A Developmental Perspective on the Postcanine Dental Proportions of *Homo naledi*

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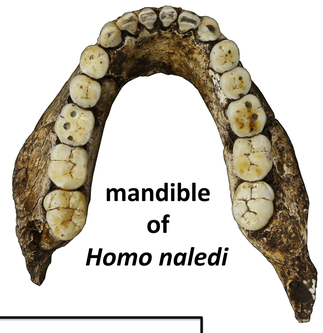
Introduction

Among the key features that differentiate australopiths (e.g., *Ardipithecus*, *Australopithecus* and *Paranthropus*) from *Homo* are:

1. Absolute and relative molar size
2. Molar proportions (i.e., molar size sequence)

Researchers have suggested that the overall anatomy of the recently discovered *Homo naledi* ties it to the genus *Homo*[1]; however, the mandibular molars present an interesting combination of small size (*Homo*-like) (Fig 1) and primitive proportions (australopith-like: i.e., $M_1<M_2<M_3$) (Fig 2).



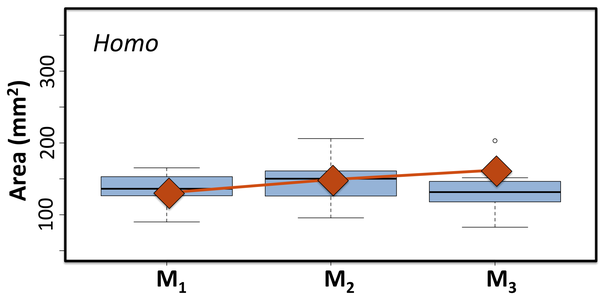


Figure 1. Mean molar areas for species in the genus *Homo*, with *H. naledi* indicated by ◆. (Species plotted: *H. sapiens, H. erectus, H. floresiensis, H. habilis, H. heidelbergensis,* and *H. neanderthalensis*)

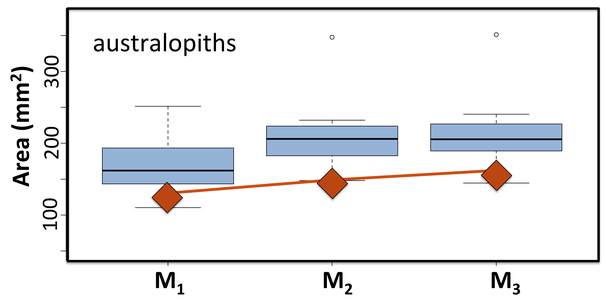
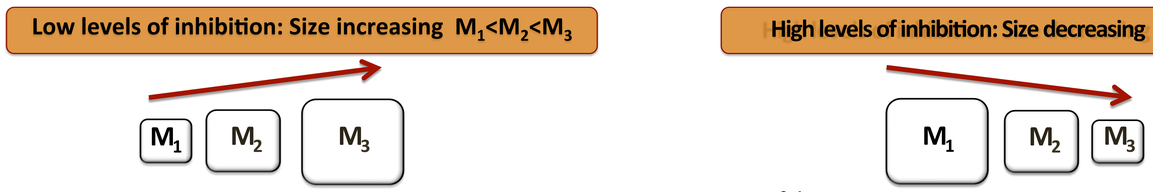


Figure 2. Mean molar areas for the australopiths with *H. naledi* indicated by ◆. (Species plotted: *Ar. ramidus, Au. afarensis, Au. africanus, Au. anamensis, Au. deyiremeda, Au. sediba, P. boisei,* and *P. robustus)*

Molar size and proportions are phenotypes that are linked through a simple developmental rule[2]:

- Relative molar proportions are controlled by an inhibitory cascade mechanism, where a previously-initiated molar influences the size of subsequently-developing molars through the balance of activator and inhibitor molecules[3].



- Hominin molar proportions fit the predictions of the inhibitory cascade[2,4].
- Molar proportions are linked to absolute M_1 size, but the relationship between M_1 size and molar proportions differs between the australopiths and *Homo*[2].
- Therefore, with the emergence of the genus *Homo,* there is a change in the developmental process regulating how molar proportions vary with absolute molar size[2].
- Because of the relationship between M_1 size and molar proportions, we can use the average size of a molar to predict the size of all remaining molars (Table 1).

Research Question

Is the developmental process (i.e., how molar proportions vary with absolute molar size) in *H. naledi* more similar to that of the australopiths or that of *Homo*?

Materials & Methods

- Published molar metrics for *H. naledi*[1] were used to calculate mean molar areas (BL x MD).
- Mean molar areas, for each molar position, were entered into the prediction spreadsheet[2] (see Table 1) to generate confidence intervals (CI) for the remaining molars from the equations provided from the australopith and *Homo* models.

Table 1. An example using the prediction spreadsheet to generate CIs for the mean M_1 area of *H. naledi* using the australopith model.

Model	Tooth Position	Tooth Area
australopith	M_1	**130.5**
‘australopith’ Or ‘*Homo*’	M_1, M_2, or M_3	Mean Molar Area

Species Mean Predicted Sizes, mm² (95% CI)		
M_1	M_2	M_3
130.5	163.3	165.0
(111.1-152.0)	(140.2-189.0)	(142.1-189.7)

Confidence Intervals

Prediction

Given its attribution to the genus *Homo*, mean molar areas and the resulting molar proportions of *Homo naledi* should fall within the CIs for the models based on *Homo* rather the australopiths.

Results

***H. naledi* mean molar areas compared to CIs generated from the “australopith” and “*Homo*” models.**

Green: fits model predictions Red: does not fit model prediction

Right-hand column indicates whether, overall, mean molar areas for M_1, M_2, and M_3 *all* fall within (✓) or outside (✗) the CI generated for each tooth position.

H. naledi Mean Molar Areas	M_1	M_2	M_3
→	130.5 mm	149.0 mm	162.1 mm

Model	Tooth Position	CI	CI	CI	Do all molars fall within CI?
australopith	M_1	—	140.2-189.0	142.1-189.7	✓
	M_2	97.6-143.4	—	123.4-178.2	✓
	M_3	108.1-150.1	136.6-185.6	—	✓
Homo	M_1	—	126.8-151.7	116.0-139.3	✗
	M_2	128.4-151.8	—	126.6-149.6	✗
	M_3	141.7-172.8	159.8-194.1	—	✗

- *H. naledi*’s mean values fall within the predicted CIs for all molars using the australopith model.
- *H. naledi*’s mean values for M_1 and M_2 fall within CIs for the *Homo* model only when predicted using M_1 or M_2, but not M_3.
- *H. naledi*’s mean value for M_3 does not fall within the CI for the *Homo* model when predicted using either M_1 or M_3.

***H. naledi’s* molar sizes and proportions are poorly predicted using the ‘*Homo*’ model and are better predicted using the ‘australopith’ model.**

Conclusions

- *H. naledi* is more similar to the australopiths in the relationship between absolute M_1 size and molar proportions.
- Our results suggest that the developmental process controlling how molar proportions vary with absolute M_1 size in *H. naledi* is more similar to that of the australopiths.
- Future research should include the deciduous premolars of *H. naledi*, as prior studies found that their size plays a key role in determining the resulting molar proportions in hominins[2].

References
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Acknowledgements: We would like to thank the following agencies for providing funds that enabled the completion and presentation of this work: the Paleoanthropology Society (ESD), ASU Graduate and Professional Student Association (ESD, CS, KP), ASU Graduate Education (ESD), the Adjunct Faculty Association (ESD), and the National Science Foundation Graduate Research Fellowship No. 2011121784 (KP). Image of the mandible of *H. naledi* kindly provided by Peter Schmidt and John Hawkes