more effective than a sophisticated sensing mechanism.

The ability to analyze long-term outcomes of evolutionary processes in stochastically fluctuating environments is of fundamental importance for understanding evolutionary biology and can, in particular, contribute important insights into the biology of pathogens. As it turns out, randomly creating phenotypic diversity—or not putting all your eggs into one basket—may be all that is necessary, and the work by Kussell and Leibler allows us to assess when this is the case.

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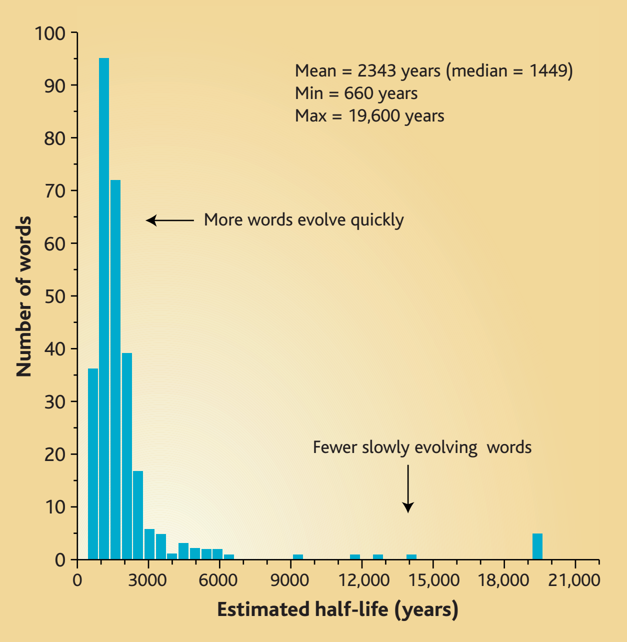
EVOLUTION

Pushing the Time Barrier in the Quest for Language Roots

Russell Gray

Questions about human origins have an enduring fascination. For centuries, scholars and laypeople have wondered where groups such as Polynesians or Indo-Europeans came from. Linguistic evidence plays a vital role in tracking the movement of people by leaving linguistic trails that are analogous to the genetic signatures that molecular biologists study. Early European explorers in the Pacific, for example, were struck by the remarkable similarities between the far-flung languages of the Pacific (the word for hand in Hawaiian and Samoan is *lima*, in Marquesan it is *'ima*, and in Tahitian *rima*). It might seem a simple matter, therefore, to trace the origin of words used in linguistic and cultural groups and thereby unravel connections between the peoples of the world that extend deep in the past. Perhaps it might even be possible to infer the initial "mother tongue" spoken before our languages diverged. Alas, the task for historical linguists and prehistorians is not this easy. First, superficial similarities in vocabulary must be separated from genuine similarities due to descent. Linguists call these genuine homologies "cognates." The diagnosis of cognates is a challenging task that requires detailed specialist knowledge to detect systematic sound correspondences. Then an even more difficult problem is encountered: The rate of vocabulary evolution is so rapid that it erases distant or "deep" historical connections.

Consider the following thought experiment: Imagine that two languages each diverge in their basic vocabulary from a common ancestor at roughly 20% every thousand years (this is a rough but not entirely arbitrary figure). After 1000 years, 64% of the languages' basic vocabulary would be cognate; after 2000 years, 41%; and after 10,000 years, just over 1%. The problem of rapid lexical decay is exacerbated by chance similarities and recent borrowings that obscure this weak historical link or "signal" (for example, the Maori and Modern Greek words for eye, *mata* and *mati*, superficially appear similar, but no one seriously postulates that this reflects some deep historical link). Instead, most linguists believe that after about 8000 to 10,000 years it is impossible to differentiate between homology and chance resemblances or borrowings. They are therefore highly skeptical of arguments for ancient language relationships, especially when cognacy judgments are made with less than the normal standard of rigor. One highly controversial example is Ruhlen's claim (*1*) that words ostensibly related to a Proto-Amerind term **t'ana* (child, sibling) provide evidence for a putative 12,000-year-old Amerind language family. As Campbell (*2*) has pointed out, the semantic variation that Ruhlen allowed (meanings including small, woman, cousin, son-in-law, old man, friend, and some 15 other terms), coupled with relatively loose phonetic matches (Ruhlen treats *tsuh-ki* and *u-tse-kwa* as related to **t'ana*), make chance resemblance highly likely.



The rate of vocabulary change. A word's half-life is the amount of time required for there to be a 50% chance that it will be replaced by a new word. Most words have a half-life of 2000 years. However, a small number of words have a half-life greater than 10,000 years. This shows that despite the fast average pace of language evolution, some meanings, like highly conserved genes, evolve at a slow rate [adapted from (*3*)]. The *y* axis is the number out of a sample of 200 meanings.

Recent work by Pagel (*3*) suggests that the prospects for discovering deep links between languages may not be quite so bleak. The calculations above assumed that all words change at the same rate. This is not realistic. Pagel adapted stochastic models of genetic evolution to the problem of lexical change. He showed that a distribution of word rates is a much better fit to the data than a single rate. This distribution has a long tail, implying that in principle there are some very slowly evolving words that remain cognate even after 20,000 years (see the figure). It is these very stable words that proponents of long-distance language relationships have focused on. However, the practical task of convincingly separating deep homologies from chance corre-

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spondences and borrowings still remains.

If words hit a time barrier when it comes to detecting linguistic links, must the deep links between languages and cultures remain forever obscured? Linguists such as Nichols (*4*) have argued that language structure holds the key to unlocking our past. By examining structural features such as the position of verbs in clauses and the presence or absence of inclusive/exclusive pronominal contrasts, Nichols claims to recognize linguistic areas and connections that are beyond the reach of the traditional comparative method with its focus on vocabulary. Although this approach appears promising, not all linguists are convinced that the structural features used by Nichols are any more stable than words. Campbell (*5*), for example, cites cases of recently diverged dialects that differ in features that are allegedly stable for periods of more than 10,000 years.

On page 2072 of this issue, Dunn *et al*. (*6*) tackle this debate in a systematic and rigorous manner, using methods derived from evolutionary biology. As Darwin noted (*7*), languages evolve in remarkably similar ways to biological species. They split into new languages, mutate, and sometimes go extinct. There are numerous historical connections between biology and historical linguistics, with linguistics often leading the way in the development of new ideas and methods (*8*). However, despite these connections, linguists have not commonly used the phylogenetic methods that have revolutionized evolutionary biology in the past 20 years [for recent exceptions, see (*9*–*11*)]. To address the problem of detecting deep signal, Dunn *et al*. borrowed two tools from their biological colleagues. First, they constructed a database of 125 structural features for 16 Austronesian and 15 Papuan languages. This enables them to avoid the charge that they merely selected a few features that happened to fit their hypotheses. The number of possible family trees of descent for even quite small numbers of languages is vast. Dunn *et al.'s* second methodological borrowing from biology was the use of a computer program to find the set of optimal trees for the Austronesian and Papuan data sets. To test whether the structural features contain a historical signal, Dunn *et al*. compared the Austronesian structure tree with the traditional classification of these languages. The resulting Austronesian structure tree matched the traditional classification quite well, which suggests that the structural features contained some historical link or signal for at least the 4000-year time depth that the Austronesian of languages studied by Dunn *et al*. are thought to have.

What about time depths beyond the reach of traditional methods? Evolutionary trees show nested patterns of descent, with the most recent divergences toward the branch tips and the most ancient at the tree base or root. The Papuan tree of Dunn *et al.* shows some geographic clustering at its tips. The signal toward the base of the tree is very weak, suggesting that few structural features support these historical links. However, the signal that is present is consistent with a scenario involving a time depth greater than 10,000 years. Dunn *et al*. are careful to emphasize that the signal is weak and discuss alternative hypotheses. Although it does not conclusively demonstrate deep historical signals in structural features, the Dunn *et al*. paper sets new standards for the systematic collection and analysis of structural features. Its approach is likely to be widely emulated by researchers working on languages in other regions. In the future we may see the development of Web-based databases for the languages of the world similar to the GenBank repository for DNA sequences. The task of making accurate inferences about our past is a demanding one that requires the integration and triangulation of inferences from genetic, linguistic, and archaeological data (*12*). The Dunn *et al*. approach is an important step forward in this interdisciplinary endeavor.

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CHEMISTRY

Better Living Through Nanopore Chemistry

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Tiny holes have huge significance—at least if you're in the business of cracking millions of barrels of crude oil into useful smaller chemical components, converting methanol into gasoline, or transforming toluene into precursors for polymers. Zeolites, the remarkable materials that catalyze these conversions, contain enormous numbers of cavities of roughly nanometer size (*1*). The cavities are uniform in size and shape and are interconnected to form extended channels or pores. The cavities and the portals between them are just the right size to imbibe oil's molecular components and process them into more useful and valuable petrochemicals.

Zeolites are mostly made from the elements of Earth's crust: silicon, aluminum, and oxygen. This makes for strong materials—in essence nanoporous rocks. But this chemical composition constrains the possible applications of these materials. For example, an important problem in chemical catalysis, especially in the area of pharmaceuticals, is the transformation of an achiral reactant selectively into just one of two possible mirror-image products ("enantioselective" catalysis). Yet purely zeolitic schemes for enantioselective catalysis are rarely, if ever, encountered.

What if the most promiscuous of elements—carbon—could be recruited for assembling zeolite-like materials? The versatility and variety of carbon chemistry—the chemistry of life—could, in principle, expand tremendously the range of compositions, architectures, and functional behavior of permanently porous crystalline materials. On page 2040 in this issue, Férey and co-workers report the latest in a series of advances in this area (*2*). The new material, called MIL-101 (where MIL stands for Matériaux de l'Institut Lavoisier), has some remarkable physical attributes. The unit cell volume is ~700,000 cubic angstroms, about 90% of it empty space once volatile solvent

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