

*The Grass Genera of the World.* By L. WATSON and M. J. DALLWITZ. C.A.B. International, Wallingford, Oxford. 1992. 1024 pages. Hardback. £75.00. ISBN 0 85198 802 4.

Here is a welcome and wonderful, robustly manufactured encyclopaedia of the phenetics of grass genera. It is the first hard-copy version of the description sets of the Watson–Dallwitz DELTA system data base of the genera of the Gramineae. It will be a treasure-trove for hunters of data about grasses, for a substantial period. We must hope that resources and enthusiasm for maintaining and improving the material will always be forthcoming. Certainly Watson and Dallwitz seem likely never to flag or fail. Their work is a fine example of what can be achieved by inspired leaders and international collaboration, using some of the best technology available for taxonomists.

After an introduction to the project, the DELTA system and other programs compatible with it, the nature and shortcomings of the data and descriptions are very honestly reviewed. The point is well put that narrower generic concepts are most effectively used as the pattern for data assembly – data on more sensibly conceived and usable genera being easily assembled by coalescence. Ah! if John Hutchinson were living at this hour! One hopes that this narrowing quirk of information science will not gradually translate itself into a philosophy or fashion of taxonomic splitting, in minds less well informed, more arthritic or, simply, narrower than that of Leslie Watson. Roll on the day, as he implicitly indicates, when data bases are all completed on a species by species level. We have but a few centuries to wait.

The character list now runs to 496 possible entries per taxon, and the descriptions as printed start with synonymy and follow a standard pattern of vegetative and reproductive morphology, before passing into anatomical data (much of it originated within this project) and then cytological, ecogeographical and economic material. Chemical data are a prominent omission, though references appear – the data base in future will no doubt extend this area considerably given the flood of facts and near-facts now coming forward. References bring up the rear. The genera are in alphabetical order, obviating the need of pagination in the index, which thus functions as a useful guide to synonymy.

Clayton's and Renvoize's *Genera Graminum* will seem to many readers and potential customers as a close competitor of this work. In fact the two are rather different. Agrostologists will need both, just as theologians find value and recreation for the mind in Concordances both with (C & R) and without (W & D) a Commentary.

Assembling specialist data bases for monographic taxonomy, like this one, could become a big business for a few substantial scientific publishers (a few spring

to mind), but broader endeavours must be appropriate work for long-term public-sector abstracting services. Even well-founded research schools in universities are too volatile to carry on with one area indefinitely (that is hardly their function). This grass work has been and is a collaborative model. International 'farming out' of suitable cases for taxonomic treatment needs to be better developed.

Buying updated tapes and printouts of data-base goods is fine for the well-endowed, much better terminalled research institute. How good that this outcome of a data base operator is a BOOK. I luxuriated in reviewing it after the work of the week was past (or postponed), the clarion call of the telephone was stilled, students and colleagues had retired to their private devices. At the weekend one can still – think. How good it was to walk away from the screen incandescent, the fax insistent, and the tidal wave of A4 that sucks at one's very juices – and read a BOOK. No battery needed. I absorbed it on a hill overlooking the sea. Not a terminal in sight. The humming sounds were made by bees. Books will survive modern man.

P. M. SMITH

*Institute of Cell and Molecular Biology  
University of Edinburgh*

*Genetic Conservation of Domestic Livestock, Volume 2.* Edited by LAWRENCE ALDERSON and IMRE BODO. Wallingford, Oxford: CAB International. 1992. 282 pages. £37.50. ISBN 0 85198 809 1.

This volume reports the proceedings of a conference held in Budapest in August, 1991. It was the first official conference of a new organization, Rare Breeds International, whose foundation illustrates the increasing interest being taken in domestic livestock conservation. The conference was a successor to one held in Britain in 1989 and reported in the first volume. (In my review of that work (1991, *Genetical Research* 57: 201), I aired, but will not reiterate, views on the value of breed conservation.) Not surprisingly, in view of the short time interval, the field has not advanced substantially. Thus there is little new and some repetition of old theory, but new conservation programmes have been organized and the volume enables those interested to keep informed.

The book is in four sections: Methodology, National and Regional Reports, Species and Breed Studies, and Biotechnology. Each comprises six or so individual chapters (papers) and a review chapter by the editors summarizing and discussing these and other papers presented at the conference. This format works well, relieving the reader of many disjointed papers and adding constructive criticism.

Most of what is written seems sensible, but there have been escapees. For example, Hodges still (cf. my comments on volume 1) writes about cloned genes and argues that: 'storing animal DNA from in-

digenous breeds in developing countries could be an effective method... If a breed were extinct, then stored DNA would be brought into the active gene pool... by insertion into embryos of another breed... There is no value in further waiting before establishing a global facility for storing and classifying animal DNA.' Would not storing semen fulfil these objectives more simply? In contrast I found Alderson's review of White Park cattle very stimulating, in particular the observations that it is both genetically distant from other British breeds and, despite its maintenance as a small population, has higher heterozygosity. There are certainly some interesting populations about.

Whilst breed conservation is mainly a topic for the enthusiast, it does raise serious population genetic interest. I noted Hedrick among the authors, for example. I hope that more is done to integrate the areas.

WILLIAM G. HILL

*Institute of Cell, Animal and Population Biology  
University of Edinburgh*

*Analysis of Human Genetic Linkage.* By JURG OTT. Second revised edition. Johns Hopkins University Press, Baltimore. 1991. US \$47.50.

The explosion of molecular markers that can be readily detected in essentially any outbred species is sparking a renaissance in genetic mapping. Much of the excitement comes for the possibility of using these maps to localize and eventually isolate genes underlying quantitative characters. These QTLs (quantitative trait loci) may range from the mundane, but tasty, genes influencing pH and soluble fruit content in tomatoes (Weller *et al.* 1988) to those with more serious consequences for humans such as high blood pressure (Hilbert *et al.* 1988). Detection of QTLs is based on associations between marker classes and phenotypic values, so that the more saturated the map, the smaller the genetic interval that bounds a QTL. While the idea of using marker-phenotype associations is obvious, there are serious complications in both obtaining a useful experimental design and in the proper analysis of the resulting data. The current favoured methods of analysis are based on generalizations (e.g. Knott and Haley, 1992) of the methods of segregation analysis developed by human geneticists (Elston, 1990) to assess the most probable genetic basis of a complex trait. The general strategy that seems to be developing for isolating QTLs is first to perform a segregation analysis on a small pilot set of data to see if there are indications of major genes. If there are, the task of constructing a relatively well saturated map of random genetic markers is undertaken and this map is subsequently used to localize the putative major loci to chromosomal regions small enough to be isolated in large cloning vectors. The statistical thread that binds these methods of analysis (segregation analysis, map construction, mapping

QTLs) is that all, for the most part, rely very heavily on maximum likelihood estimation.

Given this setting, it is timely that Jurg Ott has chosen to revise his 1985 text on statistical methods of human gene mapping. Ott focuses on maximum likelihood methods, starting with the simplest models and subsequently building on these to deal with important complications such as different recombination rates between sexes, ascertainment biases, and incomplete penetrance. The last two chapters (10 and 11) on inconsistencies and linkage analysis with disease loci are especially well done and are essential reading for anyone engaged in any aspect of genetic mapping. The author sticks entirely to his stated objectives and has produced an exhaustive review of methods for constructing genetic maps between known markers in humans. This is both the strength and weakness of the book. By limiting his attention to a particularly well defined problem with a rich statistical history, the author has, in effect, produced a wonderful treatise that serves as a case study for the development of other methods. The exciting area of mapping QTLs is essentially not covered and the powerful tool of segregation analysis is only briefly mentioned. This is rather disappointing, but to be fair to the author, Ott accomplishes his stated task – describing methods for constructing maps of known markers – superbly. Anyone with an interest in general aspects of genetic mapping will do well to peruse this book.

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J. BRUCE WALSH

*Department of Ecology and Evolutionary Biology  
University of Arizona  
Tucson, AZ 85721*