

Somatic mutation

Do plants evolve differently?

from William J. Sutherland and Andrew R. Watkinson

It has recently been stressed that single plants may consist of a mosaic of genetically different parts^{1,2}. If this is true, then the usual explanations for the operation of natural selection on animals may be insufficient to account for the process of genetic change in many plant populations. The relative importance of somatic and gametic mutations in plants cannot be assessed until the necessary measurements are made. But it is clear that somatic mutation could be important in many plant species.

Modern genetics is based on Weissmann's³ distinction between the cell line and the germ line. Mutations within cells may be expressed but are not passed on to further generations; mutations in the germ line are both expressed and transmitted to descendants. In Weissmann's theory, changes in the germ line are the sole means of evolutionary change. But Weissmann was a zoologist and applied his fundamental principle only to animals. In plants there is no distinction between the germ line and the soma. Growth occurs through the iteration of structural units (modular growth) by one or (usually) many growing points; as a consequence a mutation in a meristem may be expressed in subsequent growth and will then be contained in the pollen or ova. Thus, in plants (and some colonial animals) there is the possibility of genetic variation within an individual and, as a consequence, variation in fitness between modules.

There have been few attempts to measure genetic variability within plants, although there are indications that it may be a widespread phenomenon. Chimaera are common in two species of fern, *Matteuccia struthiopteris* and *Onoclea sensibilis*⁴; 10 out of 56 of the former and 16 out of 37 of the latter possess mutants. The rates of these mutations are high, with 0.0177 and 0.0341 mutations, respectively, per apical cell per generation. In the herbaceous perennial spring beauty (*Claytonia virginica*) 68 per cent of the population show differences in chromosome number within a plant⁵; of 8,000 plant varieties cultivated in Europe in 1899, 5,000 originated as somatic mutations⁶.

Once genetic differences exist between parts of the same plant there is the opportunity for natural selection to modify the gene frequencies within an individual by the process of differential growth. If the parts possessing the mutation grow faster the mutation may spread; if the mutation prevents successful growth then it will be eliminated — anyone possessing an

ornamental plant with variegated leaves knows that it is essential to remove branches containing normal unvariegated leaves which grow more quickly and would eventually dominate the plant.

The importance of differential growth is also shown in the case of the white clover (*Trifolium repens*) in north Wales. There is considerable genetic diversity within populations⁷ and the growth rate of different genotypes depends on the surrounding vegetation⁸. Those genotypes that grow with the grass *Holcus lanatus* produce more ramets when cultivated among *H. lanatus* than when placed among other grasses; other genotypes respond similarly to other species. Thus, the abundance and distribution of different genotypes is determined by differential growth.

In principle it is clear that evolutionary change in a population may originate from somatic mutations. It is essential that somatic mutations should be inherited both sexually and asexually and also that there is differential growth of different genotypes within the same plant. But the importance of somatic mutations is in dispute. Some argue⁹ that the role of somatic mutations is trivial, although the model on which this assertion is based does not take differential growth into account. A later model¹⁰ supports the notion that somatic mutations will produce enough variability to prevent pathogens and herbivores from adapting to all branches on individual host

trees. This model also shows that somatic mutation may be an important source of variation within trees and tree populations. It seems likely that this mechanism is unimportant for species with relatively few meristems (such as peas and maize) but more important for long-lived and extensive species. Thus, individual clones of the aspen (*Populus tremuloides*) can cover 200 acres, be comprised of 47,000 trees and may date back to the Pleistocene¹¹ — it would be incredible if each of these clones was genetically homogeneous.

Although trees provide obvious examples of large, long-lived species, somatic mutation and differential growth could also be important in stoloniferous and rhizomatous plants. Most trees are restricted by a unified architecture that limits the potential for differential growth of branches, whereas in stoloniferous species (such as clover and creeping buttercup) the individual plant fragments as it grows, thus allowing a favourable mutant to spread rapidly. □

1. Whitham, T.A., Williams, A.G. & Robinson, A.M. in *A New Ecology* (eds Price, P.W., Slobodkinoff, C.N. & Gaud, W.S.) 15 (Wiley, New York, 1985).
2. Gill, D.E. & Halverson, T.G. in *Evolutionary Ecology* (ed. Shorrocks, B.) 105 (Blackwell, Oxford, 1984).
3. Weissmann, A. *On Heredity* (Clarendon, Oxford 1883).
4. Klekowski, E.J. Jr *Evolution* 38, 417 (1984).
5. Lewis, W.H., Oliver, R.L. & Luikart, T.K. *Science* 172, 564 (1971).
6. Cramer, P.J.S. *Nature 3 Vers Vol.* 6 (Wetenschappelijke, Haarlem, The Netherlands, 1907).
7. Cahn, M.A. & Harper, J.L. *Heredity* 37, 309 (1976).
8. Turkington, R. & Harper, J.L. *J. Ecol.* 67, 245 (1979).
9. Slatkin, M. in *Evolution in Honour of John Maynard Smith* (eds Greenwood, P.J., Harvey, P.H. & Slatkin, M.) 19 (Cambridge University Press, 1984).
10. Antolin, M.F. & Strobeck, C. *Am. Nat.* 126, 52 (1985).
11. Kemperman, J.A. & Barnes, B.V. *Can. J. Bot.* 54, 2603 (1976).

William J. Sutherland and Andrew R. Watkinson are at the School of Biological Sciences, University of East Anglia, Norwich NR4 7TJ, UK.

Palaeoclimatology

Bears versus beetles

from Peter D. Moore

THE INTERNATIONAL Geological Correlation Programme recently stated the view that there were two separate warm periods during the last (Ipswichian) interglacial period, and that they can be defined on the basis of their mammalian fauna¹. The final (Devensian) glaciation is generally believed to have reached its maximum geographical extent 18,000 years ago (18,000 BP) and by 14,000 years ago Britain was essentially deglaciated. But there are many problems in elucidating the climatic sequence of the previous 200,000 years.

Fossil mammalian bones are an important source of evidence in Quaternary palaeoecology, but their use in climatic reconstruction raises some problems. Such material can be identified with con-

siderable accuracy but compared with other types of fossil evidence, such as pollen, diatoms and beetles, mammalian bones are rare. This means that sufficiently large populations of bones to allow statistical analysis at any site are infrequent, whereas smaller and more abundant fossils, such as pollen grains, lend themselves to this approach. Climatic conclusions from mammalian fossils are also complicated by the relatively large range of tolerance of mammals compared with cold-blooded invertebrates. Thus, one can argue that beetles are better climatic indicators than bears. But some aspects of climatic reconstruction in the late Quaternary are now under debate as a result of finds of mammalian bones in Britain.

Until recently it was thought that the