

land may be brought under cultivation since it is the need of the hour for feeding the growing population, to raise buffer stock and also for export. Under no circumstance shall the existing fertile land be used for industry. The concept of Special Economic Zone (SEZ), which is currently under much attention, gives

emphasis to industry alone. This approach is disastrous. In fact, we should not undermine the role of agriculture, as it alone provides the 'bread', whereas industry which gives us only 'money' does not. (iii) In some portion, ponds may be created to conserve the precious rainwater, which could be used for a variety of pur-

poses including farming, and to build up the fast depleting groundwater table.

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Taxonomy, the legacy of Linnaeus, transformed to phylogenomics

This is the tercentenary year of Carl Linnaeus, father of taxonomy, who was born in Sweden and lived from 1707 to 1778. The year 2007 therefore provides an occasion to remember the important contributions of Linnaeus to taxonomic biology, made in the mid-seventeenth century and to review their relationship to the biology of the early twenty-first century.

Linnaeus' contributions were both visionary and prolific. He initiated work to make a universal catalogue that describes and classifies all living organisms. For this, he studied thousands of specimens of plants and animals, collected by himself or obtained from botanists, explorers and correspondents in Europe, America, Pacific, Asia and Africa. His extensive comparative observations on physical forms of a large variety of plants and animals led him to devise a system of taxonomic code for treatment of each distinct organism/species. The code comprises of a name, type specimen, description and list of distinguishing features. He invented the binomial system of nomenclature in which the first name referred to genus and the second to species. He also started the convention of placing the name of the author of the species after the species name. This ensured that priority of authorship of species validated by reference to a publication was established once for all. Thanks to him, four codes of nomenclature exist now, one each for animals, plants, fungi and cultivated plants. These methodologies are best exemplified in his book entitled *Species Plantarum* published in 1753, wherein names and definite descriptions of more than 5000 species of plants are included. Since Linnaeus, each studied organisms has a name and identity, studies on living organisms have become repeatable.

Linnaeus believed that the number of species was constant, there were as many species at the beginning of life as are present now. Although he dealt with enormous variability of form demonstrated by a plethora of organisms examined by him, Linnaeus failed to perceive speciation, including common descent of several species from an ancestral species and continuum of the process of extinction of species and origin of new species, as we understand at present. In recent years, since the dawn of genomics three decades ago, taxonomy has turned into systematics. DNA sequence data are now used, in addition to morphological and biochemical features, to diagnose the identity of an organism or its parts, as well as to determine its hierarchical/phylogenomic position among related species/populations. The use of DNA sequence information, together with the conventional taxonomical tools of description, annotation and curation have made the identification of any new species more or less foolproof.

Genome sequences have been worked out now from more than 1000 species and DNA sequencing work on non-model species is rapidly growing. Nature of DNA sequences that comprise eu- and heterochromatin in chromosomes is becoming known. Genetic regulatory networks are being revealed. Functional genomics aimed at finding the roles of RNA/protein/enzyme product of specific genes is helping in these developments. Genetic linkage maps of model organisms based on conventional morphological traits, biochemical characters and DNA markers are becoming greatly detailed. Syntenic analysis is helpful in developing comparative genetic maps between related species. Sequence analyses of individual genes specified by nuclear and organelle (mitochondrion

and chloroplast) genomes is allowing the discovery of mutations present in paralogous and orthologous alleles of the given genes. Such information is allowing species-specific DNA barcodes. Comparative genomic analyses based on DNA sequences of several to many nuclear and/or organelle genes and map positions of these genes and algorithmic analyses of these data, aided by conventional taxonomic description, form a fairly rigorous technique to identify species and determine relatedness between species, genera and higher groups (families) in terms of evolutionary pathways from common ancestor(s). Notably, such analyses allowed separation of archae bacteria from other groups of bacteria. The challenging task ahead is to construct an eukaryotic tree depicting evolution among animal, plant, fungal and protist species, the major groups of eukaryotes. The science of phylogenomics has now become an integral part of taxonomy on the one hand, and genomic biology on the other.

The work of Linnaeus' organized knowledge about morphological features of identified and named plants and animals, has had a tremendous founding effect on all experimental biology. This will continue to serve as the foundation of modern genomic biology and experimental construction of new species for ecosystem services and for the benefit of human society.

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