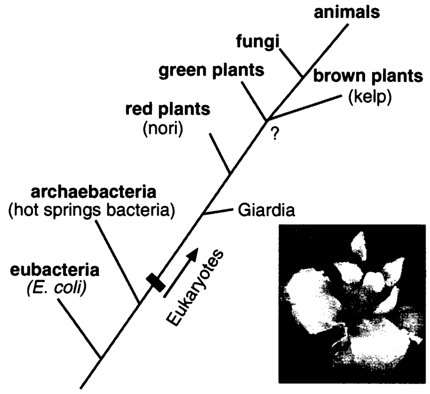
A new view of how plants are related is questioned. A model for how infants extract and use algebraic rules is proposed. A report on grant funding at the National Institutes of Health is offered, with the conclusion that "sufficient funds be provided to minimize all too costly interruptions in funding...." And a crucial control in molecular regulation studies is said to be increasingly overlooked.

Early Plant History: Something Borrowed, Something New?

In response to the article "Deep Green rewrites evolutionary history of plants" by Kathryn S. Brown (News of the Week, 13 Aug., p. 990), the statement that "plants should be divided into three kingdoms rather than one" is neither new nor particularly insightful. Botanists have long recognized that the organisms called "plants" represent a grade-level of cytological and physiological organization ("plants" = photosynthetic eukaryotes); that the various lineages that make up the "algae" are polyphyletic, each tracing its evolutionary debut back in deep time, presumably as a consequence of either a primary endosymbiotic event (leading to the red and green algae, as attested to by, among other things, their double-membrane–bound chloroplasts) or secondary endosymbiotic events (which gave rise to other lineages, such as the cryptomonads, whose chloroplasts have a nucleomorph, a nucleus-like organelle, sandwiched between their "supernumerary" second and third chloroplast membranes); and that the five- (or seven)-Kingdom system still illustrated in most introductory textbooks conflates grade (for example, "protista") with clade (for example, embryophytes). Likewise, the report that the last common ancestor of the land plants was related to modern-day Chara or Coleochaete is hardly new information, although its reconfirmation based on new molecular data is newsworthy indeed.

The new cladistic analyses of plant evolutionary relationships deserve to be reported, but it is vital that all realize that every cladogram is a hypothesis and, perhaps more important, that such hypotheses depend on both the algorithm used to generate the hypotheses (for example, the algorithim generating the reported trees has now been superseded by a much faster algorithim capable of generating shorter and more accurate hypotheses of relationship) and on the character matrix used as the basis of the analysis (such as, cladistic hypotheses will change as new data or taxa are added to the matrix). The character matrices are themselves evolving rapidly and are affected by additions of new characters, such as new gene sequences, and by the selection and definition of morphological-structural characters. Thus, the phylogeny presented as the basis for a radical shift in our understanding of green plant relationships is a transitory hypothesis that likely will be replaced by other different hypotheses. It would be far better to present that understanding as being in a dynamic state evolving in response to newly available techniques and data.



New view of plant kingdoms. Amborella, possibly the world's most primitive flowering plant (inset).

Finally, while on the subject of classification, contrary to the This Week in *Science* item in the same issue (p. 981), the cyanobacteria are not eukaryotes, but in fact are photosynthetic and oxygen-evolving prokaryotes similar in many respects to the ancient bacteria some believe evolved by means of endosymbiosis into red and green algal chloroplasts.

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Response

Niklas *et al.* contend that some of the Deep Green findings described in the News article are "neither new nor particularly insightful." That point is debatable. The findings presented at the meeting offer a more comprehensive picture of green plant phylogeny, and confirm that the common classroom view of plant classification—such that plants belong to one kingdom—is inaccurate. As the article clearly noted, the emerging phylogenetic framework is preliminary and will surely change with time. But researchers interviewed for the article suggest that current systematic methods are sufficient to ensure that cladistic analyses of plant evolutionary relationships are as reliable and valid as other types of scientific analysis, and that many branches of the tree are well supported and unlikely to change radically.

Kathryn S. Brown

Infants Learning Algebraic Rules

Gary F. Marcus *et al.* (Reports, 1 Jan., p. 77) habituated 7-month-old infants to sequences (sentences) of nonsense syllables (words) conforming either to the pattern ABA or to the pattern ABB (for example, "ga ti ga" or "ga ti ti"). Subsequently, infants were presented with additional sentences consisting entirely of new words, with half the sentences conforming to the ABA pattern and half to the ABB pattern. Infants habituated to the ABA pattern showed a marked preference for the ABB pattern, and vice versa.

The experimental results led Marcus *et al.* to conclude that infants are capable of extracting and using abstract algebraic rules such as "the first item X is the same as the third item Y." Such an algebraic rule represents a relationship between placeholders or variables for which one can substitute arbitrary values. The experimental results also suggested that infants are able to extract algebraic rules rapidly from small amounts of data.

Marcus *et al.* pointed out that, while most popular neural network models excel at capturing statistical patterns and regularities in data, they are incapable of extracting algebraic rules that generalize to new items (M. S. Seidenberg and J. L. Elman; M. Negishi; P. D. Eimas; G. F. Marcus, Letters, *Science*'s Compass, 16 Apr., p. 434). They noted, however, that certain types of connectionist architectures (*1*, *2*) that encode relationships between variables could extract such rules.

We have constructed a connectionist network architecture (*3*) derived from (*1*) and (*4*) that can readily acquire algebraic rules. The extracted rules are not tied to features of words used during habituation and generalize to new words. Furthermore, the network acquires rules from a small number of examples, without using negative evidence and without any pretraining.

What is perhaps most significant about the proposed model is that it identifies a sufficient set of architectural and representa-

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tional conditions that transform the problem of learning algebraic rules to the much simpler problem of learning to detect relevant coincidences within a spatiotemporal pattern. Our work suggests that even abstract algebraic rules can be grounded in concrete and basic notions such as spatial and temporal location and coincidence.

The representational and architectural conditions identified by the model are as follows.

1) There exist nodes that encode serial position within a sequence. Recent findings suggest that such nodes are biologically plausible (A. F. Carpenter *et al.*, Reports, 12 Mar., p. 1752).

2) The network can express bindings between a positional node and the item that occupies this position in a given sequence.

3) The bindings are expressed by means of temporal synchrony, that is, the occurrence of an item A in a particular position P in a sequence is coded by the synchronous activity of the cells encoding A and cells encoding P. There is considerable evidence that synchronization of neural activity might underlie the encoding of bindings (*1*, *5*).

4) Nodes representing positional roles and items are interconnected by means of recurrent connections mediated by intermediate (or hidden) layers of nodes.

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References and Notes

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Likelihood of NIH Extramural Funding

Biomedical scientists need an estimate of the probability that their National Institutes of Health (NIH) research grant application will be funded. Previous letters in *Science* from our caucus (16 Dec. 1994, p. 1789; 7 July 1995, p. 13) provided the success rates of NIH grant requests. This information, specifically for unamended, unsolicited investigator-initiated R01 and R29 (FIRST) NIH applications, is not readily available from the Internet or NIH publications, which usually report overall success rates of unamended as well as resubmitted new and renewal requests reviewed during a fiscal year. For example, NIH reported that for fiscal year (FY) 1998, about 31% of R01 requests were funded. These data included all new and renewal submissions, as well as solicited grant requests. We have updated the information on unsolicited new and renewal R01 and R29 applications for FY 1998 based on information provided by NIH (*1*).

Annual increases over inflation in federal NIH appropriations have raised success rates of new R01 plus R29 grant applications (that is, Type 1) from 14% (86% denied funding) in FY 1994 to 20% (80% denied funding) in FY 1998 (Table 1). There was no major change in total number of applications submitted. The table also shows the benefits of submitting or, if necessary, resubmitting, revised applications. Ultimately, about 36% of proposals were funded, a number difficult to establish accurately because the timing of submission of amended applications usually extends beyond the fiscal year, the period of reporting used by NIH.