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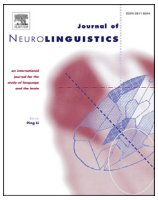

Research paper

Why only us: Recent questions and answers

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ABSTRACT

From its modern origin over sixty years ago, generative grammar has attempted to characterize the human "faculty of language" as an evolvable trait—a particular *phenotype*. This phenotype has a species-specific genetic basis, what biologists typically call a *genotype*. There are many puzzling questions about the nature of the human language genotype and phenotype, some of which are addressed in the recent book, *Why Only Us* (Berwick & Chomsky 2016). Among the most puzzling are the following: why does language occur only in humans, appearing relatively rapidly and recently in evolutionary terms, along with no apparent genomic change since its emergence? *Why Only Us* suggested that the answer to this question is that the required evolutionary innovation was simple, with most of its underpinnings antecedently in place. The key evolutionary novelty yielding the human language phenotype—perhaps the only innovation, putting to one side an important mystery regarding the origin of human concepts that were called "word-like atomic elements"—is an operation called *Merge*. Merge builds a "discrete infinity of structured expressions that are interpretable in a definite way by the conceptual-intentional system of thought and action, and by a sensory-motor system for externalization"—in short, thought linked with sound/sign (Chomsky, 2016). This may be called the "Basic Property" (BP) of human language, and it is a short answer to the question of "What evolved" for human language. The BP gives rise to the language faculty: the ability for any person to acquire any human language. We consider the language faculty the proper phenotype for analysis, and its underlying genomics, the corresponding genotype. Much confusion has arisen by conflating the properties of individually realized languages with the design of the language faculty itself, because this leads to a very different conception of the language phenotype, one inextricably linked to articulatory or vocal output modalities—the externalization of language. More broadly, WOU framed the basic evolutionary puzzles about the evolution of the language faculty in the form of answers to five additional questions: Who evolved the BP? Where and when did the BP evolve? How did it evolve? And, finally, Why? Since its publication, new evidence has accumulated in support of WOU's basic thesis, though as always many important questions remain open. Here we review this very recent evidence focusing on basic evolutionary issues, including a recurrent, but we think misguided, effort to account for the properties of the language faculty by means of cultural-biological interaction. We argue that this latter effort fails in all respects—it does not account for the properties of the language faculty, failing to rule out languages that are known to be "impossible" on other, empirical grounds, including brain imaging; and does not even make successful empirical predictions about diachronic language change.

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1. Who, where, and when: Neandertals aren't us

1.1. Divergence time and incompatibilities between humans and Neandertals

WOU suggests that Neandertals and their close extinct relatives the Denosivans were simply not us—that they did not have the BP or human language, though the speculative nature of the conclusion was emphasized. Analyses published during 2016 have strengthened this speculation, providing clarifying new details regarding the time and nature of language's emergence and the distinctiveness of *Homo sapiens* and the human genome compared to our extinct *Homo* relatives. In brief, despite inter-specific hybridization leading to about 2–3% ancient DNA in modern humans, varying of course geographically, there are significant incompatibilities between the human and the Neandertal/Denisovan genomes, enough to mark us out as a distinct species. In particular, there are apparently functionally genomic incompatibilities, for instance, in the *FOXP2* genomic region, implicated in speech, though the *FOXP2* connection to the BP, as we stressed in WOU, remains to be unraveled. Further, while the genomic differences between our closest extinct hominin ancestors and contemporary humans are slight, by using a broader population sampling base from the 1000 Genomes Project and sequencing many individuals over a more diverse set of geographic regions, we are beginning to accumulate a richer catalog of fixed genomic differences between the two groups, single nucleotide polymorphism (SNP) differences. Let us consider this evidence.

First, the date of the evolutionary split between *Homo sapiens* and Neandertals/Denisovans has been pushed much farther back in time from its traditional date of between 300,000–400,000 years ago, further separating us as a distinct species from these other groups. The sequencing of nuclear DNA material from hominin fossils found at the Spanish site *Sima de los Huesos,* or ‘pit of bones,’ has greatly extended back the divergence time between the common ancestor of modern humans and the Neandertal-Denisovan lineages. The Spanish DNA was identified as more closely related to Neandertals than Denisovans, suggesting that the time of the split between the Neandertal-Denisovan lineages was at least 381,000–471,000 years ago (Meyer et al., 2016). This in turn pushes back the split between these two species and the modern human lineage even further, far earlier than previously thought, and “suggests that the population split between archaic and modern humans occurred between 550,000 and 765,000 years ago.”

As the authors go on to say, “Such an ancient separation of archaic and modern humans is difficult to reconcile with the suggestion that younger specimens often classified as *Homo heidelbergensis*, for example Arago or Petralona, belong to a population ancestral both to modern humans and to Neanderthals” (Meyer et al. 2016, p. 506). This works out to perhaps 500,000 years of evolutionary time separating the *Homo sapiens* clade from these two extinct species—so providing more time for genomic differences to accrue, including the BP, than what was posited in WOU.

By the time of the earliest known fossil evidence for what is taken to be *Homo sapiens* in Southern Africa approximately 200,000 years ago (Tattersall, 2012), Neandertals and Denisovans had already become established in continental Europe, according to the Meyer results. After this point in time, *Homo sapiens* and individuals from the Neandertal and Denisovan lineages appear to have interbred on at least two occasions in time in at least two regions—in the Levant, approximately 100,000–125,000 years ago, and then again during at least one period after *Homo sapiens* had emigrated to Europe, 40,000–45,000 years ago (Kuhlwilm et al., 2016). Despite this interbreeding, the most recent DNA sequence comparison genomic work strongly suggests that this interbreeding led to lower fitness in the hybrid offspring (Harris & Nielsen, 2016; Sankararaman, Mallick, Patterson, & Reich, 2016). Though details regarding the cause of the reduced fitness of these hybrid individuals remains to be worked out (Harris & Nielsen, 2016), several researchers (Currat & Excoffier, 2011; Sankararaman et al. 2014) point to X-chromosome effects driving hybrid infertility: “interbreeding of Neanderthals and modern humans introduced alleles onto the modern human genetic background that were not tolerated, which probably resulted in part from their contributing to male hybrid sterility” (Sankararaman et al. 2016, 356). This effect is well known in evolutionary biology as one prime “smoking gun” signature of species separation, “Haldane's rule” (Haldane, 1922).

Two additional studies published in 2016 bolster the conclusion that *Homo sapiens* should be set apart as a different species from Neandertals and Denisovans, pointing to prominent differences in some language-related genomic regions: one analysis by Akey and colleagues (Vernot et al. 2016), and a second by Sankararaman et al. (2016) from David Reich's Harvard group, both backing up earlier work cited in WOU (Vernot et al. 2016). Both groups used the same general approach, examining the pattern of introgressed Neandertal and Denisovan DNA in modern humans, though they differ in detail. Ancient Neandertal/Denisovan DNA is not uniformly scattered through the modern human genome—there are large gaps, possibly the result of just 3–4 interbreeding events in all. In particular, Sankararaman et al. discovered that the modern human X chromosome almost entirely lacks Neanderthal DNA. This is the “Haldane's rule” pattern mentioned just above.

To be sure, some Neandertal/Denisovan genomic introgressions into the modern human genome have proved beneficial and survive to the present day in modern humans, as we noted in WOU—for example, a genomic region apparently from Denisovans that contributes to improved oxygen utilization in modern high-altitude Tibetan populations (Huérta-Sanchez et al. 2014). In any case, by carefully examining the “DNA deserts” where Neandertal/Denisovan introgression is absent, both groups came to the same conclusion that this is indeed a textbook case of what happens when two close groups, like polar bears and grizzly bears, can interbreed to some extent but are divergent species. A good litmus test for this kind of reproductive isolation shows up in the genes associated with the human testes, with 20–100 times less Neandertal DNA vs. the genes in the heart or brain. Further, crucially, the human version of the gene for FOXP2 was absent: “Four windows (1:99–112 Mb, 3:78–90 Mb, 7:108–128 Mb, and 13:49–61 Mb) are both Neanderthal and Denisovan ancestry deserts. The desert on chromosome 7 contains the FOXP2 gene, which has been hypothesized to have a role in enabling modern human