Evolutionary Genetics of Fishes

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EVOLUTIONARY GENETICS OF FISHES

Edited by Bruce J. Turner

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Preface

It is my hope that this collection of reviews can be profitably read by all who are interested in evolutionary biology. However, I would like to specifically target it for two disparate groups of biologists seldom mentioned in the same sentence, classical ichthyologists and molecular biologists.

Since classical times, and perhaps even before, ichthyologists have stood in awe at the tremendous diversity of fishes. The bulk of effort in the field has always been directed toward understanding this diversity, i.e., extracting from it a coherent picture of evolutionary processes and lineages. This effort has, in turn, always been overwhelmingly based upon morphological comparisons. The practical advantages of such comparisons, especially the ease with which morphological data can be had from preserved museum specimens, are manifold. But considered objectively (outside its context of “tradition”), morphological analysis alone is a poor tool for probing evolutionary processes or elucidating relationships. The concepts of “relationship” and of “evolution” are inherently *genetic* ones, and the genetic bases of morphological traits are seldom known in detail and frequently unknown entirely. Earlier in this century, several workers, notably Gordon, Kosswig, Schmidt, and, in his salad years, Carl Hubbs, pioneered the application of genetic techniques and modes of reasoning to ichthyology. While certain that most contemporary ichthyologists are familiar with this body of work, I am almost equally certain that few of them regard it as pertinent to their own efforts. For a while, in the 1970s, the “allozyme revolution” in evolutionary biology seemed to be having an impact on ichthyology as well, and a number of younger ichthyologists began to think in genetic terms. It is my impression that this impact is now largely spent: The recent rise of “phylogenetic systematics” with its emphasis on “derived character states” (and with, at least initially, little regard for their genetic bases) has, inadvertently and

unfortunately, revitalized the phenotypic typology that has always been present in ichthyology. This collection of reviews is thus designed, in part, to demonstrate the power of integrated genetic approaches to ichthyological problems. No morphological comparisons alone could have detected the role of ancient tetraploidy in the evolution of the salmonid or catostomid fishes, detected the existence of parthenoforms (much less probed their clonal population structure), or elucidated the role of natural selection in modulating plate numbers in stickleback populations. Moreover, morphological comparisons have already failed, and failed rather badly, to resolve the relationships of the Atlantic eels or to make much sense of the vast, and biologically important, radiations that are the cyprinid and cichlid fishes.

Most contemporary eukaryote molecular biologists concentrate their efforts on but a few species, none of them fishes. However, fishes offer a literal plethora of exciting “experimental systems” that could be exploited, and it seems worthwhile to point some of them out. For example, a process called *rediploidization* seems to be a common feature of the evolution of those groups of fishes (e.g., the salmonids) whose ancestries involved tetraploidization events. Yet how is the rediploidization achieved, and is it done the same way in different lineages? Are the extra genes deleted, mutated to functional silence (by what sort of regulatory mutations?), or are they somehow “coopted” by “ignorant” or “selfish” sequences? What fraction of duplicated genes becomes functionally specialized, as opposed to those that seem to disappear, and are there rules (other than chance) that govern this? Does the rediploidization occur at the same rate and in the same way in the highly repetitive, moderately repetitive, and “unique” portions of the genome? Gene duplication is clearly a fundamental (perhaps *the* fundamental) process in evolutionary genetics. The tetraploid fish lineages, quite literally, have duplicated genes “in spades” and might teach us much about how these are handled in a long-term evolutionary context. Equally tantalizing problems exist in other fish systems. The unisexual fishes, for example, offer opportunities to study the evolution of genomes that for the most part are not subject to the selective constraints of functional meiosis, and, moreover, are of hybrid origin. They may prove to be particularly useful systems in which to test current ideas of the evolution of gene sequences, expression, and genome organization. Similarly, it is now apparent that at least some aspects of sex determination in fishes may differ from those in mammals. What will these differences tell us about the ultimate molecular basis of the sex phenotypes? There are so many exciting questions amenable to contemporary molecular technology that the entry of molecular biology

into the evolutionary genetics of fishes is likely to be of extraordinary significance. If this book hastens that entry to even a slight extent it will have served its purpose.

Bruce J. Turner

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