bacteria. That phenobarbital activates P450 genes in animals, plants and bacteria implies that it mimics a universal regulator of growth. Second, many of the effectors cause proliferation or tumour promotion in a particular eukaryotic tissue or cell type[6]; cell proliferation is caused by chemicals that at high doses induce cancer[10]. Third, many of the chemicals that activate particular P450 genes are ligands for receptors in the nuclear receptor gene superfamily.

Therefore, the activation of genes encoding P450 as well as other drug-metabolizing enzymes by the growth effectors might be an important step, upstream in the regulatory cascade, for controlling the steady-state levels of the various transcription-activating factors. Alternatively (or additionally) the function of P450 genes might involve the metabolism of other second messengers (for example, arachidonic acid metabolites, prostaglandins, leukotrienes) in the regulatory cascade controlling cell cycle-specific genes.

The discovery of the mPPAR gene[1] brings us closer to understanding the intricate interrelationships between a huge variety of biological phenomena, ranging from bacterial growth and cell division to ischaemic heart disease. All of these processes are related to growth and differentiation, in which members of the nuclear hormone receptor superfamily and genes encoding drug-metabolizing enzymes share centre stage. It remains to be seen, however, whether the steady-state levels of most important bio-organic oxygenated growth-effector molecules are controlled by the drug-metabolizing enzymes. □

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1. Issemann, I. & Green, S. *Nature* **347**, 645–649 (1990).
2. Evans, R. M. *Science* **240**, 889–895 (1988).
3. Morris, H. R. *et al. Biochem. J.* **249**, 903–905 (1988).
4. Palmiter, R. D. & Mulvihill, E. R. *Science* **201**, 356–358 (1978).
5. Poland, A. P. & Knutson, J. C. *A. Rev. Pharmac. Tox.* **22**, 517–554.
6. Shulte-Hermann, R. *Arch. Toxic.* **57**, 147–158 (1985).
7. Nebert, D. W. & Gonzalez, F. J. *A. Rev. Biochem.* **56**, 945–993 (1987).
8. Nebert, D. W., Nelson, D. R. & Feyereisen, R. *Xenobiotica* **19**, 1149–1160 (1989).
9. Nebert, D. W. *et al. DNA Cell Biol.* (in the press).
10. Cohen, S. M. & Ellwein, L. B. *Science* **249**, 1007–1011 (1990).

PLANT ECOLOGY

Vegetation's place in history

Peter D. Moore

FOR the past 70 years there have been two strongly opposed camps among students of vegetation. The members of one group, inspired by the ideas of Clements[1], view vegetation as a set of units, associations or communities, in which the various component species have co-evolved in a manner that ensures an optimization of resource exploitation and a minimum of niche overlap. Clements regarded such integrated structures as organic entities, similar to living organisms. The alternative view, pioneered by Gleason[2], perceives vegetation as an assemblage of individual plants belonging to a variety of species, with each species distributed according to its own physiological requirements, as constrained by competitive interactions. The hypotheses have been vigorously defended by descriptive accounts of current vegetation, with various studies showing either that species tend to cluster in groups, or that they are spread as a continuum. But research into the history of vegetation, as manifested in three recent reports[3–5], may hold the ultimate key to the controversy, for it shows that post-glacial movements of species have not occurred in concert and that the timescale involved may have been too short for extensive co-evolution.

The techniques available for examining the history of a plant community depend upon timescale. When considering decades or even centuries, it may be possible to use documentary sources, but longer timescales require the use of fossil reconstruction, often involving the use of pollen stratigraphy in peats and lake sediments. In the case of the beech–hemlock (*Fagus grandifolia–Tsuga canadensis*) forests of the northeastern United States, both techniques have been applied. These two trees are currently important members of the mixed conifer–hardwood forests of the Great Lakes and New England area and their present geographical ranges are similar. They certainly seem to be strong contenders for members of an established community.

Whitney[3] has traced the history of the beech–hemlock forest of the Allegheny plateau of Pennsylvania back for 200 years using forest surveys from the early nineteenth century. At that time beech comprised about 43 per cent of the tree composition of the forest and hemlock about 20 per cent. Since then the exploitation of the area's forest resources has resulted in considerable changes favouring red maple (*Acer rubrum*), black cherry (*Prunus serotina*) and sugar maple (*A. saccharum*). But the antiquity of the beech–hemlock forest has been established and the woodland assemblage evidently pre-dates the arrival of European settlers in the area.

Analyses over longer timescales, involving the mapping of pollen abundance through the past 12,000 years, were carried out a few years ago by Jacobson, Webb and Grimm[6], and have now been reconsidered by Graham and Grimm[4]. Reconstructions of the main centres of distribution of hemlock and beech (defined as areas in which the pollen representation of these types equalled or exceeded 5 per cent of the total terrestrial pollen) show that their ranges have overlapped strongly for only about 6,000 years, and have been fully coincident for only perhaps 500 years. At the end of the Wisconsin glaciation, some 12,000 years ago, the two taxa occupied very different regions of the southeastern corner of North America, with hemlock in the elevated regions of the southern Appalachian mountain chain and beech occupying the lowland regions. Both moved gradually north, but they became important members of the same woodland 'community' only in the mid-Holocene. As Graham and Grimm point out, the response of these plant species to climatic change is essentially individualistic. Their association in the Great Lakes forests is a geologically very recent event.

The organismal concept of community is essentially dependent on the co-evolution of the component species, and the important question is whether there has been enough time to permit such mutual genetic adjustments during the limited time span of the Holocene (10,000 years). Earth's climate has been unstable for the past two million years, most of that period being characterized by glaciations. Bennett[5] proposes that the time available for evolutionary development to cope with the warm interruptions (interglacials) has been too short for most species, particularly those, such as trees, with relatively long generation times. No sooner is an assemblage of species gathered than the next cold event commences.

Species, it would seem in these unstable days, are wandering the Earth in response to their physiological limitations and their competitive capacities, complicated in some cases by sheer historical accident. Adding a time dimension to the debate about vegetation patterns makes it all the more difficult to accept the concept of organismal units that can be identified, named, classified and even sought in the fossil record. □

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1. Clements, F. E. *Carnegie Inst. Washington Publ.* **242**, 1–512 (1916).
2. Gleason, H. A. *Bull. Torrey Bot. Club* **53**, 7–26 (1926).
3. Whitney, G. G. *J. Ecol.* **78**, 443–458 (1990).
4. Graham, R. W. & Grimm, E. C. *TREE* **5**, 289–292 (1990).
5. Bennett, K. D. *Paleobiology* **16**, 11–21 (1990).
6. Jacobson, G. L., Webb, T., III & Grimm, E. C. in *North America and Adjacent Oceans During the Last Deglaciation (The Geology of North America Vol. K-3)* (eds Ruddiman, W. F. & Wright Jr, H. E.) 277–288 (Geol. Soc. Am., 1987).