

through a partnership among interested agencies of the US Federal Government; the Global Taxonomy Initiative of the Convention on Biological Diversity, a worldwide effort spun from the 1992 Rio Earth Summit; and the Global Biodiversity Information Facility, begun by the Organization for Economic Cooperation and Development in 1996 and now headquartered as an independent operation in Copenhagen.

The second phase of the full biodiversity agenda is the accelerated discovery of life forms still unknown. This achievement, the anticipated moon shot of systematic biology, is envisioned as a future goal by the organizations loosely grouped under what Bisby *et al.* [11] have called the 'Catalog of Life' initiative, and as an immediate goal with a timeline by the All Species Foundation, headquartered in San Francisco, USA [6–8,10].

The final enterprise, the electronic Encyclopedia of Life, which is already being pressed here and there, will expand upon the growing base provided by the taxonomic Catalog of Life. Covering all biological levels, from genome to ecology, it will serve as the ultimate guide to biodiversity.

New technologies

Faith in a sprint to the finish of the global census is engendered by the more advanced revolutions ongoing in bioinformatics and genomics, which together offer the means to transform the traditional methods of taxonomy. The old methods, which still prevail, have been enormously labor intensive and time consuming. To complete a taxonomic analysis of a genus or higher order taxon requires examination of the primary types of each species, subspecies and variety, which are typically scattered among museums in North America and Europe, and often in other continents. The systematist must conduct lengthy tours to examine all these specimens, or else have them sent through by hand or mail, a risky step that not all curators are willing to take. The systematist must also have access to a wide array of books and journals, many of which are old and rare. As a result, the tradition of systematics since Linnaeus has been that of arcane expertise practiced by groups of specialists working on groups of organisms to which they have devoted their professional lives.

With the new technology, the 19th century culture of taxonomy has begun to be replaced. For the first time, type specimens can be illustrated by swiftly made high-resolution digital photographs, the anatomical detail and depth of field of which are beyond those seen in specimens viewed by light microscopy. The photographs can be published on the Internet. When all the primary types of a particular group, say weevils of the family Curculionidae or grasses of the family Gramineae, are digitally photographed and online, they can be accessed immediately by anyone anywhere. When the original diagnoses from print literature are added, experts can proceed with revisions at a speed and an economy vastly greater than enjoyed in the predigital era. In one step, the practice of taxonomy is globalized and democratized and, in a sense, the type specimens are repatriated to their country of origin.

One such program already completed is the 'virtual herbarium' of the New York Botanical Garden. Almost its entire collection of type specimens of some vascular plants, representing 90 000 species, is now finished. Similar initiatives are underway in the insect collections of the Academy of Natural Sciences in Philadelphia, USA and Harvard University's Museum of Comparative Zoology. With more such projects completed, collection by collection around the world, the global iconography will come together like pieces fitted into a mosaic. The result will be the requisite foundation for a swift exploration of biodiversity on Earth and the accompanying growth of the all-species encyclopedia.

Key challenges

Construction of the complete taxonomic base will not, however, be just a smooth compilation of species. The magnitude of biodiversity and the tangle of evolutionary processes that generated it still present formidable problems. First in line is the difficulty of classifying microorganisms and many of the smallest, soft-bodied invertebrates, most of the species of which can be reliably separated only by molecular diagnosis. The difficulty has put all-species inventories out of reach in the past. However, its solution appears close at hand, thanks to the rapid advances occurring in genomics. Already, for example, tens of thousands of species from the major domains of organisms have been at least partially sequenced for small subunit rRNA genes. By April 2002, the last date for which I have seen an accounting, the genomes of no fewer than 61 species of bacteria had been completely sequenced. As the process accelerates, and the cost per base pair continues to drop, genomic data will become standard for taxonomy, as well as for phylogenetic reconstruction, across all groups of organisms.

A second barrier to the all-species inventory is the incongruence of the species concept between major groups. The classic definition of the species in sexually reproducing organisms is a closed gene pool – a population of individuals that are capable of freely interbreeding under natural conditions. This criterion works reasonably well for most animals and plants, but creates difficulties in some plant groups in which hybridization is extensive but short of total. And it fails logically, of course, in the many populations that lack sexual reproduction. The value of the classic definition of reproductive isolation is still unknown in the bulk of microorganisms, where species might have to be delineated arbitrarily by a cutoff percentage of base pairs shared by populations or some other genetic criterion.

The species problem cannot be settled in advance by any formula or legislation. It will probably be broken only as the all-species initiative evolves, illuminating the particularities of species-level variation from one phylogenetic group of organisms to another. As this knowledge grows, the difficulty of defining species will metamorphose into deeper studies of how species-level diversity arises, group by group. Meanwhile, the process of censusing can and should proceed with the best tools and species concepts at