CRITERIA TO APPLY TAXONOMIC CATEGORIES TO HUMAN FOSSILS

EMILIANO AGUIRRE

ABSTRACT. Classification of organisms must ultimately be grounded on similarities and differences of form and function. Gentic affinities are relevant and can be decisive in animal classification, but neither the magnitude nor the number of genetic mutations can constitute the essential criterion to resolve on taxonomic categories of animal organisms, since many diverse levels of organic construction mediate between genome composition and the adaptation and reproductive success of a population. Magnitude of time spans cannot be a criterion to define grades of hierarchy among taxonomic categories in organisms, since the *tempo* of diversification varies between two groups of organisms and within one stem or clade. The magnitude of morphofunctional innovations with vertical bipedality sufficies to decide at the taxonomic family level. Brain size and disproportions in the masticatory apparatus are decisive trends and combinations to distinguish *Homo* and *Paranthropus* as genera. Different conceptions in applying to fossil humans the species category are proposed to discussion.

KEY WORDS. Classification, family, genus, Hominidae, *Homo*, *Homo sapiens*, hierarchy, organism, species, taxonomy.

The aim of zoological taxonomy and nomenclature is to construct a non-equivocal language for zoologists, providing a common understanding of the terms they use to describe or analyze the animal diversity and their components.

Complex organisms must be classified attending primarily to the similarities and differences in the observable constituents and operative properties of their body as a whole, in the growing and adult states. This is valid for both living organisms (D'Ancona, 1966) and fossil remains (Simpson, 1945). Genomes are classified attending to community and differences in arrangements and operative properties of the component genes.

Museo Nacional de Ciencias Naturales, CSIC, José Gutiérrez Abascal 2, 28006, Madrid, España.

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Morphological structures as well as functional potentials are originated in and participated through the particular inherited complexes of gene chains. Genomic composition shall therefore be taken into account as an essential property of complex organic systems and their components are not to be confound by simple external, formal similarities and/or similar adaptative functions: both are related in cases of "homoplasy", a frequent instance well known and normally prevented among plant and animal taxonomists. Genetic affinity is consequently taken into account and rather decisive in animal classification.

There are essential differences in the structural composition and in the nature, subject and effects of the organic systems and of their determinant genomic systems. Magnitudes of anatomical forms and functional modes and virtualities are neither regular nor proportional to differential magnitudes in molecular genetic components. Consequently, degrees in hierarchy of genetic mutations are not decisive in animal classification.

Between a genetic mutation and the successful fertility of a population of organisms modified by its effects, a number of tests need to be overcome. First, the new mutant gene must be accepted as cooperative, functional within the whole genome and the epigenetic system. Its effects can be retarded, enhanced or otherwise influenced and modified by other genes and by the cell proteins.

Biological functions are not understood "without recourse to influences outside the genome" (Strohman, 1997). Epigenetic nets are very complex and open to environmental signals. Between the genome and the living cell an informational-operational system is recognized, which integrates environmental, intracellular and genetic information into responses of the cell activity as a whole; it also influences the genetic decoding into proteins of the cellular complex unit. It has consequently been said that the "extension of a genetic paradigm from a relatively simple level of genetic coding and decoding to a complex level of cellular behavior represents an epistemological error of the first order" (Strohman, 1997: 196). Similar considerations come again and are valid at every level of any biological organization, that is, biological operative organic subjects, multicellular and multitissular plants and animals.

In animals with complicated biological cycles, for instance, insects and placental mammals, the new mutation is required to be operative and adaptive along a chain of different operational ensembles. Adaptive efficiency and efficacy are essential in the face of either constant or changing environmental offers and pressures, beginning with initial development, while growing, in adult state and particularly in mating.

These developments, apart from leading to highly diverse magnitudes of change in organisms, obviously also take different time spans to become distinct in a group of organisms. Consequently, the time a mutation first appear, or a new taxon or clade, by no means can deserve to be a criterion for taxonomic hierarchy. This conclusion is not based on the consideration that regular and exact periodicity of genetic mutations is an assumption based on statistic inference; in any case, it cannot be extrapolated to evolutionary effects on organisms nor it can be decisive to establish grades in taxonomic hierarchy: rates of progress in evolution are diverse in different animal types.

There are risks in applying the cladistic method. The differences between two stems in a cladogram are not necessarily equivalent from a morpho-functional or organic or evolutionary point of view—nor regular chronologically. The magnitude of organic changes is independently related to the number and time of the estimated branching points.

TAXONOMIC FAMILY

These criteria can be applied to the present question of establishing a diagnose and hypodigm of the family Hominidae.

The organic differences implied in upright bipedalism, that affects almost all parts of the skeleton, many relevant anatomical regions and organic functions, reach magnitudes and derived effects that cannot be exaggerated. These are quite significant when we are to distinguish erect-bipedal primates from their closest relatives, chimpanzees and gorillas, notwithstanding their minimal genetic diversity and, consequently, sufficient and adequate as diagnostic traits to ground taxonomic distinction at the "family" level.

A pertinent observation shows that adaptation to similar ways of life and environmental limitations results in convergences in morphology and group behavior between humans and baboons, while divergences occur between humans and chimps or gorillas, the latter being closer relatives genetically and taxonomically.

Distinction between family *Panidae* including genera *Pan*, *Gorilla*, and family *Hominidae* with genera *Australopithecus* (maybe also *Paranthropus*) and *Homo* is well established and, from the viewpoint of zoological taxonomy, correct. I may say 'better adjusted' to express the matter-of-fact organic changes operated between these—genetically closest—groups of organisms.

Minor differences, in particular articulations or muscular disposition, have been observed in early human fossils. These, as well as a reasonably inferred ability to develop other alternative forms of locomotion, could obviously be expected in early bipedal generations, and cannot be used to underestimate the extent and weight of morpho-functional and behavioral consequences of erect bipedality, on which the family rank distinction for humans is grounded.

A taxonomic arrangement within family divisions based on the magnitude of organic changes can be referred to as "grade-based" classification: its divisions tend to be monophyletic as well, but are not dependent on the number nor the time of estimated branchings or cladogenetic spots. The opposition between clade-based and grade-based classifications can be fallacious. A single or last common ancestor of two or more taxa is a mental construction and cannot be decisive for taxonomical rank; the number of cladogeneses or phylogenetic branchings cannot define the ordinal step in taxonomic hierarchy. One tree may have two, three or a dozen branches originated in successive distinct divisions; all are similarly classified as branches, not as inflorescences or axis or flowers independently on the number of counted branching points. A trunk is a trunk, independently of the number of branching knots.

GENUS *HOMO*

Genera are commonly defined by distinct and durable trait combinations and by functional and morphometric trends shared by a number of species genetically related—or presumably so.

Two well-differentiated morphotypes of bipedal hominids, with obvious distinct adaptations to diverse microhabitats and resource exploitation, are recognized in fossils from less than 3 million years. These are the robust australopithecines and humans: genus *Paranthropus* and genus *Homo*, respectively. Their most relevant diagnostic traits are found in the increased size of the neurocranial vault in *Homo*; extension of surfaces for masticator muscles attachment increased in *Paranthropus*, decreased in *Homo*; frontal bone development; proportions of zygomaxillar complex and in the dental ensemble: reduced incisors and canines, enlarged molars and molariform pre-molars in *Paranthropus*; slender, decreasing molars in *Homo*.

Both differ from the *Australopithecus* morphotype, which is consistently recognized as their common ancestor. This fact supports recognition of *Paranthropus* as a genus, not just a subgenus as is frequently used. Another consideration in favor of generic distinction of *Australopithecus*, *Paranthropus* and *Homo* is based on the time of cladogenetic diversification, involving the last occurrences of the former and first occurrences of the two latter. *Paranthropus* fossils are known with dates older than 2.8 Myr in Hadar AL 438, AL 444; in Omo-Shungura upper MbB, basal MbC reaching 2.8 Myr (Suwa *et al.*, 1997); in East-Turkana below Burgi Tuff; nearing paranthropine morphology are fossils from the Grey Breccia of Makapansgat with dating around 3 Myr (Aguirre, 1970). Genus *Homo* is recognized in Chemeron Beds between 2.4-2.5 Myr (Hill *et al.*, 1992); in Shungura Fn top of MbE with more than 2.4 Myr; in Hadar AL 666 with infradate of 2.33 Myr (Kimbel *et al.*, 1997). The last occurrences of typical ("gracile") species of genus *Australopithecus* are found in the same interval: around 2.6/2.5 Myr in Sterkfontein Mb 4 is *A. africanus*; c. 2.5 Myr, *A. garhi* in Ethiopia, contemporary with stone-tools (De Heinzelin *et al.*, 1999; Asfaw *et al.*, 1999). The last evolutionary crisis of representatives of genus *Australopithecus* had probably two steps: first, variation of the stem and departure of *Paranthropus* populations at about 3 Myr; second, the appearance of genus *Homo*, and earliest lithic tool assemblages, at around 2.6 Myr (Harris, 1983). The three may have coexisted over a short time.

SPECIES

Genetic incompatibility in interbreeding, the criterion to define and distinguish Linnean species, cannot be verified in fossils. Paleontological species can only be discriminated inferentially, by evaluating patterns of morphological and morphometric differences. Comparison of magnitudes of variations between living good species may help, but cannot be decisive, since there are genetically isolated animal good species almost identical with few or single morphological variations and, on the opposite, genetically compatible polymorphic species with remarkable differences in shape and size—both domestic and wild.

Attention must be paid, when examining fossil humans, to the pattern of variation that can be inferred through space and time, further than the graphs of multivariate analysis. Unfortunately, fossil human sites do not—or very rarely—produce samples of sufficient size for reliable statistic appraises. More and more sites like "Sima de los Huesos" site in Ibeas, Sierra of Atapuerca, are needed.

A recommendation can be suggested not to assume specific—or generic, obviously—distinction between fossils, or sets of fossils, before proceeding to the deep comparative analysis, because the conclusion would be circular and critical approaches limited. Comparison can start between ensembles of fossils that are near in space and time, consequently with reasonably hypothetical genetic compatibility (Aguirre, 1993), such as the "demes" or "palaeodemes" proposed by Howell (1999). Shared traits can indicate no more than common inheritance, if variating ones are definitively distinctive, non-shared in various demes.

Since "*Homo ergaster,*" all known human fossils share the following traits: brain increase, size reduction in molar teeth and in mandibular body, long infancy, progress in tool-making with increasing diversity, definition and economy, in Africa as well as Asia and Europe. Communication and intelligent land use and inferred group cooperation to profit on naturally trapped animals in Atapuerca-Galería c. 290 Kyr and Ambrona, moreover to intentional trapping as in Torralba and Zamborino c.

200 Kyr, can reasonably be extended to other Mode 2 users and to occupants of Olorgesailie 600 Kyr. Intentional sea crossing is referred in Indonesia about 500 Kyr. Morphological variations are minor ones; most of these are shared by different populations or "demes" although with varying proportions or combinations. One case was analyzed by Martínez and Arsuaga (1997) with nine traits of the temporal bones and the distribution of their varieties in a number of groups differently defined. The total picture of the known human fossils and the populations they represent is that of a number of regional varieties of only one polymorphic species sharing clear common evolutionary trends, not at all that of a full hand of distinct contemporaneous species. The splitting and extinction of *Homo soloensis, Homo pekinensis, H. rhodesiensis, H. heidelbergensis* between 500 Kyr and 180 Kyr, *H. antecessor, H. erectus, H. mauritanicus"* between 1 Myr–0.6 Myr, is not parsimonious, and lacks solid grounds in the analysis of fossil evidence.

Differential traits of living human races were found in fossils of Mid-Pleistocene age by C. Coon (1962), frequently in the same or proximate geographic regions. He asked how far back in time those racial traits could be found in those fossils to be discover. The fossils' answer is now coming: the *antecessor* of Aurora Bed in Atapuerca with facial skeleton closely resembling Dali skull and living Chinese (Aguirre 2000, pp. 67-71), and mandibular proportions approaching Ternifine 3 and Zhoukoudian (Rosas and Bermúdez de Castro, 1999), extend Coon's recognition back to the late Early Pleistocene. These differences do not diminish the above-mentioned sharing of common trends characteristic of human genus. The most consistent taxonomic solution is to classify all those fossils in a single polymorphic species, not only similar, but the same as the living one: *Homo sapiens*, with changing varieties, or subspecies.

The evidence from mtDNA of African origin in "modern humans" is not contested. Reconsideration is recommended concerning the date of such event, since there is hard evidence of multiple "Out-of-Africa" dispersals since about 1.9 Myr (Aguirre 2000; Aguirre and Carbonell, 2001). The present global dominance of African mtDNA type could also be explained by interactions like a founder effect of a late out-of-Africa move; yet the exclusion of interbreeding with fossil populations is gratuitous and contradicts multiple evidence.

Fossil evidence also shows that neandertalian and modern morphotypes were distinct, and can be identified in fossils, since an age of more than 100/120 Kyr ago. Morphological and morphometric differences between these two types are greater than those between old populations represented by fossils not very distant in time; nevertheless, both lived in neighbor lands around the Mediterranean, using quite the same kinds of implements made with same technique, the Mode 3 Mousterian. Interbreeding cannot be excluded *a priori*; genetic isolation needs to be demonstrated, not the contrary: it could arrive no much earlier than 45/55 Kyr. Since that time, the Neanderthals can be classified as a new species, not before. Even more, neanderthalian diagnostic traits appeared successively (Condemi, 1989); trends are recognized in mid-Pleistocene populations of Europe and Africa (Rightmire, 1996) since 600 Kyr, even before. Increased genetic isolation probably was influenced by geographic barriers in glaciation's times.

There are no factual grounds to extrapolate the Neanderthal case to other fossil human populations. The morphological differences between fossil demes are not as relevant. Pre-neanderthalians are not fully the same as neanderthalians, and there is no ground for them to be considered as a different species related to their contemporaries: distinction as subspecies is consistent with the whole available evidence.

Further, the elevated shape of neural cranium, vertical forehead, chin protrusion with retractions of mandibular body, thin cortical wall in cranial and postcranial bones are all distinctive traits in modern humans. The question is whether these differences provide some base to distinguish the modern humans as species from the preceding demes in Early and Middle Pleistocene. If the answer is in the negative, then it is suggested to classify as subspecies of *Homo sapiens* the following: *H. s. rhodesiensis, H. s. heidelbergensis, H. s. pekinensis, H. s. soloensis, H. s. mauritanicus, H. s. antecessor, H. s. ergaster, H. s. erectus*. If the answer is positive, the classification of those fossil humans, as many prefer so, includes a third species: *Homo erectus* (Aiello and Dean, 1990). In this case, the latter could be recognized as a "chronospecies".

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