

# Language and genes: A new perspective on the origins of human cultural diversity

Daniel Nettle\*

Centre for Behaviour and Evolution, Newcastle University, Henry Wellcome Building, Newcastle NE2 4HH, United Kingdom

All human languages perform the same function, and the set of distinctions that they use to do so is probably highly constrained. The constraints come from the universal architecture of the human mind, which influences language form through the way it hears, articulates, remembers, and learns. However, within these constraints, there is latitude for variation from language to language. For example, the major categories of subject, verb, and object vary in their typical order, and some languages signal grammatical distinctions primarily by syntax, or the combinatorics of words, whereas others achieve this mainly through morphology, or the internal mutation of words. What determines the historical evolution of any particular language across the possibility space formed by these different options? In this issue of PNAS, Dediu and Ladd (1) present evidence suggestive of an answer that has seldom been considered before, which is that interpopulation genetic differences may play a role.

Previous work on linguistic evolution has assumed one of two background models. The first is basically chance. That is, there is a set of all language configurations consistent with the properties of the human mind, and where on that landscape a particular language moves is a random walk. Such models need not entail that all language states are equally probable or frequent. Some parts of the possibility space may impose higher learning or processing costs than others, and thus languages should be expected to spend less time in them because innovations and errors made by speakers tend to move the language away from those configurations. For example, it has been hypothesized that word orders where the object of the sentence routinely precedes the subject impose psychological costs, and this accounts for their scarcity among the world's languages (2). Similarly, there may be interactions between different linguistic parameters. An example of this is that the order of verbs and objects in a language tends to mirror the order of nouns and adpositions (words such as "on," "from," "to," and "for" in English) (3). A satisfying explanation of such a pattern is that psychological costs are lowest when the speaker can use a

parsing strategy for noun phrases that is similar to that used for verb phrases. Thus, linguistic innovations that bring these two parameters into alignment would have an elevated probability of retention.

Although the chance model predicts that some language configurations will be more common than others, it predicts no association between the state of the language and any nonlinguistic characteristic of the population that speaks it. This has been a rather strong default assumption for linguists, but it is one

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that should be interrogated with data because alternatives are perfectly cogent: after all, there are associations between acoustic attributes of the habitat and song or call type in birds (4, 5), prairie dogs (6), and macaque monkeys (7).

The second, more controversial line of research has sought to associate ecological or demographic parameters with linguistic parameters. Fought *et al.* (8) showed that languages spoken in warm climates tended to use more sonorous combinations of sounds (essentially, more vowels and fewer consonants) than languages spoken in cold climates. Languages with more sonorous sounds require lower speech volume at a given distance (9). The argument of Fought *et al.* is that in warm climates, more conversation occurs outdoors where there is more background noise, more sound dispersion, and greater interpersonal distances. This creates a context wherein innovations that increase sonority are more likely to be retained than they would be where conversation mainly occurs indoors.

Other researchers have examined the effect of population size. In genetics, small populations are more affected by genetic drift than are large populations. This makes natural selection less efficient at removing mildly deleterious mutations. An analogous effect might occur for cultural innovations in the domain of language. Nettle (10), using a computer simulation, argued that the languages of small populations might be more prone than those with many speakers to spend time in areas of the possibility space that are disfavored overall. An empirical example is object-initial word orders. Although these are rare, they appear to have arisen several times independently and always in languages with just a few hundred or few thousand speakers. Trudgill (11) argued in a similar manner, although on slightly different grounds, that small communities are disproportionately likely to have languages with unusually high or unusually low numbers of contrastive sounds. Although the empirical evidence does not appear to support his claim, it does point to interactions between sound repertoire and demography (12, 13).

The article by Dediu and Ladd (1) opens up a new, third approach to the direction of language evolution in which the evolution of a language is affected by the genetic composition of the population speaking it. There is a prior literature on language/gene correlations. However, that literature assumes a chance model for language change and a neutral model for genetic change. The correlations it seeks are the result simply of shared population history. No claim is made that anything about the genetic composition of the population actually causes languages to change in particular ways. This is where the research of Dediu and Ladd is novel. The researchers identify two genes involved in brain development, *ASPM* and *Microcephalin*, that are polymorphic in the human population. They then show that the likelihood of a language employing tonal contrasts (basically, meaning dis-

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\*E-mail: daniel.nettle@ncl.ac.uk.

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tinctions between words based on pitch patterns of individual syllables) is strongly influenced by allele frequencies for these two genes in the population of speakers. They speculate that different alleles of these genes influence the facility with which learners acquire tonal contrasts.

Any account of this kind has to overcome the generally accepted truth that any human from any population can acquire any language given input at the right stage of development. The claim of Dediu and Ladd (1) is compatible with this. All they need posit is a very slight difference in how easily speakers of different genotypes acquire this particular distinction. In populations where most people acquired tonal contrasts very easily, they would be more likely to persist relative to alternative phonological distinctions than in populations where they were acquired more slowly on average. Computer simulations confirm that a learning bias at the individual level would only have to be small for the direction of linguistic change to be affected (14, 15). Clearly, individual-level experimental research is now needed to establish that the genotypes implicated do indeed have the phenotypic effect of producing such a bias. Thus, the article by Dediu and Ladd must be regarded as hypothesis-generating rather than definitive. However, like the best hypothesis-generating work, it immediately generates testable predictions at other levels, such as longitudinal studies

of dialects and experimental work on the learning of artificial language and music.

Regardless of whether the hypothesis of Dediu and Ladd (1) is supported by further work, it will have raised the possibility of a viable category of explanation for which researchers can look for empirical evidence. Importantly, the article preserves the “psychic unity of mankind,” in that any person can learn any language, while acknowledging the by now well established fact that many human behavioral traits demonstrate heritable individual differences and thus must be underlain by genetic polymorphisms (16). The extent of human polymorphism is greater than previously thought because of the existence of many whole segments of the genome that exist in varying number in different people (17). A substantial number of human genetic polymorphisms show the signature of positive selection acting in the last few thousand years (18). This kind of work encourages us to shift our view of human evolution from something that happened and finished in the Pleistocene to a population process that continues to shape human diversity; as the great Ernst Mayr put it, from a typological to a population way of thinking (19).

In particular, findings like these suggest a greater role than previously suspected for what has been called gene–culture coevolution. This, as its name suggests, refers to situations where

the cultural evolution of practices influences, and is influenced by, the genetic composition of populations. The most famous example is the coevolution of the (cultural) trait of dairying and the (genetic) trait of lactose absorption among Northern European and African populations (20). Dediu and Ladd (1) are here hypothesizing a causal influence from the genetic to the cultural. However, there may also be influences running in the other direction. The derived haplotypes of *ASPM* and *Microcephalin* are not at fixation among humans. Although they show the hallmarks of positive selection, it is not at present clear why they have become more widespread in some populations than others, and there could be some aspect of the environments or cultural practices of different populations that modifies their selective payoffs.

The current study concerns linguistic parameters, but these are only one type of culturally transmitted element, albeit the one easiest to categorize and of which the genealogy is most tree-like and most easily ascertained. For the evolution of other cultural traits, the same three explanatory options of chance, interactions with ecology and demography, and coevolution with genes also seem to be available. It is to be hoped that more empirical work on the pattern of human cultural diversity will follow. Language may be leading the way as a “model organism” for culture more generally.

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