

PERSPECTIVES: GEOPHYSICS

Rising Through Earth's Mantle

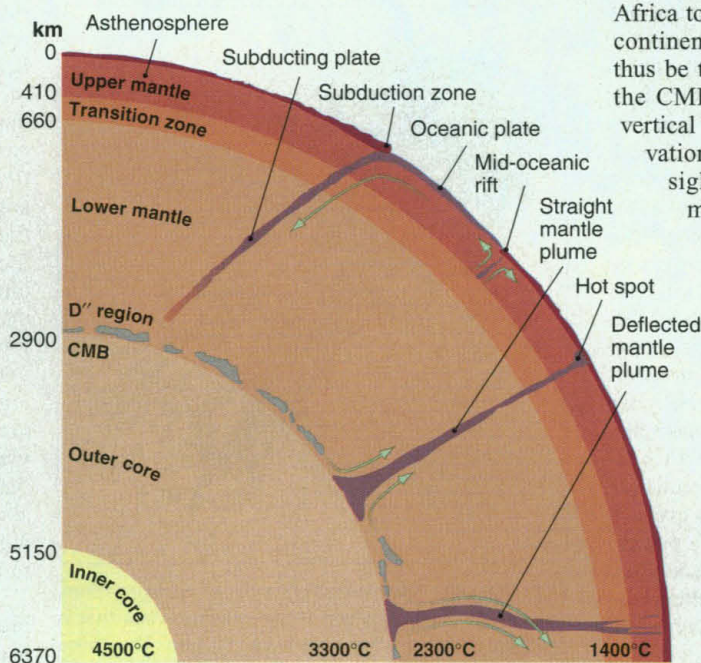
Joachim R. R. Ritter

Volcanism and the breaking of the continents continually remind us of the hot and dynamic interior of our planet. Driven by temperature and density gradients, convective currents carry vast amounts of partially molten rock through Earth's mantle (see the figure). Subducting oceanic plates have been traced during their downward flow from the top to the bottom of the mantle (1), but the nature of the upward flow is still a matter of debate. In this issue, Goes *et al.* on page 1928 (2) and Ritsema *et al.* on page 1925 (3) present fascinating seismic images that indicate large-scale upwellings of hot material in the lower mantle that extend all the way to the surface. The results are interpreted as direct evidence for the deep driving forces that cause rifting and intraplate volcanism in Central Europe and East Africa.

In recent years, advances in seismological research and geodynamical modeling have led to important refinements to the traditional layered Earth model (see the figure). Seismic tomography—a geophysical analog to medical computer tomography—has been particularly instrumental by providing detailed three-dimensional images of the spatial distribution of seismic velocities in the mantle. The seismic images can be interpreted as spatial temperature contrasts, with low velocities corresponding to high temperatures and high velocities corresponding to low temperatures. Today's images are sufficiently detailed to show the continuation of cold subduction zones across the 660-km boundary (see the figure) deep into the lower mantle and possibly even down to the core mantle boundary (CMB) (1). Geodynamical models can thus be tested and refined by seismic tomography.

These advances are helping to resolve a question that has been hotly debated for decades, namely whether material flows across the boundary between the upper

and lower mantle at 660-km depth or whether the convection patterns above and below the boundary are isolated from each other. This year, a deeper, floating boundary was proposed (4) on the basis of the observation that subducting plates can penetrate into the lower mantle (1). Further clues may come from hot spots—regions with extensive volcanism away from



Cross section through Earth. Heat from the hot outer core (~3300°C) must transverse the mantle to reach the surface. Lateral and vertical flows (indicated by arrows) compensate the temperature contrasts. Cold subducting plates and hot plumes penetrate the boundary between upper and lower mantle at 660-km depth, supporting whole mantle convection.

plate boundaries lasting for several tens of millions of years, for example, in Hawaii or Iceland. At these hot spots, mantle plumes consisting of hot mantle rock rise in a conduit of about 100- to 150-km diameter, with a temperature about 200 to 300 K higher than the surrounding mantle. Recent studies have found that at least some plumes penetrate the whole mantle in an upward direction (2, 3, 5). Geothermal models are consistent with plume-like upwellings from the CMB to the surface as a rapid carrier of heat from the core through the mantle (6).

Mantle processes may drive the Cenozoic rift systems cutting through the Central European and East African continental plates that developed during the past 40 million years and the intraplate volcanic

fields that developed at the same time. It has been suggested that both phenomena are related to active plumes or asthenospheric upwellings (or both) in the upper mantle (7, 8), but a connection to the lower mantle has remained speculative. Using data sets consisting of more than 2 million shear wave measurements, Ritsema *et al.* (3) have calculated a three-dimensional shear wave velocity model of Earth's mantle with a spatial resolution of about 500 km below Africa [see fig. 2 in (3)]. In their model, a low shear wave velocity (or increased temperature anomaly) stretches continuously from the CMB under the southeast Atlantic upward to northeast Africa to the East African rift system. The continental breakup in this region might thus be triggered by thermal anomalies at the CMB. The plume deviates from the vertical by more than 4000 km, an observation that may provide important insights into the flow patterns in the mantle and its viscosity. A possible explanation could be that the plume is deflected by the "mantle wind," that is, the large-scale mantle convection underneath Africa (9).

The seismic low-velocity anomaly underneath Europe discovered by Goes *et al.* [see fig. 3 in (2)] is most visible in the lower mantle at 600- to 2000-km depth. In the transition zone between 410 and 660 km, velocities are high; low velocities reappear in the upper mantle under the European Cenozoic rift system. The plume-like structure seems to be interrupted by the subducting African plate in the transition zone (2). This complex interaction of hot material with a subducting plate in the upper mantle could generate pockets of melt, feeding several small upper mantle plumes beneath the widely distributed Cenozoic volcanic fields in Central Europe (7).

The Central European and African plumes are obviously more complicated than simple straight tubes. With a lateral extent of more than 500 km, the observed plumes are much wider than expected, even when smearing effects inherent to global seismic tomography are accounted for. Upwelling is likely to be broad in the high-viscosity lower mantle, followed by narrowing in the low-viscosity upper mantle (10). In the upper mantle, the plume may split into several tall plumes (7, 8), as seen in local tomography studies (7). To resolve such details, high-resolution regional imaging of the interaction of plumes with mantle flow, sub-

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ducting slabs, and lithospheric plates should be performed. Carefully designed seismic field projects on the continents and in the oceans are required to achieve this challenging task. The resulting estimates of lateral and vertical mass fluxes in the mantle will provide a firmer basis for geodynamic computer models and should lead to a consistent three-dimensional Earth model.

PERSPECTIVES: EVOLUTIONARY BIOLOGY

Predictive Evolution

David M. Hillis

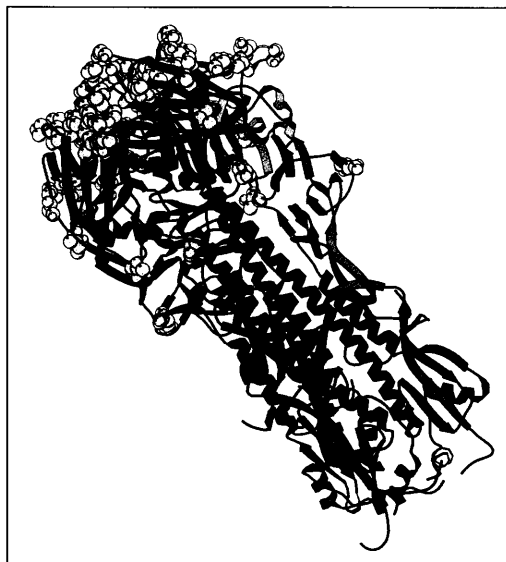
Pick up a random issue of almost any biological journal these days, and you are likely to see one or more phylogenetic trees. One of the reasons that these estimates of evolutionary history have become ubiquitous is because they are needed to make biology predictive. Just as the periodic table of elements allows chemists to make predictions about chemical reactions, so a phylogenetic tree allows biologists to make predictions about behavior, morphology, physiology, biomolecular structure, or any other biological attribute. Usually, the main difference is that chemists make predictions about reactions that have not yet occurred, whereas biologists make predictions about attributes that have already evolved, but have not yet been observed in a particular species. On page 1921 of this issue, Bush and Fitch (1) show that phylogenetic analyses of the human influenza A (subtype H3) virus can be used to make predictions about the evolutionary course of future human influenza strains. This information should prove valuable for accurately predicting the correct strains of flu virus to include in the vaccine prepared each year to protect against the upcoming influenza season.

Earlier phylogenetic studies of human influenza A (2) have shown that strains of this virus form a rather unusual phylogenetic tree. Phylogenetic trees of most viruses that have been studied to date show a continuously diverging phylogeny. For instance, the tips of the tree of human immunodeficiency virus type 1 (which represent samples of viruses taken at any one time) are more diverse and distant from one another today than they were a few decades ago [for example, (3)]. In contrast, although many different strains of influenza A may be circulating at a given time,

References and Notes

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11. I thank U. Christensen for stimulating discussions on mantle plumes.

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Defeating the flu. Molecular model of hemagglutinin, the protein on the surface of the influenza virus that is recognized by the host immune system. The three hemagglutinin chains are shown in blue, green, and red. Substitutions among 18 amino acids in hemagglutinin's HA1 domain (yellow spheres) allow influenza to avoid immune recognition in a naïve host. Consequently, there is positive selection for flu strains that have the greatest number of changes among these 18 amino acids. The model is adapted from Protein Data Bank entry 1HGG (4) and was created in MolScript (5).

most lineages do not survive to contribute to future influenza diversity. Instead, one principal (or "trunk") lineage survives and gives rise to future lineages of influenza A, whereas the other lineages quickly become extinct. The unusual shape of the influenza virus phylogenetic tree makes it easy to discern the course of past evolution. One factor influencing that course appears to be positive selection for particular changes in the amino acids in hemagglutinin, one of the two proteins that comprise the large spikes on the surface of the influenza virus (see the figure). If a person develops antibodies against a particular hemagglutinin, then the individual is much more likely to fend off infection by the viral strain carry-

ing that hemagglutinin. However, certain substitutions in the gene encoding hemagglutinin result in changes in the amino acids of this protein's HA1 domain. The altered amino acids result in a reduced immune response in an individual who has been exposed only to the hemagglutinin of an ancestral strain of influenza. Bush and Fitch found that 18 codons of the hemagglutinin gene's HA1 domain are under positive selection for changes in the amino acids that they encode. Furthermore, they established that of the strains of influenza A that are circulating at any one time, those that are most likely to be ancestral to future influenza epidemics (the surviving or trunk lineage of the phylogeny) are the ones that show the greatest number of changes among these 18 amino acids. This allowed the investigators to make predictions about which of the strains circulating today are most likely to give rise to future lineages of influenza A.

To test the effectiveness of the prediction method, Bush and Fitch examined 11 recent influenza seasons and made retrospective predictions about which of the circulating strains of influenza would be part of the future trunk lineage. The test was successful in 9 of 11 seasons. In the two unsuccessful seasons, the same isolate was chosen three seasons in a row, but only represented the correct trunk lineage in the first season it was selected. A refinement of the test that eliminates previously selected strains from consideration (on the basis that they could no longer continue to produce immune avoidance) might solve this problem. The investigators suggest another possible refinement—simply eliminate extinct lineages from the analysis. Either of these refinements might increase the performance of the method. Nonetheless, the performance of the existing test is impressive: If isolates were chosen at random, then the probability of selecting nine or more of the trunk lineages correctly is only 4.48×10^{-9} .

Bush and Fitch are careful to point out that predicting which current strain of in-

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⁶ **A Thermal Balancing Act**

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