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Two interpretations of human evolution: Essentialism and Darwinism

Maciej Henneberg

Biological Anthropology and Comparative Anatomy Research Unit, University of Adelaide, Adelaide 5005, and Department of Archaeology, Flinders University Australia; E-mail: Maciej.Henneberg@adelaide.edu.au

ABSTRACT   Despite intensive studies of a large number of fossils discovered during the 20th century there is no consensus as to the interpretation of the process of hominin evolution. Some authors see as many as six genera and some 17 species, while others argue for a single lineage from Plio/Pleistocene until today. Such diversity of interpretations of the same facts indicates lack of a uniform theoretical basis underlying studies of human evolution. Debates can be resolved using basic principles of scientific inquiry – parsimony and falsification of null hypotheses. Hypothesis testing is now possible with respect to the evolution of basic hominin characteristics such as brain size, body size and the size of the dentition that have sample sizes of a few hundred individual data points each. These characters display a continuous change with time. Analyses of variance do not falsify the null hypothesis of the existence of only one species at any time – variances around regression lines on time do not differ from the variance observed in the single species of Homo sapiens – distributions of residuals are normal. Thus, splitting of the hominin lineage into coeval species can only be based on descriptive characteristics that are liable to errors of subjective judgment.

KEY WORDS: hominin, hominid, *Australopithecus*, brain, stature

Understanding of the evolutionary process that produced modern humans is of crucial importance for the way people perceive themselves and their lives. It informs ideologies underlying political and economic decisions. Thus it is important to have this process documented and interpreted in accordance with the best rules of scientific practice. Despite over 150 years of studies of human evolution, debates on how our major traits – such as mental capacities and erect bipedal locomotion – emerged are still ongoing [Carruthers and Chamberlain 2000, Cela-Conde and Ayala 2007]. The number of validly named human species by the end of the 20th century exceeded 50 [Meikle and Parker 1994, Henneberg 1997], while it has been proposed that an even larger number should be identified [Tattersall 1987] and actually

has recently [Brown *et al.* 2004]. It does not add, though, to the clarity of the picture of our origins.

Over the last half-century several authors proposed that the parsimony and falsification of hypotheses should be applied to studies of human evolution postulating a "single species hypothesis" [Brace 1967; Wolpoff 1968, 1971]. According to Hunt [2003], Frank Livingstone proclaimed himself to be the proponent of single species hypothesis still at the beginning of the 21st century. Kevin Hunt himself argues strongly in support of the single species hypothesis using data on taxonomic diversity of large-bodied genera of mammals. Recently Holliday [2003] proposed an intermediate interpretation of hominid diversity. He used the notion of syngameon which is a network of separate cohesive taxa that exchange genes among themselves. He supported this interpretation with observations of gene flow among several species of the two genera of baboons – *Theropithecus* and *Papio* – [Jolly 1993, 2001; Jolly *et al.* 1997]. Quintyn [2009] summarized current discussions concerning hominin diversity and concluded that a temporary ban on creating new hominin taxa should be imposed until a clearer understanding of hominin variation can be reached.

Taxonomy, essentialism and the concept of species

To make sense of the variety of forms that surround us we must be able to reduce it to a manageable number of generalizing categories that can then be used in various thought processes. Thus, the human tendency to categorize: From the time platonic idealism arose in classical antiquity to the early enlightenment, the task of naturalists was perceived as that of discovering the ideal pattern of the world of living things, the "pattern of creation". Similarities among individuals were used to distil essences of ideal types of their respective kinds and those types were then organized into nested hierarchies of species, genera, families, classes, orders, phyla, etc. [Linnaeus 1758]. Thus, conceptually, the smallest unit of life was a species, not an individual. An individual was but an example of an ideal species type. Individual variation was consciously ignored for the sake of clarity. Once described, taxa became units of study for biologists. Discussions about the complexity of life in a particular region or the entire world were based on the number of species and higher taxa present in various environments, the interactions still being studied as those between particular taxa, while descriptions of evolution consist of biblical lists of who is a descendant of whom and what the family tree looks like [Henry and Wood 2007, Stanford *et al.* 2009].

As an example, following a suggestion by Robert Eckhardt:

And unto Enoch was born Irad: and Irad begat Mehujael: and Mehujael begat Methushael; and Methushael begat Lamech [*Genesis* 4:18, 1611].

Homo erctus is descended from *Homo habilis*, which in turn descended from *Australopithecus garhi* ... [Larsen 2008].

Figure 1 is an example of the classic representation of a hominin family tree. Such representation may be as well reflecting a pattern of creation. No explanations of how and why particular branches arose are given. No uncertainty as to possible mixing of categories is indicated, nor is there uncertainty indicated in separating some categories from others.

Taxa are perceived as real entities and they can only have two states: existence or
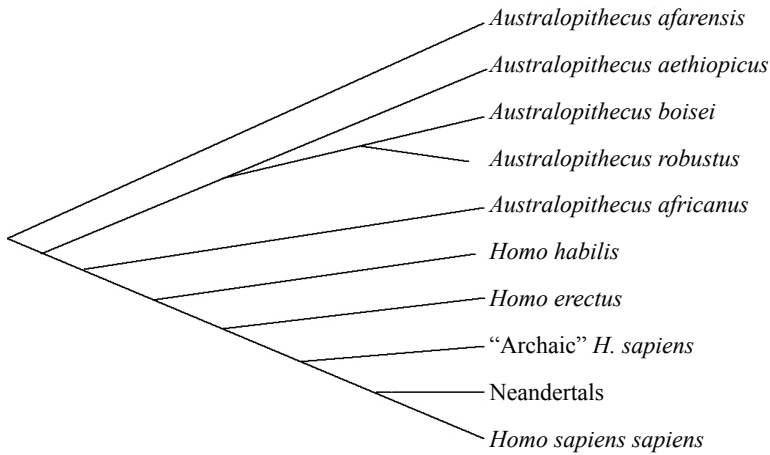
Fig. 1. Scheme originally published on page xxix of the Encyclopedia of Human Evolution and Prehistory [Tattersall *et al.* 1988] and repeated with modification in the second edition [Delson *et al.* 2000], author's own drawing. This is not evolution, this is systematics. It may as well be a "pattern of creation".

extinction; categorically yes or no. Such an approach, though producing voluminous descriptions, cannot provide explanations of the process of evolution since evolutionary mechanisms are based on individual variation and transmission of this variation from one generation of individuals to the next. It can be argued that before we can analyze anything and search for processual explanations, we must first provide a solid description. Such description, however, must be in terms that lend themselves to further productive analysis. In biology, the use of arbitrarily and sharply delimited categories is not conducive to productive analysis. It leads rather to "catastrophic" explanations in the style of George Cuvier [Brace 1981]. Taxonomic descriptions may be useful in certain applications, such as ecology, but the fact that they ignore individuals and the flow of time from generation to generation is always a limiting factor.

Currently there exist some 23 definitions of species [Mayden 1997, Quintyn 2009]. They all attempt to "salvage a Linnean rank"

[Lee 2003] in the face of the overwhelming understanding that life is variable and no stable categories actually exist. Following Lee [2003], current concepts of species can be subdivided into (1) similarity concepts using phenetic resemblance of organisms as the sole criterion, (2) cohesion concepts in which organisms are purported to share features allowing them to remain coherent from generation to generation, (3) monophyly concepts stressing membership of a single nonreticulating lineage, and (4) interbreeding concepts in which members of a species exchange genes among themselves while being reproductively isolated from others. Concepts belonging to the first three groups are valid for any taxonomic rank, not being specific to species. Depending on how strictly one defines phenetic similarity, level of cohesion or monophyletic inclusiveness, one can define supraspecific taxa (like genus) or infraspecific groupings (like races). The interbreeding concepts emphasize that actual exchange of genetic material occurs only within a species [Mayr 1969,

1995], a phenomenon which is unique to this taxonomic rank and making it the only "real" supraindividual biological unit. This is the unit of evolution because it is in the process of differential reproduction of populations isolated genetically from other populations that the adaptive change in gene pool can occur. The phylogenetic species concept stresses the same phenomenon of reproductive continuity, but from a point of view of change through time – all descendants of a particular ancestor are a taxon [Velasco 2009]. A specific variety of this approach is the genomic-phylogenetic species concept [Staley 2009] inferring evolution of an organism from sequences of its genes.

In all definitions, however, boundaries of species are imprecise because reproductive isolation is often incomplete with inter-species gene flow occurring at various rates, while it takes a minimum of three-generations for a monophyletic lineage (phylogenetic species) to separate from others [Samadi and Barberousse 2009]. In this situation, an audacious solution to the removal of the ambiguity inherent in the biological species concept has been proposed. Gonzalez-Forero [2009] postulates that in situations of relaxed reproductive isolation, some populations should be considered members of more than one species. This should be reflected in their trinomial nomenclature. An example relating to hominins would be *Homo neanderthalensis-sapiens.*

Despite a multitude of theoretical means of reconciling a descriptive platonic category with the current understanding of biology, when dealing with fossil material, only morphological similarity, and morphological variation, are available for study and must be used for testing taxonomic hypotheses. It is impossible to test directly whether a Neandertal man and a modern woman would produce fertile offspring. For a test falsifying a hypothesis of their conspecificity we must rely on secondary inferences derived from comparisons of morphology and partly reconstructed DNA sequences.

Individual variation and Darwinian view of life

In reality, only individuals exist at a particular point in time. Some of them are more similar to each other than to many other individuals. Such similar individuals can be grouped together into a *similum* [Henneberg and Brush 1994, Henneberg 1997] without any prejudice as to their formal taxonomic status. *Simila* are defined solely by mutual similarities of individuals to each other, not by a similarity of individuals to some idealized, immutable type. *Simila* are thus capable of changing continuously through time, while taxa are not because their change requires abrupt appearance of a new ideal type. In most cases of metazoans, observation of individuals over a period of their lives reveals that they mate with other members of the *similum* to produce new individuals who undergo a process of ontogenetic development and growth. During this process individuals change their physical form, physiology and behavior, sometimes to a very large extent. Depending on their sex, individuals may differ so substantially in their characteristics that they may be mistaken for different species [Manning and Dawkins 1998]. In extant organisms it is easy to study ontogenetic processes and assess sexual dimorphism, although it may happen that various ontogenetic stages, or different sexes, may mistakenly be described as separate species [Eckhardt 2000]. Even when ontogenetic

and sexual variations are known, there remains substantial interindividual variation due to both genetic polymorphism and various responses to environmental stimuli during ontogeny. This variation can hardly be categorized.

Brain size, especially when related to body size, is amongst the most prominent defining characteristics of *Homo sapiens.* Yet its variation is very substantial – CV approaches 12% [Henneberg 1990] compared with about 4% for body height and 10% for arm circumference (approximate values calculated from Frisancho [1990] data of anthropometric standards). In absolute figures, the range for modern human cranial capacity extends from 3 standard deviations (SD) below the mean at 879 ml to 3 SD above the mean at 1821 ml [Henneberg 1990]. This is more than double the minimum value. Amongst adults only about one quarter of this variation is explained by sexual dimorphism, another quarter or so can be attributed to differences among populations, while the remaining 50 percent occurs among same-sex individuals in the same population (Fig. 2, Henneberg [1990]). Were we to add variation resulting from ontogenetic doubling in brain size, what seems to be an obvious species-specific "big brain" characteristic would
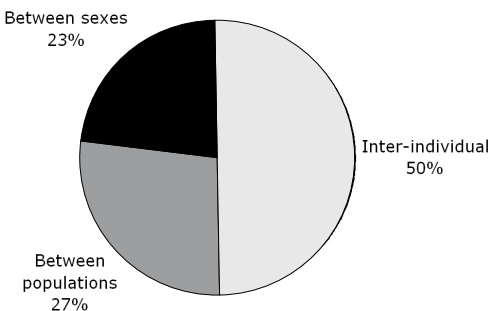
have a range of variation so wide as to be almost worthless for any diagnoses. Over centuries, the variation of brain size is further added to by microevolutionary trends. During the Holocene *Homo sapiens* cranial capacity decreased in size by about 10% from the beginning of this period to its end [Henneberg 1988, 1998] while in the Anthropocene (considered to start in the late 18th century), due to general secular increase in body size, it increased again by about 6% in some countries [Henneberg *et al.* 1985]. Such changes would be undetectable during the Plio/Pleistocene due to technical errors of dating methods that may extend to a few thousand years [Eckhardt 2000].

In paleoanthropology, when individual fossils are found, in most instances it is difficult to be sure of their sex, and their developmental age is sometimes debatable (see uncertainties in the developmental ages of the Taung Child and Nariokotome Boy, Lacruz *et al.* [2005], Walker and Leakey [1993]) and their membership of a particular local population, as opposed to some other one, unknown. Dating methods of Pliocene and Pleistocene fossils have wide error ranges, easily incorporating several hundreds of years during which microevolutionary changes could occur [Eckhardt 2000]. The situation is further complicated by the fragmentary nature of fossils. In this situation, researchers attempt to perform a multivariate assessment based on all traits that can be estimated from a given fossil. It usually takes form of a descriptive and categorical, rather than metrical, analysis and leads to attributing a fossil to an idealized taxon, usually a species. When the multivariate "appearance" of a particular fossil is somewhat different from previously described fossils it is left to an arbitrary decision of researchers whether to assign it to one of the already established "species" or

Fig. 2. Components of variance in the human brain size.

to a new one. The amount of variation that can be tolerated within one species is still debated [Cope and Lacy 1992, 1996; Albrecht and Miller 1993; Kelley 1993; Plavcan 1993; Rose and Bown 1993; Plavcan and Cope 2001; Ackermann *et al.* 2006]. Uncertainties abound, especially because there are so many different definitions of species. The Latin word *specere* means simply "a kind" or "a form", thus anything looking like a new kind or new form of organism can be designated as a new species. Since there are no two organisms that look precisely alike in all details – even identical twins differ somewhat on closer inspection – researchers must judge whether the form of this particular fossil they are trying to classify differs from other similar forms more than expected for members of the same species, or less. Some definitions of species, especially those akin to the Biological Species Concept [Mayr 1969, 1995], allow for the existence of fairly wide ranges of intraspecific variation, while others, such as especially the Phylogenetic Species Concept or morphological species concepts, may consider any "diagnosable" difference as defining a new species, thus narrowing substantially allowable ranges of intraspecific variation [Hennig 1966, Platnick 1977*a,b*, Eldredge and Cracraft 1980, Nelson and Platnick 1981, Mishler and Donoghue 1982, Mishler and Brandon 1987, De Queiroz and Donoghue 1988, Nixon and Wheeler 1990, Kimbel and Rak 1993, Mishler and Theriot 2000]. This increases the arbitrariness of decisions assigning particular specimens to previously known species or to new ones.

Once a new species is created, it replaces a particular specimen, or sample of specimens in consideration of phylogenies, that is, in descriptions of the process of macroevolution. Production of phylogenies does not explain processes of evolution but provides only a static description of its course. A phylogeny is only as good a description of the course of evolution as are the definitions of species and other taxa that are included with it. Were the taxa incorrectly identified, or incorrectly characterized, the description of the process of evolution would be faulty. Thus, any attempts at explanations of evolutionary processes operating during such phylogeny would be incorrect. In common descriptions of hominin evolution many homoplasies are identified, meaning that supposedly the same adaptations evolved separately in various hominin taxa [Holliday 2003, Lieberman *et al.* 1996]. This might be true, accepting correctness of the standard phylogeny, but it might not be true if individuals assigned to separate taxa actually belonged to a single polymorphic species that was evolving as a whole. Then, various individuals of such species are expected to have same adaptations.

Construction of phylogenies based on species that are considered ideal static descriptions of organisms of a particular "kind", imposes on the explanations of transitions from one taxon to the next abrupt, largely unexplainable events in the form of "punctuations" [Eldredge and Gould 1972] rather than adaptive processes based on generation-by-generation reproductive success of some variants over others. The use of platonic ideal entities – immutable species – prevents an understanding of the actual mechanism of evolution and factors that play a role in evolutionary changes. As Charles Darwin [1859: 485] himself remarked "… we shall at least be freed from the vain search for the undiscovered and undiscoverable essence of the term species." He also stated that he does not see any substantial difference between the notion of variety and a species. His explanation

of the way life evolves rests on the observation that individuals are variable, that they are adapted to their living conditions only to a certain degree and that those who happen to be best adapted at a given moment have greater reproductive success than others. Life consists of assemblages of individuals who, though clustering into groups based on mutual similarity, are variable and reproduce with different success that is a measure of their adaptation to momentary conditions. Those conditions change through time and thus midpoints of ranges of variation of individuals shift with the passage of time.

Identification of the human lineage

With regard to human ancestry, researchers are faced with a difficult task that automatically produces a conflict between identification of taxonomic diversity and lineage continuity. The only way to identify human ancestors in the fossil record is to find among assemblages of primate fossils from the Miocene, Pliocene and Pleistocene those skeletal remains that resemble humans more than other primates. As one goes back in time, having already identified human-like fossils at a later date, one can then try to compare even earlier fossils with those later ones and so on. Eventually, one enters the epoch that contains no fossils whose similarity to later putative human ancestors can convincingly be shown. At present, this process has reached back some 6-7 Ma, identifying forms such as *Sahelanthropus chadensis* and *Orrorin tugenensis* as possible earliest hominins (Stanford *et al.* 2009). The necessity to identify fossils somehow similar to those that are similar to humans, while the density of fossil record decreases on going back in time, reduces the reliability of the identification of the earliest human ancestors. For later periods that have more abundant fossil representation, greater number of individual fossils necessarily produces greater variability of morphological characters. This, coupled with the tendency to categorize, and with the common belief that evolution proceeds by emergence of new species, leads most researchers to splitting of the Pliocene and Pleistocene fossil record into numerous species while also recognizing that they can be organized into chronological grades [Henry and Wood 2007]. We are therefore left with a picture of human evolution in which the necessary use of similarities to identify our ancestors and the natural individual, regional, microevolutionary and sexual variation act in opposite directions – reducing and increasing postulated diversity. Disputes regarding detailed morphological, chronological and geographical characteristics of particular fossils can continue interminably, unless some generally accepted method of distinguishing intra-specific variation from inter-specific diversity can be applied.

Quantitative testing of the hypothesis of human lineage

The 20th century produced a large, temporally and geographically widespread fossil record of hominins. Thus, detailed debates regarding small number of individual fossils can be replaced by a generalizing overview using statistical methods of hypotheses testing to resolve the perennial dispute between "lumpers" and "splitters". The approach to testing hypotheses of human evolution should conform to the basic rules of scientific methodology: parsimony and null hypothesis falsification. We should use the commonly accepted approach in which a null hypothesis must be

falsified before alternative hypotheses can be entertained. In the case of fossil documentation of hominin lineage, the null hypothesis that it consisted of one species at each point in time can be reasonably built based on the general consideration of the speciosity of genera of large eurytopic mammals [Conroy 2002, Hunt 2003]. Such genera usually comprise just one or two species. This is true of the hominid genera *Pan, Gorilla* and *Pongo*.

Although the number of hominin fossils is of the order of thousands of specimens, these are fragmentary. Thus sample sizes for determination of their various detailed characteristics can be small. It is practical to analyze for the largest possible number of fossils general characteristics that can be uniformly reconstructed from various parts of skeletal elements. These are: body size and cranial capacity. The latter is still extensively used to characterize various putative hominin species [Wood and Richmond 2000]. One can add to those generalizing characteristics the direct metric characteristics of dentition since teeth preserve well in the fossil record.

The study of variation in some 210 hominin brain sizes, some 205 body size estimates and 915 sizes of dentition [Henneberg and Thackeray 1995; Henneberg and de Miguel 2004; Henneberg 1997, 2006, 2008] invariably shows that there is a gradual change in those characteristics through geological time, that distributions of individual values around regressions describing temporal changes are unimodal, normal and of the magnitude not different from that of a single modern species *Homo sapiens*. The scattergrams of body height, mass and cranial capacity (Fig. 3) illustrate temporal continuity without abrupt changes and branching.
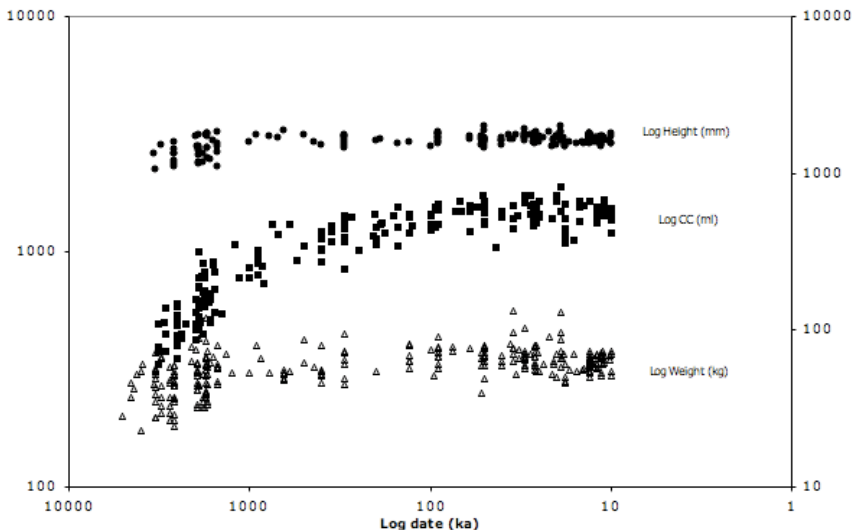
Fig. 3. Body height, mass and cranial capacity of hominins from Pliocene to the end of Pleistocene. All scales logarithmic. Note continuity of distributions and lack of branching. All available in the literature: cranial capacities of adult hominins are used ($N = 209$, as reported by de Miguel and Henneberg [2001], supplemented from more recent literature). Reconstructed body heights and weights of hominins from Mathers and Henneberg [1995] and de Miguel and Henneberg [1999].

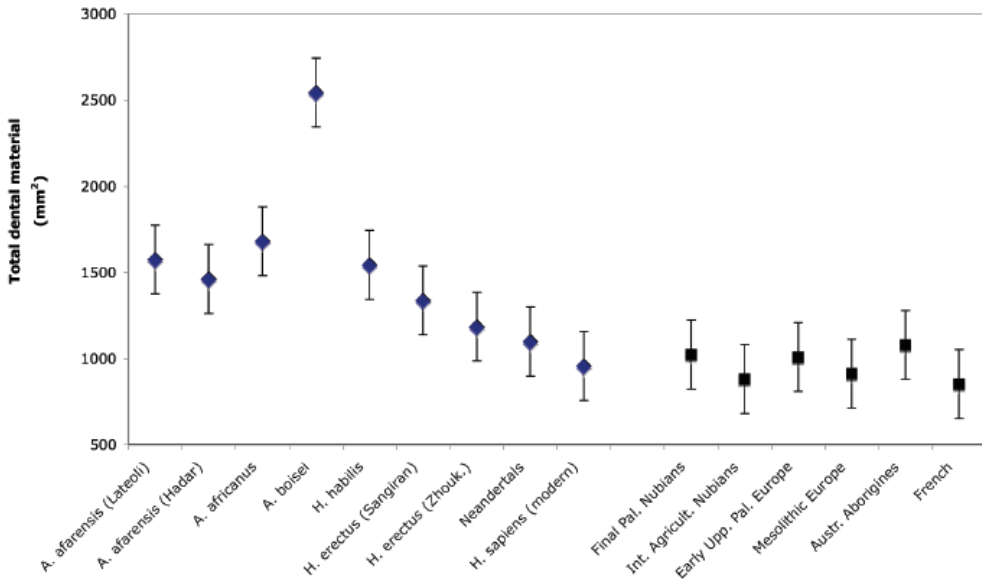Fig. 4. Average total tooth areas for various hominin taxa compared with several averages and 2 standard deviation ranges for various modern human groups. Note that differences between hominin species are of the same order as those between modern human populations. The only exception are robust australopithecines. Data for all australopithecines, *H. habilis*, *H. erectus* and *H. sapiens* (modern) from Tobias [1988], for Neandertals from Brace and Mahler [1971], for Nubians from Calcagno [1989], for Early Upper Palaeolitic and Mesolitic Europe from Frayer [1978], for Australian Aborigines and for French from Brace [1995].

The averages of the "total dental material" [Tobias 1988], that is, the sum of horizontal crown areas of all teeth, of various hominin taxa do not differ more than averages of various modern human groups (Fig. 4) with exception of the robust australopithecines. Since total dental material is a composite variable and difficult to calculate for individuals, its variation can only be estimated. Here we use an SD estimate of approximately 100 mm² derived from Brace *et al.* [1991]. When intervals of 2 SD are built around averages for various groups, most of the variation among hominin taxa averages is included in those intervals (see Fig. 4).

There is only one exception from the pattern of brain and body size change through time in the hominin lineage [Henneberg 2007, Martin 2007]. It is the single, unfossilized skeleton labeled LB1 found, together with isolated bone elements and teeth of a few other humans on the island of Flores, Indonesia in 2003–2004 [Brown *et al.* 2004, Morwood *et al.* 2004, Brumm *et al.* 2006]. Both its body size (1.06 – 1.35 m) and cranial capacity (about 430 ml) fall 3 to 5 SD below the distributions for other hominins of similar dating (Late Pleistocene) while size of the dentition is close to the average. The find has been, and still is, hotly debated as a number of authors proposed that it is a pathologically deformed individual, not a representative of a new species [Henneberg and Thorne 2004, Jacob *et al.* 2006, Weber *et al.* 2005, Hershkovitz *et al.*

2007, Martin *et al.* 2006*a,b*, Obendorf *et al.* 2008]. It has been suggested that its dating is incorrect and it is a modern human [Henneberg and Schofield 2008]. Until this debate is resolved, we can assume that this exception is a result of doubtful attribution rather than a challenge to the general picture of hominin evolution.

The recent description of a large assemblage of 4.4 Ma old fossils of the *Ardipithecus ramidus* [White *et al.* 2009] fits the pattern well. The cranial capacity of 300–350 ml and body height of 1.2 m could be predicted by extrapolating backwards in time the trends already documented (see Fig. 3).

Conclusion: A single variable, adapting lineage

It can be concluded that at no point in time since the late Miocene in the distributions of basic metric characteristics of hominins are there to be found any significant discontinuities, deviations from normality or ranges expanded beyond what is observed in the only living hominin species. Although arguments can be made that upon a study of descriptive characteristics some categorical discontinuities can be detected, the subjective nature of the descriptions makes it difficult to objectively test such arguments. Thus the null hypothesis that hominins are a single lineage cannot be falsified and must be accepted at the present time. This is the most parsimonious and simplest interpretation able to be made. It is also compatible with the way by which hominin ancestors are identified among fossils.

Since the Miocene, we are dealing with populations of interbreeding, geographically widespread ecologically eurytopic [Henneberg 2001] human individuals who, responding to the pressures of natural selection, and later to the forces of artificial selection resulting from self-amplifying feedbacks between human biology, technology and culture [Bielicki 1969, Strzałko and Henneberg 1982], change towards modern human form. The present-day human *similum* comprises a variety of individuals bearing signs of their ancestral adaptations to the same wide range of climatic and economic conditions as it was in the past, except that over time the external conditions to which adaptations occurred were different and those conditions changed over time due both to natural forces and human activities. Such an interpretation of human evolution is simpler than the long litany of fossil "species" changing abruptly and inexplicably from one to another. Most importantly, it allows us to focus attention on the processes of adaptation, explainable in terms of Darwinian mechanisms, that led from sparse populations of hunter/gatherer hominids to the widespread, very dense and numerically dominant form of large mammal.

Notes

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Streszczenie

Mimo bogactwa materiałów zgromadzonych w ubiegłym stuleciu, wśród autorów zajmujących się antropogenezą brakuje jednomyślności w rozumieniu tego procesu. Niektórzy z nich utrzymują, że w ciągu ostatnich 5 milionów lat istniało 17, lub nawet więcej gatunków homininów, inni twierdzą, że było ich znacznie mniej – może zaledwie 2, a nawet, że ewolucja człowieka przebiegła w obrębie jednej, niedzielącej się, linii rozwojowej. Różne są także interpretacje pojawienia się dwunożności i przyczyn wzrostu względnych rozmiarów mózgowia. Nadal toczą się spory o rolę neandertalczyków i pochodzenie ludzi o współczesnych cechach morfologicznych. Taka różnorodność interpretacji tej samej bazy faktograficznej wskazuje na słabość podstaw teoretycznych, jakimi posługują się zwolennicy rozmaitych koncepcji. Słabość ta wynika najprawdopodobniej z tego, że badacze antropogenezy rekrutują się spośród absolwentów wielu dyscyplin, zarówno humanistycznych jak i przyrodniczych (rzadko biologii) oraz stosują heterogeniczne paradygmaty i niejednolite definicje podstawowych pojęć, takich jak gatunek, gen czy specjacja. Przy tym, ze względu na światopoglądowe znaczenie wyjaśnienia naszego pochodzenia, istnieją uwarunkowania pozanaukowe – ideologiczne, którym różni autorzy ulegają świadomie lub podświadomie (ryc. 1).

W tej sytuacji trzeba zmierzać do rozstrzygnięcia istniejących sporów stosując podstawowe zasady postępowania naukowego – falsyfikację hipotez w oparciu o odpowiednio liczne, jednolicie mierzone lub opisywane, materiały. Takie podejście jest możliwe w stosunku do licznych już obserwacji dotyczących podstawowych cech hominidów, takich jak wielkość mózgu, rozmiary ciała i uzębienia. Cechy te zmieniały się w ciągu ostatnich 3-4 milionów lat w sposób ciągły, nie wykazując rozszczepiania w procesach specjacji. Analiza wariancji rozkładów tych cech w poszczególnych okresach chronologicznych nie pozwala odrzucić hipotezy zerowej, stanowiącej, że rozkłady te nie różnią się wielkością wariancji wewnątrzgrupowej od rozkładu charakteryzującego pojedynczy, i jedyny żyjący obecnie, gatunek *Homo sapiens* (ryc. 2). Rozkład indywidualnych rozmiarów mózgów 210 homininów wokół linii ich regresji na czas geologiczny nie różni się istotnie od rozkładu normalnego. Podobnie, rozkłady wielkości ciała po usunięciu efektu czasu (datowania) nie odbiegają od normalności (ryc. 3). Wielkość

uzębienia rozmaitych postulowanych gatunków homininów, z wyjątkiem masywnych australo-piteków, waha się w granicach nie przekraczających różnic pomiędzy rozmaitymi populacjami człowieka współczesnego (ryc. 4).

Nie da się zatem, w oparciu o te podstawowe cechy, sfalsyfikować hipotezy, że w ciągu ostatnich 3-4 milionów lat istniał w każdym momencie tylko jeden gatunek człowieka (lub jego przodka). Akceptacja hipotezy alternatywnej, o wielogatunkowości, może być rozważana tylko w oparciu o cechy bardziej szczegółowe, mierzone (opisywane) mniej obiektywnie, których próby mają mniejszą liczebność, a interpretacja wartości przystosowawczej nie zawsze jest jasna. Badania antropogenezy winny w tej sytuacji skoncentrować się na wyjaśnianiu ewolucji przystosowań ludzkich, a nie na formalnej opisowej klasyfikacji poszczególnych znalezisk.