

Book reviews

Biotechnology and the Improvement of Forage Legumes (Biotechnology in Agriculture Series 17). B. D. McKersie and D. C. W. Brown (eds). CAB International, Oxford. 1997. Pp. 444. Price £75.00, hardback. ISBN 0 85199 109 2.

McKersie, in the final chapter to this volume, concludes that biotechnology offers attractive solutions to the problems of forage production in legumes; forage quantity and quality, hardiness and sustainability. This volume reviews the state of knowledge of forage legume biochemistry and molecular biology and ends with a plea for a concerted effort towards coupling biotechnology and agronomy for the improvement of forage production systems.

As one of the largest, most diverse and economically important plant families the value of legumes as forage is amply illustrated, although most of the papers concentrate on herbaceous species (e.g. *Medicago* and *Trifolium*), rather than woody species (e.g. *Leucaena* and *Calliandra*) which have great importance in many tropical production systems. The recurrent theme of the volume is the potential role of biotechnology in resolving the classical problems of forage legume production. The editors have brought together an eclectic mixture of papers that deal with topics as varied as using alfalfa as an industrial enzyme bioreactor (Austin & Bingham) to legume breeding methods (Bowley). Biotechnology in breeding method improvement is reviewed in chapters dealing with germplasm conservation (Yamada & Okumura), somatic hybridisation and embryo rescue (Arcioni *et al.*), somatic embryogenesis (McKersie & Brown) and the use of molecular markers in alfalfa (Osbourne *et al.*). Forage quality and stress tolerance biotechnology are reviewed in chapters concerned with condensed tannin manipulation (Morris & Robbins), temperature and drought stress (Castonguay *et al.*) and salinity and aluminium stress (Bouton & Parrott). The role of biotechnology in resistance to insects (Burgess & Gatehouse), fungi (Manners & Dickman) and viruses (Forster *et al.*) is also reviewed. The final section of the book contains reviews of nitrogen metabolism (Barran & Blomfield; Vance) and signalling (Phillips & Streit), whilst Austin and Bingham raise the possibility of industrial enzymes being manufactured by fields of alfalfa and it is in this paper that an omission from the book is evident. Given that the aim of the *Biotechnology in Agriculture Series* is to review advances and current knowledge in key areas of biotechnology, a paper concerned with issues related to the release of genetically engineered organisms would have been valuable and timely given the current media interest in another legume, transgenic soy bean.

The papers in this volume are likely to appeal to post-graduate students as starting material for wider exploration

of the subject area. However, it is uncertain how far this volume will stimulate the collaboration that the editors have aspired to.

STEPHEN HARRIS
Department of Plant Sciences
University of Oxford
South Parks Road
Oxford OX1 3RB
U.K.

New Uses for New Phylogenies. Paul H. Harvey, Andrew J. Leigh Brown, John Maynard Smith and Sean Nee (eds). Oxford University Press, Oxford. 1996. Pp.349. Price £19.95, paperback. ISBN 0 19 854984 9.

In the past 40 years there has been a series of fads which have swept through Evolutionary Biology leaving their signatures on the fields like the sweeps of advantageous alleles: caryotypes/ banding, morphometrics, electrophoresis, molecular evolution, and now the conjunction of molecular sequences and phylogenetic reconstruction. In each case there has been a period of hard sell where the proponents pretend (or perhaps even believe) that their new methods will solve all of the major questions (Harding's chapter has equivalents in the earlier fads), then a mindless period of frantic data gathering, then a phase in which questions are finally addressed (or even asked), and finally a phase in which the strengths and weaknesses of the formerly new techniques are realistically assessed. Some of the chapters suggest that we may finally be getting to phase III of the shifting intellectual balance process. We can still hope that this will result in a greater increment in evolutionary understanding than the previous ones because we are now integrating many disparate fields with Evolution (e.g. Palaeontology, Systematics, Developmental Biology), and as a result have completely new sources of data, and this allows us to ask questions that we couldn't even have dreamt of asking before.

The book provides a snapshot of many of the new approaches. Examples include taking advantage of the dependence of gene tree growth and pruning rates upon N_e (Barton & Wilson, Nee *et al.*), individuals containing deleterious haplotypes or traits leave few descendants and therefore should be at the tips of haplotype networks (Crandall & Templeton), selected traits should yield different patterns than those more affected by history (Malhoutra *et al.*, Losos). Differences in evolutionary lability and changes in population structure, colonization and speciation may yield characteristic tree patterns (several authors). Host-parasite systems have been especially illuminated by the new approaches, for example we now have information on between-species transmission and recombinational events of diseases such as AIDS