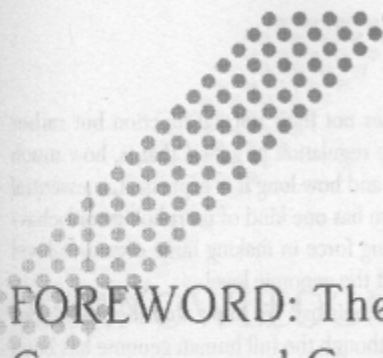




FOREWORD: The Continuity of Genomes and Genetic Resources for the New Century

Genomics promises to solve previously intractable problems in the biology of complex organisms, and in this context I believe genomics will be of high utility to conservation biology. Two important components of modern genomics can enhance the expansion of modern biology to address these important biological problems. The first concerns a new paradigm for studying organisms at a variety of levels gleaned from genomic studies. This paradigm uses the evolutionary process and evolutionary principles. The second concerns the potential availability of genetic resources from as broad an array of organisms as possible. Both of these components are relevant to conservation biology initiatives in the age of genomics.

In the study of evolution, access to the genomes of animals of the past is restricted, except for what can occasionally be gleaned from their hard parts, which are generally preserved in rocks. However, a complex record of the past is preserved in an organism's DNA. Putting some thought into what genomic information can tell us about life on this planet is of utmost importance. Because DNA carries not only the blueprint for organisms but also a record of the past, we should do everything possible to preserve these genomes and hence one aspect of the history of life on this planet.

Several initiatives exist to enhance and implement the collection and storage of genomes of a vast number of organisms, whether as actual nucleic acid samples or simply as DNA sequences. It is not entirely unreasonable to think that in the future (perhaps 50 to 100 years from now) we might be able to read the information in these genomes so as to be able to reconstruct them, either physically or computationally.

One of the great pieces of evidence to come from modern genomics for evolutionary studies is that the genes from many different organisms have a common evolutionary origin. For instance, whether you look at a bacterium or a human being, the genes specifying a protein such as triose phosphate isomerase in these two organisms have a common evolutionary ancestor. Furthermore, it is highly probable that one could take the yeast gene for triose phosphate isomerase and put it in a lobster, and it would work. This is highly probable because we know we can combine the yeast and the lobster proteins and get a functional entity out of them. That sort of experiment suggests that we can use new technology to implement a different approach to study how the biodiversity we observe every day on the planet arose.

If an organism develops a new muscle, it doesn't start from scratch and reinvent all the components of a muscle in order to provide for that new muscle. It is more likely

that the genes involved in muscle formation alter not their normal function but rather the location or timing of their expression. So the regulation of genes, that is, how much of each gene is expressed, where it is expressed, and how long it is expressed, is essential information that determines whether an organism has one kind of morphology or behavior. Natural selection can be a tremendous driving force in making large organism-level changes involving a small number of mutations at the genomic level.

What do we know about these control mechanisms? We know that they exist. But we don't know very much about them, and even though the full human genome has been sequenced, most of the information from these DNA sequences is still meaningless. Unfortunately, a computer program does not exist that can look at the human genome and determine when a particular gene is functionally important. An approach that has arisen out of modern genomics called inverse genetics promises to expand comparative biology in a direction never before imagined.

Classical genetics took organisms of the same genotype and then made changes in them, called mutations, that were then studied gene by gene. In other words, genetic researchers looked at small changes in a sea of uniformity. Inverse genetics, on the other hand, looks at constancy in a sea of noise.

One of the major goals of modern genomics is to understand the function of genes. In order to make sense of the changes and hence the function of genes in the genome of two lineages, an examination of the constant parts of their genomes in comparison to the sea of noise is essential. As many evolutionary comparisons as possible are necessary for the full extent of the approach to be efficient. Even as far away from the human lineage as the fish lineage is, the neuroendocrine system and many parts of the early embryology are much the same in the two organisms. Organisms that are considered more closely related will also share common genomic elements as well as common embryology and neurology. For instance, by putting fish genes into mice and assaying whether the transferred genes function the same as mouse genes, we confirm common functions for any gene in the genomes of organisms being compared. So it is of utmost importance to have available as many organismal genomes or genetic resources as possible.

Many examples in molecular biology demonstrate that with the new genomics we can do a new kind of genetics that amounts to crossing fish and mice and looking at recombinants. Experiments have recently been done on controlling elements in lymphocytes, with the same specific results. The advancing technology opens up the possibility of analyzing sequences of evolutionarily distant species, and the availability of as many genomes from as many taxa as possible is of paramount importance. The more combinations that can be made, the richer the comparisons will become and the more information we will obtain about gene regulation. This approach to studying genomes makes DNA from all kinds of organisms valuable.

As someone who has been involved in analyzing genomes for some time, I have concluded that of the vast sums being spent in this field by both governments and the private sector, a significant percentage should be used to encourage scientists to look at this field from an evolutionary perspective, of which conservation biology and genetic resource conservation are also a part. In addition, it is important that we move toward preserving the genomes of organisms in the living world in such a form and of sufficient quality that we can use it to enrich our knowledge of life on this planet and so our descendants can experience the vast variety of life on this planet in the future.