Introduction To Population Genetics Halliburton

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making the theory of population genetics relevant to readers this book explains the related mathematics with a logical organization it presents the quantitative aspects of population genetics and employs examples of human genetics medical evolution human evolution and endangered species for an introduction to and understanding of population genetics

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loss of biodiversity is among the greatest problems facing the world today conservation and the genetics of populations gives a comprehensive overview of the essential background concepts and tools needed to understand how genetic information can be used to conserve species threatened with extinction and to manage species of ecological or commercial importance new molecular techniques statistical methods and computer programs genetic principles and methods are becoming increasingly useful in the conservation of biological diversity using a balance of data and theory coupled with basic and applied research examples this book examines genetic and phenotypic variation in natural populations the principles and mechanisms of evolutionary change the interpretation of genetic data from natural populations and how these can be applied to conservation the book includes examples from plants animals and microbes in

wild and captive populations this second edition contains new chapters on climate change and exploited populations as well as new sections on genomics genetic monitoring emerging diseases metagenomics and more one third of the references in this edition were published after the first edition each of the 22 chapters and the statistical appendix have a guest box written by an expert in that particular topic including james crow louis bernatchez loren rieseberg rick shine and lisette waits this book is essential for advanced undergraduate and graduate students of conservation genetics natural resource management and conservation biology as well as professional conservation biologists working for wildlife and habitat management agencies additional resources for this book can be found at wiley com go allendorf populations

this two volume set winner of a 2013 highly commended bma medical book award for medicine provides an in depth look at one of the most promising avenues for advances in the diagnosis prevention and treatment of human disease the inclusion of the latest information on diagnostic testing population screening predicting disease susceptibility pharmacogenomics and more presents this book as an essential tool for both students and specialists across many biological and medical disciplines including human genetics and genomics oncology neuroscience cardiology infectious disease molecular medicine and biomedical science as well as health policy disciplines focusing on ethical legal regulatory and economic aspects of genomics and medicine volume one includes principles methodology and translational approaches takes readers on the journey from principles of human genomics to technology informatic and computational platforms for genomic medicine as well as strategies for translating genomic discoveries into advances in personalized clinical care volume two includes genome discoveries and clinical applications presents the latest developments in disease based genomic and personalized medicine with chapters dedicated to cardiovascular disease oncology inflammatory disease metabolic disease neuropsychiatric disease and infectious disease this work provides the most comprehensive guide to the principles and practice of genomic and personalized medicine highly commended 2013 bma medical book award for medicine contributions from leaders in the field provide unparalleled insight into current technologies and applications in clinical medicine full colour throughout enhances the utility of this work as the only available comprehensive reference for genomic and personalized medicine discusses scientific foundations and practical applications of new discoveries as well as ethical legal regulatory and social issues related to the practice of genomic medicine

historically viral outbreaks have affected farmed and wild shrimp stocks in the northwestern pacific coast of mexico litopenaeus stylirostris is one of the three main penaeid shrimp species in the region and represents a major component of the bulk of wild caught shrimp despite the economic importance of the species genetic diversity and population structure of l stylirostris has been poorly studied and its interactions with viral pathogens remain unexplored in this study the genetic diversity population structure and demographic history of l stylirostris populations were addressed using mitochondrial control region sequences the results showed that l stylirostris have high levels of genetic diversity and their populations are geographically structured along the gulf of california factors contributing to the observed population structure include historic geological events and contemporary physical oceanographic conditions the health status of l stylirostris populations was assessed by determining the prevalence of four of the main viral pathogens known to affect penaeid shrimp the results showed that infectious hypodermic haematopoietic necrosis virus ihhnv is highly prevalent across the geographic range while other viral pathogens are present in low levels or remained undetected based on these findings the population genetics rates of evolution and population history of ihhnv were studied using capsid region sequences the results showed that ihhnv has a high rate of nucleotide substitution comparable to rna viruses is more genetically diverse than previously reported and presents a significant subdivision among viral populations in the northwestern pacific coast of mexico this study provides important insights into the previously unexplored evolutionary and population dynamics of l stylirostris and ihnnv in the mexican northwestern pacific region

since the first publication of population genetics and fishery management in 1987 significant technological analytical and conceptual changes have occurred by explaining basic population genetics in a fisheries context the text continues to serve as an excellent starting point for approaching complex recent developments

the definitive genetics lab manual for over 50 years this user friendly volume stresses classical genetics but includes some of the recent advances related to molecular and human genetics as well drosophila and maize experiments in genetics monohybrid crosses dihybrid crosses cell reproduction mitosis meiosis in animals oogenesis and spermatogenesis meiosis in angiosperms microsporogenesis and megasporogenesis polytene chromosomes from drosophila salivary glands sex chromosomes and gene transmission the sex check a study

of sex chromatin in human cells human chromosomes linkage and crossing over genetics of ascospore color in sordaria an investigation of linkage and crossing over using tetrad analysis open ended experiments using drosophila locating a mutant gene in its chromosome isolation of dna restriction endonuclease digestion and gel electrophoresis of dna amplification of dna polymorphisms by polymerase chain reaction per and dna fingerprinting transformation of escherichia coli gene action synthesis of b galactosidase in escherichia coli chromatographic characterization of drosophila melanogaster mutants bacterial mutagenesis gene recombination in phage polygenic inheritance fingerprint ridge count population genetics the hardy weinberg principle the effects of selection and genetic drift applied human genetics for anyone interested in hands on genetics work

populations of chinook oncorhynchus tshawytscha and coho salmon o kisutch from northern california and four species of north american sturgeon were analyzed by horizontal starch gel electrophoresis the products of 53 gene loci from 27 enzyme systems were used to characterize the genetic structure of 35 groups of hatchery and wild chinook salmon the distribution of specific alleles cluster analysis based on genetic identities analyses of gene flow and gene diversity analyses indicated that groups of chinook salmon from the three major river drainages in california were genetically differentiated the products of 45 gene loci from 21 enzyme systems were used to characterize the genetic structure of 27 groups of coho salmon most of the observed genetic variation was due to rare alleles occurring in only a few groups of salmon no obvious association of specific alleles with geographic area was observed and the low level of genetic variability made patterns of genetic structure or associations among the groups of coho salmon difficult to determine the application of biochemical genetic analyses to the management of chinook and coho salmon fisheries was addressed a comparison of hatchery groups of chinook and coho salmon with wild groups in the same area revealed that hatchery stocks generally reflect the genetic structure of the local populations the genetic differentiation of chinook salmon by drainage could provide fishery scientists with a means to identify specific groups of chinook salmon the application of this technique to manage coho salmon populations is problematic at the present given the seemingly random distribution of alleles and the low levels of genetic variability the products of seven gene loci were used to identify hybridization between chinook and coho salmon in a collection of salmon from a tributary to the trinity river the implications of a group of hybrid fish in the wild were discussed in terms of genetic resource conservation and disease transmission the products of 20

gene loci were used to characterize the genetic structure and relationship of four species of sturgeon acipenser transmontanus a medirostris a fulvescens and a brevirostrum fixed allelic differences existed among the four species at several gene loci and each species could be unambiguously identified by its genetic profile

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