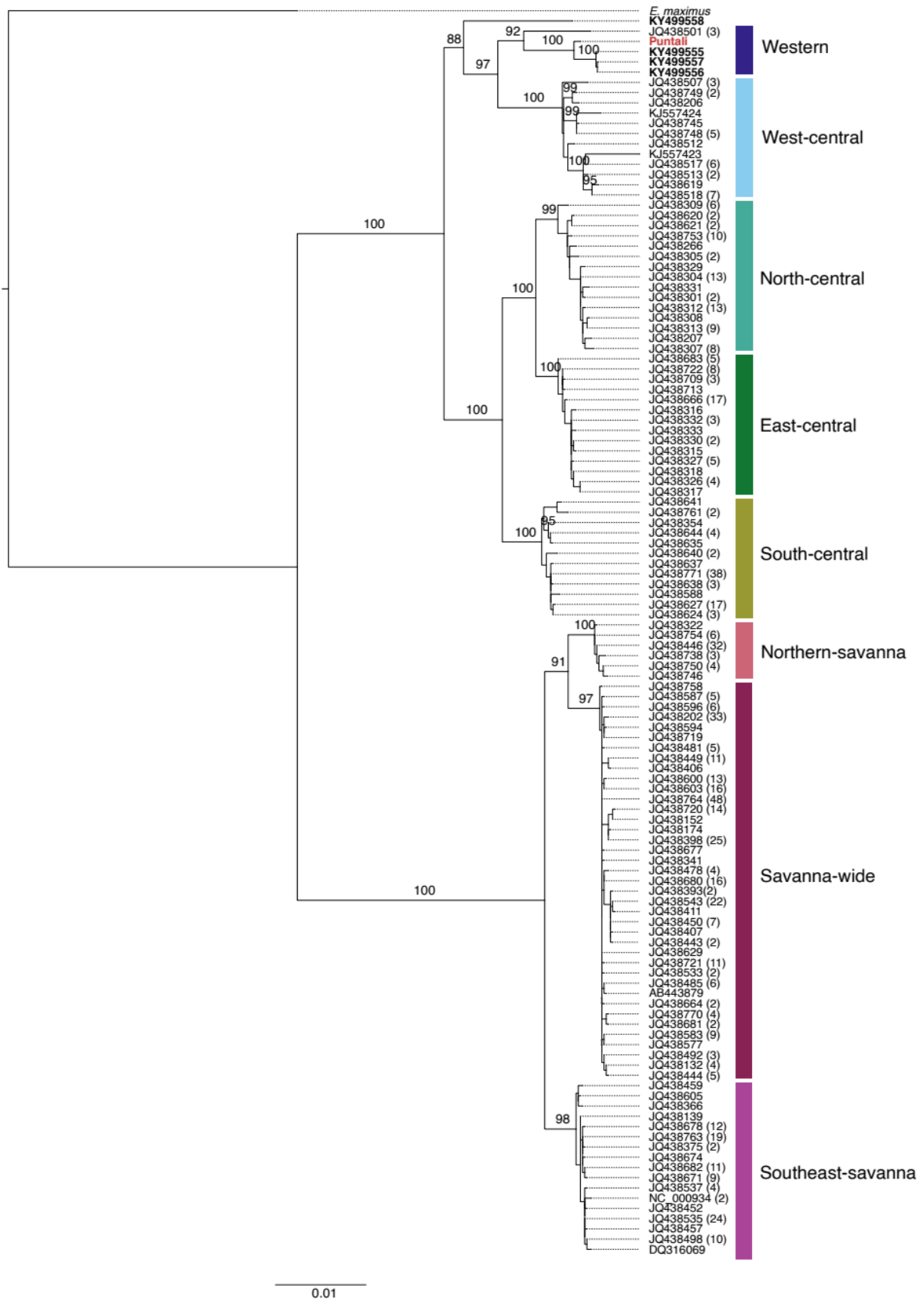


Figure S3: Maximum-likelihood phylogeny of a 4258 bp mtDNA alignment of 122 unique haplotypes. Related to Figure 2 and STAR methods. Subclade naming follows previous publications.^{S1} From the original alignment of 675 sequences, identical haplotypes

were collapsed to a single representative, with numbers indicated in parentheses. Node support is given as bootstrap value, with values lower than 85 not shown. The mainland straight-tusked elephants (**Neumark-Nord (KY499555-KY499557)** and **Weimar (KY499558)**) are indicated in bold.

| | | | | | | | | | | | | | | | |
|------------------------|----------------------------------|--|--------|------|------|------|------|------|------|------|------|------|------|------|------|
| Norwich Crag Formation | 1.9-2.2 Ma | <i>Anancus arvernensis</i> | 1385 | 0.54 | 0.00 | 0.26 | 0.00 | 0.67 | 0.02 | 0.48 | 0.01 | 0.24 | 0.01 | 0.42 | 0.02 |
| | | <i>Anancus arvernensis</i> | 7971 | 0.47 | 0.00 | 0.22 | 0.00 | 0.60 | 0.00 | 0.39 | 0.01 | 0.20 | 0.00 | 0.37 | 0.01 |
| | | <i>Mammuthus meridionalis</i> | 5988 | 0.51 | 0.01 | 0.27 | 0.00 | 0.69 | 0.00 | 0.44 | 0.00 | 0.23 | 0.00 | 0.41 | 0.01 |
| Crayford | MIS 7/6 boundary (ca. 200 ka) | <i>Mammuthus trogontherii</i> <i>/primigenius</i> | 117009 | 0.22 | 0.00 | 0.06 | 0.00 | 0.15 | 0.01 | 0.22 | 0.00 | 0.07 | 0.00 | 0.10 | 0.00 |
| | | | 5123 | 0.26 | 0.01 | 0.07 | 0.00 | 0.20 | 0.01 | 0.28 | 0.01 | 0.09 | 0.00 | 0.11 | 0.00 |

Table S1: Related to STAR methods. Ratios of amino acid D- and L-isomer (D/L) values and preparative replicate standard deviations (n=2) for the free amino acid (FAA) fraction and the total hydrolysable amino acid (THAA) fraction for individual dwarf elephant teeth from Spinagallo and Puntali caves.

| Museum | Specimen | Species | Site | Humerus TL (mm) |
|----------------------|-------------------------------|----------------------------|-------------------------------|------------------------|
| Palermo GM | 100 | <i>P. cf. mnaidriensis</i> | Puntali Cave | 590 |
| Palermo GM | 560/102 | <i>P. cf. mnaidriensis</i> | Puntali Cave | 685 |
| Palermo GM | 560/99 | <i>P. cf. mnaidriensis</i> | Puntali Cave | 610 |
| Palermo Osservatorio | GPL30 | <i>P. cf. mnaidriensis</i> | Puntali Cave | 590 |
| Milan NHM | V2873 | <i>P. cf. mnaidriensis</i> | ?Puntali Cave | 612 |
| Rome Sapienza | "RSH2" | <i>P. antiquus</i> | Tufello | 1297 |
| SMNS Stuttgart | 6616.2.12.88.1 | <i>P. antiquus</i> | Bruhl (Koller) | 1286 |
| SMNS Stuttgart | 6717.7.6.66.6 | <i>P. antiquus</i> | Rheinhausen, Osterwiesen | 1167 |
| Erkek & Lister 2021 | Riano | <i>P. antiquus</i> | Riano | 1150 |
| Erkek & Lister 2021 | Fonte Campanile I (Viterbo I) | <i>P. antiquus</i> | Fonte Campanile I (Viterbo I) | 1280 |
| Erkek & Lister 2021 | Aveley | <i>P. antiquus</i> | Aveley | 1030 |
| Erkek & Lister 2021 | Amyntaio | <i>P. antiquus</i> | Amyntaio | 1170 |
| Erkek & Lister 2021 | Neumark Nord (152-E9) | <i>P. antiquus</i> | Neumark Nord (152-E9) | 1220 |
| Erkek & Lister 2021 | Jozwin (Konin) | <i>P. antiquus</i> | Jozwin (Konin) | 1287 |
| Erkek & Lister 2021 | Neumark Nord (176-E24A) | <i>P. antiquus</i> | Neumark Nord (176-E24A) | 1270 |
| Erkek & Lister 2021 | Upnor | <i>P. antiquus</i> | Upnor | 1290 |
| Erkek & Lister 2021 | Warsaw | <i>P. antiquus</i> | Warsaw | 1162 |
| Erkek & Lister 2021 | Kiesäcker 72 | <i>P. antiquus</i> | Kiesäcker 72 | 1155 |
| Erkek & Lister 2021 | Gröbern I | <i>P. antiquus</i> | Gröbern I | 1340 |

Table S3. Total humerus length (TL) in mm. Related to Figure 1 and STAR methods.

SUPPLEMENTAL REFERENCES

- S1. Ishida, Y., Georgiadis, N. J., Hondo, T., & Roca, A. L. (2013). Triangulating the provenance of African elephants using mitochondrial DNA. *Evolutionary Applications*, 6(2), 253-265.