
Book Reviews

Managing Global Genetic Resources. Livestock. Committee on Managing Global Genetic Resources: Agricultural Imperatives, Board on Agriculture, National Research Council. National Academy Press, Washington, D.C. 1993. 276 pages. Price \$34.95. ISBN 0 309 04394 8.

Discussion of the value of conserving livestock populations and the documentation of breeds and local varieties has become a major international industry. A substantial part of the efforts of FAO in animal production are devoted to the topic; any major conference on applications of genetics in animal production includes a session or more on it (typically, but not unusually for international conferences, with much the same set of speakers each time), and there are series of international workshops for the main proponents. At the local level, societies have been established to foster common interests, and breed conservation programmes are in place, for example in farm parks where they are bred and exhibited, and in semen banks. The farm livestock conservation industry is being boosted by politically proper concerns of the general public about maintenance of 'biodiversity' (which must surely be second after 'genetic engineering' as the most overworked current topic in the biology/politics interface). What, apart from paper, are the likely products of this industry?

The first, and to me unarguable, benefit of conservation of our livestock breeds is aesthetic: it is a pleasure to be able to see variation in conformation, size, colour and horns, just as it is to see a range of species at a zoo. The only issue with this is who should bear the cost of the conservation, for questions as to whether conservation can be through living, accessible, animals, or semen in a flask in a vat of liquid nitrogen do not arise. The second benefit of conservation is as a potential genetic resource for animal production, on which there is a consensus of a sort: 'Numerous reports agree on the need to develop national and international efforts, to preserve and manage livestock genetic resources'. There are, however, different approaches, categorised as: '(1) utilizationist, the primary aim being immediate use of available genetic resources, and (2) preservationist, the primary goal being long-term preservation of genetic resources for unknown future use' (p. 42). As the utilizationist is

doing no more than making the best use of what is currently available without particular regard to the long term, it is debatable as to whether this falls within the remit of conservation: it is overtly sound breeding practice. The main problem is to get information on the existing populations, and there are commendable programmes, notably by FAO, to document characteristics and performance of livestock breeds throughout the world. The preservationist has a harder case to make, for returns are likely to be realised under some future hypothetical circumstances. We do not take out an insurance policy on our house because it *will* burn down, but because it *may* burn down; we currently want peace of mind and we hope we never need to call on it. The questions that need to be addressed are: what are the relevant long-term risks in livestock breeding, and who should pay the premiums? Both are hard questions.

I doubt that we are getting much closer to answers to them. Whilst methodology for estimating differences among populations at the neutral DNA level is developing rapidly, and should lead to nice information on the genetic distances and evolution of breeds, it will not tell us what the returns from conservation are likely to be, for that will depend on particular coding sequences. There is no good evidence that livestock breeders are yet going back to stocks in the conserved store which might have useful genes but are far behind in performance, as opposed to their national or international competitor's stock. It is moot whether unimproved populations will have anything to offer that we know or will know about. Modern molecular technology will enable us to bring individual useful genes free of background and quickly into a commercial from an unimproved population by marker assisted backcrossing, providing we have identified the genes. The technology is, however, also likely to enable us to bring in genes from different species or to make new genes, so it is hard for me to believe that the importance of conserved populations will rise. Meanwhile the debate goes on, and a lot is actually being done to conserve declining breeds in many countries.

This book comprises the report of a subcommittee on Animal Genetic Resources set up by the Committee on Managing Genetic Resources: Agricultural Imperatives, itself established by the National Research

Council in the U.S.A. It was asked to review the use, preservation and management of global genetic resources nationally and internationally, to recommend research and development needs and to present a global strategy. The subcommittee was chaired by H. A. Fitzhugh, and the other members were E. L. Henson, J. Hodges, D. R. Notter, D. Plasse, L. L. Setshwaelo, T. E. Wagner and J. E. Womack (a good mix of those who are on the conservation circuit and those who are not). The report was published in 1993 but, judging by the references, was drafted two years earlier. It comprises a lengthy summary, a main section which reviews the arguments, describes genetic and new reproductive methodology, and discusses national and international programmes. There are also appendices including useful lists of breed numbers in different species and more specialized reviews on methodology and disease transfer risks with sperm and embryos. Whilst the presentation is all very clear, it is spoilt by the inclusion of poorly printed photographs, which look as if they had been conserved for half a century when in fact they are recent. It is a very thorough review of the topic although, as one might expect from a committee, rather turgid in style. Most of what is said can be found in many other places, but the slow state of advance of value of conservation in terms of hard evidence makes that inevitable. The committee argues very strongly and cogently for the value of and need for livestock conservation, recommending 'Mechanisms must be put in place to ensure that genetic diversity of the major livestock species is maintained to support improvements in production efficiency and to accommodate future changes in selection goals.' It will be interesting to see what comes of it.

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Locus Maps of Complex Genomes: Genetic Maps, 6th Edition. Edited by STEPHEN J. O'BRIEN. New York: Cold Spring Harbor Laboratory Press 1993. Published in two forms: (1) Complete version of 1532 pages, Cloth \$175. ISBN 087969 414 9. (2) As six paperback volumes with the following contents: *Book 1 – Virus*, 195 pages with 59 maps. \$35. ISBN 0 87969 415 7. *Book 2 – Bacteria, Protozoa and Algae*, 181 pages with 27 maps. \$35. ISBN 0 87969 416 5. *Book 3 – Lower Eukaryotes*, 285 pages. \$40 ISBN 0 87969 417 3. *Book 4 – Nonhuman Vertebrates*, 332 pages with 33 maps. \$40. ISBN 0 87969 418 1. *Book 5 – The Human Maps*, 267 pages with 10 maps. \$40. ISBN 0 87969 419 X. *Book 6 – Plants*, 272 pages with 26 maps. \$40. ISBN 0 87969 414 9.

The 6th edition of *Genetic Maps* contains some 40% more information than the 5th edition of 1990, judging by the relative number of pages (1532 compared with 1103), but is printed on thinner paper

which takes up about 20% less shelf space (70 versus 90 mm) which is a significant improvement. Publishing the edition both as a single volume for libraries and in six separate paperback sections at a cheap price for such a massive amount of information means that each research group should be able to afford to have the relevant section on its own shelves.

Reviewing previous editions of this masterwork, which Stephen O'Brien edited in 1980, 1982, 1984, 1987 and 1990, one can only marvel at the Editor's persuasive ability in extracting ever more elaborate scripts for successive editions from an ever increasing number of busy authors. The new edition has added a number of new organisms: I note Coliphage 196, Bovine herpesvirus-1, and Alcelaphine herpesvirus in Book 1 (Viruses), *Bacillus megaterium* and *B. stearrowthermophilus*, *Chlamydomonas eugametos*, *C. moewusi* and *Prototheca wickerhamii* in Book 2 (Bacteria, Algae and Protozoa), *Aspergillus niger*, *Cochliobolus heterosporus*, and *Drosophila buzzatii* among Lower Eukaryotes (Book 3). New among the Non-Human Vertebrates (Book 4) are the Silver Fox, *Xenopus laevis*; and the latest human–mouse comparative map with a figure by chromosomes and a table giving human locus symbol, gene name and location, alongside mouse locus and chromosome, bovine and cat chromosomes. Book 6 (Plants) has added the apple, rice, alfalfa, peanut, potato, cowpea and mungbean. No organism has been discarded and the smallest gene map still belongs to *Meriones unguiculatus* with 4 genes forming 2 linkage groups. There are probably about 170 organisms covered, with 189 genetic maps of different kinds, and the records for most of the species now take us to mid or late 1992, making them often the most up-to-date records available. Work on some organisms is progressing very rapidly: thus the linkage map of *Arabidopsis thaliana* has increased from 93 to 140 from 1989 to 1992, and the DNA sequences of 23 of these loci have now been published. The advance for *Caenorhabditis elegans* has been equally dramatic, an increase from 830 to 982 genes in the current linkage map.

Book 5, on the Human Genome, includes a list of 740 mutations under the classification 'Morbid Anatomy' which have been mapped, compared with about 550 in the previous edition. That is an impressive enough total, and at this rate of increase many more 'morbid mutations' for us to worry about are waiting to show themselves. At mid-1992, the current volume tells us that 10410 loci in the human genome had been mapped, including 2328 genes and pseudogenes, 84 chromosomal breakpoints, 113 fragile sites and 7885 anonymous DNA segments. These are all shown in figures beside each chromosome, and the 2328 genes and pseudogenes are then listed in order by chromosome, with symbol, location and marker name. Among other tables are a listing of Polymorphic PCR-detectable markers of *Homo sapiens*, including lo-