Bigger Brains Led to Bigger Bodies?

The Correlated Evolution of Human Brain and Body Size

by Mark Grabowski

CA+ Online-Only Material: Supplement A

Most investigations of hominin brain and body size evolution assume that different selection pressures acted on each trait or that brain and body size are linked physiologically via the energetic demands of large brains. However, evidence from model organisms suggests that some genes cause variation in both brain and body size, with the result that selection on either trait can lead to a correlated response in the unselected trait. If brain and body size covariation exists in our lineage, correlated evolution could mean that changes observed in the fossil record are poor predictors of past selection pressures that produced those changes. This study shows that modern humans, chimpanzees, and all primates included here have significant and roughly similar levels of evolutionary constraints from brain and body size covariance, arguing that similar levels were present in earlier hominins. Building on these findings, results suggest that strong selection to increase brain size alone played a large role in both brain and body size increases throughout human evolution and may have been solely responsible for the major increase in both traits that occurred during the transition to *Homo erectus*. This switch in emphasis has major implications for adaptive hypotheses on the origins of our genus.

One of the most enduring questions in hominin evolution is how to explain our unique cognitive abilities. Modern humans possess the largest brains of any extant primate. At least since Darwin (1874), overall brain size has been linked with the evolution of cognition. As larger animals generally have larger brains (Jerison 1973), relative brain size—that is, enlargement of the brain beyond what would be expected by allometric scaling for body size—has often been used to compare cognition across species (e.g., Boddy et al. 2012; Montgomery et al. 2013). However, a number of recent studies propose that absolute brain size (Deaner et al. 2007; MacLean et al. 2014) and total neocortical neuron number (Herculano-Houzel et al. 2007) are better predictors of cognitive abilities. Relative brain size can also confound patterns of brain and body size evolution and lead to the assumption that relatively larger brains result from selection for increased cognitive abilities, not for reduced body sizes (Deacon 1990; Smaers et al. 2012). Along these lines, brain size apparently increased across nearly all major transitions of hominin evolution, whereas body size increased in some and decreased in others (fig. 1). This pattern of apparently independent brain and body size evolution is not unusual when compared to other mammals (Boddy et al. 2012; Smaers et al. 2012) or primates (Montgomery et al. 2010). These studies and others (Finarelli and Flynn 2009; Gonzalez-Voyer, Winberg, and Kolm 2009; Weston and Lister 2009) propose that different selection pressures on brain and body size led to the diversity of evolutionary patterns seen across a wide range of mammalian groups. Corresponding hypotheses on the ultimate causes of hominin brain size and cognitive evolution generally focus on separate selection pressures on the brain alone (e.g., Dunbar 1998) or propose that brain and body are linked physiologically through the need to satisfy the substantial energetic requirements of a large brain (e.g., Aiello and Wheeler 1995; Fonseca-Azevedo and Herculano-Houzel 2012).

However, evidence suggests that brain size and body size might not actually be independent over evolutionary time. Experimental results in model organisms have shown that selection on either brain or body size led to a correlated response in the unselected trait (Atchley 1984; Fuller 1979; Riska and Atchley 1985; Roderick 1979; Roderick, Wimer, and Wimer 1976; Wimer 1979). This effect is the result of the two traits sharing some portion of the genes that cause variation in brain and body size. The size of the correlated response depends on the degree of shared variation, largely caused by pleiotropy and manifest in the genetic correlation between traits (Atchley 1984; Atchley et al. 1984; Riska and Atchley 1985; Roderick, Wimer, and Wimer 1976; but see Hager et al. 2012). Lande (1979) was the first to explore the role of genetic brain-body correlation in hominin evolution and hypothesized that because changes

Mark Grabowski is a James Arthur Postdoctoral Fellow at the American Museum of Natural History (Central Park West/79th Street, New York, New York 10024, USA) and a Guest Researcher at the Centre for Ecological and Evolutionary Synthesis in the Department of Biosciences at the University of Oslo (PO Box 1066 Blindern, NO-0316 Oslo, Norway [mwgrabowski@gmail.com]). This paper was submitted 20 XI 14, accepted 16 VI 15, and electronically published 29 III 16.

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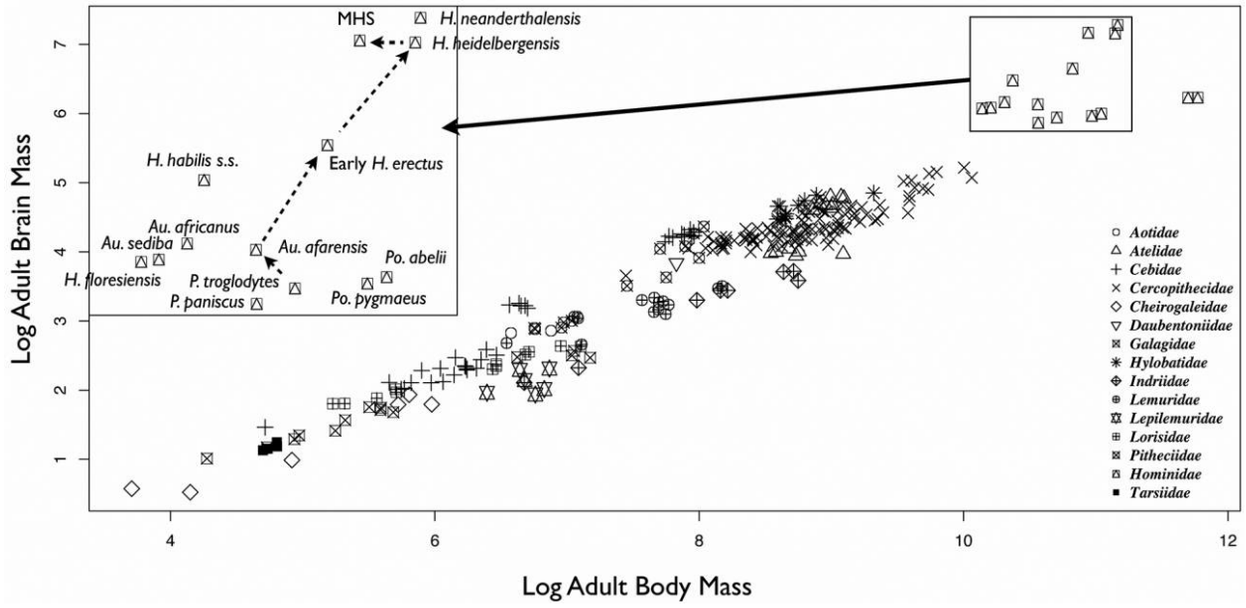

Figure 1. Natural log of mean brain mass plotted against the log of mean body mass for adult primates, including fossil hominins. *Inset*, close-up view of hominin brain-body evolution, with one hypothetical evolutionary trajectory from a *Pan*-like last common ancestor shown with arrows. Adjusted R^2 for the least squares regression of the nonhominin species is 0.935. Hominid data sources are given in table 2; other primates are from Isler et al. (2008).

in one trait lead to changes in the other, high correlations reflect a relationship that could prevent the independent evolution of either trait. In other words, brain-body pleiotropy could lead to evolutionary constraints on brain and body size evolution. An example will clarify this issue: given strong genetic covariation between brain and body size in a population, if selection was only to increase brain size, larger bodies could also evolve due to a correlated response to selection on brain size (fig. 2*A*). Given a strong level of genetic covariation, to evolve a larger brain but not a larger body (an increase in relative brain size), selection would have to be for larger brains but smaller bodies, with the latter canceling out correlated selection to increase body size (fig. 2*B*).

Lande (1979) suggested that primates in general had lower levels of brain-body correlation when compared to other mammals, and such a relationship permitted the evolution of our absolutely and relatively larger brains. Though Lande's hypothesis received a great deal of interest (Atchley et al. 1984; Jungers and Susman 1984; Riska and Atchley 1985; Shea 1983, 1984), it has one unexplored aspect that could have major consequences for our ideas about hominin brain evolution. Lande (1979) suggested that levels of genetic brain-body correlation were reduced in primates when compared to other mammals, not a complete absence of correlation. The level he proposed based on observed phenotypic correlations was around 0.2, which implies that primate brain and body size share some portion of their genetic background. Even at this relatively low level, selection on either trait would likely lead to some degree of correlated response in the other.

But the extraordinary size and complexity of the modern human brain indicates that something more than unusual selection pressures may have occurred. While genetic correlations can provide some idea of the propensity of traits to evolve together, the extent of the correlated response to selection depends on more than this one metric. Along with mutation and genetic drift, evolution occurs through natural selection acting on heritable variation in populations (Darwin 1859). How much of this variation is shared with variation in other traits (i.e., covariation), as well as the strength of selection, will determine the magnitude and direction of the response to selection (Falconer and Mackay 1996; Lande and Arnold 1983). The genetic basis of covariation between traits can evolve in response to selection pressures (Pavlicev, Cheverud, and Wagner 2011), and the results of recent studies suggest that changes in patterns of covariation likely played a major role in hominin evolution (Grabowski 2013; Grabowski, Polk, and Roseman 2011; Porto et al. 2009; Young, Wagner, and Hallgrimsson 2010). Thus, it is possible that the key to brain expansion within our lineage was a reduction in the evolutionary constraints imposed by the genetic brain-body relationship in hominins when compared to other primates. Such a change would have allowed brain and body size to respond to separate selection pressures and could have permitted the evolution of our absolutely and relatively large brains. On the other hand, if brain-body covariation exists in our lineage and was important for evolution, the changes observed in the fossil record (evolutionary patterns) may be poor predictors of past selection pressures that produced those patterns (evolutionary pro-

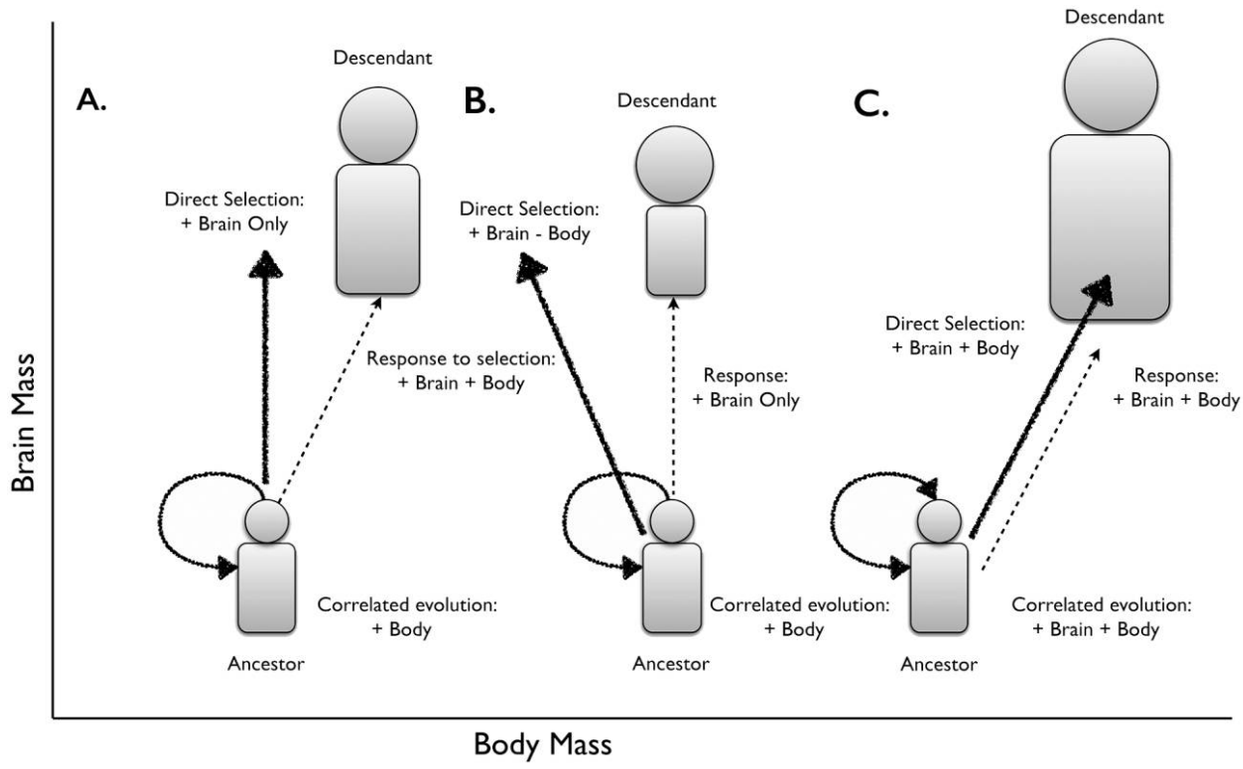

Figure 2. Three evolutionary scenarios showing the relationship between within-population genetic brain-body covariation, natural selection, and evolutionary change (the response to selection). Brain mass is on the *Y*-axis, and body mass is on the *X*-axis. Body and brain mass are assumed to be the same in all ancestors here, boldface arrows show the direction of selection, and dotted arrows show the direction of evolutionary change. Direction of arrows corresponds to directions on *X*- and *Y*-axes. During the first transition (*A*), the direction of selection is for larger brains, not for larger bodies (+ Brain Only), but larger bodies evolve due to a correlated response to selection on brain mass. Hence, change in body mass would not be adaptive. During the second transition (*B*), direct selection is for larger brains but smaller bodies (+ Brain − Body), with the latter canceling out correlated selection to increase body mass, and the end result is larger brains but body mass remaining constant. During the last transition (*C*), selection is for larger brains and larger bodies (+ Brain + Body), with correlated selection pressures and direct selection pressures building on each other, and the amount of evolutionary change is greater than possible if there was no covariation.

cesses). An increase in brain size may have been due to a correlated response to selection for increased body size or vice versa, and in either case, if changes were not the result of selection, they were not adaptive. Thus, correlated evolution potentially complicates our interpretation of the role of selection and adaptation in hominin brain-body evolution (e.g., fig. 2).

Background of My Approach

To answer these questions, I use an approach based in evolutionary quantitative genetics (Ackermann and Cheverud 2004; Hansen and Houle 2008; Lande 1979; Rolian, Lieberman, and Hallgrimsson 2010). First, I quantify patterns of variation and covariation in brain and body size across a range of captive and laboratory primates, in addition to modern humans, which estimate the underlying genetic relationships. Using these patterns, I model the effect that covariation between traits had on evolution (Hansen and Houle 2008) and test whether modern humans have a lower level of evolutionary constraints on brain and body size than other primates. Next, I explore how brain-body covariation influenced observed patterns of evolution by estimating past selection pressures that led to major hominin transitions of brain and body size (see below) using models of covariance based on extant populations. These estimates separate the response to selection (i.e., observed change) into how much change was due to direct selection on an individual trait (i.e., brain or body size) and how much change was a correlated response to selection on the other trait. In simple terms, the estimates reveal the extent to which covariation between brain and body size led to one trait being pulled along by selection on the other. Note that here and below, "brain size" and "body size" are shortened to "brain" and "body" where warranted.

The metric of natural selection used here, β, is defined as the increase in relative fitness for a proportional change in the trait of interest or as the regression slope of relative fitness on the trait (Hereford, Hansen, and Houle 2004). Relative fitness is the expected fitness of individuals that possess a certain trait value (i.e., the expected contribution of off-

spring to the next generation relative to the average of the population). To put it simply, estimates of selection as described here reveal how observed changes in traits impacted the overall fitness of the individuals that possessed them. As we are looking at both brain and body size evolution and the covariance between them, here β is a vector of values that reveal the change in relative fitness for a change in each trait while all other traits are held constant—a partial regression coefficient. Multivariate estimates of selection show the contribution of changes in each trait to relative fitness, independent of other traits. The most important point of this fitness-based definition is that if a trait has evolved as a by-product of selection on another trait (i.e., nonsignificant values of β), changes observed in this trait have little to no effect on fitness. Such a finding would present difficulties for hypotheses that see observed changes as adaptations for particular functional goals, as these changes cannot be adaptive if they have no effect on fitness. While this approach was originally devised to quantify short-term microevolutionary change, this analysis follows previous studies that have applied this approach to macroevolutionary questions in hominin (Ackermann and Cheverud 2004; Rolian, Lieberman, and Hallgrimsson 2010) and primate (Marroig and Cheverud 2004) evolution. Here, differences between taxa are the overall or net effect of natural selection, and changes observed in traits that appear to have been the result of substantial amounts of selection indicate that these changes had large fitness effects. On a longer timescale such as seen in this analysis, it is possible that some traits have changed as a result of selection on other traits, but these changes impacted fitness. While this may be true, traits that have not evolved as a result of selection are, by definition, not adaptations. Overall, this study's focus on quantifying the role of selection in producing observed change differs from previous studies that infer selection based on observed change and then use those inferences to formulate adaptive hypotheses.

Patterns of Covariation

The genetic basis of the relationships among traits is quantified by the genetic variance/covariance matrix, **G**, a symmetrical matrix with variances on the diagonal and covariances on the off diagonal. This matrix determines the predominant direction and magnitude of the response to natural selection and thus how selection on one trait tends to lead to a correlated response in the other (Steppan, Phillips, and Houle 2002 and references). Heritable variation and covariation contained in **G** lead to expressed variation and covariation in observed populations. Observed variation is described in the phenotypic variance/covariance matrix, **P**, which is the sum of **G** and environmental effects, **E**. Because accurate estimates of **G** can usually only be obtained via pedigreed populations with hundreds of families, a large amount of research discusses the validity of substituting the relatively easy to estimate **P** for **G** in evolutionary analysis (Cheverud 1988; Marroig et al. 2009; Roff 1995, 1996; Roseman 2012). While this opinion is by no means universal (e.g., Kruuk, Slate, and Wilson 2008; Willis, Coyne, and Kirkpatrick 1991), multiple studies suggest that **P** and **G** are nearly proportional for morphological traits (Cheverud 1988; Marroig et al. 2009; Roff 1995, 1996; Roseman 2012). As accurate estimates of the brain-body **G** are extremely difficult or impossible to obtain for most of the species in this analysis, this study follows a large number of previous researchers (e.g., Ackermann and Cheverud 2004; Cheverud 1995; Marroig et al. 2009; Porto et al. 2009) by substituting **P** for **G**. In addition, this study estimates **G** for one primate species for which relevant data are readily available—modern humans—along with **P** (see below).

Fossil Transitions

The sequence of early hominin evolution is contentious, particularly given a number of new discoveries that stretch the definition of *Homo* brain size—for example, the recently described Dmanisi D4500/D2600 hominin appears to be similar to australopiths (Lordkipanidze et al. 2013). Many researchers propose that *Australopithecus afarensis* is likely the ancestor of later hominins (Gabunia et al. 2000; Johanson and White 1979; Strait, Grine, and Moniz 1997; Wood and Richmond 2000). This can also be said for African and Georgian *Homo erectus* (here describing what some call *Homo ergaster* [Wood and Richmond 2000], plus the sample from Dmanisi). In between these two reasonably well-known species, there is much less certainty. *Australopithecus afarensis* may have led to *Homo habilis* sensu stricto or sensu lato (comprised of *H. habilis* s.s. and what has also been described as *Homo rudolfensis*; Wood 1992), which led to early *H. erectus* (e.g., Johanson and White 1979). The issue with this evolutionary model is that body mass based on postcranial fossils is known for only two individuals that can confidently be assigned to this species: OH 62 and KNM-ER 3735 (Grabowski et al. 2015). In addition, recent findings such as KSD-VP 1/1 (Haile-Selassie et al. 2010) increase the sample average *A. afarensis* body mass to about 7 kg larger than the current *H. habilis* s.s. average (table 2). While the evolutionary sequence leading from *A. afarensis* to a larger-brained but smaller-bodied *H. habilis* s.s. is, of course, possible, we simply do not have a large enough sample of individual postcranial fossils that can be attributed to *H. habilis* s.s. to make reliable assumptions about average body mass of this species. In addition, while there are only a few fossil individuals throughout hominin evolution for which brain and body size based on postcranial traits are known, there are none for *H. habilis* s.s. It is possible that the fossils with larger brain sizes for *H. habilis* s.s. (e.g., OH 7; Spoor et al. 2015) also had larger bodies than presently found and that those with smaller brains (e.g., KNM-ER 1813) were matched with smaller body sizes such as OH 62 and KNM-ER 3735. The issue of unmatched brain and body sizes across the hominin fossil record could lead to more error in this relationship, but every attempt was taken to use the largest sample sizes for each trait possible at this time, which should partially account for this source of error.

This study, therefore, takes the more conservative approach and investigates the transition between *A. afarensis* and early *H. erectus* (described by African and Georgian *H. erectus*; see tables A1, A2 for more information and individual brain size estimates and averages; tables A1–A3 and figs. A1–A5 are available in CA+ online supplement A), a shift in both grade and clade. While the placement of *Homo heidelbergensis* as ancestral to modern humans is also debated (e.g., Arsuaga et al. 2014; see Stringer 2012 and references), this study does not assume that the fossil hominin species involved in the evolutionary transitions are directly ancestral to modern humans, just that the direct ancestors had broadly similar brain-body size relationships. For this reason and a lack of another credible well-sampled taxa at this important time point, *H. heidelbergensis* is included here as our best current estimate of the species that bridges the gap between early *H. erectus* and modern humans.

The evolutionary transitions investigated here are between the species averages of (1) *Pan troglodytes*–like last common ancestor (LCA) and *A. afarensis*, (2) *A. afarensis* and early *H. erectus*, (3) early *H. erectus* and *H. heidelbergensis*, and (4) *H. heidelbergensis* and modern humans. It is important to note that even if the brain and body size of the LCA was substantially different from that of the modern common chimpanzee, this incorrect assumption would affect the results of only the first evolutionary transition here (LCA to *A. afarensis*) and would have no impact on the others. On the other hand, the brain and body size of the earliest possible hominins (*Sahelanthropus tchadensis*, *Orrorin tugenensis*, *Ardipithecus ramidus*) appear to be quite similar to that of common chimpanzees (Lovejoy et al. 2009; Nakatsukasa et al. 2007; Suwa et al. 2009; Zollikofer et al. 2005), and thus, using a *Pan*-like model for the overall size of these two traits is supported.

Material and Methods

To estimate **P** in modern humans, common chimpanzees, and other primates (species in table 1), brain mass and body mass data were taken from a number of sources (table A3). These include wild-caught and captive samples, but I did not pool them in this analysis (see below). Samples of 40 individuals or more of matched brain and body mass data are required to substitute **P** for **G** (Cheverud 1988), and species included here are those for which such data could be obtained. Brain masses were subtracted from body masses to produce two sets of data used in this analysis. As this study focuses on estimating the population-level genetic architecture underlying traits, sources of variation related to sex must be removed before estimating **P**. This was accomplished using the residual covariance from a MANOVA, with brain/body as the dependent variable and sex as the independent variable (Ackermann and Cheverud 2000; Marroig et al. 2009; Porto et al. 2009).

The modern human **G** was calculated using an animal model approach and data from twins. This sample (Osborne 1980) consists of measurements of cranial circumference and body mass from 136 sets of twins (61 pairs of monozygotic twins and 48 pairs of dizygotic twins; table 1), along with age, sex, population, and various other phenotypic measurements. Cranial circumference was converted to endocranial volume following Jorgensen, Paridon, and Quaade (1961) and was converted to brain mass by the multiplication of volume by the specific gravity of brain mass (1.036 g/mL; Blinkov and Glezer 1968; see also DeSilva and Lesnik 2006).

Genetic (V_G), common environmental (V_{EC}), and the remaining environmental (V_{EW}) variance components were estimated by fitting a generalized linear mixed model using a Bayesian Markov Chain Monte Carlo (MCMC) method (Hadfield and Nakagawa 2010). First, a pedigree was built from the twin data using the R package MasterBayes (Hadfield, Richardson, and Burke 2006). A mixed model was then fit with brain and body mass as the response variables, sex and population as fixed effects, and pedigree information and family as the random effects. Genetic and residual priors were set to the same value—one-half of **P**, with the off-diagonals set to 0. This choice of priors means that runs start from a point of total phenotypic variance being broken down into equal genetic and environmental components and initially assumes that there is independence between brain and body mass. Burn-in time (the number of initial iterations that were discarded as the MCMC algorithm searches for the peak of maximum likelihood) was 500,000 runs, and the total number of iterations was 1,000,000, with a thinning interval of 200 (the number of iterations that separated each sample of results taken from the model). These samples had minimal autocorrelation.

All modern human data used here were from individuals aged 15–18, an age range when the brain is no longer growing (Jolicoeur, Baron, and Cabana 1988; Leigh 2012), though the body may not have reached adult size. Age was therefore included in the model as a fixed effect but was found to be not significant (P value for interaction of age and brain mass = .942; P value for interaction of age and body mass = .612) and dropped from the model prior to running the full analysis. In addition, population was included as a fixed effect, and though it had a significant effect on brain mass (P value for interaction of population and brain mass = .0064), it had no effect on the overall results of this analysis, though our final results include both sex and population in the calculation of the modern human **G**. This is because including population in the model explains a portion of the residual environmental variance rather than affecting the estimate of the genetic component. The output of this model estimates the component of phenotypic brain and body variance due to genetic effects as well as the genetic covariance of the traits, the component that accounts for shared environment that results from twins being raised within the same family, and the environmental component. The best estimates of the genetic variances and covariances were used to fill in the elements of **G**, producing a modern human genetic brain-body variance/covariance matrix. It should be noted that the results using the genetic model of variation calculated here are contingent on the usual

Table 1. Mean integration for various primate species, with standard error in parentheses and sample size

Species	Captive sample	Wild-caught sample	Same but controlling for sex and location
Saimiri sciureus	.253 (.002); $n = 62$	.249 (.003); $n = 76$	.192 (.004)
Macaca mulatta	.399 (.008); $n = 222$	…	…
Macaca nemestrina	.481 (.061); $n = 204$	…	…
Macaca fascicularis	.439 (.012); $n = 45$	.231 (.005); $n = 83$	.282 (.005)
Cercocebus atys	.240 (.005); $n = 96$	…	…
Hylobates lar	…	.190 (.002); $n = 95$	.132 (.004)
Cebus nigritus	…	.289 (.003); $n = 87$	.280 (.004)
Galago senegalensis	…	.315 (.003); $n = 193$	.280 (.004)
Pan troglodytes	.319 (.030); $n = 65$	…	…
Homo sapiens **G**	.644 (.006); $n = 136$ twin sets	…	…
Homo sapiens **P**	.338 (.002); $n = 662$	…	…

Note. All statistics were calculated on phenotypic patterns of variance/covariance, except for modern humans, where results are shown using both the genetic (**G**) and the phenotypic (**P**) patterns. Sample sources are given in table A3, available in CA+ online supplement A.

assumptions of twin analysis—that information from twins provides estimates applicable to the population at large and that the environmental components of variance are the same in twins as in nontwins (Lynch and Walsh 1998).

In the case of brain mass and body mass, where the two traits have large differences in both the mean and the variance, standardization of variance/covariance matrices and estimates of selection is particularly important to place the results on the same scale. Numerous studies have argued for the benefits of standardizing both statistics by the trait means when comparing selection (Hereford, Hansen, and Houle 2004), evolvability (Hansen and Houle 2008), and integration statistics (Marroig et al. 2009) across traits, species, and populations. Mean standardizing places different traits on the same scale of measurement and allows for comparison of proportional changes between traits. One example of the benefits of mean standardizing can be seen in a study by Hereford, Hansen, and Houle (2004), who compared mean standardized strengths of selection from a broad range of studies on different trait categories and organisms. Fossil analyses present unique problems (see also Grabowski and Roseman 2015). It is not clear which mean to standardize by—standardizing the mean of the species from which the **P** matrices are calculated, the ancestral species mean in each transition, or everything by one set of means affects the results. Logging the data has a similar effect as mean standardization, but it is arguably more valid for evolutionary transitions such as those included here. Logging the data places everything on the same scale and acts more or less like mean standardization, with a mean that evolves continuously between species (T. F. Hansen, personal communication; see Grabowski and Roseman 2015, for more information). Note that the estimates of selection pressures after log scaling the data have no units. This is true for both the mean-standardized and the log-scaled cases. As such, both **P** and **G** were standardized by logging the data before analysis.

To test whether captivity affects brain-body covariation and thus the relevance of using a sample of *Pan* brain and body masses from primate research centers (table A3) to infer how covariation affects evolution in the natural world, this study compares one metric of evolutionary constraints, the mean integration statistic (see below) for wild-caught primate species, with the data collected from primate research centers (table A3). The wild-caught species data are taken from Isler et al. (2008) and are the species with the largest sample sizes. For these data, endocranial volume was reported in cubic centimeters and here was converted to grams by scaling it by the specific gravity of brain mass as above, and sex, as well as the sex and location the individual was recovered from, were included as dependent variables in the MANOVA model to control for variation due to these sources. While only two of the species included here overlap in both sets of data, overall comparisons could reveal systematic effects of captivity on mean brain-body integration.

Estimates of fossil hominin brain and body mass averages were taken from a number of sources, along with estimates of averages for modern humans and *Pan troglodytes*, and are given in table 2 with references. In all cases, brain mass was subtracted from body mass.

Analysis

Estimating Magnitudes of Brain-Body Integration

Mean integration is the average relative degree to which evolvability (the ability of traits to evolve in the direction of selection; Hansen and Houle 2008) is reduced due to conditioning on other traits under simulated stabilizing selection (i.e., through constraints via the **G** matrix) over a large number of random directions. It therefore quantifies how covariation between traits might affect evolutionary responses.

Estimates of mean brain-body integration were calculated following Hansen and Houle (2008) for modern humans, chimpanzees, and other extant primates (table 1) using calculated **P** matrices, as well as the **G** matrix for modern humans. This was accomplished using the simulation approach of Grabowski, Polk, and Roseman (2011), following Hansen and Houle (2008).

Mean integration is described by the following equation:

$$1-\mathbf{E}\left[\left(\beta'\mathbf{G}\beta\beta'\mathbf{G}^{-1}\beta\right)^{-1}\right]. \quad (1)$$

Table 2. Species designation, date range, average brain and body mass with sample size, and body mass free of brain mass

Designation	Date range (Ma)	Mean brain mass (g)	Mean body mass (g)	Mean body-brain mass (g)
Australopithecus afarensis[a]	3.7–3.0	462.1 ($n = 5$)	39,100 ($n = 12$)	38,637.9
Australopithecus africanus[a]	3.0–2.5	476.6 ($n = 9$)	30,500 ($n = 5$)	30,023.4
Australopithecus sediba[b]	1.98	435.1 ($n = 1$)	25,800 ($n = 2$)	25,364.9
Homo habilis s.s.[c]	2.3–1.6	652.03 ($n = 6$)	32,600 ($n = 2$)	31,948.0
Early *Homo erectus*[d]	1.9–1.5	774.7 ($n = 9$)	51,000 ($n = 7$)	50,225.3
Homo erectus[e]	1.9–.05	1,026.7 ($n = 36$)	51,400 ($n = 9$)	50,373.3
Homo heidelbergensis[f]	.6–.1	1,286.7 ($n = 21$)	70,600 ($n = 12$)	69,313.3
Homo neanderthalensis[f]	.2–.03	1,454.5 ($n = 27$)	72,109 ($n = 23$)	70,654.5
Homo floresiensis[g]	.018	440.3 ($n = 1$)	27,500 ($n = 1$)	27,059.7
Modern humans[h]	…	1,299.0 ($n = 662$)	57,849.1 ($n = 51$)	56,550.1
Pan troglodytes[i]	…	379.4 ($n = 65$)	44,967 ($n = 60$)	44,587.6

Note. Extant data is the between-sex average. Taxa in boldface are used in the evolutionary transitions in figure 1 and the main analyses. All endocranial volumes (cm^3) were converted to grams following DeSilva and Lesnick (2006) where applicable. See tables A1, A2 in CA+ online supplement A for more information and complete references.

[a] Mean brain mass following Holloway, Broadfield, and Yuan (2004). Mean body mass following Grabowski et al. (2015).

[b] Mean brain mass following Berger et al. (2010). Mean body mass following Grabowski et al. (2015).

[c] Mean brain mass following data from Holloway, Broadfield, and Yuan (2004) supplemented by Spoor et al. (2015). Mean body mass following Grabowski et al. (2015).

[d] Mean brain mass following data from Holloway, Broadfield, and Yuan (2004), supplemented by Spoor et al. (2007), and Lordkipanidze et al. (2013). Mean body mass following Grabowski et al. (2015).

[e] Mean brain mass following de Sousa and Cunha (2012). Mean body mass following Grabowski et al. (2015).

[f] Mean brain mass following de Sousa and Cunha (2012). Mean body mass following Skinner and Wood (2006).

[g] Mean brain mass following Kubo, Kono, and Kaifu (2013). Mean body mass following Grabowski et al. (2015).

[h] Between-sex mean brain mass following Bischoff (1880). Average worldwide population body mass following Ruff, Trinkaus, and Holliday (1997).

[i] Between-sex mean brain mass from this study (see table A3 for more information). Between-sex mean body mass of wild chimpanzee subspecies following Smith and Jungers (1997).

Here, **G** is the additive genetic variance/covariance matrix for brain and body mass (or **P**, in the case of simulations using the **P** matrix), and β is the selection vector (Hansen and Houle 2008). The selection vectors were created by drawing entries in the vector of selection gradients from a random normal distribution with a mean of 0 and a standard deviation of 1, normalized to unit length, and then applied to each species' **G** matrix using equation (1) to calculate the required statistic. The average values were calculated by repeating this procedure 1,000 times and taking the mean value of all the repetitions (Hansen and Houle 2008).

Estimating Past Selection Pressures on Brain and Body Mass

To test how any covariation between brain and body mass found above affected the evolutionary trajectory of hominins, estimates of past selection pressures required to produce observed morphological differences were calculated following Lande (1979):

$$\beta = \mathbf{G}^{-1}[z_i - z_j], \tag{2}$$

where β is the directional selection gradient, $\mathbf{G}^{-1}$ is the inverse of the additive genetic variance/covariance matrix, and $z_i - z_j$ is the difference in population means for the two species in the comparison. Here, β is an estimate of the forces of directional selection on brain or body mass that resulted in a particular evolutionary transition, taking into account covariance between traits and removing the effects of indirect selection pressures on other traits.

The metrics used here for quantifying the effects of covariation on evolution and past selection pressures are related, as the first reveals the extent to which evolvability (the ability to evolve in the direction of selection; Hansen and Houle 2008) is reduced by evolutionary constraints resulting from covariation, while the second provides a picture of how covariation led to differences between observed evolutionary change and the directions and magnitudes of selection that caused these changes. All standard errors and tests of significance were conducted using a parametric bootstrap routine (Efron and Tibshirani 1993) with 10,000 replications.

Results

Magnitudes of Brain-Body Integration

Modern humans do not have significantly lower magnitudes of mean phenotypic brain-body integration than *Pan*, and both fit within the range of other primates included here for both captive and wild-caught samples (table 1). All of the primate species had a level of mean integration that was significantly different from 0, with an average mean integration level of 0.36 (on a scale of 0–1) for laboratory individuals, 0.25 for wild-caught adult individuals (modern humans were obviously excluded from this calculation), and 0.24 with sex and location controlled for. The two species for which both captive and wild-caught data were available did not have the same pattern of mean integration results (*Saimiri sciureus*: 0.253 versus 0.249 [0.192 with both sex and location]; *Macaca fascicularis*: 0.439 versus 0.231 [0.285 with both sex and location]). Concentrat-

ing on only modern humans, mean phenotypic integration was 0.338, and mean genetic integration using **G** was almost twice as high at 0.645.

Past Selection Pressures on Brain and Body Mass

For all but one of the transitions included here, selection acted to increase average brain mass but not average body mass (fig. 3*B*, 3*C*). This is true even for the *Australopithecus afarensis* to early *Homo erectus* transition, with a significant increase in brain and body mass (almost ~70% increase in brain mass and ~30% increase in body mass; fig. 3*A*), and occurs regardless of whether a modern human phenotypic (fig. 3*B*), genetic (fig. 3*C*), or chimpanzee (fig. A1*B*) model of variation is used in the calculation. The one transition where selection acted to increase both brain mass and body mass was early *H. erectus* to *Homo heidelbergensis*, given a phenotypic model of variation (fig. 3*B*), with a large increase in brain mass (~66%) and a substantial increase in body mass (almost 40%; fig. 3*A*). On the other hand, given the genetic model (fig. 3*C*), selection on body mass is always to reduce body mass, even for the transitions where body mass is increasing—*A. afarensis* to early *H. erectus* and early *H. erectus* to *H. heidelbergensis*. This is because, given the genetic model of variation, selection to increase brain mass was so substantial during these transitions that negative selection on body mass was required to keep the body from getting too big.

The effect of covariation on brain-body evolution is highlighted when compared to the hypothetical case where covariation was removed (fig. A2). Here, while selection on brain mass is not noticeably different from the result when covariance is included, selection on body mass is completely different

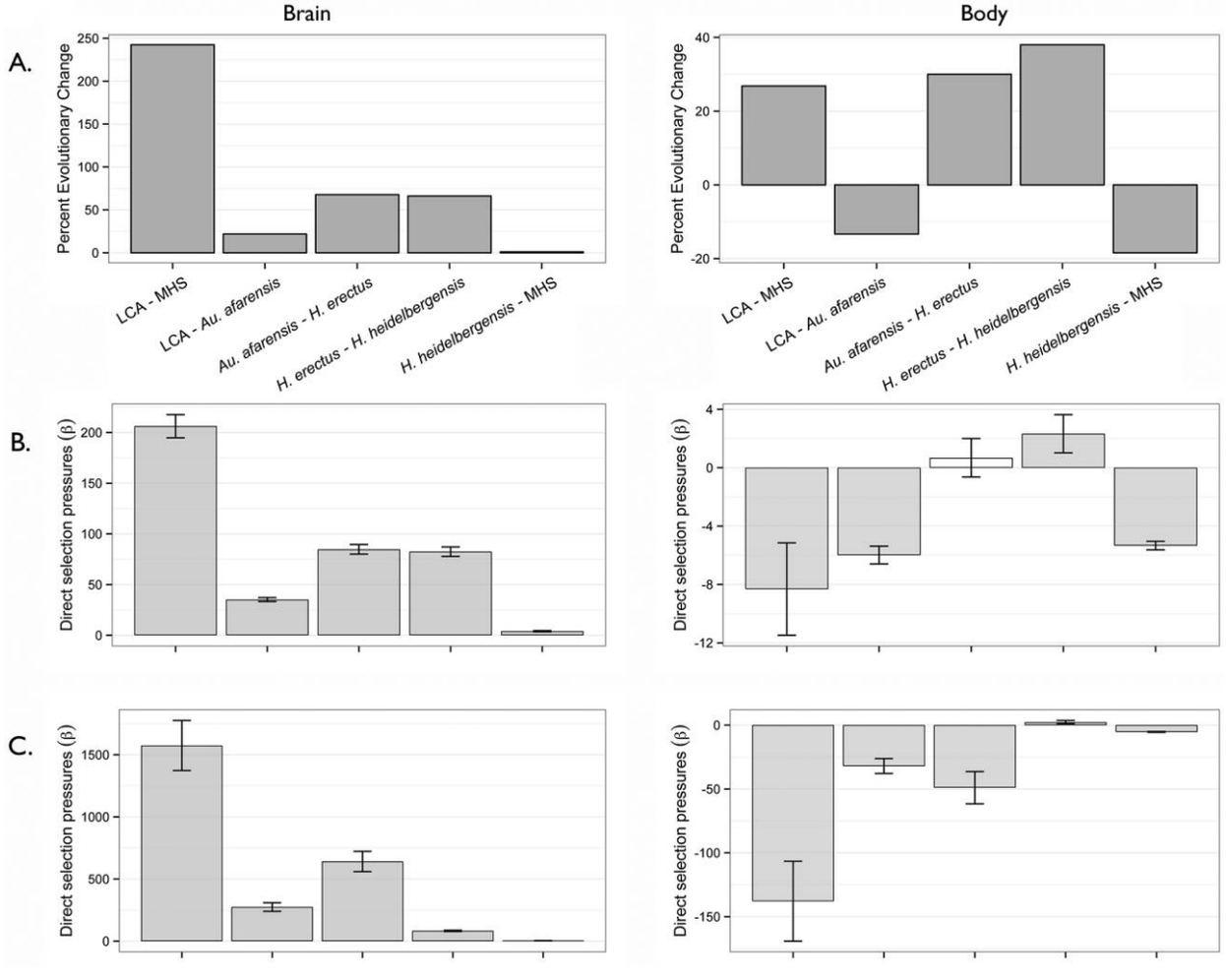

Figure 3. *A*, Percent evolutionary change in brain (left plot) and body (right plot) mass for each of the evolutionary transitions shown here. Percent evolutionary change can be compared between brain and body. *B*, Direct selection pressures required for evolutionary changes shown in *A*, with standard error bars using the modern human phenotypic model of variation (**P**). *C*, Direct selection pressures required for evolutionary changes shown in *A*, with standard error bars using the modern human genetic model of variation (**G**). The top row and bottom two rows are matched pairs; transition labels refer to bars above and below. The shaded columns are significantly different from 0. Note that β values are on the log scale to allow for comparisons and thus do not have units.

and now mirrors the pattern of evolutionary change. Notably, though strong selection to increase both brain and body mass can be seen for the early *H. erectus* to *H. heidelbergensis* transition regardless of whether phenotypic covariance is included (cf. figs. 3*B*, A2*B*), including covariation substantially reduces the amount of selection required to increase body mass for this transition.

Discussion

There are two main findings of this study: first, modern humans do not have a lower magnitude of mean brain-body integration than common chimpanzees, and both species fit within the range of other primates included in this analysis. This result suggests that hominins were also not unique in this regard and that the increase in relative brain size observed during hominin evolution took place through selection acting within similar levels of evolutionary constraints due to brain and body size covariance. The second main finding is that strong selection to increase brain size alone played a large role in both brain and body size increases throughout hominin evolution and may have been solely responsible for the major increase in brain and body size near the origins of our genus. This result suggests that evolutionary patterns do not always reflect the processes that underlie them, findings that could have major implications for hypotheses on the ultimate causes of brain and body size evolution in the hominin lineage.

Was the Key to Brain Expansion within Our Lineage a Reduction in Evolutionary Constraints Imposed by the Genetic Brain-Body Relationship?

Contrary to expectations based on previous analyses of other morphological regions (Grabowski, Polk, and Roseman 2011; Porto et al. 2009), modern humans do not have a lower level of mean phenotypic brain-body integration than common chimpanzees or other primates (table 1), and values for all species are significantly different from 0. Thus, assuming that **P** reflects **G** in a similar way across the diverse range of species included here (see below), there is no evidence that natural selection for the independent evolution of brain and body size in hominins led to a lower magnitude of brain-body covariance. This result suggests that all primates possess a similar magnitude of evolutionary constraints on brain-body evolution due to brain-body covariance and that brain size variation within our genus came about through natural selection working within existing evolutionary constraints.

While wild-caught samples had on average lower levels of mean phenotypic brain-body integration than captive samples, there was no consistent pattern in the species for which both captive and wild data could be obtained. In addition, there are nonoverlapping species in each group that had similar levels of integration. These results argue that it is acceptable to use captive common chimpanzee brain and body size data as a substitute for wild-caught data in analyses focusing on phenotypic patterns of variation and covariation. Based on similarities between modern humans and chimpanzees, the most parsimonious interpretation of these results is that brain-body covariation in early hominins was similar to these extant models, and brain and body size would likely have evolved while maintaining the same covariance relationships.

While these findings are suggestive as to levels of mean phenotypic brain-body integration in fossil hominins, evolution occurs through selection and other evolutionary forces acting on genetic, not phenotypic, variance and covariance. Therefore, the consequences of these results for evolution depend on how similar **P** is to **G**. Numerous studies suggest that phenotypic patterns are similar to genetic patterns (Cheverud 1989; Lande 1979; Lande and Arnold 1983; Porto et al. 2009; Roff 1995, 1996), and based on this reasoning, the substitution of **P** for **G** occurred in a multitude of analyses (e.g., Ackermann and Cheverud 2004; Marroig, de Vivo, and Cheverud 2004; Porto et al. 2009; Rolian, Lieberman, and Hallgrimsson 2010). However, pattern similarity between **P** and **G** does not mean similar levels of mean integration. Cheverud (1988) suggested that **G** and **P** are related through the equation $\mathbf{G} = \mathbf{P} \times h^2$, where h^2 = heritability. Thus, differences in heritability between traits would be translated into differences in estimates of genetic variances and covariances.

Here, mean genetic integration in modern humans was almost twice as high as phenotypic integration (0.645 vs. 0.338; table 1). In addition to differences due to scaling **P** by heritability, given monozygotic and dizygotic twin data such as that used here, estimates of genetic variance (V_G) may be due to additive, dominance, and epistatic components, and thus, additive genetic variance and covariance may be overstated if there are large magnitudes of the latter two components (Falconer and Mackay 1996). This upward bias in the estimates of additive genetic variance could affect both variance and covariance and lead to a higher mean integration statistic. Modern humans' cranial circumference likely has a very low or not significant dominance component as the correlation between parents and offspring (a relationship that has no dominance component), since this trait is the same as between full siblings (0.68 in both cases; Sharma and Sharma 1984), though a small fraction may be due to epistatic effects (Falconer and Mackay 1996). With regard to body mass, one study (Kaur and Singh 1981) found that for mass alone, parent-offspring correlations were lower than between siblings (0.34 for parent-offspring, 0.38 for full-sibs), arguing that some dominance may be present (though another study found the opposite pattern of results; Sharma et al. 1984).

Because of the possibility of upward bias in the mean integration statistic for **G** and the relationship between **P** and **G** (where **P** must be equal to the estimate of **G** in the absence of environmental effects), results for the mean integration statistic and past selection pressures (see below) using these two estimates can be thought of as upper and lower boundaries revealing the importance of underlying genetic relationships for evolution. This is similar to heritability estimates calcu-

lated using twin data, which provide the upper limit for estimates of heritability (broad-sense heritability; Falconer and Mackay 1996). Taken together, genetic and phenotypic modern human results, complemented by the phenotypic results for both captive and wild primates, argue that hypotheses as to the ultimate causes of hominin brain evolution must account for the fact that brain and body size are not independent.

How Well-Matched Are the Observed Changes in Brain and Body Size in the Hominin Fossil Record to the Selection Pressures That Produced Those Changes?

Results suggest that major transitions in hominin brain evolution were the consequence of strong selection to increase brain size, and a substantial portion of average body size increases were the result of correlated effects, not independent selection to increase body size. This pattern can even be seen for the transition to early *Homo erectus*, an increase in body size that many regard as one of the defining features of our genus (e.g., Antón, Potts, and Aiello 2014). Here, selection to increase brain size alone was responsible for the increases in both brain and body size. An absence of selection to increase body size near the origins of our genus suggests that overall body size changes at this point were not adaptive. These findings appear robust, as they are consistent assuming either a modern human phenotypic (fig. 3*B*), genetic (fig. 3*C*), or common chimpanzee phenotypic model of variation (fig. A1*B*). In fact, given the modern human genetic model (fig. 3*C*), selection to increase brain size during major transitions included here was so large that correlated effects that would substantially increase body size had to be kept in check by substantial negative selection on the body, even for transitions where body size was increasing (i.e., the transitions to and from early *H. erectus*).

On the whole, brain-body covariation led to substantial differences between observed changes in hominin body size evolution and the selection pressures that produced those changes (fig. 3). This is especially apparent when comparing the selection results including covariation to the hypothetical situation where covariation was removed (fig. A2)—removing covariation leads to selection mirroring the pattern of change. On the other hand, patterns of change appear to accurately reflect selection during brain size evolution. This result is because the magnitudes of selection to increase brain size for all transitions included here were so large that correlated effects due to selection on body size had only the smallest impact on the rapidly increasing brain. Taken together, these findings imply that changes in brain size, but not body size, seen over the course of hominin evolution can be taken as evidence of strong natural selection.

Taking a step back, the selection results suggest that across a range of possible levels of brain-body covariation, (*a*) all major increases in average body size during hominin evolution were solely the result of a correlated response to strong selection to increase average brain size, with selection for smaller body size to keep body size from getting too big in some cases (based on the genetic model of variation), or (*b*) strong selection to increase brain size played a large role in both brain and body size increases throughout hominin evolution and may have been solely responsible for the major increase in brain and body size near the origins of our genus (based on the phenotypic model of variation). While the results shown here cannot be used to choose between these two possibilities, the latter would seem to be more appropriate based on current evolutionary hypotheses and the possibility of inflation in the magnitude of mean integration for the genetic estimate of variation.

Ultimate Causes of Hominin Brain and Body Size Evolution: An Increasingly Hungry Brain?

Overall, results of this analysis provide new insight into the ultimate causes of hominin brain and body evolution. While evolutionary questions often ask why—what caused evolutionary events—the avenue taken here can inform us about how evolutionary events took place. This emphasis is important because unification of proximate factors and ultimate causes of evolution (Lynch and Walsh 1998; Tinbergen 1963) and tests of adaptive hypotheses (Lande and Arnold 1983) remains the goal of evolutionary biology. Strong selection to increase overall brain size was apparently the primary force in much of hominin brain-body evolution. This result supports ultimate hypotheses such as those that propose that selection to increase both overall brain size and cognitive abilities was the result of the need to negotiate increased social (e.g., Dunbar 1998) or ecological (Antón and Snodgrass 2012) complexity. But the fact that the increase in body size near the origins of our genus may have been solely the result of correlated evolution (or at the very least, covariation played a major role in body size evolution) does easily fit with most adaptive hypotheses that address the causes of body size evolution in the hominin lineage. Combining all the results of this study, it appears that modern humans and likely earlier hominins had a similar or even greater magnitude of evolutionary constraints on brain and body size due to covariance as other primates in spite of often antagonistic selection pressures on brain and body size. Because of this relationship, at several important transitions in hominin evolution, strong selection to increase brain size apparently pulled body size along with it. The question is, why?

One reason might be energetics. Larger brains are energetically expensive to maintain (Aiello and Wheeler 1995) and grow (Kuzawa et al. 2014). Around 20% of the resting metabolic rate is due to the energetic costs of the brain in adult humans. The cost is even higher in infants (slightly over 52%), and it peaks at 66% during childhood (Kuzawa et al. 2014). To put these figures in context, the cost of the brain in other adult primates is 9% or lower (Mink, Blumenschine, and Adams 1981). In addition, recent evidence (Kuzawa et al. 2014) suggests that increases in brain and body sizes during development are closely linked in modern humans and may be to some extent among the other great apes. Brain metabolism and

body size growth negatively covary during development in our species, suggesting that the high costs of the developing brain require a reduction in the amount of energy used for body growth (Kuzawa et al. 2014). It may simply be that a larger brain requires a larger body to meet its increasing energetic demands, and evolutionary constraints due to brain-body covariation are one way of maintaining this relationship.

Evolving larger brains likely required an increase in diet quality (Aiello and Wheeler 1995) or quantity (Fonseca-Azevedo and Herculano-Houzel 2012), allowing for an expanded energy budget (Aiello and Wells 2002). As diet quantity is limited by the hours per day an animal can devote to feeding (Fonseca-Azevedo and Herculano-Houzel 2012), a shift in quality to a more nutrient-rich source is one way around this energetic constraint, and such a change is hypothesized to occur at the origins of *Homo* (Aiello and Wheeler 1995). Larger average body size (see Grabowski et al. 2015) near this important evolutionary transition could have been part of a shift in foraging strategy (Aiello and Wheeler 1995)—both body sizes and higher-quality diets are associated with greater home range size in primates (Antón, Leonard, and Robertson 2002). Rather than an increase in body size being merely a reflection of greater home range size or increased diet quality, it may have been the other way around, with this increase in body size allowing early *Homo* to shift its preferred diet to higher-quality sources such as meat. Under this scenario, rapidly increasing brain size was the driving force behind the shift to intensive carnivory (Braun et al. 2010; Domínguez-Rodrigo 1997; Ferraro et al. 2013), providing access to a greater total energy budget for running both a larger body and a larger brain (Pontzer et al. 2010). Thus, advances such as hunting (e.g., Shipman 1986) and the postcranial changes that likely coincided with this development (e.g., Bramble and Lieberman 2004; Roach et al. 2014) were simply ways of feeding an ever more energetically expensive brain. Changes in life-history schedules (O'Connell, Hawkes, and Blurton Jones 1999) and reproduction strategies (Hawkes et al. 1998), such as cooperative breeding (Isler and Van Schaik 2012), that are unique to our genus or unique among primates both allowed for and were the result of our ancestors' increasingly larger brains.

The suggestion that increased body size in early *Homo* was not adaptive is consistent with suggestions that increasing body size increases daily energetic costs (Aiello and Key 2002), which were not offset by improvements in walking and running performance (cf. Bramble and Lieberman 2004; Pontzer 2012). In fact, larger body sizes present in early *Homo* may increase locomotor cost, given that longer lower limbs were apparently already present in some australopith individuals (Pontzer 2012). The pattern of hominin brain-body evolution also supports this hypothesis—there is currently no evidence of an early hominin with a large brain but a small body. On this point, the transition from *Homo heidelbergensis* to modern humans bears a second look. Here, a very slight increase in brain size was paired with a large decrease in body size (~20%). It may be that the large increase in body size during the transition that resulted in *H. heidelbergensis* was due to the increasing energetic requirements of substantial brain expansion (as suggested by the results showing a large portion of the total amount of change in body size here was the result of a correlated response to selection to increase brain size; fig. 5), along with changes in body size and shape due to new environments or behaviors. Both changes in body shape with the origins of modern humans (Arsuaga et al. 1999; Bonmatí et al. 2010; Carretero et al. 2012) and the impact of cultural innovations that occurred during this transition could have enabled the evolution of smaller body size (Frayer 1981; Ruff et al. 1993) while maintaining the energetic requirements of a large brain.

Additionally, though we lack a reliable estimate for body size in *Homo habilis* s.s. (or non-*erectus* early *Homo* in the parlance of Antón, Potts, and Aiello [2014]), if we assume that, on average, larger brains in this species were found atop body sizes similar to australopiths, recent findings indirectly reinforce the hypothesis that a shift in dietary ecology potentially contributed to the evolution of larger brains. Stable isotopic analyses of hominin enamel (Cerling et al. 2013; Sponheimer et al. 2013; Wynn et al. 2013) suggest that early *Homo* focused on a particular part of the broad spectrum of dietary variation that was present in earlier eastern African australopiths. If this portion of the dietary spectrum was composed of higher-quality foods, it may have permitted some level of brain expansion without the requirement of a larger body. The point should be made here that covariance among traits is not an absolute constraint on the independent evolution of brain and body size, as evident in *H. heidelbergensis* and possibly *H. habilis* s.s. This is true for any trait—only the highest levels of correlation would completely inhibit any level of independent evolution. The genius of our genus may simply have been to find a way of working around existing evolutionary constraints on brain size.

It should be noted that this analysis assumes an *Australopithecus afarensis*–like ancestor for early *H. erectus*. Some researchers argue that *Australopithecus africanus* from South Africa is a more suitable ancestor for early *Homo* (e.g., Skelton and McHenry 1992). Though average brain size for *A. africanus* is slightly larger than for *A. afarensis*, its average body size is 9 kg smaller (table 2). Because the increase in body size is so substantial for the *A. africanus*–early *H. erectus* transition (30.5 to 51.0 kg), selection only on brain size is not enough to cause a ~70% increase in body size given a modern human phenotypic model of variation (fig. A3*B*). It is clear that this result would occur at some point—as the body size of the ancestor decreases, a greater amount of selection on body size is needed to evolve it into the descendant. On the other hand, the results using the genetic model mirror previous findings—selection on the brain is so strong that negative selection on the body is needed to counter correlated effects (fig. A3*C*). In addition, when comparing the phenotypic model results removing covariance (fig. A4*B*) to a model including it (fig. A3*B*), covariance substantially decreases the amount of selection on body size needed for this evolutionary

transition. In other words, if *A. africanus* was the ancestor of early *H. erectus*, covariance between brain and body size might have reduced the amount of selection required to increase body size for this important evolutionary transition, as it does for early *H. erectus* to *H. heidelbergensis* (see also fig. 2*C*). Hence, whatever taxa came before early *H. erectus*, covariation between brain and body size played a major role in this evolutionary transition.

Taken together, results shown here suggest that evolutionary scenarios that interpret the increase in body size near the origins of *Homo* as adaptive (e.g., Antón, Potts, and Aiello 2014; Pontzer 2012) may be inconsistent with the evidence (see also Grabowski et al. 2015). Selective pressures undoubtedly played a role in refining the morphological changes that came with larger body size in response to changing functional demands, but they do not appear to be the driving force behind this change. What was? The answer appears to be an increasingly energetically voracious brain.

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Comments

Bárbara Costa, Daniela Rossoni, and Gabriel Marroig
Departamento de Genética e Biologia Evolutiva, Instituto de Biociências, Universidade de São Paulo, Rua do Matão, 277, 05508-900, São Paulo, Brazil (gmarroig@gmail.com). 14 IX 15

Quantitative Genetics, Selection, and Macroevolution

Quantitative genetic theory provides a valuable framework to understand the evolution of complex morphological traits. The evolution of a set of quantitative characters can be described by a multivariate extension of the breeder's equation: $\Delta\bar{z} = \mathbf{G}\beta$ (Lande 1979; Lande and Arnold 1983), where $\Delta\bar{z}$ is the vector of mean differences between generations, **G** is the additive genetic variance-covariance matrix, and β is a vector of directional selection gradients operating on each trait. The direction and the magnitude of evolutionary response ($\Delta\bar{z}$) depend on the intensity and direction of selection (β) as well as the genetic architecture of the traits (**G**), described in terms of variances and covariances (Lande and Arnold 1983). The role of genetic covariances among traits in determining the evolutionary response to selection can be seen in figure 4. In this hypothetical example, there are two positive correlated phenotypes, x and y, with their distribution in two species represented by ellipses. Traits in species A are more strongly correlated than in species B. Note that selection (β) is pushing both species to an increase in their y-trait averages, but their evolutionary responses to selection ($\Delta\bar{z}$) are quite different. The key feature here is that evolution in each trait is the result of not only direct selection but also selection on traits it genetically covaries with (see Cheverud 2004; Lande and Arnold 1983).

Grounded in quantitative evolutionary theory, Grabowski answered two major and related questions concerning hominin brain and body size evolution. First, he points out that these two traits covary within populations and that this covariation might have influenced the ancestral species' evolutionary response to selection. Taking into account this covariation among traits, Grabowski went further and reconstructed past selective pressures (β) acting along four branches of the hominin evolution: (1) *Pan troglodytes*–like LCA and *Australopithecus afarensis*, (2) *A. afarensis* and early *Homo erectus*, (3) early *H. erectus* and *Homo heidelbergensis*, and (4) *H. heidelbergensis* and modern humans. The β value estimates the force of directional selection on individual traits and therefore allows one to infer whether changes in one trait are due to direct or indirect selection. Grabowski's results suggest that strong selection for increased brain size played a large role in both brain and body size evolution in the hominin tribe. In his view, strong selection for increased brain size caused a major increase in brain and body size near the origins of our genus (*Homo*).

In his work, Grabowski highlighted the importance of covariation on brain-body evolution in an elegant way, when he compares it to a hypothetical scenario in which this covariance was removed. The big picture is that direct selection pressures required to increase brain mass for each of the lineages of the hominin tested were not noticeably different from the result when covariance is included. On the other hand, selection pressures to produce observed evolutionary changes on body mass for those same lineages were completely different after removing covariance. This is particularly interesting because along major lineages of hominin evolution, brain size increased, whereas body size increased in some lineages and decreased in others. Therefore, according to Grabowski, evolutionary patterns (fossil records) do not always reflect the

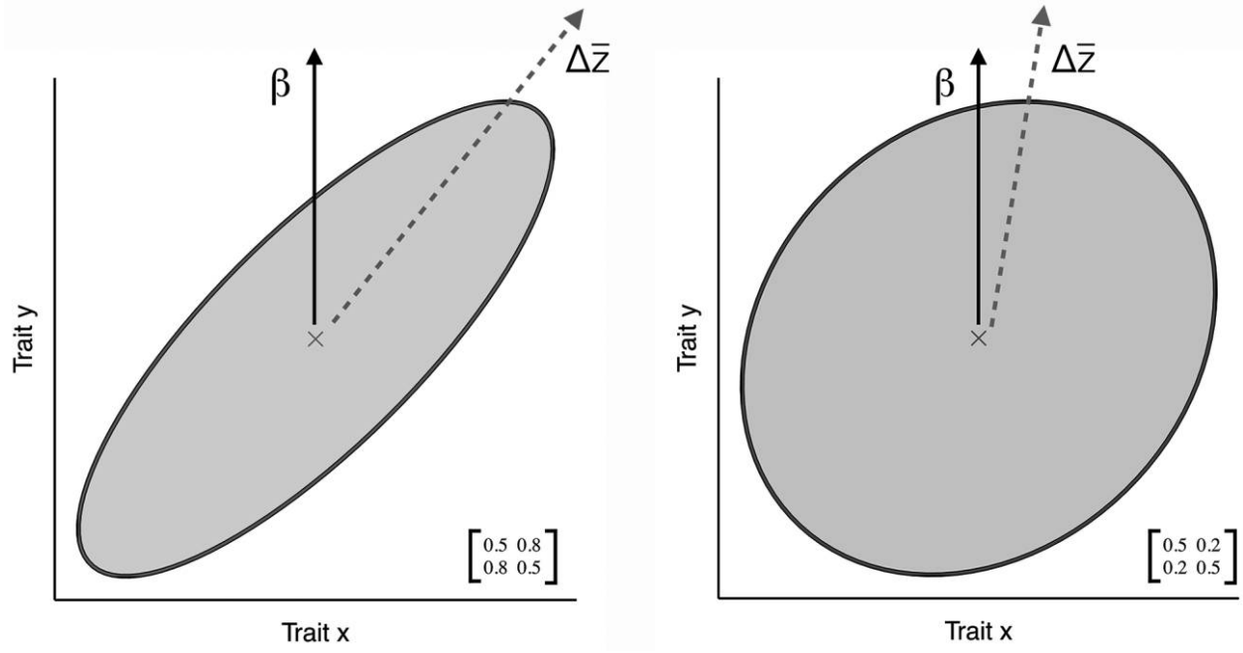

Figure 4. Hypothetical example of covariation between two traits (x and y) for species A (left) and species B (right) represented by ellipses. Covariation values are represented on the right corner of each ellipse. Note that traits are more tightly associated in species A than in B. The small × in the center of each ellipse represents the mean values for traits x and y. Boldface arrows show the direction of selection (β), and dotted arrows show the direction of evolutionary response to selection ($\Delta\bar{z}$). For details, see the main text. A color version of this figure is available online.

evolutionary process (e.g., natural selection) that produced them. By the same token, however, one shortcoming in Grabowski's contribution is the lack of other important traits, such as long bones and pelvis shape, traits that have been previously identified as potentially important to the evolution of human bipedalism. We know that identifying traits under selection is dependent on incorporating traits that are under selection on the system description (Lande and Arnold 1983). If at least one trait left out of the analyses is under appreciable directional selection and is correlated with other traits under study, the response of the characters under observation may be partly due to the correlation with the unmeasured trait (Lande and Arnold 1983). This, of course, is not a fatal criticism of the current contribution, since as Lande and Arnold (1983) commented, "a partial resolution of the influence of phenotypic correlations between characters is better than none at all" and paves the way for future studies.

In the context of retrospective selection analyses, it is worth noting the importance of controlling for noise in the estimates (Marroig, Melo, and Garcia 2012). It is especially recommended in those works addressing evolution on multiple quantitative traits, since they require larger sample sizes. This problem is exacerbated whenever matrix inversion is required, as in directional selection reconstruction analysis (Marroig, Melo, and Garcia 2012).

It is important to emphasize that selection reconstruction in macroevolutionary scenarios is still underexplored in evolutionary literature, especially when we consider the inclusion of fossil data, as recently done by Grabowski in this article and Grabowski and Roseman (2015). The reason behind this is probably the difficulty of obtaining the **G** matrix empirically (de Oliveira, Porto, and Marroig 2009). Besides, reconstructing past selection is dependent on the stability of the **G** matrix. The multivariate breeder's equation was originally developed for microevolutionary timescales (typically a few generations), and evolutionary constancy (or proportionality) of the **G** matrix as well as similarity with its phenotypic counterpart (**P** matrix) are important premises for the application of quantitative genetic approaches to study macroevolution (de Oliveira, Porto, and Marroig 2009; Lande 1979; Porto et al. 2009). However, analyses of **P** matrices in broad phylogenetic context have proven valuable for comparative approaches to the evolution of trait covariances (Steppan, Phillips, and Houle 2002). Moreover, as pointed out by Grabowski, there is a substantial literature (e.g., Cheverud 1988, 1996; Jones, Arnold, and Bürger 2003; Lovsfold 1986; Marroig and Cheverud 2001) indicating that **P** matrices can be used as a surrogate for **G** matrices. In the last decade, similarity between **P** and **G** has been consistently demonstrated (particularly for the mammalian class). Similarity between the **P** matrices of different species has been consistently demonstrated for more than 15 mammalian orders, including primates, rodents, and marsupials (de Oliveira, Porto, and Marroig 2009; Goswami 2006; Marroig and Cheverud 2001; Porto et al. 2009, 2015).

Therefore, Grabowski's work should be viewed as a guide on how to perform evolutionary quantitative approaches involving extinct and extant lineages. Selection reconstruction can be extremely useful in understanding patterns of multivariate selection in a macroevolutionary context and in helping discern among competing adaptive hypotheses.

Jeremy DeSilva
Department of Anthropology, Dartmouth College, 6047 Silsby Hall, Hanover, New Hampshire 03755, USA (jeremy.m.desilva@dartmouth.edu). 8 IX 15

Written in the style of the great evolutionary biologist Russell Lande, Mark Grabowski uses quantitative genetics to dive deep into the covariation between brain and body size and examine its implications for hominin evolution. What he reveals is that humans are just like other primates in possessing a relatively strong link between brain and body size. However, contrary to the argument that has often been posited—that brain increase was at times a nonadaptive by-product of increased body size—Grabowski flips the scenario and presents evidence that natural selection has acted directly on brain size, with body size increase being the side effect. These findings have important implications for understanding why and how our genus evolved and should challenge the field to consider whether we are even asking the right questions about the selective regimes that led to *Homo*. I would like to raise four points:

1. It is often stated that australopiths had brains that are ape sized and that hominin encephalization is a *Homo* phenomenon. However, compared with modern chimpanzees or the presumed hominid LCA (as evinced by *Rudapithecus* or *Ardipithecus*), australopiths had brains that were ~20% larger. Figure 3 appears to show the same (albeit weaker) selective pressures on brain : body in the LCA–*Australopithecus afarensis* transition as in the *A. afarensis*–*Homo erectus* transition. Why then the emphasis on *Homo*? What might this analysis tell us about australopiths and their brains?

2. Grabowski states, "There is currently no evidence of an early hominin with a large brain but a small body." The species that immediately comes to mind as traditionally fitting this description is, of course, *Homo habilis*. But, as Grabowski notes, there are no definitive skeletons of *H. habilis*. Susman (2008) and Susman and Stern (1982) might disagree, however, and have argued that OH 7, OH 8, and OH 35 belong to the same individual. Given Spoor et al.'s (2015) recent reconstruction of the OH 7 cranium (729–824 cm^3) and regression-based estimates of the OH 8 foot and the OH 35 tibia around 30–32 kg (McHenry 1992), this collection of fossils would challenge Grabowski's assertion that such a hominin does not exist. However, my colleagues and I have proposed, based on the relative development of the hand and foot bones in the OH 7/OH 8 assemblage, that OH 8 is likely from an older, arthritic female (DeSilva et al. 2010) and is not associated with the juvenile remains from OH 7. Furthermore, using body mass equations from McHenry and Berger (1998) and minimum dimensions from the eroded OH 7 capitate, OH 7 was likely >40 kg, quite a bit larger than the OH 8 individual. Thus, OH 8 is probably too small to have been associated with OH 7, and as predicted by Grabowski, the large-brained OH 7 belonged to an individual with a larger body size than the small-bodied OH 62 and KNM-ER 3735. Now, for the caveats: (1) Tocheri et al. (2008) note that the capitate OH 7R may not even be from the same individual as OH 7 and is likely to be from a smaller individual than the OH 7 hand, further supporting Grabowski's assertions. (2) Moyà-Solà et al. (2008) have argued that the OH 7 hand is from a robust australopith and is not even associated with the OH 7 craniodental remains. If true, then the Middle Bed I deposits of FLK NN are a mixed assemblage of multiple individuals representing at least two genera of hominin, and as argued by Grabowski, we are still without an *H. habilis* skeleton. Associated skeletons from early *Homo* should thus be quite high on the paleoanthropological wish list, which leads to my third point.

3. I am curious how *Homo naledi* (Berger et al. 2015) fits into Grabowski's analysis. *Homo naledi* is a rather small-brained hominin (465–560 cm^3), with a body mass estimated to have been slightly larger than South African australopiths. How might *H. naledi* fit into a South African evolutionary scenario in which *Australopithecus africanus*–*Australopithecus sediba*–*H. naledi* and *H. erectus* (or some variant of that) are the ancestor-descendant transitions being evaluated? Grabowski's paper has a strong eastern African bent to the narrative of human evolution. However, given the new (but undated) fossils from *H. naledi* and recent cladistic work proposing *A. sediba* as an ancestor to *Homo* (Dembo et al. 2015), it would be worth re-evaluating some of the conclusions of this paper with the now exceptionally rich and growing South African record. I am not arguing that South Africa is the source of *Homo*, but I am suggesting that the flood of discoveries in the last decade have at the least swayed, if not fully uprooted, some of our phylogenetic trees and should force us to consider multiple ancestor-descendant scenarios.

4. Finally, while encephalization captures our attention and our inquiry, one of the more underappreciated and ignored changes to the human brain is its recent abrupt shrinkage. Every Anthro 101 student learns that Neanderthals had larger brains than humans, but few learn that contemporaneous Pleistocene *Homo sapiens* (i.e., Cro-Magnon) also had significantly larger brains than humans have today. The average modern human brain size has reduced by nearly 20% since its peak ~30,000 years ago. While some have argued that this is a result of body size decrease (Ruff, Trinkaus, and Holliday 1997), others have challenged this also using a quantitative genetics model (Hawks 2011). I am quite interested in whether Grabowski's analysis could also be used to examine brain reduction, which would have implications for both testing causative hypotheses for brain reduction in Holocene humans and

assessing the likelihood of, if not the circumstances behind, the evolution of small-brained hominins such as *Homo floresiensis*.

Ultimately, my comments are not a critique of Grabowski's paper but an invitation for him to expand his approach to address additional questions that could be answered using these methods. I applaud Dr. Grabowski for publishing this important work and look forward to a healthy discussion in these pages of *Current Anthropology*.

Suzana Herculano-Houzel
Instituto de Ciências Biomédicas, Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil (suzanahh@gmail.com). 28 VIII 15

From Bigger Brains to Bigger Bodies

Scientists have long sought the most distinguishing feature of the human brain, the one characteristic responsible for our humanity. For a few decades, it appeared that this feature was the size of the human brain relative to the body. While gorillas have bodies up to three times as heavy as the human body, it is our brain, not theirs, that is three times as large; humans are the most encephalized species (Jerison 1973). That observation started a tradition of considering that human evolution involved a preferential and very rapid expansion of the brain away from the mass supposedly required to run the body, thus endowing humans with "excess brain mass" to dedicate to solving problems.

The logic behind this argument is that across species, larger bodies usually come with larger brains. This is a strong allometric relationship of exponent around 0.75, depending on the exact species analyzed: brain mass scales with body mass raised to an exponent of 0.5 to 0.9 (Herculano-Houzel, Manger, and Kaas 2014). Such a strong relationship implies that there are genetic mechanisms at play that control brain and body mass together. If that is the case, then how could the human brain break the rule and increase so much in size relative to its body? Is there a particularly weak correlation between brain and body mass across human individuals, such that positive selection for one could really leave the other behind?

In this article, Mark Grabowski provides an answer to this question: covariance of brain and body mass in humans, at 0.338, is not particularly weaker than that found in other extant primate species, between 0.240 and 0.481 (and 0.319 in the chimpanzee). Given these values, Grabowski then uses a simple model to estimate past selection pressures required to produce the changes in brain and body mass observed in the fossil record. He finds that most major transitions in hominin evolution can be explained as a consequence of strong selection for larger brains but not larger mass, whether or not body mass also increased, despite the not particularly low covariance between brain and body mass across modern humans. Covariance of these parameters in modern humans, and thus supposedly in ancestral hominins, is strong enough to suppose that selection for larger brain mass alone can result in increased body mass in some cases and is so strong that body mass still increases along with the brain even when the model predicts simultaneous selection for smaller bodies.

The new findings by Grabowski add to the evidence provided by Montgomery et al. (2010) that there has been independent evolution of brain and body size in primates, in the sense that although brain volume tends to increase, body size increases in some transitions and decreases in others. In particular, Montgomery et al. (2010) indicate that the evolution of small relative brain size in gorillas was a consequence of body mass increasing to a greater extent than brain mass—in the opposite direction of the pattern found by Grabowski, who did not include gorillas in his analysis. The possibility that gorillas underwent an increase in body mass that was uncoupled from an increase in brain mass due to energetic constraints is something that we have suggested previously (Fonseca-Azevedo and Herculano-Houzel 2012). It will be interesting to see whether, behind this unusual evolutionary path, there is any evidence of a particularly low covariance of brain and body mass in extant gorillas; according to Grabowski's new findings, even in the face of not particularly weak covariance, strong selection for one but not the other would still be enough to uncouple the trajectories of brain and body mass in gorilla evolution.

An important problem that is central to the evolution of larger brains and bodies, and one that Grabowski introduces but does not explore, is how covariance and scaling relationships within a species translate into covariance and scaling relationships across species in evolution. The difficulty is that covariance between brain and body mass across individuals of a species, the subject of his study, is far weaker than covariance between brain and body mass across species. Perhaps as a consequence of this differential covariance at different taxonomic levels, much steeper allometric exponents relate brain mass and body mass across species (0.5 to 0.9) than across individuals of the same species (~0.2 to 0.4, when significant at all; Riska and Atchley 1985). This is an important issue too often left out in studies of evolution. If evolution happens through positive selection within a population, the result of that selection (the allometric scaling across species) should be simply a continuation of the allometric scaling across individuals of a population. In contrast, we have recently found that this is not the case: while rodent species with larger brains also have larger bodies and more brain neurons that are on average larger, mouse individuals with larger brains have neither significantly larger bodies nor more neurons; instead, those individuals with more neurons have smaller (not larger) neurons (Herculano-Houzel et al. 2015).

This implies that selection for more brain neurons within a population is not automatically synonymous with selection for larger brains and larger bodies. The opposite trends of scaling within and across species challenge the notion that

the size of brain and body are firmly controlled by the same genes. It is probable that brain and body are much less constrained than usually suspected, and some level of self-organization is likely to be involved. If our findings about intraspecific variation turn out to apply to other species as well, and to humans in particular, the evolution of larger bodies with larger brains made of more neurons will have to stop being considered as a single package, while mechanisms must be in place that make one still be accompanied by the other. One possibility, as Grabowski shows, is that low levels of covariance may still turn out to be enough to make selection for one variable be accompanied by concerted changes in other variables—and so, bigger brains will still often come in bigger bodies.

Simon Neubauer
Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology, Deutscher Platz 6, 04103 Leipzig, Germany (simon.neubauer@eva.mpg.de). 30 VIII 15

While selection is often inferred from observed evolutionary changes, possible causes of these changes and evolutionary processes can be meaningfully discussed only after we have an idea about selection pressures and the adaptiveness of a given trait. The allometric relationship and physiological linkage between brain and body size (e.g., Aiello and Wheeler 1995; Armstrong 1983; Fonseca-Azevedo and Herculano-Houzel 2012; Gould 1975; Isler et al. 2008; Martin 1983) are important issues in analyses of hominin brain and body size evolution. Mark Grabowski models and discusses the role of selection that generated the observed changes for main transitions during hominin evolution. This is a welcome approach that attempts to take into account potentially confounding effects of covariation between brain and body size.

Evolutionary models can only be as good as the empirical data and the suitability of assumptions they are based on. The first main result of this study, which states that modern humans and extinct hominins do not have lower levels of mean brain-body integration, relies on the notion that phenotypic brain-body covariation in captive chimpanzees is representative of wild chimps. This assumption is backed by data on other primates. However, mean integration is shown to be quite variable between species and is on average higher in captive than in wild-caught samples. Data from one of the two species for which wild-caught and captive samples are available are consistent with higher integration in the latter, but the other species shows a similar level for both samples. More data of captive and wild-caught samples from the same species are therefore required to reinforce similar integration levels. However, I do agree that the presented data suggest a higher level of brain-body covariation for humans than for (wild) chimpanzees, definitely not vice-versa. Grabowski's choice to use both, a modern human model and a chimp model (as well as a human genetic model), should cover the possible variation in hominins, in my opinion.

Regarding results of past selection pressures, it is worth noting that both brain and body size estimates for fossils come with potential (sometimes significant) estimation errors. Grabowski et al. (2015) were successful in updating and improving body mass estimates, but likewise, the effects of small sample sizes should not be neglected when analyzing species means and variances, as, for example, Neubauer et al. (2012) pointed out for endocranial volumes in *Australopithecus africanus*. While evolutionary changes in brain and body size across the investigated evolutionary transitions seem quite stable by trend, it would be interesting to check whether and how numerical variation or uncertainties caused by required reconstruction and small samples affect results on selection. The same applies for uncertainties caused by brain and body size data captured from different—not the same—individuals.

Grabowski considered four major evolutionary transitions, as many researchers agree that *Australopithecus afarensis* as well as early *Homo erectus* are the ancestors of later hominins and that *Homo heidelbergensis* or a similar hominin in terms of the size relationship between brain and body bridges the gap to modern humans. This decision circumvents the problems with other fossils, especially around the origin of our genus, which are difficult to sort and controversially discussed or for which it is challenging to group cranial and postcranial remains together (e.g., Antón, Potts, and Aiello 2014; Leakey et al. 2012; Lordkipanidze et al. 2013; Spoor et al. 2007, 2015; Wood and Collard 1999; Wood and Lonergan 2008; Wood and Richmond 2000). However, these transitions are somewhat "unreal" large evolutionary jumps, omitting important fossils in between. How can the results based on unreal evolutionary jumps inform our interpretation of the ultimate causes and evolutionary processes that actually happened in real time? This question relates not only to the origin of our genus but also to other evolutionary time periods. While Grabowski used early (African and Georgian) *H. erectus* for his main evolutionary transitions, it becomes more and more evident that within this long-standing species, variation concerning dental as well as postcranial growth patterns, brain ontogeny, and life history was neither ape-like nor human-like nor on a continuum in between (e.g., Hublin, Neubauer, and Gunz 2015). This poses the question of how different selection pressures and covariation between traits formed evolutionary processes within *H. erectus* that could be investigated using similar modeling techniques. Furthermore, the transition from *H. heidelbergensis* to recent modern humans is a somewhat unreal evolutionary jump that does not take into consideration that gracilization occurred within modern humans, the earliest *Homo sapiens* having on average both larger brains and bodies than we have nowadays (e.g., Henneberg 1988; Ruff, Trinkaus, and Holliday 1997).

Grabowski highlights what his results mean for evolutionary scenarios near the origin of our genus. The idea that body size increase is adaptive at this point in time (Antón, Potts, and

Aiello 2014; Pontzer 2012) seems inconsistent with the presented data. The conclusion of an energetically voracious brain driving a significant amount of the evolutionary changes, including body size increase at the origin of *Homo* (and in general during hominin evolution), is intriguing and raises interesting questions about how it can be achieved that adult body size is pulled along with increasing adult brain size during an individual's development (e.g., see Cunnane and Crawford 2014; Kuzawa et al. 2014). In addition to new fossil discoveries and reanalyses of known fossils with new methods, I think this and other modeling studies will reveal noteworthy information to better interpret evolutionary scenarios of how brain size, body size, life history, energy allocation, developmental patterns, and social and cognitive abilities jointly changed over time.

Reply

The absolutely and relatively larger brains of modern humans are widely recognized as one of the hallmarks of our species, along with bipedalism, extreme sociality, and our command of technology. Consequently, there has been intense and sustained interest in the evolution of this fundamental human trait. Similarly, the large increase in body size that occurred near the origins of our genus has its own set of adaptive hypotheses as to its causes and consequences. Importantly, with the exception of hypotheses that explain increases or decreases in brain size as due to allometric scaling with body size (though generally leaving the underlying cause of this scaling unexplored) or propose a physiological link, these two traits are generally regarded as independent and able to evolve in response to their own selective pressures. This study makes two overall points as simply but as strongly as possible. First, that covariation plays a fundamental role in evolution and should be acknowledged in forming and testing evolutionary hypotheses, including in our own lineage. Second, the changes observed in the fossil record (evolutionary patterns) may be utterly distinct from the past selection pressures that produced those patterns (evolutionary processes), and it is only through uniting pattern and process within a framework of theoretical evolutionary biology that we can begin to test hypotheses of adaptation. Both are topics that are not commonly discussed in the majority of the paleoanthropological literature or training, and I believe it is to our detriment as a discipline. In what follows, I focus on what I see as the major points that run throughout the comments in order of their appearance.

Statistical Noise

Costa, Rossoni, and Marroig point out that controlling for noise in the estimates of selection is vital for providing accurate estimates of evolutionary quantities. As the number of traits increases, the number of individuals used to estimate covariance matrices—**P** or **G**—must increase as well or the last few dimensions/eigenvalues will be dominated by noise. Calculating directional section gradients requires matrix inversion, which leads to the smallest (and most poorly estimated) dimensions/eigenvalues dominating the resulting analysis. Here there are only two traits and thus two dimensions, making noise less of an issue, as implied by Costa, Rossoni, and Marroig. Moreover, the proposed noise-correction method of Marroig, Melo, and Garcia (2012) requires many more traits than two to function. This is not a problem with this method, as it is designed to deal with the problem of higher-dimensional covariance matrices, and I fully stand behind their sentiment. In fact, simulation studies done by collaborator Dr. Arthur Porto and myself suggest that sample size is vitally important to produce precise and unbiased estimates of numerous evolutionary parameters. Many studies have left the effects of small sample sizes unacknowledged.

Ape-Sized Australopiths

DeSilva correctly notes that it is often suggested that australopiths had ape-sized brains, with the main increase in brain size coming with the origins of our genus. This occurs even in publications that show that australopiths had absolutely larger brains than chimpanzees (e.g., McHenry and Coffing 2000), as can be seen in table 2. One of the causes of this may be earlier studies focused on smaller sample sizes of both chimpanzees and fossil hominins. Larger samples of chimpanzee brains (e.g., DeSilva 2011; see table 2) show earlier averages (e.g., 410.3 g from Aiello and Dean [1990] vs. 380 g from table 2) were quite high. Larger samples of australopiths show the opposite pattern, from 415 g in *Australopithecus afarensis* (Aiello and Dean 1990) to a current best estimate of 462.1 based on five individuals.

Another reason for this suggestion may be the compounding of absolute and relative brain size (relative to body size). My colleagues and I recently (Grabowski et al., forthcoming) explored the causes of primate brain-body allometry using phylogenetic comparative methods based on a range of possible evolutionary models and estimated and accounted for observational error in both brain and body size. The effects of controlling for phylogeny and observation error were substantial, and our analysis yielded a novel 3/5 scaling exponent for primate brain-body evolutionary allometry. There are two main implications of this new scaling exponent. First, biological interpretations based on 2/3 (e.g., Jerison 1973) or 3/4 (e.g., Martin 1981) scaling need to be reassessed. Second, it allowed us to recalculate encephalization quotients using the latest estimates of brain and body sizes for fossil hominins. Updated encephalization quotients are shown in table 3, a modified version from our publication (Grabowski et al., forthcoming). It also reproduces previous encephalization estimates based on either Jerison's 2/3 or Martin's 3/4 scaling from Aiello and Dean (1990). These results show that earlier

estimates of encephalization based on either a 2/3 or 3/4 scaling depict both *A. afarensis* and *Australopithecus africanus* as being slightly less encephalized than common chimpanzees. This contrasts with our new estimates that show that greater encephalization appears at least by the australopiths, with early hominins substantially more encephalized than previously thought. If australopiths already had larger brains than other primates, DeSilva then asks, "Why then the emphasis on *Homo*?" The answer is that brain size appears to increase dramatically near the origins of our genus, both absolutely and relatively (table 3), and continues to do so until decreasing slightly within our species. Our dramatically larger brain sizes are what make us who we are, and the evolutionary history of this distinctly human trait has led to a multitude of adaptive hypotheses that can be tested.

South African Fossil Record

DeSilva brings up the expanding South African hominin fossil record, including *Homo naledi*, which possessed a brain that overlapped in size with australopiths, with a body mass described as that of a small modern human population in Berger et al. (2015). With regard to DeSilva's proposed South African evolutionary scenario, *A. africanus–A. sediba–H. naledi–H. erectus*, as can be seen in table 2, *A. africanus* is larger in terms of both average brain size (40 g) and average body size (5 kg) than *A. sediba*. As discussed above, while it is possible that a smaller-brained and smaller-bodied species could evolve from a larger-brained and larger-bodied species (as DeSilva notes took place within one species—anatomically modern humans), *A. sediba* fossils (where brain size is based on one individual and body size is based on two individuals) may be sampling from the low end of the size spectrum, and their smaller sizes misrepresent the species as a whole. There is also the issue with dates for *A. sediba*, which appears at around the same time as *H. erectus*, though this taxa could have originated at an earlier point (Berger et al. 2010). With regard to including *H. naledi*, I am going to err on the side of caution here—first and foremost, because of a lack of published date, but also because preliminary results using the same approach as Grabowski et al. (2015) suggest that the currently published body size estimates of *H. naledi* are far too high (M. Grabowski, unpublished data). If South African hominins are placed in the evolutionary sequence that leads to *Homo*, I am inclined to support the transition from *A. africanus* to *H. erectus*, and this sequence was included in CA+ supplement A.

Pattern versus Process

Herculano-Houzel relates my findings to that of Montgomery et al. (2010), who used ancestral state reconstructions to show that brain and body size have both increased and decreased in primate evolution, as appears to have happened over the course of human evolution. It is important to note here that the referenced study focused on the pattern of evolution, rather than the evolutionary process that resulted in this pattern, as well as assumed a particular pattern of evolution—Brownian motion. Pattern does not necessarily imply processes. Natural selection acting on covariance between traits, in addition to other evolutionary forces such as genetic

Table 3. Average endocranial volume (ECV), brain mass, and body mass (with sample size) for common chimpanzees, fossil hominins, and modern humans; previous encephalization quotient (EQ) estimates using Jerison's 2/3 and Martin's 3/4 allometric equations; and new encephalization quotients from our best-supported 3/5 equation

Designation	Mean ECV (cm^3)	Mean brain mass (g)	Mean body mass (kg)	EQ (Jerison's 2/3 scaling)[a]	EQ (Martin's 3/4 scaling)[a]	EQ (current best-fit 3/5 slope)[b,c]
Pan troglodytes	366.2	379.4 ($n = 65$)	45.0 ($n = 60$)	3.01	2.38	2.40
Australopithecus afarensis	446.0	462.1 ($n = 5$)	39.1 ($n = 12$)	2.44	1.87	3.18
Australopithecus africanus	460.0	476.6 ($n = 9$)	30.5 ($n = 5$)	2.79	2.16	3.81
Australopithecus sediba	420.0	435.1 ($n = 1$)	25.8 ($n = 2$)	…	…	3.85
Homo habilis s.s.	624.3	652.0 ($n = 6$)	32.6 ($n = 2$)	4.31	3.38	4.97
Early *Homo erectus* (African + Georgian)	747.8	774.7 ($n = 9$)	51.0 ($n = 7$)	…	…	4.55
Homo erectus	991.0	1,026.7 ($n = 36$)	51.4 ($n = 9$)	4.40	3.34	6.00
Homo floresiensis	425.7	440.3 ($n = 1$)	27.5 ($n = 1$)	…	…	3.75
Homo heidelbergensis	1,242.0	1,286.7 ($n = 21$)	70.6 ($n = 12$)	…	…	6.22
Homo neanderthalensis	1,404.0	1,454.5 ($n = 27$)	72.1 ($n = 23$)	…	…	6.94
Homo sapiens	1,349.0	1,397.6 ($n = 122$)	57.8 ($n = 51$)	8.07	6.28	7.61

Note. Modified from Grabowski et al. (forthcoming). The 2/3 allometric equation is from Jerison (1973), and the 3/4 allometric equation is from Martin (1981).

[a] Following Aiello and Dean (1990).

[b] Based on brain and body size averages on left compiled in Grabowski et al. (forthcoming), except for worldwide average of modern human brain size, based on 122 populations from Beals, Smith, and Dodd (1984) and comments therein.

[c] Encephalization quotients for current best-fit slope were calculated from our equation $EQ = ECV/e^{(0.60 \times \ln(\text{body mass}) - 1.402)}$, with body mass in grams.

drift, could be responsible for observed evolutionary changes (e.g., Weaver, Roseman, and Stringer 2007). While Montgomery et al. (2010) and several recent works on rates of brain and body size evolution have used patterns of evolution to suggest that these two traits can evolve independently from each other, even suggesting a decoupling over macroevolutionary time (Gonzalez-Voyer, Winberg, and Kolm 2009), this analysis shows the distinction between pattern and process. Here, results argue that selection is actually compensating for brain-body covariation and that the response to selection (and thus the patterns of evolution) is the result of the interplay between these two factors. Rather than selection breaking down pattern of brain-body covariation to allow for brain size to evolve with greater independence from body size, the evolution of our lineage took place within these constraints. It was the result of strong direct selection to increase brain size, often along with relatively small amounts of negative direct selection to reduce body size in order to compensate for correlated effects, and brain-body covariation necessitated greater amounts of selection when both traits were evolving in antagonistic directions.

Interspecific Brain-Body Allometry

Herculano-Houzel also claims that my study does not explore how covariance within species translates into covariance and scaling relationships across species—in other words, how intrapopulation covariation may lead to macroevolutionary patterns of brain-body allometric scaling. I do, in fact, relate within-population brain-body variation to interspecific patterns of macroevolution within the context of an explicit evolutionary model, though it does not focus on interspecific brain-body allometry. This study models brain-body variation and covariation within each fossil species based on our extant comparative sample—here, modern human phenotypic and genetic patterns of variation and covariation and chimpanzee phenotypic patterns. Thus, turning to figure 1, one can imagine that around each species mean is a distribution of brain and body size variation akin to that seen in the left plot of figure 4. Selection on the pattern of within-population variation and covariation leads to evolutionary changes between one fossil species and its descendant, with the descendant taxon having its own pattern of variation and covariation on which later selection could act. Figure 5 summarizes the findings of this study, showing the interaction between selection and intraspecific patterns of variation and covariation.

While Herculano-Houzel argues that her lab's results (Herculano-Houzel et al. 2015) showing that individual mice within a population with larger brains have neither significantly larger bodies nor more neurons is contrary to the idea that brain and body size are closely linked (Herculano-Houzel et al. 2015), this finding is contrary to the results of numerous analyses using the same model organism and much larger sample sizes (e.g., a phenotypic correlation of 0.34 ± 0.4 using a sample of 1,466 adult mice in Riska and Atchley [1985]). This lack of a pattern might be due to the small sample sizes (19 mice) used in this study (Herculano-Houzel et al. 2015).

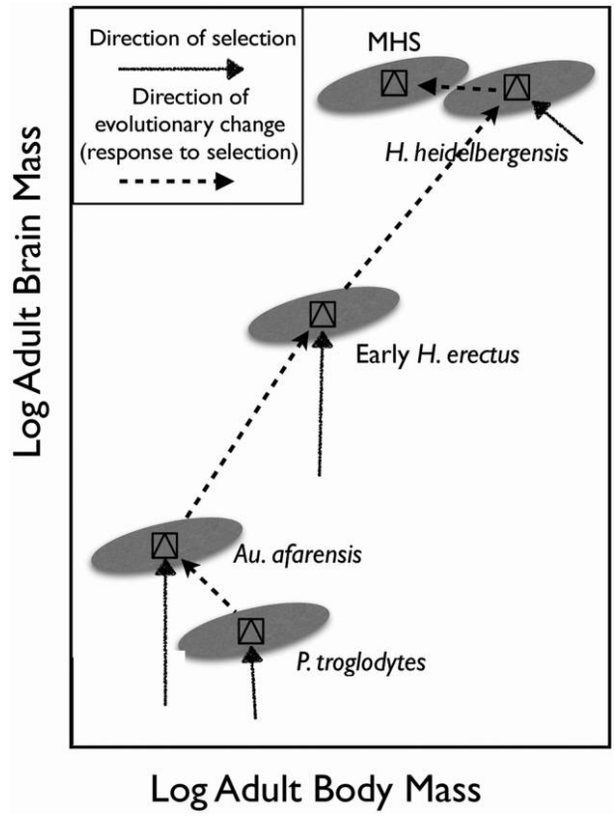

Figure 5. Modified version of the inset from figure 1, displaying the overall findings of this study. Brain mass is on the *Y*-axis, and body mass is on the *X*-axis. Symbols show fossil means, with pattern of variation and covariation around each mean. As shown in the key, boldface arrows represent the overall amount and direction of selection on each mean; dotted arrows represent the direction of evolutionary change that results from selection on the mean at the start of the transition. This figure shows how brain-body variation and covariation within each fossil species lead to differences between the direction of selection and the direction of evolutionary change. As discussed in the main text and seen here, strong selection to increase brain size alone played a major role in both brain and body size increases throughout human evolution and may have been solely responsible for the major increase in both traits that occurred during the transition to early *Homo erectus*. A color version of this figure is available online.

Estimation Errors and Evolutionary Transitions

Neubauer makes the point that brain and body size estimates come with estimation errors, which can then complicate estimates of selection. These errors can be caused by reconstruction (e.g., of endocranial volumes) and prediction (e.g., with regard to fossil body mass) as well as error around mean esti-

mates that increases with decreasing sample sizes. Issues relating to small sample sizes in analyses of hominin fossils is a particularly important point (Grabowski and Roseman 2015; Grabowski et al. 2015; Neubauer et al. 2012). Neubauer also suggests that some evolutionary transitions I included were unrealistic because they omitted important fossils in between the transitions included here, though he notes that species diagnosis as well as matching postcranial remains with cranial remains are particularly problematic in early hominin evolution. The previous comment regarding estimation errors is intimately related to his second point. In working on Grabowski et al. (2015), it became clear that there are few fossils with matched cranial and postcranial remains from which body size predictions could be calculated, and species designations for a significant portion of the fossil postcranial material are highly disputed. In Grabowski et al. (2015), we took a very conservative approach and used only the individual fossils with the most reliable attributions in calculating the species means, because species designation is a critical issue when determining characteristics of a species and differences between species. The current work took a similar approach, but this meant that *Homo habilis* sensu stricto, sensu lato, or what is sometimes called non-*erectus* early *Homo* (Antón, Potts, and Aiello 2014) were not included, as body size estimates for these groups are either based on too few individuals to be considered reliable (e.g., $n = 2$ for *H. habilis* s.s.) or made up of fossils with species designations so disputed that some may actually be *H. erectus* or not *Homo* at all (see Grabowski et al. 2015). Calculating precise and unbiased averages for hominin fossil taxa does not just depend on including the largest possible number of individuals or minimizing the error of the individual estimates—it is also vitally important that the fossil belongs to that group in the first place.

—Mark Grabowski

References Cited

Ackermann, Rebecca Rogers, and James M. Cheverud. 2000. Phenotypic covariance structure in tamarins (genus *Saguinus*): a comparison of variation patterns using matrix correlation and common principal component analysis. *American Journal of Physical Anthropology* 111(4):489.

———. 2004. Detecting genetic drift versus selection in human evolution. *Proceedings of the National Academy of Sciences of the USA* 101(52):17946–17951. doi:10.1073/pnas.0405919102.

Aiello, Leslie, and Christopher Dean. 1990. *An introduction to human evolutionary anatomy*. London: Academic Press.

Aiello, Leslie C., and Cathy Key. 2002. Energetic consequences of being a *Homo erectus* female. *American Journal of Human Biology* 14(5):551–565. doi:10.1002/ajhb.10069.

Aiello, Leslie C., and Jonathan C. K. Wells. 2002. Energetics and the evolution of the genus *Homo*. *Annual Review of Anthropology* 31(1):323–338. doi:10.1146/annurev.anthro.31.040402.085403.

Aiello, Leslie C., and Peter Wheeler. 1995. The expensive-tissue hypothesis: the brain and the digestive system in human and primate evolution. *Current Anthropology* 36(2):199–221.

Antón, Susan C., William R. Leonard, and Marcia L. Robertson. 2002. An ecomorphological model of the initial hominid dispersal from Africa. *Journal of Human Evolution* 43(6):773–785. doi:10.1053/jhev.2002.0602.

Antón, Susan C., Richard Potts, and Leslie C. Aiello. 2014. Evolution of early *Homo*: an integrated biological perspective. *Science* 345(6192):1236828. doi:10.1126/science.1236828.

Antón, Susan C., and J. Josh Snodgrass. 2012. Origins and evolution of genus *Homo*. *Current Anthropology* 53(suppl. 6):S479–S496. doi:10.1086/667692.

Armstrong, E. 1983. Relative brain size and metabolism in mammals. *Science* 220:1302–1304. [SN]

Arsuaga, J. L., I. Martínez, L. J. Arnold, A. Aranburu, A. Gracia-Téllez, W. D. Sharp, R. M. Quam, et al. 2014. Neandertal roots: cranial and chronological evidence from Sima de los Huesos. *Science* 344(6190):1358–1363. doi:10.1126/science.1253958.

Arsuaga, Juan-Luis, Carlos Lorenzo, José-Miguel Carretero, Ana Gracia, Ignacio Martínez, Nuria García, José-María Bermúdez de Castro, and Eudald Carbonell. 1999. A complete human pelvis from the Middle Pleistocene of Spain. *Nature* 399(6733):255–258. doi:10.1038/20430.

Atchley, William R. 1984. The effect of selection on brain and body size association in rats. *Genetics Research* 43(3):289–298.

Atchley, William R., Bruce Riska, Luci A. P. Kohn, A. Alison Plummer, and J. J. Rutledge. 1984. A quantitative genetic analysis of brain and body size associations, their origin and ontogeny: data from mice. *Evolution* 38(6):1165–1179.

Beals, Kenneth L., Courtland L. Smith, and Stephen M. Dodd. 1984. Brain size, cranial morphology, climate, and time machines. *Current Anthropology* 25(3):301–330.

Berger, Lee R., Darryl J. de Ruiter, Steven E. Churchill, Peter Schmid, Kristian J. Carlson, Paul H. G. M. Dirks, and Job M. Kibii. 2010. *Australopithecus sediba*: a new species of *Homo*-like australopith from South Africa. *Science* 328(5975):195–204. doi:10.1126/science.1184944.

Berger, Lee R., John Hawks, Darryl J. de Ruiter, Steven E. Churchill, Peter Schmid, Lucas K. Delezene, Tracy L. Kivell, et al. 2015. *Homo naledi*, a new species of the genus *Homo* from the Dinaledi Chamber, South Africa. *eLife* 4:e09560. doi:10.7554/eLife.09560.

Bischoff, Theodor L. W. 1880. *Das Hirngewicht des Menschen: eine Studie*. Bonn, Germany: Neusser.

Blinkov, Samuil M., and Il'ya I. Glezer. 1968. *The human brain in figures and tables: a quantitative handbook*. New York: Basic.

Boddy, A. M., M. R. McGowen, C. C. Sherwood, L. I. Grossman, M. Goodman, and D. E. Wildman. 2012. Comparative analysis of encephalization in mammals reveals relaxed constraints on anthropoid primate and cetacean brain scaling. *Journal of Evolutionary Biology* 25(5):981–994. doi:10.1111/j.1420-9101.2012.02491.x.

Bonmatí, Alejandro, Asier Gómez-Olivencia, Juan-Luis Arsuaga, José Miguel Carretero, Ana Gracia, Ignacio Martínez, Carlos Lorenzo, José María Bérmudez de Castro, and Eudald Carbonell. 2010. Middle Pleistocene lower back and pelvis from an aged human individual from the Sima de los Huesos site, Spain. *Proceedings of the National Academy of Sciences of the USA* 107(43):18386–18391. doi:10.1073/pnas.1012131107.

Bramble, Dennis M., and Daniel E. Lieberman. 2004. Endurance running and the evolution of *Homo*. *Nature* 432(7015):345–352. doi:10.1038/nature03052.

Braun, David R., John W. K. Harris, Naomi E. Levin, Jack T. McCoy, Andy I. R. Herries, Marion K. Bamford, Laura C. Bishop, Brian G. Richmond, and Mzalendo Kibunjia. 2010. Early hominin diet included diverse terrestrial and aquatic animals 1.95 Ma in east Turkana, Kenya. *Proceedings of the National Academy of Sciences of the USA* 107(22):10002–10007. doi:10.1073/pnas.1002181107/-/DCSupplemental.

Carretero, José Miguel, Laura Rodríguez, Rebeca García-González, Juan Luis Arsuaga, Asier Gómez-Olivencia, Carlos Lorenzo, Alejandro Bonmatí, Ana Gracia, Ignacio Martínez, and Rolf Quam. 2012. Stature estimation from complete long bones in the Middle Pleistocene humans from the Sima de los Huesos, Sierra de Atapuerca (Spain). *Journal of Human Evolution* 62(2):242–255. doi:10.1016/j.jhevol.2011.11.004.

Cerling, Thure E., Fredrick Kyalo Manthi, Emma N. Mbua, Louise N. Leakey, Meave G. Leakey, Richard E. Leakey, Francis H. Brown, et al. 2013. Stable isotope-based diet reconstructions of Turkana Basin hominins. *Proceedings of the National Academy of Sciences of the USA* 110(26):10501–10506. doi:10.1073/pnas.1222568110.

Cheverud, James M. 1988. A comparison of genetic and phenotypic correlations. *Evolution* 42(5):958–968.

———. 1989. A comparative analysis of morphological variation patterns in the papionins. *Evolution* 43(8):1737–1747.

———. 1995. Morphological integration in the saddle-back tamarin (*Saguinus fuscicollis*) cranium. *American Naturalist* 145(1):63–89.

———. 1996. Quantitative genetic analysis of cranial morphology in the cotton-top (*Saguinus oedipus*) and saddle-back (*S. fuscicollis*) tamarins. *Journal of Evolutionary Biology* 9(1):5–42. [BC/DR/GM]

———. 2004. Darwinian evolution by the natural selection of heritable variation: definition of parameters and application to social behaviors. In *The origins and nature of sociality*. Robert W. Sussman and Audrey R. Chapman, eds. Pp. 140–157. New York: Aldine. [BC/DR/GM]

Cunnane, Stephen C., and Michael A. Crawford. 2014. Energetic and nutritional constraints on infant brain development: implications for brain expansion during human evolution. *Journal of Human Evolution* 77:88–98. [SN]

Darwin, Charles. 1859. *On the origins of species by means of natural selection*. London: J. Murray.

———. 1874. *The descent of man: and selection in relation to sex*. 2nd edition. London: J. Murray.

Deacon, Terrence W. 1990. Fallacies of progression in theories of brain-size evolution. *International Journal of Primatology* 11(3):193–236.

Deaner, Robert O., Karin Isler, Judith Burkart, and Carel van Schaik. 2007. Overall brain size, and not encephalization quotient, best predicts cognitive ability across non-human primates. *Brain, Behavior and Evolution* 70(2):115–124. doi:10.1159/000102973.

Dembo, Mana, Nicholas J. Matzke, Arne Ø. Mooers, and Mark Collard. 2015. Bayesian analysis of a morphological supermatrix sheds light on controversial fossil hominin relationships. *Proceedings of the Royal Society B: Biological Sciences* 282:20150943. [JD]

de Oliveira, Felipe Bandoni, Arthur Porto, and Gabriel Marroig. 2009. Covariance structure in the skull of Catarrhini: a case of pattern stasis and magnitude evolution. *Journal of Human Evolution* 56(4):417–430. [BC/DR/GM]

DeSilva, Jeremy, and Julie Lesnik. 2006. Chimpanzee neonatal brain size: implications for brain growth in *Homo erectus*. *Journal of Human Evolution* 51(2):207–212. doi:10.1016/j.jhevol.2006.05.006.

DeSilva, Jeremy M. 2011. A shift toward birthing relatively large infants early in human evolution. *Proceedings of the National Academy of Sciences of the USA* 108(3):1022–1027. doi:10.1073/pnas.1003865108.

DeSilva, Jeremy M., Bernhard Zipfel, Adam P. Van Arsdale, and Matthew W. Tocheri. 2010. The Olduvai Hominid 8 foot: adult or subadult? *Journal of Human Evolution* 58:418–423. [JD]

de Sousa, Alexandra, and Eugénia Cunha. 2012. Hominins and the emergence of the modern human brain. *Progress in Brain Research* 195:293–322. doi:10.1016/B978-0-444-53860-4.00014-3.

Domínguez-Rodrigo, Manuel. 1997. Meat-eating by early hominids at the FLK 22 *Zinjanthropus* site, Olduvai Gorge (Tanzania): an experimental approach using cut-mark data. *Journal of Human Evolution* 33(6):669–690. doi:10.1006/jhev.1997.0161.

Dunbar, Robin I. M. 1998. The social brain hypothesis. *Evolutionary Anthropology* 6:178–190.

Efron, Bradley, and Robert Tibshirani. 1993. *An introduction to the bootstrap*. New York: Chapman & Hall.

Falconer, Douglas S., and Trudy F. C. Mackay. 1996. *Introduction to quantitative genetics*. 4th edition. Essex: Longman.

Ferraro, Joseph V., Thomas W. Plummer, Briana L. Pobiner, James S. Oliver, Laura C. Bishop, David R. Braun, Peter W. Ditchfield, et al. 2013. Earliest archaeological evidence of persistent hominin carnivory. *PLoS ONE* 8(4): e62174. doi:10.1371/journal.pone.0062174.s008.

Finarelli, John A., and John J. Flynn. 2009. Brain-size evolution and sociality in carnivora. *Proceedings of the National Academy of Sciences of the USA* 106(23):9345–9349. doi:10.1073/pnas.0901780106.

Fonseca-Azevedo, Karina, and Suzana Herculano-Houzel. 2012. Metabolic constraint imposes tradeoff between body size and number of brain neurons in human evolution. *Proceedings of the National Academy of Sciences of the USA* 109(45):18571–18576. doi:10.1073/pnas.1206390109.

Frayer, David W. 1981. Body size, weapon use, and natural selection in the European Upper Paleolithic and Mesolithic. *American Anthropologist* 83(1): 57–73.

Fuller, John L. 1979. Fuller BWS lines: history and results. In *Development and evolution of brain size*. Martin E. Hahn, Craig Jensen, and Bruce C. Dudek, eds. Pp. 187–204. New York: Academic Press.

Gabunia, Leo, Abesalom Vekua, David Lordkipanidze, Carl C. Swisher III, Reid Ferring, Antje Justus, Medea Nioradze, et al. 2000. Earliest Pleistocene hominid cranial remains from Dmanisi, Republic of Georgia: taxonomy, geological setting, and age. *Science* 288(5468):1019–1025.

Gonzalez-Voyer, Alejandro, Svante Winberg, and Niclas Kolm. 2009. Distinct evolutionary patterns of brain and body size during adaptive radiation. *Evolution* 63(9):2266–2274. doi:10.1111/j.1558-5646.2009.00705.x.

Goswami, Anjali. 2006. Morphological integration in the carnivoran skull. *Evolution* 60(1):169–183. [BC/DR/GM]

Gould, S. J. 1975. Allometry in primates, with emphasis on scaling and the evolution of the brain. *Contributions to Primatology* 5:244–292. [SN]

Grabowski, Mark, Kevin G. Hatala, William L. Jungers, and Brian G. Richmond. 2015. Body mass estimates of hominin fossils and the evolution of human body size. *Journal of Human Evolution* 85:75–93. doi:10.1016/j.jhevol.2015.05.005.

Grabowski, Mark, and Charles C. Roseman. 2015. Complex and changing patterns of natural selection explain the evolution of the human hip. *Journal of Human Evolution* 85:94–110.

Grabowski, Mark, Kjetil L. Voje, and Thomas F. Hansen. Forthcoming. Evolutionary model testing and correcting for observation error support a 3/5 brain-body scaling for primates. *Journal of Human Evolution*. doi:10.1016/j.jhevol.2016.03.001.

Grabowski, Mark W. 2013. Hominin obstetrics and the evolution of constraints. *Evolutionary Biology* 40:57–75. doi:10.1007/s11692-012-9174-7.

Grabowski, Mark W., John D. Polk, and Charles C. Roseman. 2011. Divergent patterns of integration and reduced constraint in the human hip and the origins of bipedalism. *Evolution* 65(5):1336–1356. doi:10.1111/j.1558-5646.2011.01226.x.

Hadfield, J. D., and S. Nakagawa. 2010. General quantitative genetic methods for comparative biology: phylogenies, taxonomies and multi-trait models for continuous and categorical characters. *Journal of Evolutionary Biology* 23(3):494–508. doi:10.1111/j.1420-9101.2009.01915.x.

Hadfield, J. D., D. S. Richardson, and T. Burke. 2006. Towards unbiased parentage assignment: combining genetic, behavioural and spatial data in a Bayesian framework. *Molecular Ecology* 15(12):3715–3730. doi:10.1111/j.1365-294X.2006.03050.x.

Hager, Reinmar, Lu Lu, Glenn D. Rosen, and Robert W. Williams. 2012. Genetic architecture supports mosaic brain evolution and independent brain-body size regulation. *Nature Communications* 3:1079. doi:10.1038/ncomms2086.

Haile-Selassie, Yohannes, Bruce M. Latimer, Mulugeta Alene, Alan L. Deino, Luis Gibert, Stephanie M. Melillo, Beverly Z. Saylor, Gary R. Scott, and C. Owen Lovejoy. 2010. An early *Australopithecus afarensis* postcranium from Woranso-Mille, Ethiopia. *Proceedings of the National Academy of Sciences of the USA* 107(27):12121–12126. doi:10.1073/pnas.1004527107.

Hansen, T. F., and D. Houle. 2008. Measuring and comparing evolvability and constraint in multivariate characters. *Journal of Evolutionary Biology* 21(5):1201–1219. doi:10.1111/j.1420-9101.2008.01573.x.

Hawkes, K., J. F. O'Connell, N. G. Blurton Jones, H. Alvarez, and E. L. Charnov. 1998. Grandmothering, menopause, and the evolution of human life histories. *Proceedings of the National Academy of Sciences of the USA* 95(3):1336–1339.

Hawks, John. 2011. Selection for smaller brains in Holocene human evolution. arXiv:1102.5604. [JD]

Henneberg, Maciej. 1988. Decrease of human skull size in the Holocene. *Human Biology* 60:395–405. [SN]

Herculano-Houzel, Suzana, Christine E. Collins, Peiyan Wong, and Jon H. Kaas. 2007. Cellular scaling rules for primate brains. *Proceedings of the National Academy of Sciences of the USA* 104(9):3562–3567. doi:10.1073/pnas.0611396104.

Herculano-Houzel, Suzana, Paul R. Manger, and Jon H. Kaas. 2014. Brain scaling in mammalian evolution as a consequence of concerted and mosaic changes in numbers of neurons and average cell size. *Frontiers in Neuroanatomy* 8:77. [SH-H]

Herculano-Houzel, Suzana, Débora J. Messeder, Karina Fonseca-Azevedo, and Nilma A. Pantoja. 2015. When larger brains do not have more neurons: increased numbers of cells are compensated by decreased average cell size across mouse individuals. *Frontiers in Neuroanatomy* 9:1–12. doi:10.3389/fnana.2015.00064.

Hereford, Joe, Thomas F. Hansen, and David Houle. 2004. Comparing strengths of directional selection: how strong is strong? *Evolution* 58(10): 2133–2143. doi:10.1111/j.0014-3820.2004.tb01592.x.

Holloway, Ralph L., Douglas C. Broadfield, and Michael S. Yuan. 2004. *Brain endocasts: the paleoneurological evidence*, vol. 3 of *The human fossil record*. Hoboken, NJ: Wiley.

Hublin, Jean-Jacques, Simon Neubauer, and Philipp Gunz. 2015. Brain ontogeny and life history in Pleistocene hominins. *Philosophical Transactions of the Royal Society B: Biological Sciences* 370:20140062. [SN]

Isler, Karin, E. Christopher Kirk, Joseph M. A. Miller, Gene A. Albrecht, Bruce R. Gelvin, and Robert D. Martin. 2008. Endocranial volumes of primate species:

scaling analyses using a comprehensive and reliable data set. *Journal of Human Evolution* 55(6):967–978. doi:10.1016/j.jhevol.2008.08.004.

Isler, Karin, and Carel P. Van Schaik. 2012. How our ancestors broke through the gray ceiling. *Current Anthropology* 53(suppl. 6):S453–S465. doi:10.1086/667623.

Jerison, Harry J. 1973. *Evolution of the brain and intelligence*. New York: Academic Press.

Johanson, D. C., and T. D. White. 1979. A systematic assessment of early African hominids. *Science* 203(4378):321–330.

Jolicoeur, P., G. Baron, and T. Cabana. 1988. Cross-sectional growth and decline of human stature and brain weight in 19th-century Germany. *Growth, Development, and Aging* 52(4):201–206.

Jones, Adam G., Stevan J. Arnold, and Reinhard Bürger. 2003. Stability of the **G**-matrix in a population experiencing pleiotropic mutation, stabilizing selection, and genetic drift. *Evolution* 57(8):1747–1760. [BC/DR/GM]

Jorgensen, Jørgen Balslev, Erling Paridon, and Flemming Quaade. 1961. The correlation between external cranial volume and brain volume. *American Journal of Physical Anthropology* 19:317–320.

Jungers, William L., and Randall L. Susman. 1984. Body size and skeletal allometry in African apes. In *The pygmy chimpanzee*. Randall L. Susman, ed. Pp. 131–177. New York: Springer.

Kaur, D. P., and R. Singh. 1981. Parent-adult offspring correlations and heritability of body measurements in a rural Indian population. *Annals of Human Biology* 8(4):333–339.

Kruuk, Loeske E. B., Jon Slate, and Alastair J. Wilson. 2008. New answers for old questions: the evolutionary quantitative genetics of wild animal populations. *Annual Review of Ecology, Evolution, and Systematics* 39:525–548. doi:10.1146/annurev.ecolsys.39.110707.173542.

Kubo, Daisuke, Reiko T. Kono, and Yousuke Kaifu. 2013. Brain size of *Homo floresiensis* and its evolutionary implications. *Proceedings of the Royal Society B: Biological Sciences* 280(1760):20130338. doi:10.1016/j.jhevol.2008.08.015.

Kuzawa, Christopher W., Harry T. Chugani, Lawrence I. Grossman, Leonard Lipovich, Otto Muzik, Patrick R. Hof, Derek E. Wildman, Chet C. Sherwood, William R. Leonard, and Nicholas Lange. 2014. Metabolic costs and evolutionary implications of human brain development. *Proceedings of the National Academy of Sciences of the USA* 111(36):13010–13015. doi:10.1073/pnas.1323099111.

Lande, Russell. 1979. Quantitative genetic analysis of multivariate evolution, applied to brain : body size allometry. *Evolution* 33(1):402–416.

Lande, Russell, and Stevan J. Arnold. 1983. The measurement of selection on correlated characters. *Evolution* 37(6):1210–1226.

Leakey, Meave G., Fred Spoor, M. Christopher Dean, Craig S. Feibel, Susan C. Antón, Christopher Kiarie, and Louise N. Leakey. 2012. New fossils from Koobi Fora in northern Kenya confirm taxonomic diversity in early *Homo*. *Nature* 488:201–204. [SN]

Leigh, Steven R. 2012. Brain size growth and life history in human evolution. *Evolutionary Biology* 39(4):587–599. doi:10.1007/s11692-012-9168-5.

Lofsvold, David. 1986. Quantitative genetics of morphological differentiation in *Peromyscus*. I. Tests of the homogeneity of genetic covariance structure among species and subspecies. *Evolution* 40(3):54–67. [BC/DR/GM]

Lordkipanidze, David, Marcia S. Ponce de León, Ann Margvelashvili, Yoel Rak, G. Philip Rightmire, Abesalom Vekua, and Christoph P. E. Zollikofer. 2013. A complete skull from Dmanisi, Georgia, and the evolutionary biology of early *Homo*. *Science* 342(6156):326–331. doi:10.1126/science.1238484.

Lovejoy, C. Owen, Gen Suwa, Scott W. Simpson, Jay H. Matternes, and Tim D. White. 2009. The great divides: *Ardipithecus ramidus* reveals the postcrania of our last common ancestors with African apes. *Science* 326(5949):73–106. doi:10.1126/science.1175833.

Lynch, Michael, and Bruce Walsh. 1998. *Genetics and analysis of quantitative traits*. Sunderland, MA: Sinauer.

MacLean, Evan L., Brian Hare, Charles L. Nunn, Elsa Addessi, Federica Amici, Rindy C. Anderson, Filippo Aureli, et al. 2014. The evolution of self-control. *Proceedings of the National Academy of Sciences of the USA* 111(20):E2140–E2148. doi:10.1073/pnas.1323533111.

Marroig, G., M. de Vivo, and J. M. Cheverud. 2004. Cranial evolution in sakis (*Pithecia*, Platyrrhini). II. Evolutionary processes and morphological integration. *Journal of Evolutionary Biology* 17(1):144–155. doi:10.1046/j.1420-9101.2003.00653.x.

Marroig, Gabriel, and James M. Cheverud. 2001. A comparison of phenotypic variation and covariation patterns and the role of phylogeny, ecology, and ontogeny during cranial evolution of new world monkeys. *Evolution* 55(12):2576–2600. [BC/DR/GM]

———. 2004. Did natural selection or genetic drift produce the cranial diversification of Neotropical monkeys? *American Naturalist* 163(3):417–428. doi:10.1086/381693.

Marroig, Gabriel, Diogo A. R. Melo, and Guilherme Garcia. 2012. Modularity, noise, and natural selection. *Evolution* 66(5):1506–1524. doi:10.1111/j.1558-5646.2011.01555.x.

Marroig, Gabriel, Leila T. Shirai, Arthur Porto, Felipe B. de Oliveira, and Valderes De Conto. 2009. The evolution of modularity in the mammalian skull. II. Evolutionary consequences. *Evolutionary Biology* 36(1):136–148. doi:10.1007/s11692-009-9051-1.

Martin, R. D. 1981. Relative brain size and basal metabolic rate in terrestrial vertebrates. *Nature* 293(5827):57–60.

———. 1983. Human brain evolution in an ecological context. 52nd James Arthur Lecture on the Evolution of the Human Brain. American Museum of Natural History, New York. [SN]

McHenry, Henry M. 1992. Body size and proportions in early hominids. *American Journal of Physical Anthropology* 87:407–431. [JD]

McHenry, Henry M., and Lee R. Berger. 1998. Body proportions in *Australopithecus afarensis* and *A. africanus* and the origin of the genus *Homo*. *Journal of Human Evolution* 35:1–22. [JD]

McHenry, Henry M., and Katherine Coffing. 2000. *Australopithecus* to *Homo*: transformations in body and mind. *Annual Review of Anthropology* 29:125–146. doi:10.1146/annurev.anthro.29.1.125.

Mink, Jonathan W., Robert J. Blumenschine, and David B. Adams. 1981. Ratio of central nervous system to body metabolism in vertebrates: its constancy and functional basis. *American Journal of Physiology* 241(3):R203–R212.

Montgomery, Stephen H., Isabella Capellini, Robert A. Barton, and Nicholas I. Mundy. 2010. Reconstructing the ups and downs of primate brain evolution: implications for adaptive hypotheses and *Homo floresiensis*. *BMC Biology* 8(1):9. doi:10.1186/1741-7007-8-9.

Montgomery, Stephen H., Jonathan H. Geisler, Michael R. McGowen, Charlotte Fox, Lori Marino, and John Gatesy. 2013. The evolutionary history of cetacean brain and body size. *Evolution* 67(11):3339–3353. doi:10.1111/evo.12197.

Moyà-Solà, Salvador, Meike Köhler, David M. Alba, and Sergio Almécija. 2008. Taxonomic attribution of the Olduvai Hominid 7 manual remains and the functional interpretation of hand morphology in robust australopithecines. *Folia Primatologica* 79:215–250. [JD]

Nakatsukasa, Masato, Martin Pickford, Naoko Egi, and Brigitte Senut. 2007. Femur length, body mass, and stature estimates of *Orrorin tugenensis*, a 6 Ma hominid from Kenya. *Primates* 48(3):171–178. doi:10.1007/s10329-007-0040-7.

Neubauer, Simon, Philipp Gunz, Gerhard W. Weber, and Jean-Jacques Hublin. 2012. Endocranial volume of *Australopithecus africanus*: new CT-based estimates and the effects of missing data and small sample size. *Journal of Human Evolution* 62(4):498–510. doi:10.1016/j.jhevol.2012.01.005.

O'Connell, J. F., K. Hawkes, and N. G. Blurton Jones. 1999. Grandmothering and the evolution of *Homo erectus*. *Journal of Human Evolution* 36(5):461–485.

Osborne, Robert Travis. 1980. *Twins: black and white*. Athens, GA: Foundation for Human Understanding.

Pavlicev, Mihaela, James M. Cheverud, and Günter P. Wagner. 2011. Evolution of adaptive phenotypic variation patterns by direct selection for evolvability. *Proceedings of the Royal Society B: Biological Sciences* 278(1713):1903–1912. doi:10.1098/rspb.2010.2113.

Pontzer, Herman. 2012. Ecological energetics in early *Homo*. *Current Anthropology* 53(suppl. 6):S346–S358. doi:10.1086/667402.

Pontzer, Herman, Campbell Rolian, G. Philip Rightmire, Tea Jashashvili, Marcia S. Ponce de León, David Lordkipanidze, and Christoph P. E. Zollikofer. 2010. Locomotor anatomy and biomechanics of the Dmanisi hominins. *Journal of Human Evolution* 58(6):492–504. doi:10.1016/j.jhevol.2010.03.006.

Porto, A., H. Sebastião, S. E. Pavan, J. L. VandeBerg, G. Marroig, and J. M. Cheverud. 2015. Rate of evolutionary change in cranial morphology of the marsupial genus *Monodelphis* is constrained by the availability of additive genetic variation. *Journal of Evolutionary Biology* 28(4):973–985. [BC/DR/GM]

Porto, Arthur, Felipe B. de Oliveira, Leila T. Shirai, Valderes De Conto, and Gabriel Marroig. 2009. The evolution of modularity in the mammalian skull. I. Morphological integration patterns and magnitudes. *Evolutionary Biology* 36(1):118–135. doi:10.1007/s11692-008-9038-3.

Riska, Bruce, and William R. Atchley. 1985. Genetics of growth predict patterns of brain-size evolution. *Science* 229(4714):668–671. doi:10.1126/science.229.4714.668.

Roach, Neil T., Madhusudhan Venkadesan, Michael J. Rainbow, and Daniel E. Lieberman. 2014. Elastic energy storage in the shoulder and the evolution of high-speed throwing in *Homo*. *Nature* 498(7455):483–486. doi:10.1038/nature12267.

Roderick, Thomas H. 1979. Genetic techniques as tools for analysis of brain-behavior relationships. In *Development and evolution of brain size*. Martin E. Hahn, Craig Jensen, and Bruce C. Dudek, eds. Pp. 133–145. New York: Academic Press.

Roderick, Thomas H., Richard E. Wimer, and Cynthia C. Wimer. 1976. Genetic manipulation of neuroanatomical traits. In *Knowing, thinking and believing*. L. Petrinovich and J. L. McGaugh, eds. Pp. 143–178. New York: Plenum.

Roff, Derek A. 1995. The estimation of genetic correlations from phenotypic correlations: a test of Cheverud's conjecture. *Heredity* 74(5):481–490.

———. 1996. The evolution of genetic correlations: an analysis of patterns. *Evolution* 50(4):1392–1403.

Rolian, Campbell, Daniel E. Lieberman, and Benedikt Hallgrimsson. 2010. The coevolution of human hands and feet. *Evolution* 64(6):1558–1568. doi:10.1111/j.1558-5646.2010.00944.x.

Roseman, Charles C. 2012. The soundness of the Cheverud conjecture and its implications for the study of human evolution. *American Journal of Physical Anthropology* 147(S54):252.

Ruff, Christopher B., Erik Trinkaus, and Trenton W. Holliday. 1997. Body mass and encephalization in Pleistocene *Homo*. *Nature* 387(6629):173–176. doi:10.1038/387173a0.

Ruff, Christopher B., Erik Trinkaus, Alan Walker, and Clark Spencer Larsen. 1993. Postcranial robusticity in *Homo*. I. Temporal trends and mechanical interpretation. *American Journal of Physical Anthropology* 91(1):21–53. doi:10.1002/ajpa.1330910103.

Sharma, K., P. J. Byard, J. M. Russell, and D. C. Rao. 1984. A family study of anthropometric traits in a Punjabi community. I. Introduction and familial correlations. *American Journal of Physical Anthropology* 63(4):389–395. doi:10.1002/ajpa.1330630406.

Sharma, K., and J. C. Sharma. 1984. Familial resemblance for head size in a Punjabi population of India. *Annals of Human Biology* 11(6):577–580.

Shea, Brian T. 1983. Allometry and heterochrony in the African apes. *American Journal of Physical Anthropology* 62(3):275–289. doi:10.1002/ajpa.1330620307.

———. 1984. An allometric perspective on the morphological and evolutionary relationships between pygmy (*Pan paniscus*) and common (*Pan troglodytes*) chimpanzees. In *The pygmy chimpanzee*. Randall L. Susman, ed. Pp. 89–130. New York: Springer.

Shipman, Pat. 1986. Scavenging or hunting in early hominids: theoretical framework and tests. *American Anthropologist* 88(1):27–43.

Skelton, Randall R., and Henry M. McHenry. 1992. Evolutionary relationships among early hominids. *Journal of Human Evolution* 23(4):309–349.

Skinner, Matthew M., and Bernard Wood. 2006. The evolution of modern human life history. In *The evolution of human life history*. Kristen Hawkes and Richard R. Paine, eds. Pp. 331–400. Santa Fe, NM: School of American Research.

Smaers, Jeroen B., Dina K. N. Dechmann, Anjali Goswami, Christophe Soligo, and Kamran Safi. 2012. Comparative analyses of evolutionary rates reveal different pathways to encephalization in bats, carnivorans, and primates. *Proceedings of the National Academy of Sciences of the USA* 109(44):18006–18011. doi:10.1073/pnas.1212181109.

Smith, Richard J., and William L. Jungers. 1997. Body mass in comparative primatology. *Journal of Human Evolution* 32(6):523–559. doi:10.1006/jhev.1996.0122.

Sponheimer, Matt, Zeresenay Alemseged, Thure E. Cerling, Frederick E. Grine, William H. Kimbel, Meave G. Leakey, Julia A. Lee-Thorp, et al. 2013. Isotopic evidence of early hominin diets. *Proceedings of the National Academy of Sciences of the USA* 110(26):10513–10518. doi:10.1073/pnas.1222579110.

Spoor, F., M. G. Leakey, P. N. Gathogo, F. H. Brown, S. C. Antón, I. McDougall, C. Kiarie, F. K. Manthi, and L. N. Leakey. 2007. Implications of new early *Homo* fossils from Ileret, east of Lake Turkana, Kenya. *Nature* 448(7154):688–691. doi:10.1038/nature05986.

Spoor, Fred, Philipp Gunz, Simon Neubauer, Stefanie Stelzer, Nadia Scott, Amandus Kwekason, and M. Christopher Dean. 2015. Reconstructed *Homo habilis* type OH 7 suggests deep-rooted species diversity in early *Homo*. *Nature* 519(7541):83–86. doi:10.1038/nature14224.

Steppan, Scott J., Patrick C. Phillips, and David Houle. 2002. Comparative quantitative genetics: evolution of the **G** matrix. *Trends in Ecology and Evolution* 17(7):320–327.

Strait, David S., Frederick E. Grine, and Marc A. Moniz. 1997. A reappraisal of early hominid phylogeny. *Journal of Human Evolution* 32(1):17–82.

Stringer, Chris. 2012. The status of *Homo heidelbergensis* (Schoetensack 1908). *Evolutionary Anthropology* 21(3):101–107. doi:10.1002/evan.21311.

Susman, Randall L. 2008. Brief communication: evidence bearing on the status of *Homo habilis* at Olduvai Gorge. *American Journal of Physical Anthropology* 137:356–361. [JD]

Susman, Randall L., and Jack T. Stern. 1982. Functional morphology of *Homo habilis*. *Science* 217(4563):931–934. [JD]

Suwa, Gen, Berhane Asfaw, Reiko T. Kono, Daisuke Kubo, C. Owen Lovejoy, and Tim D. White. 2009. The *Ardipithecus ramidus* skull and its implications for hominid origins. *Science* 326:68. doi:10.1126/science.1175825.

Tinbergen, N. 1963. On aims and methods of ethology. *Zeitschrift für Tierpsychologie* 20:410–433. doi:10.1163/157075605774840941.

Tocheri, Matthew W., Caley M. Orr, Marc C. Jacofsky, and Mary W. Marzke. 2008. The evolutionary history of the hominin hand since the last common ancestor of *Pan* and *Homo*. *Journal of Anatomy* 212:544–562. [JD]

Weaver, Timothy D., Charles C. Roseman, and Chris B. Stringer. 2007. Were Neandertal and modern human cranial differences produced by natural selection or genetic drift? *Journal of Human Evolution* 53(2):135–145. doi:10.1016/j.jhevol.2007.03.001.

Weston, Eleanor M., and Adrian M. Lister. 2009. Insular dwarfism in hippos and a model for brain size reduction in *Homo floresiensis*. *Nature* 459(7243):85–88. doi:10.1038/nature07922.

Willis, John H., Jerry A. Coyne, and Mark Kirkpatrick. 1991. Can one predict the evolution of quantitative characters without genetics? *Evolution* 45(2):441–444.

Wimer, Cynthia. 1979. Correlates of mouse brain weight: search for component morphological traits. In *Development and evolution of brain size*. Martin E. Hahn, Craig Jensen, and Bruce C. Dudek, eds. Pp. 147–162. New York: Academic Press.

Wood, Bernard. 1992. Origin and evolution of the genus *Homo*. *Nature* 355(6363):783–790. doi:10.1038/355783a0.

Wood, Bernard, and Mark Collard. 1999. The human genus. *Science* 284:65–71. [SN]

Wood, Bernard, and Nicholas Lonergan. 2008. The hominin fossil record: taxa, grades and clades. *Journal of Anatomy* 212:354–376. [SN]

Wood, Bernard, and Brian G. Richmond. 2000. Human evolution: taxonomy and paleobiology. *Journal of Anatomy* 197:19–60.

Wynn, Jonathan G., Matt Sponheimer, William H. Kimbel, Zeresenay Alemseged, Kaye Reed, Zelalem K. Bedaso, and Jessica N. Wilson. 2013. Diet of *Australopithecus afarensis* from the Pliocene Hadar Formation, Ethiopia. *Proceedings of the National Academy of Sciences of the USA* 110(26):10495–10500. doi:10.1073/pnas.1222559110.

Young, Nathan M., Gunter P. Wagner, and Benedikt Hallgrimsson. 2010. Development and the evolvability of human limbs. *Proceedings of the National Academy of Sciences of the USA* 107(8):3400–3405. doi:10.1073/pnas.0911856107.

Zollikofer, Christoph P. E., Marcia S. Ponce de León, Daniel E. Lieberman, Franck Guy, David Pilbeam, Andossa Likius, Hassane T. Mackaye, Patrick Vignaud, and Michel Brunet. 2005. Virtual cranial reconstruction of *Sahelanthropus tchadensis*. *Nature* 434(7034):755–759. doi:10.1038/nature03397.