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Biology in Focus Chapter 21: The Evolution of Populations

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Natural Selection

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Chapter 23: The Evolution of Populations This chapter begins with the idea that we focused on as we closed the last chapter: Individuals do not evolve! Populations evolve. The Overview looks at the work of Peter and Rosemary Grant with Galápagos finches to illustrate this point, and the rest of the chapter examines the change in populations over time.

Evolution Of Population Chapter Test

Evolution Of Populations Test B Answers [MOBI] Chapter Test B Evolution Of Populations Answer The I B and I 0 alleles made up 134 percent and 605 percent of the alleles respectively, and all of the frequencies added up to 100 percent A change in this frequency over time would constitute Evolution Of Populations Chapter Test B Answers

Chapter Test B Evolution Of Populations Answer

In population genetics, the term evolution is defined as a change in the frequency of an allele in a population. Using the ABO blood type system as an example, the frequency of one of the alleles, IA, is the number of copies of that allele divided by all the copies of the ABO gene in the population.

The Evolution of Populations | Biology for Majors II

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Intraspecific genetic diversity is an important attribute of natural populations and is deemed critical for their adaptive potential and persistence. However, we have limited empirical understanding of the impact of genetic diversity on population performance under different conditions. For my dissertation, I conducted long-term laboratory experiments with populations of the flour beetle Tribolium castaneum to test the consequences of genetic variation for population dynamic stability and niche evolution. In Chapter 1, I show that genetic variation prevented population extinction in a novel habitat. In addition, genetically diverse populations were more stable, both in a novel heterogeneous habitat and in their ancestral habitat. In the ancestral habitat, alleles from a single founding lineage dominated the dynamics, leading to increased stability of genetically diverse populations. However, such as selective effect was not observed in the novel heterogeneous habitat. Therefore, while genetic variation within populations increased their stability and persistence, the magnitude of the impact and its mechanism depended on the selective habitat. In Chapter 2, I ask whether genetic variation also facilitates resource niche expansion, i.e., use of a novel resource. Using stable carbon isotopes, I analyzed diets of beetles sampled from the above experiment and quantified the rate of change in resource use. Contrary to theoretical predictions, I found that genetic variation for resource use had no effect on the rate of niche evolution. Furthermore, behavioral niche expansion accounted for most of the adaptation to the novel resource, and the behavioral change hindered subsequent evolutionary change in resource use. It is thus apparent that in the short term, behavioral plasticity in niche use may impose far greater constraints on niche evolution than the amount of standing genetic variation. Mathematical models predict that intraspecific competition generates selection for niche evolution, and that genetic variation increases the response to selection. Therefore, I hypothesized that the impact of genetic variation on resource niche evolution may depend on the degree of intraspecific competition. In the final chapter of this thesis, I describe results of an experiment to test this hypothesis. I found that genetic variation and competition indeed interacted to increase the rate of niche expansion in T. castaneum, but that their impacts were temporally variable. Furthermore, the two factors acted on different components of niche evolution: while competition only affected the degree of niche expansion, genetic variation also promoted maintenance of individual variation in resource use. In summary, my thesis describes experiments to test for the ecological and evolutionary impacts of intraspecific genetic variation; and its interaction with behavioral plasticity, intraspecific competition, and resource availability. Genetic diversity and behavioral plasticity are common features of living organisms, and therefore it is vital to understand their combined consequences for population ecological and evolutionary dynamics. In addition, natural populations often face intense competition for limited resources. Hence the experimental results presented here can help us to better understand how populations overcome these resource constraints, given their specific genetic composition. Biologists are increasingly aware that the intricate connection between ecological and evolutionary dynamics is important to gain a more complete understanding of population biology. The work described here represents one of the few experiments providing such detailed mechanistic understanding of the interactions between- and consequences of - key ecological and evolutionary parameters. Finally, the results have important implications for conservation biology, because they show that the effects of genetic diversity can vary greatly depending on a number of population and environmental parameters.

Biology for AP® courses covers the scope and sequence requirements of a typical two-semester Advanced Placement® biology course. The text provides comprehensive coverage of foundational research and core biology concepts through an evolutionary lens. Biology for AP® Courses was designed to meet and exceed the requirements of the College Board's AP® Biology framework while allowing significant flexibility for instructors. Each section of the book includes an introduction based on the AP® curriculum and includes rich features that engage students in scientific practice and AP® test preparation; it also highlights careers and research opportunities in biological sciences.

Today many school students are shielded from one of the most important concepts in modern science: evolution. In engaging and conversational style, Teaching About Evolution and the Nature of Science provides a well-structured framework for understanding and teaching evolution. Written for teachers, parents, and community officials as well as scientists and educators, this book describes how evolution reveals both the great diversity and similarity among the Earth's organisms; it explores how scientists approach the question of evolution; and it illustrates the nature of science as a way of knowing about the natural world. In addition, the book provides answers to frequently asked questions to help readers understand many of the issues and misconceptions about evolution. The book includes sample activities for teaching about evolution and the nature of science. For example, the book includes activities that investigate fossil footprints and population growth that teachers of science can use to introduce principles of evolution. Background information, materials, and step-by-step presentations are provided for each activity. In addition, this volume: Presents the evidence for evolution, including how evolution can be observed today. Explains the nature of science through a variety of examples. Describes how science differs from other human endeavors and why evolution is one of the best avenues for helping students understand this distinction. Answers frequently asked questions about evolution. Teaching About Evolution and the Nature of Science builds on the 1996 National Science Education Standards released by the National Research Council--and offers detailed guidance on how to evaluate and choose instructional materials that support the standards. Comprehensive and practical, this book brings one of today's educational challenges into focus in a balanced and reasoned discussion. It will be of special interest to teachers of science, school administrators, and interested members of the community.

"A central goal of evolutionary biology is to understand how organisms adapt to their environment. Though much progress has been made in answering this question, many aspects of the process of adaptation remain mysterious. This is especially true for biologists' understanding of the genetic basis of adaptation in natural populations of organisms. My dissertation integrates phenotypic and genetic perspectives to advance our understanding of selection and adaptation in natural populations of organisms. I take multiple approaches to this question, combining meta-analysis, population surveys, and manipulative experiments in the field. In my first chapter, I explore the consequences of natural selection on genetic variants. In many population genetic models, selection is parameterized as the selection coefficient, s. Through a meta-analysis of over 3000 selection coefficients from 79 studies, I reveal generalities about how natural selection operates at the genetic level. I relate these results to population genetic theory and studies of phenotypic selection, and provide recommendations for the calculation, interpretation, and reporting of selection coefficients. In my second chapter, I consider natural selection and adaptation within a rapidly moving hybrid zone between two races of Heliconius erato butterfly that differ in colour pattern. Because the genetic loci responsible for variation in colour pattern in H. erato are well characterized, I consider selection at the phenotypic and genetic levels simultaneously. I develop new statistical methods for quantifying hybrid zone position and shape and apply these to show that over the last 15 years the H. erato hybrid zone has grown wider while its movement has slowed. I show that this is due to a decrease in the strength of selection on colour pattern and the underlying colour-pattern allele. I then use remotely-sensed data on forest loss and productivity to test hypotheses about the ecological forces that influence hybrid zone dynamics. In my final chapter, I examine whether phenotypic and genetic change are predictable. I take an experimental approach, using a large-scale, long-term, eco-evolutionary field study with Anolis sagrei lizards. Anoles are an exemplar of parallel evolution across an adaptive radiation, and their interactions with competitor and predator species have been well-studied in within-generation experiments. This provides clear predictions for how these ecological interactions might drive adaptive evolution over multiple generations. I test these predictions by manipulating the presence and absence of predator and competitor species in a factorial design across 16 small islands in the Bahamas. I measure changes in a suite of morphological traits relevant to habitat use and performance, and use DNA sequencing to characterize changes in allele frequency across the genome. Despite strong and consistent effects of predators and competitors on behavior, diet, and population size in A. sagrei, I found that phenotypic and genetic change were difficult to predict in advance. Phenotypic change was related to variation in vegetation structure and lizard densities across islands, making a priori prediction challenging. Genetic change, on the other hand, was unpredictable and unrelated to either our experimental manipulations, phenotypic change, or environmental differences. My work reveals the necessity of ecological data and knowledge of natural history for predicting natural selection, and shows how field experiments can be used to test and clarify hypotheses about how natural selection operates. Overall, my dissertation demonstrates that integrating phenotypic and genetic perspectives can help biologists understand how natural selection operates in the wild. In particular, it shows the value of combining these perspectives with detailed ecological data, novel statistical techniques, and experimentation to directly test hypotheses about evolution in natural populations"--

Concepts of Biology is designed for the single-semester introduction to biology course for non-science majors, which for many students is their only college-level science course. As such, this course represents an important opportunity for students to develop the necessary knowledge, tools, and skills to make informed decisions as they continue with their lives. Rather than being mired down with facts and vocabulary, the typical non-science major student needs information presented in a way that is easy to read and understand. Even more importantly, the content should be meaningful. Students do much better when they understand why biology is relevant to their everyday lives. For these reasons, Concepts of Biology is grounded on an evolutionary basis and includes exciting features that highlight careers in the biological sciences and everyday applications of the concepts at hand.We also strive to show the interconnectedness of topics within this extremely broad discipline. In order to meet the needs of today's instructors and students, we maintain the overall organization and coverage found in most syllabi for this course. A strength of Concepts of Biology is that instructors can customize the book, adapting it to the approach that works best in their classroom. Concepts of Biology also includes an innovative art program that incorporates critical thinking and clicker questions to help students understand--and apply--key concepts.

A recent focus on contemporary evolution and the connections between communities has sought to more closely integrate ecology with evolutionary biology. Studies of coevolutionary dynamics, life history evolution, and rapid local adaptation demonstrate that ecological circumstances can dictate evolutionary trajectories. Thus, variation in species identity, trait distributions, and genetic composition may be maintained among ecologically divergent habitats. New theories and hypotheses (E.G., metacommunity theory and the Monopolization hypothesis) seek to understand better the processes occurring in spatially structured environments and how dispersal contributes to ecology and evolution at broader scales. As few empirical studies of these theories exist, this work seeks to further test these concepts. Spatial and temporal dispersal are the mechanisms connecting habitats to one another. Both processes allow organisms to leave suboptimal or unfavorable conditions, and enable colonization and invasion, species range expansion, and gene flow among populations. Freshwater zooplankton typically develop resting stages as part of their life that allow organisms to disperse both temporally and spatially. Additionally, because many species are cyclically parthenogenetic, they make excellent model organisms to study in a controlled environment. Here, I use freshwater zooplankton communities to examine the mechanisms and consequences of dispersal and to test these nascent theories on the influence of spatial structure in natural systems. In Chapter one, I use field experiments and mathematical models to determine the movement vectors and range of adult zooplankton dispersal over land. Chapter two uses statistical models with field and mesocosm experiments to examine prolonged dormancy in "Daphnia pulex." I show that variation in dormant egg hatching is substantial among populations in nature and can be attributed to genetic differences among the populations. Chapters three and four explore the consequences of dispersal at multiple levels of biological diversity. Chapter three looks at population level consequences of dispersal over evolutionary time on current patterns of population genetic differentiation. I test two alternative hypotheses addressing why nearby populations of "Daphnia" exhibit high population genetic differentiation. Finally, chapter four is a case study of how dispersal has influenced patterns of variation at the community, trait and genetic levels of biodiversity in a lake metacommunity. [The dissertation citations contained here are published with the permission of ProQuest llc. Further reproduction is prohibited without permission. Copies of dissertations may be obtained by Telephone (800) 1-800-521-0600. Web page: http://www.proquest.com/en-US/products/dissertations/individuals.shtml.].

The advent of large-scale population genomic datasets has enabled detailed inferences regarding human evolutionary history. Demographic changes and positive selection have left their marks on the genome and we can now begin to decipher them. In this dissertation, I present the work I have completed on the topic of human population genomic inference. In chapter 1, I begin by reviewing the importance of human genetic variation and the factors that influence it, focusing on the effects of demographic changes and positive selection. Chapter 2 describes an analysis of genetic ancestry in a worldwide sample of human populations. I show that mitochondrial lineage tests overlook large amounts of variation in genetic ancestry. In chapter 3, I focus on inferences regarding the effective sex ratio in the recent evolutionary past. I present a reanalysis of SNP and resequencing data that resolves a set of conflicting results from previous studies. Using coalescent simulations, I present a model of a recent male bias in effective population size, coupled with an earlier female bias, which is consistent with existing genetic variation on the X chromosome and the autosomes. In chapter 4, I present a comprehensive study of the performance of a battery of neutrality test statistics under a wide range of realistic models of positive selection in recent human evolution. I demonstrate that existing tests perform better than expected for detecting the signatures of a soft sweep from standing variation. Then, I develop a genome-wide approach, the Cumulative Selection Score (CSS), for combining the signals from multiple neutrality test statistics to detect the signatures of positive selection with greater accuracy. By implementing this approach in genomic variation data for chromosome 2, I show that the CSS can be applied to whole-genome datasets. I conclude in chapter 5 by discussing the potential of population genomic inferences and the future of the field.

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Each test question is answered in complete detail with easy-to-follow, easy-to-grasp explanations. - The book"s glossary allows for quicker, smarter searches of the information you need most TABLE OF CONTENTS INTRODUCTION: PREPARING FOR THE SAT II: BIOLOGY E/M SUBJECT TEST About the SAT II: Biology E/M Format of the SAT II: Biology E/M About this Book How to Use this Book Test-Taking Tips Study Schedule Scoring the SAT II: Biology E/M Scoring Worksheet The Day of the Test CHAPTER 1 - CHEMISTRY OF LIFE General Chemistry Definitions Chemical Bonds Acids and Bases Chemical Changes Laws of Thermodynamics Organic Chemistry Biochemical Pathways Photosynthesis Cellular Respiration ATP and NAD The Respiratory Chain (Electron Transport System) Anaerobic Pathways Molecular Genetics DNA: The Basic Substance of Genes CHAPTER 2 - THE CELL Cell Structure and Function Prokaryotic Cells Eukaryotic Cells Exchange of Materials Between Cell and Environment Cellular Division Equipment and Techniques Units of Measurement Microscopes CHAPTER 3 - GENETICS: THE SCIENCE OF HEREDITY Mendelian Genetics Definitions Laws of Genetics Patterns of Inheritance, Chromosomes, Genes, and Alleles The Chromosome Principle of Inheritance Genes and the Environment Improving the Species Sex Chromosomes Sex-linked Characteristics Inheritance of Defects Modern Genetics How Living Things are Classified CHAPTER 4 - A SURVEY OF BACTERIA, PROTISTS, AND FUNGI Diversity and Characteristics of the Monera Kingdom Archaebacteria Eubacteria The Kingdom Protista The Kingdom Fungi CHAPTER 5 - A SURVEY OF PLANTS Diversity, Classification, and Phylogeny of the Plant Kingdom Adaptations to Land The Life Cycle (Life History): Alternation of Generations in Plants Anatomy, Morphology, and Physiology of Vascular Plants Transport of Food in Vascular Plants Plant Tissues Reproduction and Growth in Seed Plants Photosynthesis Plant Hormones: Types, Functions, Effects on Plant Growth Environmental Influences on Plants and Plant Responses to Stimuli CHAPTER 6 - ANIMAL TAXONOMY AND TISSUES Diversity, Classification, and Phylogeny Survey of Acoelomate, Pseudocoelomate, Protostome, and Deuterostome Phyla Structure and Function of Tissues, Organs, and Systems Animal Tissues Nerve Tissue Blood Epithelial Tissue Connective (Supporting) Tissue CHAPTER 7 - DIGESTION/NUTRITION The Human Digestive System Ingestion and Digestion Digestive System Disorders Human Nutrition Carbohydrates Fats Proteins Vitamins CHAPTER 8 - RESPIRATION AND CIRCULATION Respiration in Humans Breathing Lung Disorders Respiration in Other Organisms Circulation in Humans Blood Lymph Circulation of Blood Transport Mechanisms in Other Organisms CHAPTER 9 - THE ENDOCRINE SYSTEM The Human Endocrine System Thyroid Gland Parathyroid Gland Pituitary Gland Pancreas Adrenal Glands Pineal Gland Thymus Gland Sex Glands Hormones of the Alimentary Canal Disorders of the Endocrine System The Endocrine System in Other Organisms CHAPTER 10 - THE NERVOUS SYSTEM The Nervous System Neurons Nerve Impulse Synapse Reflex Arc The Human Nervous System The Central Nervous System The Peripheral Nervous System Some Problems of the Human Nervous System Relationship Between the Nervous System and the Endocrine System The Nervous Systems In Other Organisms CHAPTER 11 - SENSING THE ENVIRONMENT Components of Nervous Coordination Photoreceptors Vision Defects Chemoreceptors Mechanoreceptors Receptors in Other Organisms CHAPTER 12 - 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Founded in 1959 with the purpose of disseminating the most recently developed scientific information to groups in industry, government, high schools, and universities, REA has since become a successful and highly respected publisher of study aids, test preps, handbooks, and reference works. REA"s Test Preparation series includes study guides for all academic levels in almost all disciplines. Research & Education Association publishes test preps for students who have not yet completed high school, as well as high school students preparing to enter college. Students from countries around the world seeking to attend college in the United States will find the assistance they need in REA"s publications. For college students seeking advanced degrees, REA publishes test preps for many major graduate school admission examinations in a wide variety of disciplines, including engineering, law, and medicine. 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Species introductions can provide unplanned and occasionally replicated experiments that can be studied to understand fundamental ecological and evolutionary processes associated with range expansions in the natural world. The cichlid species flock of Lake Malawi consists of an estimated 451-800 species and is a textbook example of explosive speciation that has been studied as a model system of evolution in the past three decades. In addition, fish are of major socio-economic importance to Malawian people, and they form an important source (circa 70%) of animal protein in their diet. Furthermore, fisheries activity employs 3% of the country's population and contributes to 4% of the country's Gross Domestic Product (GDP). This thesis studies a well documented, human mediated introduction of a rocky-shore, plankton-feeding cichlid fish Cynotilapia afra into Lake Malawi National Park. This introduction has important evolutionary and ecological consequences on the native populations of Pseudotropheus zebra, and here I investigate its population genetic impacts using contemporary molecular genetic tools and analyses. Three hypotheses were tested: 1. Introduction events are usually associated with a small founder population size, and the resulting genetic bottleneck is expected to reduce genetic variation of C. afra in the introduced range. 2. The invasive scenario during the introduction followed a stepping stone pattern, or alternatively, it occurred as several independent introductions of C. afra in Lake Malawi National Park. 3. Introgressive hybridisation between C. afra and P. zebra may have facilitated the introduction of the invading C. afra population and restored its depleted genetic variation associated with the founder event. Furthermore, the gene pool of C. afra has more non-native genetic material as compared to P. zebra. Samples were collected from six native and four introduced populations of C. afra, as well as three native populations of P. zebra. The latter species is from a different genus, although laboratory experiments indicate that both species hybridise in laboratory conditions. Sequence variation in the mitochondrial DNA (mtDNA) control region was analysed using 15 individuals per sample population and 60 individuals per sample population were genotyped at six microsatellite loci. These data were analysed to test the three hypotheses and identify potential source populations, infer introduction patterns (stepping stone or independent), and deduct whether introgressive hybridisation may have facilitated the founder event and subsequent establishment of C. afra in the invasive range in Lake Malawi Natural Park. The three data chapters in this thesis discuss the findings of the mtDNA sequence study (Chapter 2) and the microsatellite study (Chapter 3). In Chapter 4, I analyse the microsatellite data in further detail and consider the role of introgression by using Bayesian analysis tools. The mtDNA study presented in Chapter 2 reveals that C. afra and P. zebra mtDNA sequences show high levels of lineage sorting (i.e. the DNA sequences of both species are remarkably distinct). This finding is in sharp contrast to previous studies on Lake Malawi rock-dwelling cichlids which have shown that cichlid species share the same or very similar mtDNA haplotypes. Furthermore, the introduced populations showed a higher sequence and haplotype diversity than their native counterparts. This analysis suggests that elevated gene diversity was largely due to C. afra populations being founded by individuals from several genetically distinct and geographically separate populations. In Chapter 4, I discuss the role of introgressive hybridisation with native P. zebra, and its impact on mtDNA variation in the introduced C. afra gene pool. In Chapter 3, I show that in contrast to the signal obtained from the mtDNA, the genetic variation at the microsatellite loci exhibited a significant reduction in the introduced range. Introduced C. afra populations have a lower mean effective number of alleles (ne) than C. afra populations in their native range. I use an approximate Bayesian analysis and show compelling evidence that at least two independent introductions have contributed to the introduced C. afra gene pool, a conclusion that is supported by high probability values. This conclusion differs from that of previous studies which suggested a stepping stone introduction pattern around Thumbi West Island. Surprisingly, a population of C. afra at Domwe Island was founded by a source population from Thumbi West Island, and this stepping stone introduction pattern is supported with a high probability (95%). Microsatellite analysis furthermore suggests that the founder event of C. afra in Lake Malawi National Park was associated with strong genetic drift associated with a genetic bottleneck. I was not able to detect this signal from the mtDNA genetic marker alone, which showed an increase in genetic variation at the mtDNA due to different source populations contributing to the founder event (see Chapter 2). These combined studies reported in Chapter 2 and 3 thus demonstrate that microsatellites may be well-suited to investigate questions related to conservation issues such as bottlenecks associated with founder events, while mtDNA is more suited to reveal the evolutionary processes and establish different source populations that have contributed to the introduction. In Chapter 4, I analyse the level of genetic differentiation at microsatellite loci, and show that the introduced C. afra and native P. zebra populations at Thumbi West Island are genetically more similar (G'ST=0.36+/-0.05) than the species-pair at Otter point (G'ST=0.94+/-0.18) and Domwe Island (G'ST=0.55+/-0.09). In addition, C. afra and P. zebra at Thumbi West Island showed a lower genetic distance than allopatric C. afra or P. zebra populations from Otter point and Domwe Island. Further analysis using a Bayesian assignment approach supports previous findings and demonstrates the likelihood of introgressive hybridisation between an introduced C. afra and a native P. zebra population at Thumbi West Island. No evidence of introgression is found at Otter point and Domwe Island, where the C. afra and P. zebra populations show distinct genetic structure. The occurrence of introgressive hybridisation at Thumbi West between species from distinct genera shows that translocations can have a dramatic impact even on the gene pools of heterospecific recipient populations. The results from this work have crucial implications in evolution of cichlid fishes and in invasion biology when predicting the evolution of invasiveness. In summary, the thesis shows that hybridisation, as well as the introduction of multiple genetically differentiated source populations has increased the genetic diversity of introduced C. afra populations, and this may have facilitated their establishment in Lake Malawi National Park. Translocation of cichlid species in Lake Malawi can have a dramatic impact even on heterospecific gene pools.

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