

Preface

Evolutionary genetics straddles the two fundamental processes of life, development (the transition from egg to adult) and reproduction (the generation of eggs from adults), and scrutinizes, from an evolutionary perspective, the nature and consequences of the twin genomic attributes of expression and replication, respectively. Moreover, development and reproduction in the living world occur in, and are shaped by, the context of the ecology of organisms. Given this vast domain of evolutionary genetics, it is not surprising that its practitioners often work on very different issues, using varied approaches and methodologies. Historically, the early focus of evolutionary genetics was on heredity, more specifically on deducing the population-level consequences of Mendelian inheritance within families. The descendent lineages of these early studies in population and quantitative genetics can be categorized, for heuristic purposes, as efforts to understand the consequences of natural selection, and these lineages constitute a major 'tribe' within evolutionary genetics. These lines of investigation address the broad issue of how the distribution of genotypes in a population changes under the influence of a given fitness function acting on it. A contrast to this focus on the consequences of natural selection is provided by studies-sometimes characterized as evolutionary ecology-that attempt to understand how and why particular fitness functions are defined on the distribution of phenotypes in a population by its ecology. Studying how the interaction between phenotype and environment results in a fitness function is essentially an exercise in understanding the causes of natural selection. Connecting the causes and consequences of natural selection, or, to put it another way, extrapolating a fitness function defined

on a distribution of phenotypes to the corresponding underlying distribution of genotypes, is important to a fuller understanding of the evolutionary process. Basically, making this extrapolation requires not only a detailed understanding of the genome, but also an understanding of how genomes direct the development of phenomes through their expression in a given ecological context, also referred to as understanding the genotype-to-phenotype map. Approaches addressing this issue constitute a relatively young 'tribe' within evolutionary genetics, and rudimentary empirical tools required to study genotype-to-phenotype mapping have only recently become available.

In the past, the domains of evolutionary genetics (in terms of understanding the consequences of selection) and evolutionary ecology (understanding the causes of selection) were separated by a conceptual and empirical gulf owing to the paucity of information about, and understanding of, the genotype-to-phenotype map. Classical quantitative genetics was, in a sense, a clever and useful way of bypassing the expression aspect of the genome (genotype-to-phenotype map) by treating it as a black box, although with time the shortcomings of this approach have become clearer. Classical developmental genetics tended to focus on the genotype-to-phenotype map for exclusively morphological traits, and has led to a greatly refined understanding of the ontogeny of form. What has been lacking is an understanding of the ontogeny of function, and through it the ontogeny of life histories in meaningful ecological contexts, an approach that has been termed developmental evolutionary biology. Today, with the increasing ability to empirically study the sequences and temporal patterns of expression of entire genomes, we are finally at the threshold of a 'complete' evolutionary genetics, encompassing both the expression and replication aspects of genomes.

I sincerely hope that this work of mine will be helpful to all students, teachers and the general readers alike.

—Author