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Flying into the Future

This cover of *Science* shows a fly providing the support system for a hang-gliding man. It provides a symbol for the symbiotic relationship between studies on humans and the model systems in less complex taxa such as fruit flies, yeast, and bacteria. Because humans are not available for the genetic engineering, tissue homogenizing, cell cycle interruptions, and other manipulations on which modern biology has depended, other species provided the experimental material with which the genetic code was unraveled, the enzymes involved in glycolysis were isolated, and the genes involved in development were tested. Although these organisms were interesting in themselves, the value of their biology was enhanced when it became apparent that all living things are more alike than they are different. A molecular biologist might say, "If you've seen one species, you've seen them all."

That statement is, of course, a gross oversimplification because the differences between species are not only interesting but highly relevant to such modern problems as extrapolating rat carcinogenesis tests to human disease prevention. The similarities are still striking, however. The homeobox, part of the control mechanism for organization during development, was initially discovered in fruit fly research when mutant flies with legs growing out of their heads were observed and similar genes were subsequently discovered in other organisms. Because homeotic mutants in humans would usually die in utero, the fly has become one example of a model system for exploring biology that is relevant but difficult, illegal, or impossible to study in humans. More than 400 genes have already been identified that are highly similar in the human and the fly and there will be many more. Because the fruit fly has 165 megabases of DNA in contrast to the 3000 megabases of human DNA, the fly is obviously a far simpler organism to study and manipulate. However, it is sufficiently complicated that it can mimic many of the behavioral and biological aspects of its more complex counterparts. Anyone with a flyswatter knows that the flight information and landing computation of a fly would elicit the admiration of any flight controller. The learning and memory of a fly are fleeting and not likely to get a fly through first grade, but they exist and can be manipulated genetically and biochemically.

The identification of genes in *Drosophila* and its uses as an experimental tool are described by Merriam, Ashburner, Hartl, and Kafatos. The information on the advances in the human genome map since last year and a summary of mapping and sequencing in the fruit fly are shown in a wall chart elucidated by a team of experts under the leadership of Senior Editor Barbara Jasny. Some legal problems are discussed by Leslie Roberts, and a pullout section on databases is included. The importance of getting the information into databases and the need for money and incentives to make these databases up to date is discussed by Pearson and co-workers in a Perspective. By means of new technologies, many being developed for the Human Genome Initiative, the sequencing and mapping of the fruit fly should advance greatly in the next few years, a great boon to research in *Drosophila*. Thus, contrary to some critics, the Human Genome Initiative, with its technological and intellectual advances, should provide benefits to the study of other biological systems.

The converse is also true. Already we learn a great deal about the human from our understanding of the biodiversity, morphology, and behavior of what are frequently called "lower" species. That will become increasingly true as previously uncharted regions of the human genome are subjected to the new technologies. Some of the genes will be immediately recognized by their sequence similarities to genes in other organisms such as the fly. The symbiotic relationship between the information from the fly and other species to the human genome is a powerful testimony to the farsightedness of the National Institutes of Health in funding research in all species.

When grants are written on studies of such systems as yeast, nematodes, bacteria, and *Drosophila*, it is the practice to explain how the work will relate to human health, which is the justification for the National Institutes of Health. The Human Genome Initiative is thus a logical closing of the loop that relates the biology of other species to human health. There is some argument about how fast or how efficiently this project might proceed, but there is no doubt that the mutual information exchange between scientists studying humans and those studying other organisms is to the advantage of all.—DANIEL E. KOSHLAND, JR.