Book reviews

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 theologists find value and recreation for the mind in 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-

Genetic Conservation of Domestic Livestock, Volume 2. Edited by LAWRENCE ALDERSO 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, Genetic 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.
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in both obtaining a useful experimental design and in 
references 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 
e.g. I hope that more is done to integrate the 
areas.

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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 under-
lying quantitative characters. These QTLs (quan-
titative 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 general-
izations (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 under-
taken 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 
(seggregation 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 recom-
bination 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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