

Could There Have Been Human Families Where Parents Came from Different Populations: Denisovans, Neanderthals or Sapiens?

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Abstract. No later than ~500kya the population of *Homo sapiens* split into three lineages of independently evolving human populations: Sapiens, Neanderthals and Denisovans. After several hundred thousands years, they met several times and interbred with low frequency. Evidence of coupling between them is found in fossil records of Neanderthal – Sapiens offspring (*Oase 1*) and Neanderthal – Denisovans (*Denisova 11*) offspring. Moreover, the analysis of ancient and present-day population DNA shows that there were several significant gene flows between populations. Many introgressed sequences from Denisovans and Neanderthals were identified in genomes of currently living populations. All these data, according to biological species definition, may indicate that populations of *H. sapiens sapiens* and two extinct populations *H. sapiens neanderthalensis* and *H. sapiens denisovensis* are one species. Ontological transitions from pre-human beings to humans might have happened before the initial splitting of the *Homo sapiens* population or after the splitting during evolution of *H. sapiens sapiens* lineage in Africa. If the ensoulment of the first homo occurred in the evolving populations of *H. sapiens sapiens*, then occasionally mixed couples (Neanderthals – Sapiens or Denisovans – Sapiens) created relations that functioned as a family, in which children could have matured.

Keywords: Neanderthals; Denisovans; *Homo sapiens*; interbreeding; gene flow; ensoulment.

Introduction

In the Middle (770–129kya) and Late (129–11,7kya) Pleistocene era, fossil records of *Homo sapiens* individuals were found e.g.: in Marocco (*Jebel Irhoud, Rabat, Dar-es-Soltan II, El-Aliya and Témara*), in Southern Africa (*Florisbad, Klasies River Mouth, Border Cave*), in East Africa (*Eliye Springs, Ngaloba, Omo Kibish, Guomde, Herto, Singa*), in Western Asia (*Misliya Cave, Mugharet es-Skhul, Qafzeh Cave, Manot Cave*) (Hershkovitz et al. 2015, 216, Hershkovitz et al. 2018, 1, Stringer 2016, 3–6), in Europe (*Apidima Cave, Oase 1*) (Fu et al. 2015, 1, Harvati et al. 2019, 1), in Asia (*Ust'-Ishim, Tianyuan*) (Slon et al. 2018, figure 1). Neanderthal fossil sites from Middle and Late Pleistocene are known from e.g.: Europe (*Sima de los Huesos, El Sidrón, Les Cottés, Spy, Goyet, Feldhofer, Vindija*), Asia (*Mezmaiskaya, Chagyrskaya, Altai, Shanidar, Tabun, Dederiyeh, Kebara, 'Ein Qashish, Amud Caves*) (Been et al. 2017, 1,5, Mafessoni et al. 2020, 15132, Slon et al. 2018, figure 1, Solecki 1963, 179). Denisovans are only known from a distal manual phalanx (*Denisova 3*), three molars (*Denisova 2, Denisova 4 and Denisova 8*), and a fragment of a long bone (*Denisova 11*) all excavated at Denisova Cave in the Altai Mountains in southern Siberia (Reich et al. 2010, 1058, Slon et al. 2017, 1, Slon et al. 2018, 1).

Identification of ancient DNA in the fossils of the hominins and sequencing genomes¹ from the present individuals of geographically diverse human populations allowed the discovery that interbreeding between different lineages of homo such as Sapiens, Neanderthals and Denisovans occurred (Green et al. 2010, 1, Meyer et al. 2012, 1, Prüfer, 2014, 1, Reich 2010, 1). Studies of nuclear and mitochondrial DNA enable the detection of not only the sequences that are shared from a common ancestor but also the introgressed sequences. An introgression takes place when individuals from distinctly evolved populations interbreed in contact zones so some DNA sequences can flow from one population to the other one, and might become present in a gene pool² of a population through following generations. Each

¹ Genome is the genetic material of an organism (Merriam-Webster Collegiate Dictionary).

² Gene pool is the collection of genes in an interbreeding population that includes each gene at a certain frequency in relation to its variants (Merriam-Webster Collegiate Dictionary).

detected introgressed sequence is proof of an interbreeding event, because there is no other natural process among hominins which could explain gene flow between individuals.

Data from human fossils record (genetic, anatomical, archeological, geological) and also from historical climatic fluctuations and animal fossils enable us to predict how evolution of hominin population may have progressed. The estimation of the human population mutation rate per generation and calibration of data thanks to fossil evidence allow estimation of the probable time of divergence between populations. According to the concept of biological species and paying attention to theological considerations of humans origins, created by God in His image, we could postulate how the first person or couple looked; when and where may have lived; whether they had a rational soul; and could undergo *caritas* with God.

In this paper, evidence of Neanderthal and Denisovan sequences existing in contemporary human populations will be presented. Some of these introgressed DNA fragments will be mentioned in this article. Next, the divergence times between populations of Sapiens, Denisovans and Neanderthals and main gene flows which occurred between them after divergence of their lineages will be shown. The second part will describe a concept of multi-regional evolution of hominins in Africa; a consideration of the biological species concept; a view on the theological origin of humans with regard to poly- and monogenism; and a brief reflection on signs of “intelligent” Neanderthal activity. A final reflection will be presented on the time of ontological transition from pre-humans to humans.

1. Evidence of Neanderthal and Denisovan sequences in genomes of present-day populations

In 2015, the 1000 Genomes Project was completed. This resulted in the reconstructed genomes of 2,504 present-day individuals from 26 populations around the world. It provided a global reference for human genetic variation (The 1000 Genomes Project Consortium 2015, 68). Thanks to this project, among the genomes of present-day humans populations, inherited sequences

from Neanderthals have been identified: Africans (17 Mb³ on average per individual); Europeans (51 Mb on average per individual); East Asians (55 Mb on average per individual); and South Asians (55 Mb on average per individual). The signal of Neanderthal ancestry detected in Africans is a sign of human back-migration to Africa which came after the split of Europeans and East Asians, from a population related to the European lineage (Chen et al. 2020, 3–4). Glacial events which occurred around 106–94kya, 89–73kya, 59–47kya and 45–29kya may have contributed to the potential gene flow back into Africa (Timmermann and Friedrich 2016, 94). The modest 8% enrichment of Neanderthal ancestry in present-day Asians compared to Europeans is explained by a single wave of Neanderthal admixture occurring after the out-of-Africa dispersal into the ancestors of Asians. (Chen et al. 2020, 9, Meyer et al. 2012, 5, Petr et al. 2018, 1641, Vernot and Akey 2015, 450).

The Denisovan sequence which was identified in African samples (1.2 Mb on average per individual) is similar to the amount in non-African individuals (~1 Mb on average per individual) (Chen et al. 2020, 4), except for the Papuans, which have ~ 30 Mb per individual. This can be explained by independent waves of Denisovan admixture from a population closely related to the Altai Denisovans to the ancestors of present-day East Asians; whereas the component more distantly related to the Altai Denisovans forms the major part of the Denisovan ancestry in Papuans (Browning et al., 2018, 7).

The evidence of Neanderthal and Denisovan sequence presences in all sequenced genomes of present-day populations illustrated here indicate that all people living nowadays are descendants of populations in which interbreeding between Sapiens with Neanderthals and Denisovans occurred.

2. Estimates of split times between populations of hominins

The full suite of derived Neanderthal features (anatomical and functional modules) did not emerge as a single package, but those different features

³ Mb is a mega base pairs (= 1,000,000 bp).

appeared separately and at different times. In particular, Neanderthal facial morphology, dental and mandibular features evolved first, followed by changes in the neurocranium (Arsuaga et al. 2014, 1358, 1362). New hominin remains of at least five individuals from Jebel Irhoud (Morocco) are dated to 315 ± 34 kya. The Irhoud fossils are evidence of the early phase of *H. sapiens* evolution in Africa, because of their elongated rather than globular braincase shapes. Their brain size fell within the range of present-day humans. Whereas their facial, mandibular and dental morphology align with an early anatomically modern humans from Ethiopia Omo Kibish dated 195 ± 5 kya and Herto dated 160–154 kya. It corroborates the interpretation of the fragmentary specimen from Florisbad (South Africa) as an early *H. sapiens*, tentatively dated to 259 ± 35 kya. As in the Neanderthal lineage, facial morphology was established early on, and evolution in the last 300 kya primarily affected the braincase, brain connectivity, organization and development. Brain shape evolved gradually within the *H. sapiens* lineage, reaching present-day human variation between about 100–35 kya (Grün et al. 1996, 500, Hublin et al. 2017, 289, 291, McDougall et al. 2005, 733, Neubauer et al. 2018, 1, Scerri et al. 2018, 583, White et al. 2003, 742).

DNA from Sima de los Huesos hominins (early Neanderthals or closely related to the ancestors of Neanderthals) indicate that the population divergence between Neanderthals and Denisovans predates 430 kya (Meyer et al. 2016, 504, 506). The estimates of Neanderthal population divergence times from the common ancestors shared with the Denisovans is around 440 kya (95% confidence interval, 484–367 kya) according to Hajdinjak et al. (2018, 5). This data is consistent with the divergence time of between 473–381 kya calculated by Prüfer et al. (2014, 44). Estimates of the divergence time between ancestors of Sapiens and ancestors of both Neanderthals and Denisovans are: about 530 kya (95% confidence interval, 565–503 kya) (Hajdinjak et al. 2018, 5), between 765–550 kya (Prüfer et al. 2014, 44), 640–484 kya (Kuhlwilm et al. 2016, 432). In the view of these data, the last common ancestor of Sapiens, Neanderthals and Denisovans lived until around 500 kya (figure 1).

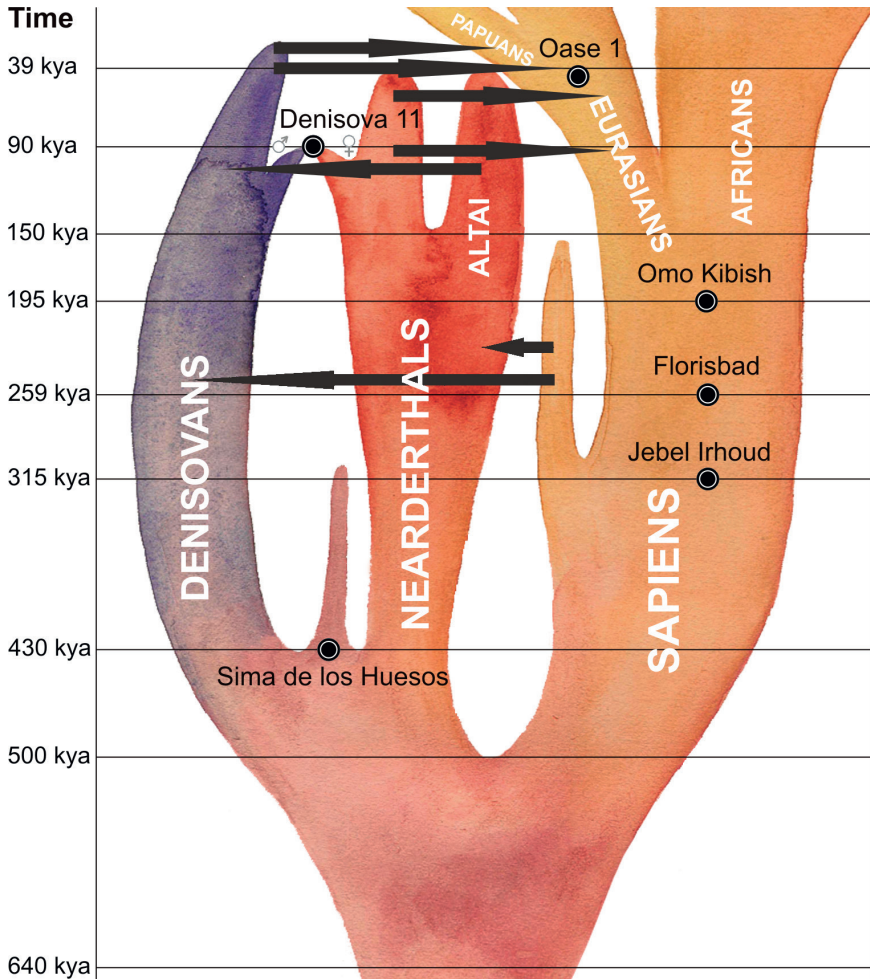


Figure 1. Phylogenetic tree of *Homo sapiens* species. Black arrows: gene flow between populations. *Denisova 11* had a Denisovan father and Neanderthal mother

3. Adaptive introgressions

Most of the gene flow has probably occurred intermittently, often in both directions and across a geographic range. Hominin groups met and had offspring on many occasions in the Late Pleistocene, but the extent of

gene flow between the groups was generally low (Prüfer et al. 2014, 48). Introgressed sequences are under the pressure of a purifying selection to remove genetic material, which indicate that the Sapiens, Neanderthal and Denisovans alleles⁴ were often not tolerated in each other's genetic background. Introgressed sequences could have been transmitted successfully to next generations because individuals which carried them have benefits over those who didn't have these introgressed sequences. This process is adaptive when such introgressed alleles are maintained by natural selection. It is necessary to find associations between introgressed DNA and a phenotype⁵ to confer a fitness⁶ advantage.

There has been identification of 13 African-specific, 38 non-African specific and 31 African-European shared high frequency Neanderthal haplotypes⁷ which are targets of adaptive introgression, such as the ultraviolet-radiation sensitivity gene *POU2F3*⁸ and immune related genes *TLR1/6/10*⁹ (Chen et al. 2020). Neanderthal introgression also reintroduced thousands of ancestral hominin alleles lost in the Sapiens out of Africa bottleneck¹⁰ (Rinker et al. 2019, 1). More genes were introgressed from Neanderthals into Sapiens than in the other direction (Hajdinjak et al. 2018, 6). Gene flow (in the amount of 0,1–2,1% of the genome) from a population that diverged early from other Sapiens to ancestors of Neanderthal from the

⁴ An allele is a variant of a given gene (Wikipedia).

⁵ Phenotype is the physical expression of one or more genes (Merriam-Webster Collegiate Dictionary).

⁶ Fitness is the capacity of an organism to survive and transmit its genotype to reproductive offspring as compared to competing organisms (Merriam-Webster Collegiate Dictionary).

⁷ A group of alleles of different genes on a single chromosome that are closely enough linked to be inherited, usually as a unit (Merriam-Webster Collegiate Dictionary).

⁸ *POU2F3* is a transcription factor that mediates keratinocyte differentiation and proliferation, and the archaic haplotype is at 66% frequency in East Asians but almost absent in Europeans (Racimo et al. 2015, 12).

⁹ *TLR1/6/10* haplotype occurs with a frequency of 39% in East Asians, 22% in Europeans and 17% in South Asians. Toll-like receptors play a key role in the innate immune system, and *TLR1* and *TLR6* are well-characterized non-viral receptors; whereas *TLR10* is a possible receptor for influenza and other pathogens (Gittelman et al. 2016, 3379).

¹⁰ A population bottleneck is an event that drastically reduces the size of a population. It causes a decrease in the gene pool of the population because many alleles that were present in the original population are lost (Nature Education).

Altai Mountains (Kuhlwilm et al. 2016, 431) occurred at 270–200kya (Hubisz et al. 2020, 9, Posth et al. 2017, 1). Among introgressed segments to Altai Neanderthals, the *FOXP2* was identified (Kuhlwilm et al. 2016, 432), which encodes a transcription factor that could have contributed to the evolution of human speech (Wolfgang 2011, 415).

Gene flow from an ancestor of the Altai Neanderthals into Denisovans genome occurred, and it was estimated that a minimum of 0.5% of the Denisovan genome was contributed by Neanderthals. Particularly strong signals of that gene flow are found in the human leucocyte antigen (HLA) region and the CRISP gene cluster on chromosome 6 (Prüfer et al. 2014, 46–47, Slon et al. 2018, figure 4).

Gene flow events (marked by black arrows in figure 1) are evidence that, during successful interbreeding between populations of Denisovans, Neanderthals and Sapiens, specific genes were transferred between populations.

4. Interbreeding events between populations of hominins

Neanderthals were inhabiting Eurasia and Sapiens were inhabiting Africa. Migrating out of Africa, Sapiens dispersed through the Levant. The earliest fossil with Sapiens features is known from the Apidima Cave in southern Greece, dated to more than 210kya (Harvati et al., 2019, 1). The earliest modern human fossils (a maxilla and associated dentation) at Levant were found at Misliya Cave (Israel) and were dated to 194–177kya (Herskovitz et al. 2018, 1). The *Qafzeh* and *Skhul* fossils were dated to 135–90kya (Grün et al. 2005, 316, Marcier et al. 1993, 169, Valladas et al. 1998, 69–75) and the Manot Cave fossils were dated to 55kya (Herskovitz et al. 2015, 216). Dating of contexts associated with the Neanderthal fossils from *Tabun*, *Dederiyeh*, *Kebara*, *Ein Qashish* and *Amud Caves* suggests that Neanderthals existed in that region between ca. 80 and ca. 55kya (Been et al. 2017, 1,5). The bulk of Neanderthal gene flow into Sapiens could have occurred around 70–47kya (Kuhlwilm et al. 2016, 433, Vernot and Akey 2014, 1, Villanea and Schraiber, 2019, 1). Hajdinjak et al. infer that the majority of Neanderthal gene flow happened after they separated from a common ancestor with

the Altai Neanderthal from Siberia around 150kya, but before the split from a common ancestor with *Mezemaiskaya 1* (North Caucasus) at least 90kya (Hajdinjak et al. 2018, 5). Later, around 50–45kya, Sapiens spread further into the rest of Eurasia, replacing the Neanderthals by about 39 kya (Higham et al. 2014, 1). Genetic analysis of an approximately 42–39ky-old modern human from Romania (*Oase 1*) suggests that this individual had a Neanderthal ancestor as fourth-, fifth- or sixth-degree relative. This is evidence that interbreeding between Neanderthals and modern humans also happened in Europe at a later point in time (Fu et al. 2015, 3–4).

It was estimated that a consequence of interbreeding was reduction to at least 40% of the median Neanderthal fitness compared to the median modern human (Harris and Nielsen 2016, 883, 889, Juric et al. 2016, 1, Kuhlwilm et al. 2016, 432). One of the factors which could explain a fast disappearance of Neanderthals in Europe was proposed by Greenbaum et al. (2019). After one hundred thousand years of largely independent evolution, Neanderthals and Sapiens likely acquired immunity to different suites of pathogens. During their close contact in Levant, specific pathogens carried by them could have been transmitted between them causing diseases, so it stopped Sapiens migration. Sapiens may have overcome the disease burden, becoming resistant to Neanderthal-specific pathogens through immune-related adaptive introgression processes sooner than Neanderthals. So they migrated to Europe and Asia, carrying contagious diseases to which Neanderthals, living outside the contact zone in Levant, were intolerant (Greenbaum et al. 2019, 2–3).

The fragment of a long bone (*Denisova 11*) shows that it comes from a female, at least 13 years old at death, who had a Denisovan father and Neanderthal mother closely related to Neanderthals who lived later in Europe than the Altai Neanderthal found in the Denisova Cave (figure 1). The finding of a first-generation Neanderthal-Denisovan offspring among the small number of archaic specimens sequenced to date provides direct evidence for genetic mixture between Neanderthals and Denisovans. This suggests that mixing among archaic and modern hominin groups may have been frequent when they met (Slon et al. 2018, 1, 2, 4–5).

Early Sapiens who migrated outside Africa also met Denisovans whose genome contained about 0.37% of introgressed Sapiens sequence (Hubisz et al. 2020, 10). These contacts also occurred later, as mentioned above, with gene flow in the opposite direction. Nowadays, Papuans have introgressed Denisovans genome fragments in amounts significantly greater than any other contemporary humans (Browning et al., 2018, 7, Chen et al. 2020, 4).

5. Multi-regional evolution of *Homo sapiens* in Africa

The great tropical forests and hyper-arid regions of Africa are biogeographic barriers to species that are adapted to savanna and savanna-woodland-mosaic habitats (Berger et al. 2017, 5, Scerri et al. 2018, 583). During the climatic oscillations of the Pleistocene (2580–11,7kya) distinct savannah refugia were present in West, East, Southern and South-West Africa. The East African environmental was most unstable, in contrast to a stable, long-standing savannah refuge in the South (Lorenzen et al. 2012, 3656). Extremely arid conditions in tropical East Africa (Lake Malawi) occurred in several discrete episodes between 135–76kya. During the Late Pleistocene (126–11,7kya) and Holocene (11,7–0kya), every ~21ky the Earth's axial precession decreased¹¹ and a corresponding higher boreal summer insolation intensified rainfall in northern Africa, the Arabian Peninsula and the Levant, thus generating habitable savannah-type corridors. Such climate change may have stimulated the expansion and migrations of human populations (Scholz et al. 2007, 16416, Timmermann and Friedrich 2016, 92).

Early *Homo sapiens* fossils do not demonstrate a simple linear progression towards contemporary human morphology. Recent archeological and genetic data are consistent with the view that our species originated and diversified with strongly subdivided (i.e. structured) small hominin populations across Africa, whose connectivity changed through time. For millennia, semi-isolated populations, in which evolution may at times have progressed independently,

¹¹ Axial precession is a gravity-induced, slow, and continuous change in the orientation of an astronomical body's rotational axis. The precession is the major cause of the climate oscillation on the Earth having a period of 19-23ky (Wikipedia).

were connected by sporadic gene flows (Berger et al. 2017, 6 Chen et al. 2020, 9, Scerri et al. 2018, 582–583, Skoglund et al. 2017, 1, Stringer 2016, 1). This concept is called “African multiregionalism” (Stringer 2016, 7).

6. The Biological species concept

According to Ernst Mayr, “species are groups of actually or potentially interbreeding natural populations, which are reproductively isolated from other such groups” (Mayr, 1942). In his biological species concept, Mayr stressed the intrinsic reproductive isolation aspect, which is the end point of speciation. Emergence of a new species is a continuum process in which metapopulation lineages evolve separately (de Queiroz 2005, 6604) accumulating differential adaptation to different environments or diverging mating systems (Darwin 1875). Between metapopulations, lineages could involve migrations and thus hybridizations. Even Mayr later wrote: “...for it seems as if some part of the genotype of the 2 species is not affected by the hybridization. The 2 species, in such a case, seem to remain “reproductively isolated”, in the sense that they do not fuse into a single population, in spite of the leakage of certain genes” (Mayr 1982). Dobzhansky (1937, 312) famously stated that: “Species is a stage in a process, not a static unit.” Some acknowledge that species boundaries do not necessarily extend across the entire genome; alleles at some loci can be exchanged between species, so it is better to consider species boundaries as semipermeable (Barton and Hewitt, 1981, 119, Gompert et al. 2017, 213, Hamlin et al. 2020, 147, Harrison 1990, 98–99, Harisson and Larson 2014, 797, Key 1968, 19, Mallet et al. 2015, 147, Roux et al. 2016, 1, Wu 2001, 853, Zachos 2018, 815).

If speciation means evolving from gene flow to no gene flow, then the current amount of gene flow between two entities could be taken as a measure of the speciation stage (Galtier 2018, 658). At an intermediate stage, loci¹² involved in reproductive isolation (species barriers) experience

¹² Locus – the position in a chromosome of a particular gene or allele (Merriam-Webster Collegiate Dictionary)

little or no gene flow, whereas neutral loci can be freely exchanged between the diverging populations (Coyne and Orr 2004). Haldane's rule states that "when F1 offspring¹³ of two different animal races one sex is absent, rare, or sterile, that sex is the heterozygous sex" (Haldane 1922, 101). There is a clear tendency for restricted introgression on X (or Z¹⁴) chromosomes relative to autosomes (Gompert et al. 2017, 217). A gene flow at incompatible alleles and at linked loci will tend to be more strongly reduced on sex chromosomes (Presgraves 2018, 3823). A closely related observation is the large X effect stating that there is a disproportionate contribution of X/Z-chromosome in fitness reduction of heterogametic hybrids (Coyne and Orr 2004, Presgraves 2018, 3823). Species are expected to accumulate reproductive isolation with increasing evolutionary divergence (Coyne and Orr 1997, 295, Moyle and Nakazato 2010, 1521), suggesting that introgression should become attenuated with increasing evolutionary age among species (Hamlin et al. 2020, 148). Conspecific mate preference is ubiquitous and may be one of the earliest reproductive isolating mechanisms to evolve between populations (Schumer et al. 2017, 10940). Hybrid male sterility reflects the rapid differentiation in the genetics of spermatogenesis. In general, the number of species pairs yielding hybrid male sterility is much larger than those yielding inviability or hybrid female sterility (Wu 2001, 860). Late stages of speciation are characterized by genome-level reproductive isolation that is often due in part to strong assortative mating (Gompert et al. 2017, 218, Schumer et al. 2017, 10936).

In present-day humans the largest deserts of Neanderthal ancestry are on the X chromosome, where the mean Neanderthal ancestry is about a fifth of the autosomes. It could be explained by the "large X effect", where the X chromosome was more resistant to introgression of Neanderthal ancestry than autosomes. If male hybrid sterility is contributing to these observations, a prediction is that the responsible genes will be

¹³ An F1 hybrid is the first filial generation of distinctly parental types (Wikipedia).

¹⁴ The ZW sex-determination system (birds, some fish, some crustaceans, and some reptiles), females have a pair of dissimilar ZW chromosomes, and males have to similar ZZ chromosomes (Wikipedia).

disproportionally expressed in testes. It was found that only genes that are specific to testes were enriched in regions of low Neanderthal ancestry (when compared with all other genes expressed in the same tissue). It was shown that interbreeding of Neanderthals and Sapiens introduced alleles into Sapiens genetic background that were not tolerated, which probably resulted in part from their contributing to male hybrid sterility. This may explain why a proportion of Neanderthal ancestry is up to 8% higher in present-day Asian populations compared to European ones. Asian population sizes were smaller than European populations, which could have resulted in less efficient selection to remove Neanderthal-derived deleterious alleles (Sankararaman et al. 2014, 356).

High coverage (~3%) of Sapiens to Neanderthals introgression on the X chromosome have been observed for both Altai and Vindija samples. Although the Vindija sample is younger by 70kya than the Altai sample, it shows no depletion of Sapiens ancestry on the autosomes, suggesting that negative selection did not cause a significant loss of Sapiens introgressed regions during that interval. However, some individual chromosomes did show decreases in coverage from Altai to Vindija, with the largest drop on the X chromosome. An interesting question is whether the observed absence of negative selection reflects healthy variation introduced by Sapiens into the Neanderthal genome, or a Neanderthal population that was too small for efficient removal of deleterious variants (Hubisz et al. 2020, 9–10).

An analysis of the present-day populations of genomes and the ancient genomes extracted from hominins fossils shows evidence of the gene flows: from Sapiens to the ancestors Altai Neanderthals and Denisovans, from Neanderthals to ancestors of Eurasians Sapiens, from Neanderthals to Denisovans and from Denisovans to ancestors of Asian Sapiens (black arrows in figure 1). The real admixture history is likely to have been more complex. Most of the gene flow probably occurred intermittently, often in both directions and across a geographic range. Hominin groups met and had offspring on many occasions in the Late Pleistocene¹⁵ (129-11,7kya),

¹⁵ Late Pleistocene is currently estimated to span the time between ca. 129–11,7kya (Wikipedia).

but the extent of gene flow between the groups was generally low (Prüfer et al. 2014, 48). From known fossils, ancient offspring between Sapiens and Neanderthals is known in 39–42kya Sapiens from Romania (Oase 1). This individual had a Neanderthal ancestor as fourth-, fifth- or sixth-degree relative. A first-generation offspring called *Denisova 11* was also found who had a Neanderthal mother and a Denisovan father.

Up to the extinction of Neanderthals and Denisovans, existence of a complete reproductive isolation between them and Sapiens has not been observed. As mentioned above, there is evidence not only of neutral gene flows between these group of homo but also of many adaptive introgressions from Neanderthal to Sapiens and Denisovans and from Sapiens to Neanderthal (e.g. *FOXP2*, which encodes a transcription factor that could have contributed to the evolution of human speech). This may have caused that process of speciation to be less advanced. Also, introgression events between Sapiens and Neanderthals have been noticed which concern the X chromosome. It is known that the sex chromosome's isolation barrier is the least permeable in relation to other chromosomes. All of this evidence indicates than it could not be certainly stated that these groups are, beyond question, different species. Rather it may be said that Sapiens, Neanderthals and Denisovans are separately evolving metapopulation lineages which, during their evolutionary processes, developed adaptive features and to some degree reproductive isolation (e.g. conspecific mating preference), but the speciation process probably wasn't finished before the Neanderthal and Denisovan extinctions. So, it might be assumed that one *Homo sapiens* species exists which embraces such metapopulations as present-day *Homo sapiens sapiens*, ancients *Homo sapiens neanderthalensis* and *Homo sapiens denisovensis*.

7. Biological polygenism and theological monogenism

The human person, created in the image of God, is a being at once corporeal and spiritual (Catechism of the Catholic Church, 360). The immaterial nature of a human soul places it outside the realm of the biological sciences, so

evolutionary considerations are only concerned with evolution of the matter of the human body. Joseph Ratzinger (1964, 194) clearly distinguishes between biological polygenism and theological monogenism. Biological polygenism states that an evolving population or a group of populations was the origin of humans. Theological monogenism holds that, in one or two individuals, God immediately created a soul. According to Ratzinger, “it is highly probable, the hominization, which had its origin in biological population, makes possible that genius *blitz* of transcendental thinking occurred for the first time in one or two individuals. Biological polygenism and theological monogenism are not excluding antithesis, because the plane of its questions not completely overlap” (Sánchez 2014, 482). What Ratzinger called a *blitz* John Paul II named “ontological leap [...] the moment of transition to the spiritual” (John Paul II 1996, 6). This one or these two persons could then have interbred with other members of their biological species and have fertile offspring with rational souls.

8. Do the signs of Neanderthal intelligent activity exist?

According to Wrangham’s hypothesis (Carmody and Wrangham, 2009, 379, Wrangham, 2009), fire was a central evolutionary force toward larger human brains: eating cooked foods made early hominin digestion easier, and the energy formerly spent on digestion was freed up, enabling their energy-expensive brains to grow. The Middle Paleolithic¹⁶ Neanderthals had the ability to make, conserve, and transport fires during successive occupations or at different sites (Roebroeks and Villa, 2011, 5209–5211). The discovery from Poggetti Vecchi (~171kya) provides evidence that Neanderthals had cognitive abilities to choose the appropriate very tough wood and to process it with fire to produce tools (Aranguren et al. 2017, 2054). Also, a 50kya tar-hafted flint tool found off the present-day Dutch coastline demonstrate complex Neanderthal technology and advanced intelligence competency (Niekus et al. 2019, 22081). In Bruniquel Cave in southwest France, 336 metres from

¹⁶ The Middle Paleolithic spanned from 300 to 50 kya.

the entrance of the cave, annular constructions made of broken stalagmites and several traces of fire were found. The regular geometry of the structures strongly suggests intentional construction at 176,5kya ($\pm 2,1$ kya). Early Neanderthals were the only human population living Europe during this period. These findings suggest that the Neanderthal groups responsible for these constructions had a level of social organization which included complex spatial organization, fire use, and deep karst occupation (Jaubert et al. 2016, 111–114). New finds of Sapiens fossils from the Apidima Cave in southern Greece, dated to more than 210kya (Harvati et al., 2019, 1), call into question whether Neanderthals were responsible for the constructions in the Bruniquel Cave because no human fossils were found there.

Despite distinct differences in ossicle morphology, likely associated with convergent¹⁷ brain expansion, there is no evidence for differences in the auditory sensitivity level in the lower frequencies between Sapiens and Neanderthals. This may suggest consistent aspects of vocal communication in the two species (Stoessel et al. 2016, 11493). Vowels are the core of speech production and are required to effectively transmit consonantal acoustics. Together they enable a phonologically encoded lexicon, which is then subject to syntax. The anatomical studies concerning reconstructions of vocal tract structures in ancient and recent Sapiens and Neanderthals provide suggestive but indirect evidence of the potential for complex vocal communication in Neanderthals (Barney et al. 2012, 95–96, Boë et al. 2002, 564, Boë et al. 2019, 7).

Some signs of possible intelligent Neanderthal activity were mentioned above. Yet, the question remains open how to interpret these signs in the context of the Neanderthal cognitive abilities and what is the nature of these abilities. It would be interesting to perform a comparative analysis of signs of intelligent activity and culture between the African lineage of Sapiens and the European/Asian lineage of Neanderthals; but it is beyond the scope of this paper.

¹⁷ Convergent evolution creates analogous structures that have similar form or function but were not present in the last common ancestor of those groups (Wikipedia).

9. When could an ontological leap have been?

Populations of *H. sapiens sapiens* did not reach the end of the speciation process by the time of *H. sapiens neanderthalensis* and *H. sapiens denisovensis* extinction, because evidence of interbreeding between them has been found. In the contact zones between these populations, mixed couples were occasionally created. They had fertile offspring who transmitted inherited genes into subsequent generations. All present-day populations of *H. sapiens sapiens* whose genomes have been examined up to date have introgressed sequences from populations of Neanderthals and Denisovans.

Muller said: “Rational ensoulment could have take place prior to the achievement of the final physical form of the human race, or even after this had been achieved” (Müller 2010, 321). The most distant point of ensoulment might be ca. 640-500kya. when the last common ancestor of *Homo sapiens* lived. If the first human population, which received souls from God, lived before divergence into Sapiens, Denisovans and Neanderthals, then all these subsequent populations have to be treated equally from an ontological perspective. After several hundred thousands of years of independent evolution, they occasionally contacted each other, interbreeding to create families and nurture children. In this case, populations of *H. sapiens sapiens*, *H. sapiens neanderthalensis* and *H. sapiens denisovensis* are understood as persons who make personal relations and share an identical ontological nature. Moreover, they would be equal in the dignity of being created in the image and likeness of God, and in the grace of Christ’s redeeming sacrifice. Clearly there would be some anatomical, cultural and cognitive differences. These variations between them would be greater than between the most contemporary discrepant human populations. But even different languages, customs and behaviour would not be the obstacle to create relations firm enough to successfully raise children, as explained before.

In the second option, the moment of ensoulment was after the split of the *H. sapiens sapiens* population from the ancestors of Denisovans and Neanderthals, e.g. in the time of living sapiens individuals found in *Jebel Irhoud*, *Florisbad* or *Omo Kibish*. How could we interpret mixed relations

created between populations of Sapiens, Denisovans and Neanderthals? Should we call them zoophilic¹⁸ (Austriaco 2019, 211)? The concept of zoophily concerns the idea of having an attraction to or preference for animals, which are different species to *Homo sapiens*. Because diverging metapopulation lineages of Neanderthals, Denisovans and Sapiens, as outlined above, may be considered as one *Homo sapiens* species, there is no reason whatsoever to formally call the sexual relations between these populations as zoophilic.

It should be kept in mind that, tens of thousands of years ago, the human perception of morality was by far distinct from the modern human consciences. In the areas of contact between evolutionary distinct populations, there would also have been mixed mating between Neanderthals, Denisovans and Sapiens. The innate necessity of mating and reproduction could have exceeded the need to live in personal relationships and the need of mutual understanding. Even if a person entered into a relationship with a ‘non-person’, such a person might have seen this as inappropriate, but not necessary understood this relation in the category of a sin. It is known that the human conscience developed in a moral sense: Lamech’ view (Gen 3,19–24) – Old Testament Law (Ex 21,24–25; Deut 19,21) – Jesus’ commandment (John 13,34). It is likely at the time of the interbreedings between Sapiens, Neanderthals and Denisovans, their consciences were not yet able to see their relationships accurately. The human nature wounded by original sin misses the choice of the reasonable good. In these non-personal relationships, parents successfully nurtured their children, as evidenced by the fact that every person living today has, in their genome, a fragment of the Neanderthal and Denisovan sequence, because one of his or her ancestors must have been a Neanderthal or Denisovan. Of course, the individual contributions in building relationships in a mixed couple were disproportionate. Certainly, a person (Sapiens) would contribute more than

¹⁸ How can we understand interbreeding among our ancestors, identical with us in respect of behaviour, with contemporary hominin populations such as Neanderthals and Denisovans? In theological comprehension, such a situation should be recognized as zoophilic. (Own translation from Polish.)

they receive from a ‘non-person’ Neanderthal or Denisovan. Among populations of *H. sapiens sapiens*, with rational souls, there would be a prevailing preference to create personal bounds which were, for them, definitely more beneficial, desirable and gave their children the community in which they could successfully grow and progress.

The presented results of biological discoveries concerning human (body) evolution leave open the way to theological and philosophical consideration when an ontological leap could have been made. It is possible that it may have occurred before splitting the ancestors of Sapiens from the common ancestors of Neanderthals and Denisovans or it may have happened after this splitting in a metapopulation of Sapiens lineage.

Conclusion

Evidence of several documented gene flows between *H. sapiens sapiens* and two extinct populations *H. sapiens neanderthalensis* and *H. sapiens denisovensis* and discoveries of human record fossils of *Oase 1* and *Denisova 11* indicate that they probably were one biological species of *Homo sapiens*. There is no known time when ensoulment could have taken place. If the “ontological leap” took place before the splitting of *Homo sapiens* populations into Sapiens, Denisovans and Neanderthals, then all descendants of these populations are persons who have souls created by God. If “spiritual transitions” have taken place during evolution of *Homo sapiens sapiens* lineage in Africa after splitting Sapiens from the ancestors of Neanderthals and Denisovan, then relations between mixed couples (Neanderthals and Sapiens or Denisovans and Sapiens) were between one parent who did not have a rational soul (non-person being) and the other one who had it (person being). In such a parental relationship their children, who would be persons with rational souls, could have grown in a community called a family. Maybe the theological reflection is now facing a similar challenge as in time after the discovery of Americas, when there were discussions about the nature and the dignity of indigenous people from newly-explored continents. Pope Paul III in bull *Sublimis Deus*, from June 2, 1537 wrote that “the Indians are

truly men”. Do Neanderthals and Denisovans have the same God-given dignity and rational souls as present living men?

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