results of Parigi *et al.*, the laboratory techniques they describe could pave the way toward new possibilities in the fields of quantum information science and quantum optics (*5*–*8*). These results show how one can convert a purely thermal light field, which possesses no nonclassical properties, into a light field with strongly nonclassical features. This work thus constitutes a step toward the development of techniques for "quantum state engineering," that is, the creation of states with specified quantum properties. States of this sort are expected to play a key role in quantum computing, quantum cryptography, and control of quantum systems.

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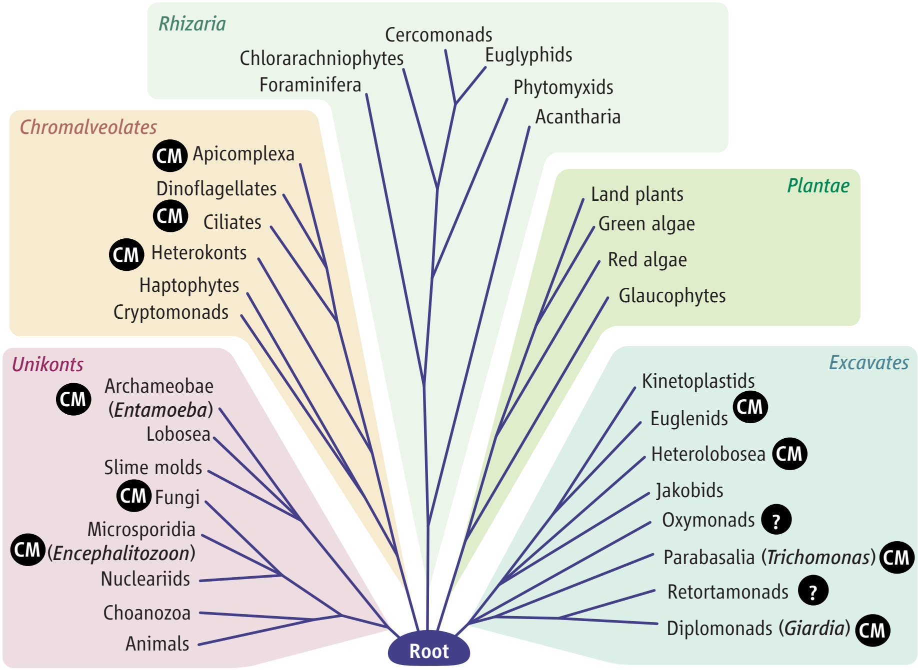
GENOMICS

Deep Questions in the Tree of Life

Now that the genome of a unicellular parasite has been deduced, can it resolve the debate on the origin of eukaryotes?

Patrick J. Keeling



Eukaryotic evolution. The hypothetical evoultionary tree consists of five "supergroups" based on several kinds of evidence (*15*). The branching order of supergroups is unresolved, implying that the relationships are unknown rather than a simultaneous radiation. CM indicates the presence of cryptic mitochondria (hydrogenosomes or mitosomes). A question mark indicates that no organelle has yet been found.

A genome sequence might provide answers to major questions about the biology and evolutionary history of an organism. Alternatively, it might reveal more problems than solutions, and its true value then lies in identifying what questions to ask. Perhaps the most interesting genomes do both: They are a panacea and a Pandora's box. On page 1921 in this issue, Morrison *et al.* (*1*) describe such a genome from the diplomonad protist *Giardia lamblia*, a human intestinal parasite. The compact *Giardia* genome is replete with information ranging from the simplicity of its molecular systems to how the parasite interacts with its environment. However, the evolutionary history of *Giardia* is not so clearly written in the genome, reigniting a smoldering debate about the origin of *Giardia* and its relationship to other eukaryotes.

The evolution of *Giardia* has commanded a level of attention matched by few other organisms because it differs from the "textbook" eukaryote in many ways. Most notably, there are no mitochondria in *Giardia* or its relatives, in keeping with its tolerance for low levels of oxygen (*2*). The absence of this organelle took on new significance with the Archezoa hypothesis, which proposed that *Giardia* (and certain other protists) diverged from other eukaryotes before the endosymbiotic origin of mitochondria, and was therefore ancient and primitively amitochondriate (*3*). Early molecular phylogenies supported this view, placing *Giardia* and other Archezoa at the base of eukaryotic evolution (*4*, *5*). The case seemed closed: *Giardia* arose from the prokaryote-eukaryote transition, one of the greatest transformations in evolution.

The Archezoa hypothesis proved too good to be true. Nuclear genes phylogenetically related to mitochondrial homologs were discovered in Archezoa, including *Giardia* (*4*, *5*). The protein products of such genes have been localized to double membrane–bounded organelles (hydrogenosomes or mitosomes) in all major Archezoan groups, and similar structures were found in distantly related eukaryotes (see the figure). Some of these organelles and their metabolic activities are well characterized (e.g., *Trichomonas* hydrogenosomes), but the functions of other cryptic organelles remain elusive (e.g., *Entamoeba* mitosomes). In *Giardia*, proteins involved in iron-sulfur cluster assembly and protein folding appear closely related to mitochondrial homologs and localize to a relict mitosome (*6*, *7*). Interestingly, the *Giardia* genome contains little else of identifiable mitochondrial ancestry: No other functions can be predicted and protein-import complexes are reduced or highly divergent (*1*, *8*).

The other implication of the Archezoa hypothesis—that *Giardia* is an early branching eukaryote—has attracted even more controversy. The "deep" position of some Archezoa has been convincingly undermined

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by showing that they belong elsewhere in the phylogenetic tree, the clearest case being the relationship between microsporidia and fungi (*5*). For *Giardia*, such a specific alternative is not so clear-cut, but the genome may provide clues. Diplomonads may belong to a group of protists known as excavates, specifically related to Parabasalia such as *Trichomonas* (*9*, *10*). Like *Trichomonas*, the *Giardia* genome does not encode myosin (which is rarely absent from eukaryotic genomes) and encodes a bacterial arginine metabolism pathway, supporting a close relationship. This does not preclude an early divergence for both *Giardia* and parabasalids, for this depends on where the root of the eukaryotic tree lies, which is difficult to resolve. Indeed, there are doubts about how phylogenetic reconstruction methods can determine this root, given the unequal rates of sequence evolution and great genetic distance between eukaryotes and prokaryotes (*11*). There are also difficulties inherent in reconstructing the history of divergent genes with current phylogenetic methods, and large amounts of data that violate evolutionary models can generate well-supported errors (*12*). Morrison *et al.* show high levels of divergence in much of the *Giardia* genome, so although the genome may contain data to reconstruct *Giardia*'s history, it will be a challenge to use it.

The outcome of this debate affects not only our understanding of early eukaryotic evolution, but also our view of *Giardia* biology. Simple characteristics could be primitive or derived via reduction, alternatives with very different meanings. The simplicity of *Giardia*'s molecular systems differs from that of known derived parasites (*1*, *13*). However, different lineages can follow different reductive paths (*14*), so determining *Giardia*'s origins independently of its simplicity is essential. Given the depth of these questions, the new life that Morrison *et al.* have breathed into the debates is welcome, and will ensure continued attention on both a fascinating cell and the origin of eukaryotes.

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PHYSICS

Does Our Universe Allow for Robust Quantum Computation?

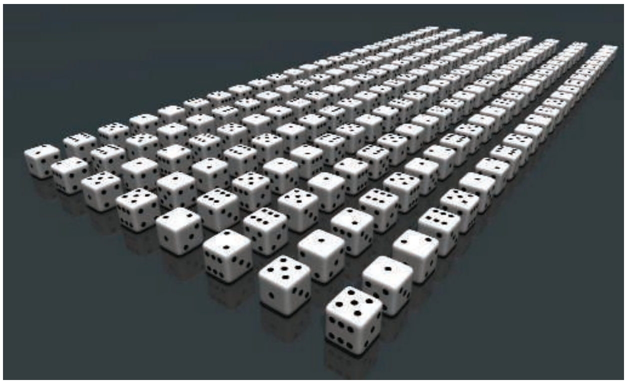
An approach for analyzing quantum decoherence may help push the boundaries of quantum computing.

Dave Bacon

Computers operating purely according to the laws of quantum theory might break modern cryptographic codes (*1*), revolutionize quantum chemical calculations (*2*), and overturn the most basic limits to computing (*3*). Standing in the way of creating these dream machines is the fact that quantum computers do not like to maintain their quantum nature, but instead have a propensity to decay into machines obeying the classical laws of physics. This obstacle is known as quantum decoherence, and on page 1893 of this issue, Emerson *et al.* (*4*) report a way to analyze various quantum processes to find the ones that can stand up to this decay.

The solution to the problem of quantum decoherence, at least in theory, has been known for more than a decade and is encoded in a famous theorem for fault-tolerant quantum computation (*5*–*8*). This "threshold" theorem says that multiple quantum systems can be used to simulate a single error-free quantum system. Left out, however, is the question of whether the theorem actually holds in an experimental setting: Does our universe allow for robust quantum computation?

This is a hard question because the cost (the number of experiments needed) of characterizing the properties of quantum systems useful for fault-tolerant computation rises exponentially with the number of quantum systems (*9*, *10*). Emerson *et al.* have found a way to probe quantum processes that has a cost that, contrariwise, scales polynomially in the number of quantum systems (that is, a much lower cost per quantum system). Although this method throws away a certain amount of information, it also retains much of the relevant information. Thus, the authors have opened the door on a new era where quantum devices can be rapidly characterized as useful or not useful for the task of building



Quantum casino. Emerson *et al.* propose a new scheme in which the evolution of a quantum system is symmetrized to eliminate unwanted information. The operations for a single qubit are shown as transforms of a gambling die. All 192 such operations on a die are displayed, 24 rotations and eight reflections of a die through a plane (which are impossible in our world and why you won't find those dice on a casino table). The procedure of Emerson *et al.* can be thought of as randomly selecting one die for each quantum bit in the system from the 192 choices and then applying the transform corresponding to that die to a corresponding quantum bit.

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