Open Access

OBM Genetics

LIDSEN Publishing Inc.

Review

Anatomical Variation, Hominins, Species, and Self-Domestication

Niccolo Caldararo *

Department of Anthropology, San Francisco State University, 1600 Holloway, S.F., Ca. 94132, USA; E-Mail: cald@sfsu.edu

* **Correspondence:** Niccolo Caldararo; E-Mail: cald@sfsu.edu

Academic Editor: Joep Geraedts

Special Issue: Feature Papers of OBM Genetics in 2021

OBM Genetics
2022, volume 6, issue 1
doi:10.21926/obm.genet.2201145

Received: October 19, 2021
Accepted: December 27, 2021
Published: January 11, 2022

Abstract

The evolution of hominins, members of the zoological tribe Hominini, has been a much-studied topic, and the construction of phylogenetic trees has been the key method in molecular evolutionary studies. How scientists determine the phylogenetic trees are governed by the assumptions they place on the construction of similarities and differences in morphological traits, the differences in the number of base pairs in the genomes, and the number of similar gene clusters that code for traits (haplotypes) or are error sequences (SNPs). Among the several methods employed for the construction of a phylogenetic tree, mathematical methods (utilized for sorting data, including fabrication of algorithms) are the most significant ones; also, the nature of population structuring plays an important role in the evolutionary process. In this paper, I will not only describe the drawbacks of current assumptions in hominin evolution during the Middle Pleistocene era (based on fossil evidence) but also the aspects of brain evolution and the self-domestication of our species. The evolution of the brain is usually associated with an increase in neurons and other types of cells associated with signal processing (connectivity) and memory. Assessing actual neuron counts in fossils is challenging; moreover, new research has shown decreased neuron numbers in the neocortex and demonstrated large counts in the cerebellum, leading to a decreased focus on brain size. The idea of increased brain size in the Pleistocene era without a substantial increase in the evidence of cognitive activity in complex behavior residues might be explained by increased myelination to provide additional insulation in Ice Age conditions and faster transition of signals due to increased competition for reduced food supplies. Other cold-adaptation features can also be noted. Such a model can provide a new approach to assess the apparent brain size reduction in the Upper Paleolithic period.

Keywords
Phylogenetics; genetics; population; suicide; abortion; demes; brain size variation and ability

1. Introduction

With the discovery of the Feldhofer cave fossils in the Neander Valley (Neanderthal means the valley of) in Germany in 1856 and the later finds, including Dubois's discovery in Indonesia of what he called *Homo erectus*, the attempt to understand the tempo and mode of human evolution became a process of debate and study. Thus, the nature of human origins and the number of hominin species became a controversial topic. Preexisting ideas, some religious and some ideological, seeped into the analysis, leading to a contest of the many origins of hominids; these ideas were divided into polygenic and monogenic schemes early on. A "Presapiens" ancient root was proposed, with the idea of an early human-like big brain as opposed to a linear and progressive development of humanity from an ape-like small-brained ancestor; this was reinforced by the "discovery" of the Piltdown fraud. Based on this concept, Louis Leakey presented his Kanam Man, which was fit into the scheme with Piltdown; Michael Hammond [1] and Frank Spencer [2] providing detailed reviews of the history. What I want to do here is place today's dominant paradigm of human evolution, the "bushy tree", in contrast with the concept of human variation and speciation.

2. Phylogenetics, Populations, and the Idea of Race

Let us begin with population assumptions. Usually, the scientists constructing algorithms to chart human evolution make the assumption that the fertility of early human populations mirrored that of contemporary modern populations. This fertility factor, which is measured on certain groups like the surviving hunter-gatherers, is then utilized for predicting the increase of human populations over time. It is also employed to assess the number of generations necessary to produce a specific number of mutations that could be used to construct nodes of speciation in the past. This is usually couched in terms of fitness, as Ewbank [3] does. Fitness is equated with reproduction, and Ewbank [3] utilized the reproductive rate of certain groups in Ukraine and Kenya as models to establish the "growth rate" or the increase in numbers.

One drawback of this assumption is that we do not know the population histories of hominid groups in the past; some may have had rates like today's modern humans in Ukraine or Kenya, or of today's Hadza, or perhaps more like the gorilla, orangutans, or lemurs. What we do know is that some human populations exhibit either very slow or nil growth rates. This is demonstrated by Codrington [4], who cites reports on some Melanesian groups where the women practiced abortion or infanticide so often that the population hardly grew, was stable, or had to import children from other islands. Thus, looking at population diversity in space and time has resulted in a number of false starts in understanding human evolution.

For some scientists like Carleton S. Coon [5], population diversity meant speciation; according to them, certain human groups were regarded as proto-species, which meant that certain species evolved at different regions at different times from a single species. However, molecular pieces of evidence suggested that population diversity reflected a dynamic nature of social and ecological adaptations and not incipient speciation [6]; only 6.3% of the total genetic variation was explained by differences among major populations, whereas 94% of human genetic diversity was observed within these very large groups. Therefore, this leads to the question of whether the diversity shown by fossils from the Middle Pleistocene (Mid-Pleistocene) era is evidence of large-scale speciation over time as some have proposed [7, 8], or is it the root of contemporary population diversity? This pertains to the latest additions to the Mid-Pleistocene hominin family, the Harbin cranium [9], and that from Nesher Ramla [10]. Are they two different species with similar traits, some of which are common to many fossils considered *Homo erectus* or later fossils? Can we call them Neanderthal (*Homo neanderthalensis* to some), Presapiens, or Archaic Homo, but with some significant variations? It must be noted that they are widely separated in geographic location but dated to approximately the same time. While our samples of the Mid-Pleistocene era are very few in numbers compared to that of recent human populations, even of the past 50,000 years, calling any of these fossils representative of species seems unwarranted.

Apart from the above-mentioned factors, one other factor affecting the phylogenetic tree construction is the use of measurements. So, if one makes assumptions about fertility or traits that define a species, then the measurements of fossils based on these become the evidence for species designation. During this process, trait measurements are entered into a database, and the software clusters the data, as usually k-means, to arrive at points for comparison. Arriving at k-means distinguishes data entries by an estimation process built into the design of the algorithm [11, 12]; these can be constructed as “medoids” as in Partitioning Around Medoids (PAM) or Environment for DeveLoping KDD-Applications Supported by Index-Structures (ELKI) [13] that measures the degree of dissimilarity of the dataset, again a level of parsing designed by the programmers. All this reinstates the fact that the processes of trait selection, measurement, and program design are dependent on human assumptions. In the 1980s, people called this “garbage in, garbage out.” In the 1960s, when I was learning Fortran and Basic languages, we were constantly reminded of Keynes’ warning, “do not mistake probability for reality.” Creating programs is simply a tool for examining our data; it cannot become a replacement for it. People have the tendency to overlook evidence from fossils and rely on what they consider less subjective interpretations derived from molecular data. However, here too, we are dependent on assumptions. How many base pair variations make a species? Caldararo and Gabow questioned this in 2000 and reported that the assertion of 24 base pair differences between Neanderthal DNA and reference human DNA could not be defended using the Biological Species Concept, as chimpanzees from different populations, with more than 24 base pair variations, were still interfertile [14]. This argument has been opposed by those who consider hybrids to be dead-ends and lacking (or showing reduced) in fitness. However, this is also not defensible, as fitness is a relative point dependent on environmental stasis or change.

Other essential foundations of phylogenetic computations base their ideas of gene flow and speciation on concepts drawn from plant or animal-based studies, where populations separate into closed reproductive units [15]. This may be the result of competition for resources and, in humans, warfare [16, 17]. How this idea applied to the selection and creation of sub-population groups of limited gene flow was summarized by Howell [18]. Calibration of nodes of separation is not only based on the assumption of neutral theory, which was questioned recently [19] but also on theoretical expansions or contractions of hominid populations in the past [20]. The neutral theory is based on the simple assumption that most of the variations within and between species are the result of random genetic drift. Some efforts to produce a more robust definition of how neutral theory could apply to selection and evolution seem interesting [21]. However, ideas of speciation and hybridization have become more complex in recent years, as questions of stability of hybrids and of reduced introgression have indicated the presence of genomic resistance in some cases, including the case of fertile offspring [22]. The concept of differential introgression indicates that alleles at some loci introgress more than others [23]. This certainly undermines the Biological Species Concept or at least subjugates it to a genomic organization over time. However, we must understand why such resistance takes place, that is, is such differential behavior related to surrounding genes or introns and is a mechanism for stability, or is it based on some other aspect of gene biochemistry? A promising reassessment of many of these assumptions affecting phylogenetic analysis has appeared recently [24] and may lead to the rectification of some of the distortions presently affecting research. The re-evaluation of the genetic diversity of human populations in Africa throws new light on the potential dynamic gene flow among Mid-Pleistocene populations and gives a fresh perspective to understanding the potential of hybridization and population diversity in the past.

There has been an emphasis on trends in speciation in hominin groups by most researchers, with the exception of Wolpoff [25]. The opposite approach is to focus on the occurrence of stabilizing selection, demonstrated by Edward Blyth in his 1835 and 1837 papers. Stabilizing selection is observed when the population stabilizes on a particular trait and genetic diversity decreases. Therefore, it has been easier to demonstrate in populations that have adapted to environmental conditions. It is the antithesis of change or evolution, as individuals meeting the "survival of the fittest" standard under selective pressures produce stability; this concept explains the successful adaptation of hominin populations from two million years ago to the present. H.C. Bumpus recorded these processes with English sparrows in his famous experiments using the bimodal distribution curve. Yet environments change, as do selection pressures and evolution.

While language has been argued to be the essential element of human evolution [26-28], associated with everything from successful hunting to fireside chats producing solidarity in action, one function has been largely overlooked, i.e., the integration of members of different groups. I mention this in regard, for example, to the exchange of spouses between hostile or adjacent foraging groups. This also explains the survival of populations spread thinly across the globe from the Cape of Africa to Japan and England, indicating that mutual survival under harsh conditions could have been a very adaptive trait. Here, language could have facilitated integration, especially the ability to learn new languages both as children and as adults [29].

The idea of integrating into foreign groups, especially of females into hostile neighbors as mate exchange, requires not only language but also consciousness to be liable to acceptance of variation and adaptability [30]. In fact, human consciousness is often described as if it were a magical production, incapable of quantification, yet in its malfunctions, it does seem to display elements of function like any other biological system. In a study, Kotchoubey [31] asserts that human consciousness must be seen as an adaptive system. This is supported by several other studies by Luria [32] and Sacks [33, 34] and a few in experimental research [35], where different parts of the brain are removed and behaviors were assessed. Examples like the study of twins John and Michael in Sacks' description who translate rhythms into algorithms of their own language, victims of Korsakov's syndrome, the spectrum of isolation of autistic patients, and the musical references of idiot savants are windows into the origins of human awareness. The failure to understand these as variations of modal human consciousness is derived from the abandonment of searching ways of being in the past in contemporary pathologies. Sacks revitalizes this idea in his autistic patients. The lack of a comprehensive view of pathologies of consciousness gives rise to ignorance of variations of reality formation seen only in another area of research, i.e., trance analysis and induced states of consciousness—from sensory deprivation to the ingesting of psychomimetic/psychotomimetic drugs [36]. Fabbro et al. [37] attempted a comprehensive overview of this problem, but definitions of states of perception and pathological variations undermine a clear assessment.

Most challenging is the problem of associating an individual view of the world with that of others. Laing [38], like Sacks, tried to derive from pathological conditions a contrast that could be used as an evolutionary formula—the general view of certain pathologies versus the specific view of the social norms. The nature of human consciousness makes it difficult for "us" to conceive it in other animals for just the same reasons that ideas animals lacked a mind could have been so strongly held. Now evidence of one central element of mind, self-recognition has been shown in fish [39] Similar arguments had been made before this time about the mentality of serfs and after about Africans [40], indicating the issue to be that of exclusivity.

3. Evolutionary Rates and Demes

Estimation of population size and changes in population over time affect assumptions in phylogenetics concerning rates of change, especially mutational rates and selection (as well as "neutral" effects, as in drift). Recent studies have discovered widespread transcriptional scanning in the testes, resulting in the elimination and control of germline mutations [41]. The lack of concern for stability in the selection and normative adaptation to environments is characteristic of all models of human evolution on which the phylogenetic relations of speciation are based. This characteristic has been widely discussed by Caldararo in a recent paper [42]; however, all the modern program algorithms used for the construction of phylogenetic trees are based on this very characteristic. For example, in a recent study of facial recognition technology, the software had significant demographic effects, mainly high reliability on African Americans and low on people of Indian subcontinent origin [43, 44]. Some efforts, such as those based on maximum likelihood analysis [45], have verified Neanderthal admixture, but the situation remains complex given the arguments of evidence of long-term selection against Neanderthal introgression [46]. Studies have computed various times for admixture and promoted numerous admixture events [47]. In their study, Petr et al. [46] have addressed many of the distortions created by earlier assumptions in analytic programs applying to DNA of Neanderthal and modern human samples; issues addressed included comparisons among different geographic populations and dilution of Neanderthal genes. Taskent et al. [48] have also reviewed the work on introgression between Neanderthals and anatomically modern humans (AMH) and concluded that there was more than one introgression event, probably several. Durvasula and Sankararaman [49] have added some interesting information to this process by attempting to recover introgression signals in African populations by novel means. Hubisz et al. [50] have attempted to identify the flow of genetic traffic from archaic hominins to AMH. The above-mentioned studies indicate that further revelations about the evolutionary process can be expected in the future; however, it also brings up a curious question. Since "introgression" means the transfer of genetic information from one species to another resulting from hybridization events or backcrossing, it can be understood that previous studies assumed Neanderthals to be a different species than early *Homo sapiens* populations. If we assume that by Neanderthals we mean *Homo sapiens neanderthalensis*, then there can be no "introgression" as defined. Significant literature and debate have resulted because of this issue over the past 30 years, without leading to any resolution [23].

However, we cannot ignore either fossil evidence or biology in this pursuit. This was demonstrated by recent studies focusing on variation control in oocytes; these studies indicated that selection is going on constantly to control variation that would lead to non-functionality or disrupt stability. In mitochondrial DNA (mtDNA), mutations disrupt the efficient function of the very limited space available and create a high genetic load that could "imperil survival of the species" [51]. Wallace [51] argues that the process of variation control occurs in the ovaries, where the proto-oocytes and oocytes with the most severe mutations are selectively eliminated. If there is so close a selection and lack of room for functional variation, how did the macrohaplotypes evolve, and do people in these macrohaplogroups differ in the functional efficiency of their mitochondria? In both oocytes and sperm, the close editing of mutations reduces or eliminates the strength of assumed action of neutrality in phylogenetics; therefore, the importance of selection in developing algorithms for human evolution must be reexamined.

This idea of the formation of demes and limited gene flow due to hostile attitudes [52, 53] is contradicted by our knowledge of mate exchange among hostile human groups in the ethnohistorical record. The essential nature of the "Out of Africa" scenario is one where replacement is the key process, i.e., the local populations were replaced by the migrating African populations, with little, if any, interbreeding [53]. Fried [54] cites several examples where warring groups traditionally exchanged brides. Such customs might be a part of the drive for mate diversity seen in most social systems, leading to great genetic variation in modern humans. Studies focusing on fitness and reproduction have highlighted general concepts of the struggle for mates, inter and intragroup violence to gain females, and a basic sense that all humans have always maximized their potential to produce offspring [55]. Trivers [56] has produced some of the more explicit scenarios of this view, leading to the coining of the term "parental investment." Yet the life of the individual is seldom acknowledged. Instead, we find mathematical computations as if all beings were computers calculating the fine advantages of how to pass on their "selfish genes" [56, 57]. While this might be true in some cases, the lust for life for pleasure and for producing few but high-quality offspring is only barely mentioned. It is the focus on R-selection instead of K-selection and ignoring any conscious self-reflection in other species that dominates these views. The variation in the meaning of the terms R and K selection adds to the challenge further [58]. Humans are generally considered to be K-selected with significant investment to offspring; however, this is a relative measure, as apes are considered more K-selected than most monkey species. Interestingly, few studies have been conducted on the reproductive status and selection in humans. Nettle and Pollet [59] studied reproductive success and wealth in the population of Great

Britain and observed significant differences between males and females. However, human history also demonstrates close relatives killing each other; recorded examples are those of royalty: Herod the Great's murder of his sons, or of the English princes by Richard III, and others listed in the pages of Brentano, 1964 [60]. More general examples are the inter-group and inter-tribal "feuds" of the Yanomamo, where whole family units were massacred [61]. The nature of society is forced into a basic monogamous idealized, Western unit; this type of structure ignores the significant variations in contemporary society and ethnohistorical evidence, as for instance, the substantial contributions of extended families in raising children and sharing of co-wives among the Pondo [62].

4. Gene Frequencies, Speciation, and Character Traits

Here, we come to another aspect of gene flow leading to evolutionary changes. Wolpoff [25] argued that the genetic differences in the chimpanzee and *Homo sapiens* genomes were too few to allow for dynamic speciation within the hominids. This argument was supported by Caldararo et al. [14] in 2000 in relation to the decision of Krings et al. [63] to choose 24 base pair differences to determine speciation when chimpanzee populations were still interfertile with many more differences. Recent research into chimpanzee genetic evolution has demonstrated a complicated picture of introgression among populations over the past 500,000 years [64]. Wolpoff [25] suggested that most of the variation in the past two million years was caused by changes in gene frequencies of alleles and that these seldom reached the level of speciation events. He emphasized the contradiction of a co-adapted genetic system model of species with the genetic variability of local populations. This scenario is complicated by the fact that identification of species is a subjective process, as Caldararo pointed out in a recent paper [42]. The numerous changes in species designation of specific fossils further substantiate this. Investigation of these fossils indicates that some have undergone changes from Neanderthal to *Homo erectus* to *Homo antecessor* or *Homo heidelbergensis*. This results in a dizzying exercise of comparing Oakley's charts [65], with a recent attempt to clarify distinctions by Parins-Fukuchi et al. [66]. The fact that we are dealing with paleospecies whose fertility cannot be determined by observation makes it even more complicated, though Parins-Fukuchi [66] summarizes attempts to do so. Gingerich [67, 68] cautioned against making such distinctions, arguing a gradual transition similar to early mammals with intermediate forms as the most likely evolutionary model for hominids. He stressed that divisions among hominids were "arbitrarily divided segments of an evolving lineage…" Could hominids termed *Homo ergaster* and *Homo erectus* in Africa and Asia, respectively, at the same time produce fertile young? Who knows? In this context, continuity based on morphological gradation across regions has been a major point of argument [69, 70]. The fact that it was argued for more than a century that Neanderthals were a separate species who did not contribute to the modern human genome has been overturned should be a telling lesson. We know that Neanderthal and Denisovan genes have been found in modern humans, so why do we still refer to them as separate species?

In a recent article, Michael Hammer [71] has described hybrid models for introgression of genes from Middle Pleistocene hominids as a means to understand a more complex process of hominid evolution. Here, I use this model to indicate gene flow from a genetically different population to another, and not, as some do, from one species to another, which confuses not only the idea of hybridization but also the Biological Species Concept. This approach seems to make sense, as human contemporary morphological and genetic diversity can be seen as a result of microevolutionary selective adaptation to a variety of climates, pathogens, diet, and social pressures (mate exchange, language, war, and sedentism). These are linked as late-appearing features of human experience, especially sedentism, and it is a part of the idea of self-domestication, which was promoted by Wilson [72] and described for some traits in Caldararo's 2005 [73] paper. This idea of humans as social actors within society-oriented consciousness is essentially what Freud described in the development and evolution of the superego to control the instincts, without which he argued no civilization could arise [74]. However, he was reprised by Humphrey [75], in a more modern context, and Laing [38], especially regarding self-consciousness and the pathology of being seen; this was first noted by George Berkeley as "esse est percipi" or "to be is to be perceived." But it is compelling to compare the evolution of eusocial conditions in humans with various mechanisms, such as social conditions. For example, it seems logical to parallel ant eusocial environments, where ants domesticate other species with human social complexity and self-domestication [76]. Attempts have been made recently to apply the same principle on early hominid evolution [77] by combining it with a "neural crest hypothesis." These attempts are confused by the myriad selective agents and ideas of directed evolution, though one might conceive of a paradigm as proposed by Darlington [78] of a "period of self-acceleration." During this period, an explosive organic evolutionary process for bipedalism followed by a hiatus and then a secondary "pulse" driven by population increase occurred. Theories of specific developmental schemes like that of Haeckel are not new, though Gould [79] pointed out problems in arranging trends of adaptations by aligning features in ontogeny, contributed by heterochronic processes, as related outcomes. De Beer [80] focused on the confusing nature of the appearance of embryonic characters in adult stages when comparing animals as different as the ostrich and penguin; this is a form of neoteny, which does not necessarily indicate adaptation to similar selective pressures. Johnsson et al. [81] have shown the evidence for a universal genetic mechanism behind the hominin evolution, Wilkins et al. [82] have proposed is both indirect and weak at best.

Nevertheless, the theory, as related to neural crest genes [82], depends on a specific agency in reference to adaptation. The proposed mutations in the genes related to development from the neural crest take place in a vacuum and are influenced by a "key" gene *BAZ1B.* While it is known that mutations can influence adaptation, this can only happen in an adaptive landscape. Human intervention across a long period and diverse environments must have resulted in the formation of different human groups in a typical process. Some improvement in survival and reproduction must have been made with the assistance of human agency. Wilkins et al. [83] suggest a "multi-stage process" of "breed formation." However, since the lack of uniformity could lead to an accident, their suggestion seems another example of overreach frequently found in the history of biology [84]. It is also known that genes can have multiple effects, such as they can be a part of polygenic influences and epigenetic interaction, yet all this must be linked to selective advantage. It was suggested in 2017 [85] that reduced brain size could be a consequence of self-domestication; this was confirmed by a study of behavioral changes in wild and domestic fowl [86], indicating that the reduction in brain size could take place in the absence of an identifiable selective pressure. My suggestion here is that the reduction in brain size in the Middle Pleistocene era is related to adaptation to cold, which is a more logical explanation. Yet studies of human contemporary cranial variation suggest that variations occur mainly due to drift, migration, and gene flow [87], reducing the effects of selection. Still, recent studies question the robust nature of reliance on theories of neutrality [88]. The question of why human brain size seems to have plateaued after reaching modern volumes (over 1,000 ccs) almost a million years ago, remains unclear, as does the obvious explosion of complex social life and technology after 10,000 BP. However, if we accept Flynn's [89] argument regarding intelligence and ability being a consequence of social context, then this explosion becomes understandable. Therefore, we do not have to create special conditions of brain reorganization or connectivity that cannot be resolved by fossil evidence or search databases in DNA analysis using questionable evolutionary algorithms. Connectivity and brain plasticity are certainly essential to understand cultural and individual adaptations, especially under stress and relearning [90]. Emphasis on the size of the brain and gross numbers of neurons has given way to analysis of specific biomarkers and recently to significant differences in cell type, for example, gene expression in oligodendrocytes over other primates [91]. Rather, the increase in the ability of human beings, as Flynn has demonstrated for the past 100 years, simply becomes the consequence of modifications of enculturation and related conditioning methods.

Another theory related to social life is the social brain theory of Dunbar and associates [92], according to which, the prefrontal cortex (PFC) enlarged as a result of selection pressure for increased social complexity. A major drawback of this theory is that our brains and the PFC increased over time when human groups were quite small, i.e., they were mobile, hunter-gatherer units. One would expect, if the theory was correct, that the PFC would have increased during the latter part of human evolution, certainly in response to sedentism, food production, and food sharing. The fact that we find larger brains in highly social animals indicates a possible pre-adaptation, thereby supporting the Dunbar theory; however, it lacks a convincing selective mechanism as in increased hunting efficiency, mating success, surveillance of disease in conspecifics.

Also, the social brain theory was contradicted by Semendeferi et al. [93] and Herculano-Houzel [94], who found that humans did not have larger PFC than gorillas, chimps, or orangs; Herculano-Houzel [94] demonstrated that the human PFC does not have more neurons than other primate species.

What is more problematic is the idea that a single gene regulatory network of genes [82], leading to significant disabilities in mutant conditions, could be combined to produce functional organisms and the assumption that an accidental combination of these genes in humans would lead to the domestication of other animals. The authors of this work seem to believe that by noting experimental manipulating genes (and natural mutations), producing pathological conditions in other species, they have revealed the genetic evolutionary history of *Homo sapiens*. This is quite an assertion, as they ignore the substantial influences and complexity of the polygenic nature of many of these pathological conditions. For example, while picking the Waardenburg syndrome (prevalence 1 in 42,000), they neglected to add that this condition leads to four different types of syndrome, including association with Hirschsprung's disease that causes a congenital lack of nerves in the intestines leading to bowel dysfunction [95, 96].

This theory (Domestication Syndrome) of a jumble of dysfunctional mutations leading to human social behavior, can be compared with more established modes of new functions, as in gene duplication [97] and co-option of existing genes; however, it is usually limited to related functions, as in the evolution of venom in wasps [98]. In addition, new genes are often created de novo, as in the artic cod discovered by Helle Tessane [99]. Research focusing on the dog has challenged the behavioral aspects of this theory [100], and the central trait proposed for humans, i.e., passivity, is difficult to support. Self-domestication may be a form of domestication, but a few studies have indicated that it is part of the process of eusocial evolution [85].

Like Pinker's [101] "better angels" concept, few researchers have argued that humans have experienced reduced aggressiveness over the past two million years, 50,000 years, etc. These studies have limitations like the lack of uniform and multiple samples over the past two million years. However, the opposite argument of humans becoming more aggressive can also be made, especially as they have become members of larger social groups and have recruited more fighters both for internal war and external conquest. In my opinion, it might seem logical that only a European could argue that humans have become more peaceful given the brutality and savagery of the colonial wars since 1492 and the Wars of the Reformation. Davidson's [102] brief outline of the ruination of African societies from the 15th century onward gives a taste for this unbounded aggression which has been reviewed elsewhere [103].

In a recent article, Caldararo [42] placed emphasis on determining the traits for differentiating hominin as species. Many people use the terms, such as primitive character or plesiomorphy, symplesiomorphy, derived or apomorphies, shared derived synapomorphy, uniquely derived autapomorphies, or novelties as if they identified specific items that were easily described and agreed upon [26]. However, such arguments lack comprehensive information on population variation. Of this dilemma, Lieberman [104] noted that the "…choice of characters poses the greatest obstacle to resolving evolutionary relationships among human taxa." Yet the abandonment of references to population variation in contemporary populations has a history, one that became tinged in controversy [105].

Questions regarding the age of introgression have been proposed to eliminate the idea of the recent hybridization of modern humans and Neanderthals [105]. In this scenario, genes believed to be Neanderthal or Denisovan were argued to be derived from an earlier, more diverse last common ancestor of Neanderthals, Denisovans, and modern humans. A study by Posth et al. in 2019 depicts this scenario [106], wherein three species B, C, & D are derived from an ancestor species A (Chart 1).

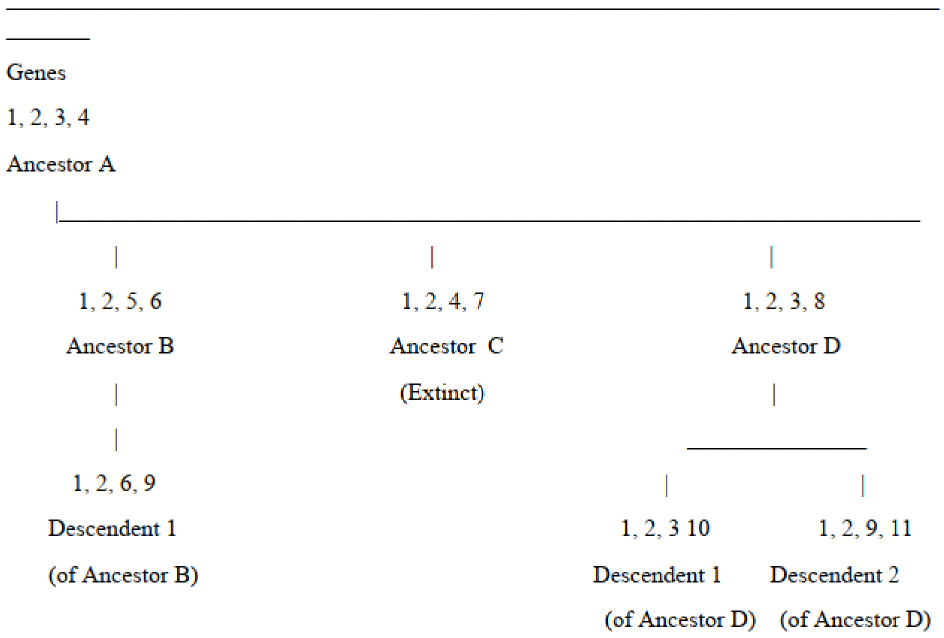

Chart 1 Here, we have an ancestor species A from which three species are derived: B, C, & D.

Here, genes 1, 2, 3, and 4 are the ancestral genes. Genes 1 and 2 are retained as conservative genes and appear in each descendent species after being inherited directly from the ancestor. Genes 5, 6, 7, 8, 9, 10, and 11 are mutations appearing in the individual histories of the separate species. In the Vernot et al. 2016 [107] chart, the lines from Neanderthals and Denisovans indicate "introgression" of mutations, newly produced in these hominids, into populations of early *Homo sapiens* at some time in the past. This process of introgression is a distinctly different process from genes being transmitted via sexual mating of hominids that are interfertile, as Vernot et al. [107] assume. However, as mentioned above, this term can be confusing.

The proposal of the Vernot et al. study is found in two parts; on the one hand; they eliminate the bias variations in the D-Loop of their very degraded fossil sample, which has been difficult to date. Second, they assume this unique individual possesses sequences that are also found in all later hominins. This is a surprising finding, almost too good to be true, and generally, such discoveries do prove later to be the product of wishful thinking even in the hands of the most accomplished scientists [108]. But finally, the age of the sample is the central issue; if it is not as old as they assume, then the results are more than suspect. However, Yang et al. [109] studied the same ancient structure model and demonstrated that it was unlikely to explain the Neanderthal and non-African genetic similarity.

Another problem that is associated with specific trait comparisons and employing them to identify transitions in phylogenetics is the nature of complexes of traits that produce combinations of physiological features. One of these that has become popular is the idea of self-domestication in our species [110]. While Caldararo described this trend in human evolution [73], noting its origins in work by Wilson [72], he developed this concept in more detail in a later book [85] by expressing concern with both the behavioral and physiological interrelation. Recent studies [111] have attempted to determine genetic origins and polygenic functions during the evolution of embryological modifications of gene action, mostly surrounding the modern human face and the neural crest. This approach, which has been questioned in the past, places significant importance on orthogenic trends (or also known as orthogenetic evolution), where evolution is seen as directional and self-correcting [79].

Studies of gene action and the association and causation of variants have questioned some claims regarding disease and gene effects [112]. Association and causation, especially where polygenic interaction is concerned, form a complex issue and should be carefully approached. Another drawback of these studies is that several of the traits, associated with their key gene *BAZ1B*, are still found in many contemporary humans, for example, prognathic faces in many recent AMH populations [113]. Another study pointed out that the variations in the nasal index do not relate to concepts of geographic races but show environmental sensitivity [114, 115]. Another trait indicating self-domestication is tooth size, but as Brace [116] has argued, teeth played a mechanical role in other facets of culture than being related to food processing, and the wearing of Neanderthal anterior teeth is an illustration of this. Some contemporary populations have also used their teeth in this way, as in the Inuit [117]. Gómez-Robles [118] and her associates found that the increase in brain size and the size of the tooth were not correlated with the rates of change in human evolution. Ungar [119] also makes an argument that tooth size and mandible shortening are related to diet. Brace and Nagai [120] demonstrated that at around 300 B.C.E., the Yayoi brought rice farming to Japan when their teeth were 10% larger than that of the Jomon population resident aboriginals. Brace and Ryan [121] demonstrated that differences in tooth size were present in most contemporary human populations and could be related to body size and sexual dimorphism. A reverse association to that of Wilkins et al. [82] concerns the adrenal glands and diet. We know that in some animals, the adrenal function has seasonal variations, for example, variations associated with hibernation [122]. But we also know from experimental work that a high-fat diet increases adrenal function; thus, a shift to cereals from a diet of meat and fat could produce some telling physiological changes [123]. For example, hyperpigmentation can result from adrenal insufficiency, which is seen in Addison’s disease and Cushing’s disease, where the cause is adrenal hyperstimulation. This contradictory situation is explained by how the body processes adrenocorticotropic hormone (ACTH) and related proteins in each of the above-mentioned conditions [124]. Adrenal ablation and certain conditions of adrenal insufficiency demonstrate the remarkable effects of adrenal function, from easy fatigability, anorexia, and diarrhea to emotional problems. Given the claims of Wilkins et al. [82] regarding the role of this glandular system, we should expect more specific evolutionary relationships.

Similar theories have been produced around the differences in growth patterns of modern humans and Neanderthals, especially in the dentition and brain. Hublin et al. [125] note that “… the hemochorial placenta is often considered a response to the needs of the fast-growing embryonic brain…” However, Garrett et al. [126] have found that the eutherian placenta is associated with changes in the pace of life and life events, where maternofetal interdigitation and placental invasiveness are associated with reduced offspring production early in life and increased lifespan. Hublin et al. [125] ignore modern human diversity in their argument on the differences in dental maturity between Neanderthals and modern humans. Jung et al. [127] and Chaillet et al. [128] demonstrate considerable ethnic diversity between Neanderthals and modern humans. Also, Hublin et al. [125] argue that brain shape can be used to distinguish Neanderthals from modern humans. However, this seems premature given not only the small number of Neanderthal brain samples and brain estimates obtained from instrumentation but also the remarkable plasticity and variation of modern human brains, the effects of diet and lifestyle [129], and the suggestion that Neanderthal introgression has had an influence on modern human “globularity” [130]. The idea of “globularity” reminds one of the craniology of the past with ideas of “roundheads” (brachycephalic) replacing “longheads” (dolicocephalic) during the change from hunting and gathering to agriculture [131]. Changes in neonatal development, and the comparisons drawn between Neanderthals and modern humans, may be related to changes in body size and related altriciality as seen in ursids [132]. But even in these studies performed by scholars like Hublin et al. [125] an artificial type of human is compared with a small sample of Neanderthals. Since terms like “children” and “adolescent” are often used in these comparisons addressing puberty, it should be noted that there are substantial variations in human puberty from precocious to late or delayed puberty [133], and changes in median dates of puberty in recent history have been noted [134].

In looking for evolutionary relationships and selective pressures for color variation in humans and its potential association with self-domestication, we might focus on other vertebrates that have complex societies and eusocial lives. One of these is cichlid fish, where we find color change to be associated with reproductive status and agonistic behavior. In aggressive encounters, individuals signal aggressive status by changing color—a mechanism for reducing injury and engagement [135]. While this has no obvious analog with human behavior or coloration, we might expect some parallels in vertebrate adaptations in eusocial contexts. Here, we find none, perhaps, but we do see a relevant adaptation where we lack such Darwinian explanations in the domestication theories.

In fact, as Liebermann [136] puts it, “many researchers [137] thus consider *Homo sapiens* to be a morphologically diverse species with archaic and anatomically modern grades.” And, in his 2019 article, Caldararo argues that no amount of mathematical jiggling can demonstrate a clear separation between the Upper Paleolithic premodern populations and present-day humans. Still, Liebermann’s [136] claim that he has discovered clear autapomorphies is only achieved by the subjective limitation of those current *Homo sapiens* populations and individuals who do not fit his categories. Another trait supposedly associated with neural crest-driven self-domestication is the reduction in tooth size. So, we see face reduction, cranial shape, tooth size all fail to relate to domestication in humans. Also, we find a major problem with the idea of white skin or patching pigmentation, unless the authors [82] of a study conducted on rhesus monkeys believe that the monkeys are domesticated, as we find such pigmentation common in them [138]. Obviously, human populations vary considerably in pigmentation due to environmental factors [139].

The lack of a population approach to human evolution, due to the smaller number of fossil samples and isolated parts, has given the discipline of paleoanthropology a distinct character of emphasizing a few traits in idealized AMH, ignoring others and their lack of appearance in contemporary populations. This complex situation regarding traits of premoderns and AMH is what we might expect given that both populations, being widespread species, have had to adapt to conditions, such as changing climates, over time. And, in the past 50,000 years of the spread of AMH, the climate has only moderated in the last 10,000 years.[140] suggest the chin of AMH could also be used as one of the *Homo sapiens* autapomorphies, but as Thayer and Dobson [141] contradicted this due to the considerable population variation in contemporary populations. What is more important is that some fossils long identified as premodern (Neanderthal) like from St. Cesaire have chins that fall with contemporary human variation (see Thayer and Dobson [141]). It is clear that the “chin” of St. Cesaire is within this series of variations. Wider views on the nature of human cranial and skeletal diversity focus on the idea of “modernity”, where populations became sedentary [142]; others are critical of what modernity is and how it has been characterized [143](Figure 1).

Fig. 10-5. *Distribution curves connected with the process of stabilizing selection.*

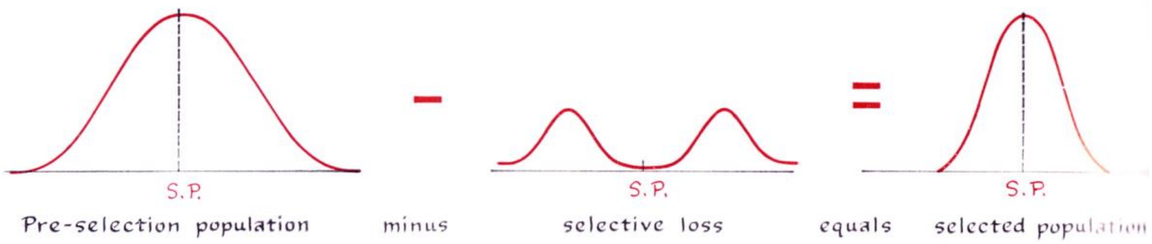

Figure 1 This illustration of stabilizing selection is from Bumpus [144], modified by Hardin [145, 146]. See below.

Still, Zanella et al. [111] have done an elegant job discussing the function of the *BAZ1B* gene and its relationship with other genes and functions. However, establishing it as a primary mover is perhaps unfounded. It brings up a number of problems related to phylogeny and ontogeny. For example, which came first, domestication of other animals or self-domestication? If we look at other social animals, e.g., insects, the origins of complex behavior appear in parasitoidism, as Farris and her colleagues have suggested [147], which apparently is linked to complex processing in the mushroom bodies of the insect brain. The development of these bodies is a characteristic of the social behavior of insects, but not entirely limited to them. Caldararo recently [85] paralleled this with the rise of hunting and gathering in premodern Homo since the complex process of hunting and gathering under scarcity conditions could lead to brain evolution. Yet this association is not true in the case of termites, another highly social insect, whose eusocial evolution seems to be a defensive development against their chief enemy, ants [148]. A degree of association between predation and sociality is seen in some spiders and fish. The problem here is the occurrence of a lag 10,000 years ago between large brains and the development of complex sedentary human societies. The time frame seems too short. Of course, we could simply argue that the products of initial human evolutionary cognition in the Upper Pleistocene era were directed only to toolmaking and other intellectual exercises, without any materialist outcomes. But discussions of human consciousness are so idealized that they are entirely subjective. When I was born, the Diagnostic and Statistical Manual of Mental Disorders (now the DSM-5) was less than a half-inch thick; today, it is over 5 inches thick. One might wonder if we as a species have become crazier since the end of the Second World War or we have discovered a myriad number of ways of performing our cognitive apparatus.

The small problem is that other mammalian social hunters like wolves and hunting dogs display little brain evolution over their canid and felid relatives [149, 150]. Often the idea of language as an aid to hunting is suggested, and various scenarios have been produced to give language a selective advantage in human evolution [151, 152]. In some cases, due to a lack of evidence of complexity, theories have been proposed by placing a mutation closer to the idea of social complexity after 50,000 B.P. [153].

5. Man's Uniqueness

Man's unique nature is widely accepted by several intellectuals, including Darwin and his defender Huxley. Huxley put forward a number of arguments to explain the seemingly great chasm separating man from other animals, the primates in particular. Darwin's book, *Descent of Man*, mainly focused on this issue. Today, we find a host of books trumpeting man's great abilities and dominance over nature. In 1941, Julian Huxley published a volume of essays by a variety of scholars on the subject. In his introduction, he states that the unity of man and animal proposed by Darwin and Thomas Huxley was only accomplished by their endeavor to not exaggerate human abilities or denigrate those of animals.

Caldararo made the same effort whenever unique views on traits and behaviors were presented, such as hair or keeping pets in man [73, 85, 154]. The essential problem does not reside with the traits or abilities described, such as language or big brains, but with the desire to find a unique place in nature, as Julian Huxley so clearly states. As Bickerton [152] notes, other animals also have language; however, as Deacon [27] painstakingly describes, the way that language gives us organizational abilities seems so overwhelmingly triumphant that any parallel with other animals seems absurd.

I do not depreciate the ability provided by language; rather, I think it is overblown. Yet as we do for many human abilities, such as "thinking", designing and making tools, music, or math, we tend to remark on the complexity of the language we have produced and forget its components and development. Vygotsky [155] noted the close and uneven development of this ability, requiring conditioning (as also described by Luria [32]) in the development of the human infant. In this case, the growth of the mastery of language seems like a recapitulation of the evolution of human consciousness, though the term "recapitulation" has too negative a connotation to be used with freedom (the idea was given serious expression by von Monkow in 1911 [156]). Nevertheless, as Oliver Sacks [157] describes the cases of individuals who display abnormalities of these components of human consciousness, the fragments expose the true nature of that ability. The Great Mental Calculators or Calculating Prodigies demonstrate unique abilities to produce computations of numbers, in primes, for example, that astound and surprise anyone. Are they visualizing the numbers, or since they cannot accomplish the simplest of arithmetic operations, are they "counting" by a music-like means, as Sacks suggests? To visualize Eratosthenes' sieve would be logical, but one must know the relationships of the numbers to recognize their commonality or composite nature.

Yet another problem is our ability to assess adequately the cognitive skills and perceptions of other animals. This is demonstrated in the research of Tomasello et al. [158], where they speak of children of 14 months "understanding" adult intentionality or producing "rational imitation"; however, using these terms distorts the behavior observed [159] in the same way as using similar terms for birds is considered anthropomorphic or projection. However, in recent years, we have discovered novel means of gaining access to many animals' cognitive life, as in the "representations" of rats in decision-making via hippocampal generation or as described by Kay et al. [160] in "generative representation", where memory is evoked in the process of future action.

The complex actions involved in the problem-solving skills of New Caledonian crows is another example, which, even a decade ago, would have been considered to be “anthropomorphic” in nature [161].

Some explanations of human uniqueness are associated with the size of the body, brain, and longevity. Often sociality is also linked to human uniqueness, which is similar to the case of naked mole rats who are uniquely long-lived, highly social, and naked—all traits similar to humans. The blindness of these rats and the fact that they live underground are ignored. One of these features, longevity, is common among many rodents, squirrels, beavers (also highly social), and porcupines [162], naked mole rats are easier to study because of their lab colonies and small size.

The evolution of the brain is usually associated with an increase in neurons and other cell types associated with signal processing and memory. As we cannot assess the actual neuron counts in fossils, and new research has shown decreased neuron numbers in the neocortex and demonstrated large counts in the cerebellum, focus on brain size has changed [94]. The idea of increased brain size in the Middle Pleistocene era, without a substantial increase in evidence of cognitive activity in complex behavior residues, might be explained by increased myelination to provide additional insulation in Ice Age conditions and faster transition of signs due to increased competition for reduced food supplies [163]. Research has indicated that compared with chimpanzees, human myelination is exceptional [164]. This would account for the leveling off of brain size noted after 50,000 B.P., where we enter the last glacial period and then a decrease to current brain sizes. As cold conditions in general dissipated and became seasonal and moderate; significant insulation would have been less of a selective advantage.

6. Abilities, Time, Superorganism and Scale, and a Conclusion

In his 2017 book*, Big Brains and the Human Superorganism*, Caldararo agreed with E.O. Wilson that the scale and physiology of the human body could explain much of the human abilities that seem so stupendous compared with other animals. As an example, he points out [165] that ants could hardly master fire given their size in relation to the temperatures created by fire. Their ability to control fire and use it systematically would be limited by how short their appendages are compared with the heat of a fire. I know of no one who has tested this theory, but it seems reasonable.

Two other elements of the domestication theory in humans need addressing; one is floppy ears; obviously, our ears are quite within the range of normal primate variation, and the second element is docility. Humans are not docile; we are very violent primates. Organized by language and culture, we are the most destructive and deadly animal on the planet. I made a more detailed critique above.

However, one may argue that the abilities to organize and control the environment are not specific to the human species but are accidental and might not ever be reproduced. This was suggested in Caldararo’s 2017 [85] book as well, and I think that it can be compared to an insight provided by Oliver Sacks regarding the special abilities of idiot savants and related pathologies [157]. Sacks notes that F.W. H. Myers, in his work on genius, found that such abilities could often be a temporary condition and disappear spontaneously. This gives rise to the question that if humans could be isolated from culture and language, could they reproduce the engine of ability they provide?

We should also think about domestication as several types. Self-domestication is considered a special form related to the eusocial environment of superorganisms. Here, while docility is reserved for co-specifics of a group, violence, and aggression are tools for the perpetuation of superorganism.

Perhaps the most disturbing fact about the theory of domestication proposed by Wilkins et al. [82] and modified to human self-domestication by later researchers [166, 167] is the idea that a group of mutations, mostly disruptive to the fitness of the organism, in combination could create traits that produce the characters of some modern human populations. I should note that Wilkins is in general agreement with Wrangham on the issue of the mechanisms of animal domestication but they have some differences.

The idea that Europeans, generally supposed here as White people of Caucasians, could be the product of such a cache of accidental combinations of mutations, which otherwise could be detrimental, is strangely reminiscent of a social evolutionary theory promoted by the founder of the Nation of Islam, Wallace Fard Muhammad. This theory argued that White people (Europeans) were the product of mutations, and all the terrors of Africans and other non-Europeans could be traced to the consequences, which were not only limited to the physical traits of Europeans but also reflected in their exploitive behavior, etc. [168]. Strange indeed.

Author Contributions

The author did all the research work of this study.

Competing Interests

The author has declared that no competing interests exist.

References

1. Hammond M. The shadow man paradigm in paleoanthropology, 1911-1945. In: Bones, bodies, behavior: Essays on biological anthropology. Madison: The University of Wisconsin Press; 1988. pp.117-137.
2. Spencer F. The shadow man paradigm in paleoanthropology. In: Bones, bodies, behavior. Madison: University of Wisconsin Press; 1988. pp.84-116.
3. Ewbank D. Measuring selection in human populations using the growth rate per generation. Philos Trans R Soc Lond B Biol Sci. 2016; 371: 20150148.
4. Codrington RH. The Melanesians. Cambridge: Clarendon Press; 1891.
5. Coon CS. The origin of races. New York: Alfred A. Knopf; 1962.
6. Lewontin RC. The apportionment of human diversity. In: Evolutionary biology. New York: Springer; 1972. pp.381-398.
7. Tattersall I. Species recognition in human paleontology. J Hum Evol. 1986; 15: 165-175.
8. Tattersall I. The many faces of Homo habilis. Evol Anthropol. 1992; 1: 33-37.
9. Ni X, Ji Q, Wu W, Shao Q, Ji Y, Zhang C, et al. Massive cranium from Harbin in northeastern China establishes a new Middle Pleistocene human lineage. Innovation. 2021; 2: 100130.
10. Hershkovitz I, May H, Sarig R, Pokhojaev A, Grimaud-Hervé D, Bruner E, et al. A middle pleistocene homo from Nesher Ramla, Israel. Science. 2021; 372: 1424-1428.

11. Bradley PS, Fayyad UM. Refining initial points for k-means clustering. In: ICML’98. Burlington: Morgan Kaufmann Publishers; 1998. pp.91-99.
12. Celebi ME, Kingravi HA, Vela PA. A comparative study of efficient initialization methods for the k-means clustering algorithm. Expert Syst Appl. 2013; 40: 200-210.
13. Van der Laan M, Pollard K, Bryan J. A new partitioning around medoids algorithm. J Stat Comput Simul. 2010; 73: 575-584.
14. Caldararo N, Gabow S. Mitochondrial DNA analysis and the place of Neandertals in Homo. Ancient Biomol. 2000; 3: 135-158.
15. Chepko-Sade BD, Halpin ZT. Mammalian dispersal patterns: The effects of social structure on population genetics. Chicago: University of Chicago Press; 1987.
16. Alexander RD. Evolution of the human psyche. In: The human revolution. Princeton: Princeton University Press; 1989. pp.455-513.
17. Williams GC. Sex and evolution. Princeton: Princeton University Press; 1975.
18. Howell FC. Paleo-demes, species clades, and extinctions in the Pleistocene hominin record. J Anthropol Res Das. 1999; 55: 191-243.
19. Chen J, Glémin S, Lascoux M. From drift to draft: How much do beneficial mutations actually contribute to predictions of Ohta’s slightly deleterious model of molecular evolution? Genetics. 2020; 214: 1005-1018.
20. Weaver TD, Roseman CC, Stringer CB. Close correspondence between quantitative-and molecular-genetic divergence times for Neandertals and modern humans. Proc Natl Acad Sci USA. 2008; 105: 4645-4649.
21. Johri P, Charlesworth B, Jensen JD. Toward an evolutionarily appropriate null model: Jointly inferring demography and purifying selection. Genetics. 2020; 215: 173-192.
22. Runemark A, Vallejo-Marin M, Meier JI. Eukaryote hybrid genomes. PLoS Genet. 2019; 15: e1008404.
23. Harrison RG, Larson EL. Hybridization, introgression, and the nature of species boundaries. J Hered. 2014; 105: 795-809.
24. Scerri EM, Thomas MG, Manica A, Gunz P, Stock JT, Stringer C, et al. Did our species evolve in subdivided populations across Africa, and why does it matter? Trends Ecol Evol. 2018; 33: 582-594.
25. Wolpoff MH. Multiregional evolution: The fossil alternative to Eden. In: The human evolution. Princeton: Princeton University Press; 1989. pp.62-108.
26. Klein RG. The human career. Chicago: University of Chicago Press; 1989.
27. Deacon TW. The symbolic species. New York: W.W. Norton & Co; 1997.
28. Wrangham RW. Targeted conspiratorial killing, human self-domestication and the evolution of groupishness. Evol Hum Sci. 2021; 3: e26.
29. Hagen LK. The bilingual brain: Human evolution and second language acquisition. Evol Psychol. 2008; 6: 43-63.
30. Herdt G. Secrecy and cultural reality: Utopian ideologies of the New Guinea Men's House. Ann Arbor: University of Michigan Press; 2003.
31. Kotchoubey B. Human consciousness: Where is it from and what is it for. Front Psychol. 2018; 9: 567.
32. Luria AR. The working brain. Harmondsworth: Penguin Books; 1973.
33. Sacks O. The man who mistook his wife for a hat. New York: Harper & Row; 1985.

34. Sacks O. Hallucinations. New York: Vintage Books; 2013.
35. Von Bonin G. The cerebral cortex. Springfield: Charles C. Thomas; 1960.
36. Caldararo N. A mental ethnography. Palgrave/Macmillan. 2022.
37. Fabbro F, Cantone D, Feruglio S, Crescentini C. Origin and evolution of human consciousness. Prog Brain Res. 2019; 250: 317-343.
38. Laing RD. The divided self. Baltimore: Pelican Books; 1965.
39. Masonari K, Hoffa T, Takeyama T, Awata S, Tanaka H, Asai J, et al. If a fish can pass the mark test, what are the implications for consciousness and self-awareness testing in animals? PLoS Biol. 2019; 17: e3000021.
40. Firmin JA. The equality of the human races. Oxfordshire: Taylor & Francis; 2000.
41. Xia B, Yan Y, Baron M, Wagner F, Barkley D, Chiodin M, et al. Widespread transcriptional scanning in the testis modulates gene evolution rates. Cell. 2020; 180: 248-262.
42. Caldararo N. Probability, populations, phylogenetics, and hominin speciation. Hum Biol. 2018; 90: 129-155.
43. Grother P, Ngan M, Hanaoka K. Face recognition vendor test (FVRT): Part 3, demographic effects [Internet]. Gaithersburg: National Institute of Standards and Technology; 2019. Available from: https://nvlpubs.nist.gov/nistpubs/ir/2019/NIST.IR.8280.pdf.
44. Metz C. Can artificial intelligence be bias-free [Internet]? New York: The New York Times; 2021. Available from: https://www.nytimes.com/2021/03/15/technology/artificial-intelligence-google-bias.html?searchResultPosition=1.
45. Lohse K, Frantz LA. Neandertal admixture in Eurasia confirmed by maximum-likelihood analysis of three genomes. Genetics. 2014; 196: 1241-1251.
46. Petr M, Pääbo S, Kelso J, Vernot B. Limits of long-term selection against Neandertal introgression. Proc Natl Acad Sci USA. 2019; 116: 1639-1644.
47. Ziętkiewicz E, Yotova V, Gehl D, Wambach T, Arrieta I, Batzer M, et al. Haplotypes in the dystrophin DNA segment point to a mosaic origin of modern human diversity. Am J Hum Genet. 2003; 73: 994-1015.
48. Taskent O, Lin YL, Patramanis I, Pavlidis P, Gokcumen O. Analysis of haplotypic variation and deletion polymorphisms point to multiple archaic introgression events, including from Altai Neanderthal lineage. Genetics. 2020; 215: 497-509.
49. Durvasula A, Sankararaman S. Recovering signals of ghost archaic introgression in African populations. Sci Adv. 2020; 6: eaax5097.
50. Hubisz MJ, Williams AL, Siepel A. Mapping gene flow between ancient hominins through demography-aware inference of the ancestral recombination graph. PLoS Genet. 2020; 16: e1008895.
51. Wallace DC. Mitochondrial DNA variation in human radiation and disease. Cell. 2015; 163: 33-38.
52. Stringer C. Lone survivors. New York: St. Martin's Press; 2012.
53. Stringer C. Why we are not all multiregionalists now. Trends Ecol Evol. 2014; 29: 248-251.
54. Fried M. The notion of tribe. Menlo Park: Cummings Publishing Co.; 1975.
55. Geary DC, Vigil J, Byrd-Craven J. Evolution of human mate choice. J Sex Res. 2004; 41: 27-42.
56. Trivers R. Social evolution. Menlo Park: The Benjamin/Commings Publishing Co.; 1985.
57. Dawkins R. The selfish gene. 2nd ed. Oxford: Oxford University Press; 1989.
58. Parry GD. The meanings of r-and K-selection. Oecologia. 1981; 48: 260-264.

59. Nettle D, Pollet TV. Natural selection on male wealth in humans. Am Nat. 2008; 172: 658-666.
60. Brentano R. The early Middle Ages 500-1000. New York: The Free Press of Glencoe; 1964.
61. Chagnon NA. Yanomamo: The fierce people. New York: Holt, Rinehart and Winston; 1968.
62. Hunter M. Reaction to conquest: Effects of contact with Europeans on the Pondo of South Africa. Oxford: Oxford University Press; 1936.
63. Krings M, Stone A, Schmitz RW, Krainitzki H, Stoneking M, Pääbo S. Neandertal DNA sequences and the origin of modern humans. Cell. 1997; 90: 19-30.
64. De Manuel M, Kuhlwilm M, Frandsen P, Sousa VC, Desai T, Prado-Martinez J, et al. Chimpanzee genomic diversity reveals ancient admixture with bonobos. Science. 2016; 354: 477-481.
65. Oakley KP. Frameworks for dating fossil man. Chicago: Aldine Publishing Company; 1968.
66. Parins-Fukuchi C, Greiner E, MacLatchy LM, Fisher DC. Phylogeny, ancestors, and anagenesis in the hominin fossil record. Paleobiology. 2019; 45: 378-393.
67. Gingerich PD. Species in the fossil record: Concepts, trends, and transitions. Paleobiology. 1985; 11: 27-41.
68. Gingerich PD. The stratophenetic approach to phylogeny reconstruction in vertebrate paleontology. In: Phylogenetic analysis and paleontology. New York: Columbia University Press; 1979. pp.41-78.
69. Jelínek J. The east and southeast Asian way of regional evolution. Anthropos. 1982; 21: 195-212.
70. Wolpoff MH, Wu X, Thorne AG. Modern Homo sapiens origins: A general theory of hominid evolution involving the fossil evidence from East Asia. In: The origins of modern humans: A world survey of the fossil evidence. New York: Alan R. Liss, Inc.; 1984. pp.411-483.
71. Hammer MF. Human hybrids. New York: Scientific American; 2016. pp.44-49.
72. Wilson PJ. The domestication of the human species. New Haven: Yale University Press; 1988.
73. Caldararo N. Hair, human evolution, and the idea of human uniqueness. Evol Anthropol. 2005; 14: 132-133.
74. Freud S. Civilization and its discontents. New York: W.W. Norton; 1962.
75. Humphrey N. The inner eye: Social intelligence in evolution. Oxford: Oxford University Press; 1986.
76. Caldararo N. The tendency to make man an exception. In: Primatology: Theories, methods and research. New York: Nova Publishers; 2009. pp.113-128.
77. Sánchez-Villagra MR, van Schaik CP. Evaluating the self-domestication hypothesis of human evolution. Evol Anthropol. 2019; 28: 133-143.
78. Darlington PF. Rates, patterns, and effectiveness of evolution in multi-level situations. Proc Natl Acad Sci USA. 1976; 73: 1360-1364.
79. Gould SJ. Ontogeny and phylogeny. Cambridge: Harvard University Press; 1977.
80. De Beer GR. Embryos and ancestors. Oxford: Clarendon Press; 1958.
81. Johnsson M, Henriksen R, Wright D. The neural crest cell hypothesis: No unified explanation for domestication. Genetics. 2021; 219: iyab097.
82. Wilkins AS, Wrangham RW, Fitch WT. The “domestication syndrome” in mammals: A unified explanation based on neural crest cell behavior and genetics. Genetics. 2014; 197: 795-808.
83. Wilkins AS, Wrangham R, Fitch WT. The neural crest/domestication syndrome hypothesis, explained: Reply to Johnsson, Henriksen, and Wright. Genetics. 2021; 219: iyab098.

84. Athreya S, Hopkins A. Conceptual issues in hominin taxonomy: Homo heidelbergensis and an ethnobiological reframing of species. Am J Phys Anthropol. 2021; 175: 4-26.
85. Caldararo N. Big brains and the human superorganism. Lanham: Lexington Books; 2017.
86. Caldararo N. Preliminary observations on the behavior of feral chickens (Jungle Fowl) on the island of Kauai: Reflections on domestication as complexity. Int J Environ Sci Nat Resour. 2017; 4: 107-111.
87. Zichello JM, Baab KL, McNulty KP, Raxworthy CJ, Steiper ME. Hominoid intraspecific cranial variation mirrors neutral genetic diversity. Proc Natl Acad Sci USA. 2018; 115: 11501-11506.
88. Kern AD, Hahn MW. The neutral theory in light of natural selection. Mol Biol Evol. 2018; 35: 1366-1371.
89. Flynn JR. Are we getting smarter? Cambridge: Cambridge University Press; 2012.
90. Arnsten AF, Paspalas CD, Gamo NJ, Yang Y, Wang M. Dynamic network connectivity: A new form of neuroplasticity. Trends Cogn Sci. 2010; 14: 365-375.
91. Berto S, Mendizabal I, Usui N, Toriumi K, Chatterjee P, Douglas C, et al. Accelerated evolution of oligodendrocytes in the human brain. Proc Natl Acad Sci USA. 2019; 116: 24334-24342.
92. Powell J, Lewis PA, Roberts N, García-Fiñana M, Dunbar RI. Orbital prefrontal cortex volume predicts social network size: An imaging study of individual differences in humans. Proc Royal Soc B Biol Sci. 2012; 279: 2157-2162.
93. Semendeferi K, Lu A, Schenker N, Damásio H. Humans and great apes share a large frontal cortex. Nat Neurosci. 2002; 5: 272-276.
94. Herculano-Houzel S. The human advantage. Cambridge: MIT Press; 2016.
95. Shah KN, Dalal SJ, Desai MP, Sheth PN, Joshi NC, Ambani LM. White forelock, pigmentary disorder of irides, and long segment Hirschsprung disease: Possible variant of Waardenburg syndrome. J Pediatr. 1981; 99: 432-435.
96. Pina-Garza JE. Lower brainstem and cranial nerve dysfunction. In: Fenichel's clinical pediatric neurology. Amsterdam, Netherlands: Elsevier; 2013.
97. Gregory TR. Macroevolution and the genome. In: The evolution of the genome. Amsterdam: Academic Press; 2005. pp.679-729.
98. Martinson EO, Kelkar YD, Chang CH, Werren JH. The evolution of venom by co-option of single-copy genes. Curr Biol. 2017; 27: 2007-2013.e8.
99. Levy AM. Genes from the junkyard. Nature. 2019; 574: 314-316.
100. Wheat CH, Fitzpatrick JL, Rogell B, Temrin H. Behavioural correlations of the domestication syndrome are decoupled in modern dog breeds. Nat Commun. 2019; 10: 2422.
101. Pinker S. The better angels of our nature. New York: Penguin Books; 2015.
102. Davidson B. The lost cities of Africa. Boston: Little Brown & Co.; 1970.
103. Caldararo N. War or religion in different cultural contexts: Discerning war, violence, empires or proselytizing & religious cults from archaeology and literature. Insights Anthropol. 2020; 4: 207-223.
104. Lieberman DE. Testing hypotheses about recent human evolution from skulls: Integrating morphology, function, development, and phylogeny. Curr Anthropol. 1995; 36: 159-197.
105. Leroi AM. On human diversity. Scientist. 2005; 19: 16-17.
106. Posth C, Wißing C, Kitagawa K, Pagani L, van Holstein L, Racimo F, et al. Deeply divergent archaic mitochondrial genome provides lower time boundary for African gene flow into Neanderthals. Nat Commun. 2017; 8: 16046.

107. Vernot B, Tucci S, Kelso J, Schraiber JG, Wolf AB, Gittelman RM, et al. Excavating Neandertal and Denisovan DNA from the genomes of Melanesian individuals. Science. 2016; 352: 235-239.
108. Bradt S. Molecular analysis confirms T. Rex's evolutionary link to birds [Internet]. Cambridge: Harvard University; 2008. Available from: https://news.harvard.edu/gazette/story/2008/04/molecular-analysis-confirms-t-rexs-evolutionary-link-to-birds/.
109. Yang MA, Malaspinas AS, Durand EY, Slatkin M. Ancient structure in Africa unlikely to explain Neanderthal and non-African genetic similarity. Mol Biol Evol. 2012; 29: 2987-2995.
110. Wrangham RW. The goodness paradox: How evolution both made us more and less violent. London: Profile Books; 2019.
111. Zanella M, Vitriolo A, Andirko A, Martins PT, Sturm S, O'Rourke T, et al. Dosage analysis of the 7q11. 23 Williams region identifies BAZ1B as a major human gene patterning the modern human face and underlying self-domestication. Sci Adv. 2019; 5: eaaw7908.
112. Barsh GS, Cooper GM, Copenhaver GP, Sirugo G, Tang H, Williams SM. Evaluating the strength of genetic results: Risks and responsibilities. PLoS Genet. 2019; 15: e1008437.
113. Spoor F, Leakey MG, Leakey LN. Correlation of cranial and mandibular prognathism in extant and fossil hominids. Trans R Soc South Africa. 2005; 60: 85-89.
114. Franciscus RG, Long JC. Variation in human nasal height and breadth. Am J Phys Anthropol. 1991; 85: 419-427.
115. Leong SC, Eccles R. A systematic review of the nasal index and the significance of the shape and size of the nose in rhinology. Clin Otolaryngol. 2009; 34: 191-198.
116. Brace CL. The stages of human evolution. Englewood Cliffs: Prentice-Hall; 1967.
117. Wood SR. Tooth wear and the sexual division of labour in an Inuit population. Burnaby: Simon Fraser University; 1984.
118. Gómez-Robles A, Smaers JB, Holloway RL, Polly PD, Wood BA. Brain enlargement and dental reduction were not linked in hominin evolution. Proc Natl Acad Sci USA. 2017; 114: 468-473.
119. Ungar P. Evolution's bite: A story of teeth, diet, and human origins. Princeton: Princeton University Press; 2017.
120. Brace CL, Nagai M. Japanese tooth size: Past and present. Am J Phys Anthropol. 1982; 59: 399-411.
121. Brace CL, Ryan AS. Sexual dimorphism and human tooth size differences. J Hum Evol. 1980; 9: 417-435.
122. Saboureau M, Bobet JP, Boissin J. Cyclic activity of adrenal function and seasonal variations of cortisol peripheral metabolism in a hibernating mammal, the hedgehog (Erinaceus europaeus L.). J Physiol. 1980; 76: 617-629.
123. Swierczynska MM, Mateska I, Peitzsch M, Bornstein SR, Chavakis T, Eisenhofer G, et al. Changes in morphology and function of adrenal cortex in mice fed a high-fat diet. Int J Obes. 2015; 39: 321-330.
124. Tepperman J. Metabolic and endocrine physiology. 4th ed. Chicago: Year Book Medical Publishers; 1980.
125. Hublin JJ, Neubauer S, Gunz P. Brain ontogeny and life history in Pleistocene hominins. Philos Trans R Soc B. 2015; 370: 20140062.
126. Garratt M, Gaillard JM, Brooks RC, Lemaître JF. Diversification of the eutherian placenta is associated with changes in the pace of life. Proc Natl Acad Sci USA. 2013; 110: 7760-7765.

127. Jung YH, Cho BH. Radiographic evaluation of third molar development in 6-to 24-year-olds. Imaging Sci Dent. 2014; 44: 185-191.
128. Chaillet N, Nyström M, Demirjian A. Comparison of dental maturity in children of different ethnic origins: International maturity curves for clinicians. J Forensic Sci. 2005; 50: 1164-1174.
129. Beals KL, Smith CL, Dodd SM, Angel JL, Armstrong E, Blumenberg B, et al. Brain size, cranial morphology, climate, and time machines [and comments and reply]. Curr Anthropol. 1984; 25: 301-330.
130. Gunz P, Tilot AK, Wittfeld K, Teumer A, Shapland CY, Van Erp TG, et al. Neandertal introgression sheds light on modern human endocranial globularity. Curr Biol. 2019; 29: 120-127.
131. Howells W. Mankind in the making: The story of human evolution. Harmondsworth: Penguin Books; 1959.
132. Li P, Smith KK. Comparative skeletal anatomy of neonatal ursids and the extreme altriciality of the giant panda. J Anat. 2020; 236: 724-736.
133. Palmert MR, Boepple PA. Variation in the timing of puberty: Clinical spectrum and genetic investigation. J Clin Endocrinol Metab. 2001; 86: 2364-2368.
134. Brix N, Ernst A, Lauridsen LL, Parner E, Støvring H, Olsen J, et al. Timing of puberty in boys and girls: A population-based study. Paediatr Perinat Epidemiol. 2019; 33: 70-78.
135. Maan ME, Sefc KM. Colour variation in cichlid fish: Developmental mechanisms, selective pressures and evolutionary consequences. Semin Cell Dev Biol. 2013; 24: 516-528.
136. Liebermann DE, McBratney BM, Krovitz G. The evolution and development of cranial form in Homo sapiens. Proc Natl Acad Sci USA. 2002; 99: 1134-1139.
137. Wolpoff MH, Hawks J, Frayer DW, Hunley K. Modern human ancestry at the peripheries: A test of the replacement theory. Science. 2001; 291: 293-297.
138. Montagna W. The skin of nonhuman primates. Am Zoo. 1972; 12: 100-124.
139. Jablonski N. Skin: A natural history. Berkeley: University of California Press; 2006.
140. Schwartz JH, Tattersall I. The human chin revisited: What is it and who has it? J Hum Evol. 2000; 38: 367-409
141. Thayer ZM, Dobson SD. Geographic variation in chin shape challenges the universal facial attractiveness hypothesis. PloS ONE. 2013; 8: e60681.
142. Mirazon Lahr M. The shaping of human diversity: Filters, boundaries and transitions. Philos Trans R Soc Lond B Biol Sci. 2016; 371: 20150241.
143. Pearson OM. Postcranial remains and the origin of modern humans. Evol Anthropol. 2000; 9: 229-247.
144. Bumpus HC. The elimination of the unfit as illustrated by the introduced House Sparrow Passer domesticus. Woods Hole: Marine Biology Laboratory; 1899. pp.209-226.
145. Hardin G. Biology: Its principles and implications. 2nd ed. San Francisco: Freeman; 1966.
146. Bumpus HC. The variations and mutations of the introduced sparrow: Passer domesticus. Woods Hole: Marine Biology Laboratory; 1898. pp.1-16.
147. Farris SM, Schulmeister S. Parasitoidism, not sociality, is associated with the evolution of elaborate mushroom bodies in the brains of hymenopteran insects. Proc Royal Soc B. 2011; 278: 940-951.
148. Engel MS, Barden P, Riccio ML, Grimaldi DA. Morphologically specialized termite castes and advanced sociality in the Early Cretaceous. Curr Biol. 2016; 26: 522-530.

149. Finarelli JA, Flynn JJ. Brain-size evolution and sociality in Carnivora. Proc Natl Acad Sci USA. 2009; 106: 9345-9349.
150. Van Schaik CP, Isler K, Burkart JM. Explaining brain size variation: From social to cultural brain. Trends Cogn Sci. 2012; 16: 277-284.
151. d'Errico F, Vanhaeren M, Henshilwood C, Lawson G, Maureille B, Gambier D, et al. From the origin of language to the diversification of languages. In: Becoming eloquent: Advances in the emergence of language, human cognition, and modern cultures. Amsterdam: John Benjamins Publishing Co.; 2009. pp.13-68.
152. Bickerton D. Language and species. Chicago: University of Chicago Press; 1992.
153. Klein RG. Language and human evolution. J Neurolinguistics. 2017; 43: 204-221.
154. Caldararo N. Complex animal societies, domestication and human uniqueness. J Primatol. 2012; 1: 103.
155. Vygotsky LS. Mind in society. Cambridge: Harvard University Press; 1978.
156. Von Monakow C. Localization of brain functions. J Psychol Neurol. 1911; 17: 185-200.
157. Sacks O. The man who mistook his wife for a hat. Oxfordshire: Routledge; 1985.
158. Tomasello M, Carpenter M, Call J, Behne T, Moll H. Understanding and sharing intentions: The origins of cultural cognition. Behav Brain Sci. 2005; 28: 675-691.
159. Herschensohn J. Review of the language instinct. Mod Lang J. 2007; 91: 486-487.
160. Kay K, Chung JE, Sosa M, Schor JS, Karlsson MP, Larkin MC, et al. Constant sub-second cycling between representations of possible futures in the hippocampus. Cell. 2020; 180: 552-567.
161. von Bayern AM, Danel S, Auersperg AM, Mioduszewska B, Kacelnik A. Compound tool construction by New Caledonian crows. Sci Rep. 2018; 8: 15676.
162. Gorbunova V, Bozzella MJ, Seluanov A. Rodents for comparative aging studies: From mice to beavers. Age. 2008; 30: 111-119.
163. Stiefel KM, Torben-Nielsen B, Coggan JS. Proposed evolutionary changes in the role of myelin. Front Neurosci. 2013; 7: 202.
164. Miller DJ, Duka T, Stimpson CD, Schapiro SJ, Baze WB, McArthur MJ, et al. Prolonged myelination in human neocortical evolution. Proc Natl Acad Sci USA. 2012; 109: 16480-16485.
165. Wilson EO. Sociobiology. Cambridge: Harvard University Press; 1976.
166. Theofanopoulou C, Gastaldon S, O'Rourke T, Samuels BD, Messner A, Martins PT, et al. Self-domestication in Homo sapiens: Insights from comparative genomics. PloS ONE. 2017; 12: e0185306.
167. Benítez-Burraco A, Lattanzi W, Murphy E. Language impairments in ASD resulting from a failed domestication of the human brain. Front Neurosci. 2016; 10: 373.
168. Beynon ED. The voodoo cult among negro migrants in Detroit. Am J Sociol. 1938; 43: 894-907.