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PALMER KIDD

An Aging World Oxford University Press
"Now in full color, this new edition of Human evolutionary genetics has been brought up-to-date with the many advances and discoveries made since the publication of the highly regarded first edition. The focus of the book is human genetic diversity: the mechanisms that generate it, how we study it, its implications in evolution, and its implications today. It will be an invaluable resource for anyone studying human evolution, genetic variation, population genetics, and biological anthropology"--
Human Evolutionary Biology Academic Press
Longevity and the rate of senescence are determined by the

ecological conditions experienced during a population's recent evolutionary history, and are intrinsically linked to other components of life history and to fitness. These traits should be examined in an ecological context, in which other aspects of the life history are taken into account. However, although many mutations which promote longevity in model organisms disrupt mechanisms that are involved in responding to environmental change, trade-efts associated with increased lifespan have typically been examined in benign laboratory conditions. In the nematode Caenorhabditis elegans, long-lived, stress resistant age-1 (hx546) mutants can compete with wild type worms in favourable growth conditions, but display fitness costs when populations are periodically starved. By monitoring temporal changes in genotype frequencies, I have established that age-1 mutants can have higher fitness than the wild type strain if mixed genotype populations are exposed to periods of thermal or oxidative stress when food is available. Genotype- by-environment interactions, and spatial and temporal distributions of the FOXO transcription factor DAF-16, suggest that this is because age-1 mutants are more able to survive, develop and reproduce during and/or after exposure to environmental stress, due to increased expression of genes involved in somatic maintenance and repair.

Using population projection matrices, I have demonstrated that the age- 1 (hx546) mutant allele can confer a selective advantage over the wild type genotype when populations experience abiotic stress, even if periods of starvation are frequently endured. This is the first demonstration that a long-lived, laboratory-derived mutant can have higher fitness than a wild type genotype under specific environmental conditions. The results imply that, if genetic variation is present in populations which encounter harsh conditions, increased longevity can evolve as a consequence of selection for greater resistance to stress. I have also established that the effects of mutations which promote longevity on the ability to tolerate environmental stress can be context dependent, and that long-lived age-1 (hx546) mutants display increased cold tolerance, relative to wild type worms, due to increased expression of 119 desaturase genes and additional transcriptional targets of DAF-16. The results presented in this thesis suggest that genetic and life history responses to environmental stress deserve a more prominent role in evolutionary studies of ageing.

Biological Evolution Taylor & Francis

In Fragile X-Associated Tremor Ataxia Syndrome (FXTAS), the editors present information on all aspects of FXTAS, including clinical features

and current supportive management, radiological, psychological, and pathological findings, genotype-phenotype relationships, animal models and basic molecular mechanisms. Genetic counseling issues are also discussed. The book should serve as a resource for professionals in all fields regarding diagnosis, management, and counseling of patients with FXTAS and their families, as well as presenting the molecular basis for disease that may lead to the identification of new markers to predict disease risk and eventually lead to target treatments.

Biology for AP ® Courses

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Darwin's theory of evolution by natural selection was based on the observation that there is variation between individuals within the same species. This fundamental observation is a central concept in evolutionary biology. However, variation is only rarely treated directly. It has remained peripheral to the study of mechanisms of evolutionary change. The explosion of knowledge in genetics, developmental biology, and the ongoing synthesis of evolutionary and developmental biology has made it possible for us to study the factors that limit, enhance, or structure variation at the level of an animals' physical appearance and behavior. Knowledge of the significance of variability is crucial to this emerging synthesis. Variation situates the role of

variability within this broad framework, bringing variation back to the center of the evolutionary stage. Provides an overview of current thinking on variation in evolutionary biology, functional morphology, and evolutionary developmental biology Written by a team of leading scholars specializing on the study of variation Reviews of statistical analysis of variation by leading authorities Key chapters focus on the role of the study of phenotypic variation for evolutionary, developmental, and post-genomic biology *Genomics of Beta Vulgaris Crop Types* Cambridge University Press Multiple Sclerosis (MS) is a demyelinating disease of the central nervous system with autoimmune etiology. It affects approximately 2.3 million people worldwide, but prevalence is distributed unequally with countries closer to the equator manifesting a lower prevalence of MS. The Italian island of Sardinia is an exception, with prevalence rates that are among the highest in the world. Sardinia is inhabited by a unique, isolated population that was founded approximately 10,000 years ago. The reasons for this enrichment of MS cases in Sardinia are unknown. Like most complex diseases, MS has both genetic and environmental components of susceptibility. To date, research has uncovered the identity of 114 Single Nucleotide Polymorphisms

(SNPs) which tag loci that explain approximately 27% of the genetic factors that drive MS susceptibility, in populations of Northern European ancestry. With the exception of the effect exerted by polymorphisms in the Human Leukocyte Antigen DRB1gene, these genetic susceptibility alleles have small to moderate effect sizes (Odds Ratio range 1.03 to 1.34) and are largely common in the population (Risk Allele Frequency range 0.09 to 0.95). There are multiple reasons to explore the hypothesis that the Sardinian population may be enriched for the risk alleles that drive MS susceptibility, such as the high prevalence of MS and predictions made by population genetics theory with regard to the genetic landscape of isolated populations. Past studies in the genetics of MS in Sardinia have uncovered regions of the genome with possible roles in MS pathogenesis that display little overlap with regions identified in other populations. In the present study, I examined the presence of established MS-associated SNPs in a dataset of 19 multiplex Sardinian families. Although the Northern European-derived risk variants are present in Sardinians, these are able to differentiate patients from unaffected Sardinian individuals only when considered cumulatively, with the use of a weighted genetic burden score. The presence of multiple MS cases in the same family afforded us the opportunity to search for

genetic variation that affected relative pairs may share from a common ancestor. Five regions with suggestive amounts of allele sharing were detected (logarithm of the odds (LOD*) score >= 1); fine-mapping underneath these linkage peaks identified four genes that may be relevant in MS pathogenesis in Sardinia (EPHA7 on 6q16.1, JAZF1 on 7p15.1, KLRC2 on 12p13.2 and CD226 on 18q22.2). Interestingly, the chromosome 12 peak spans the natural killer cell gene cluster at that location. I therefore used whole exome sequencing data of the affected individuals from 5 of the Sardinian multiplex families to search for rare, nonsynonymous variants. I identified two variants in IKZF1 at 7p12 and MANBA at 4q24, two genes that are implicated in MS via the established associations. These variants are conserved and predicted to be probably damaging to the protein product. I also found a range of variants in the genes underneath the linkage peaks, highlighting the importance of cumulative assessments of the burden of rare and common variants in disease. In total, these data indicate that the overall MS susceptibility landscape in Sardinia is not markedly different from that of outbred European populations, and likely includes both common and rare risk alleles. However, these data also highlight the utility of multiplex families from an isolated population in the initial

identification of possible risk alleles. Replication in large population samples is required to assess the relevance of the identified variants in MS pathogenesis.

Human Evolutionary Genetics John Wiley & Sons

A pioneering proposal for a pluralistic extension of evolutionary theory, now updated to reflect the most recent research. This new edition of the widely read Evolution in Four Dimensions has been revised to reflect the spate of new discoveries in biology since the book was first published in 2005, offering corrections, an updated bibliography, and a substantial new chapter. Eva Jablonka and Marion Lamb's pioneering argument proposes that there is more to heredity than genes. They describe four “dimensions” in heredity—four inheritance systems that play a role in evolution: genetic, epigenetic (or non-DNA cellular transmission of traits), behavioral, and symbolic (transmission through language and other forms of symbolic communication). These systems, they argue, can all provide variations on which natural selection can act. Jablonka and Lamb present a richer, more complex view of evolution than that offered by the gene-based Modern Synthesis, arguing that induced and acquired changes also play a role. Their lucid and accessible text is accompanied by artist-physician Anna Zeligowski's lively drawings, which humorously and effectively illustrate the

authors' points. Each chapter ends with a dialogue in which the authors refine their arguments against the vigorous skepticism of the fictional “I.M.” (for Ipcha Mistabra—Aramaic for “the opposite conjecture”). The extensive new chapter, presented engagingly as a dialogue with I.M., updates the information on each of the four dimensions—with special attention to the epigenetic, where there has been an explosion of new research. Praise for the first edition “With courage and verve, and in a style accessible to general readers, Jablonka and Lamb lay out some of the exciting new pathways of Darwinian evolution that have been uncovered by contemporary research.” —Evelyn Fox Keller, MIT, author of Making Sense of Life: Explaining Biological Development with Models, Metaphors, and Machines “In their beautifully written and impressively argued new book, Jablonka and Lamb show that the evidence from more than fifty years of molecular, behavioral and linguistic studies forces us to reevaluate our inherited understanding of evolution.” —Oren Harman, The New Republic “It is not only an enjoyable read, replete with ideas and facts of interest but it does the most valuable thing a book can do—it makes you think and reexamine your premises and long-held conclusions.” —Adam Wilkins, BioEssays

Animal Homosexuality

Springer Science & Business Media

A look into the phenomena of sex and reproduction in all organisms, taking an innovative, unified and comprehensive approach.

Mathematical Population Genetics 1 Cambridge University Press

This volume of Methods in Cell Biology, the second of two parts on the subject of zebrafish, provides a comprehensive compendia of laboratory protocols and reviews covering all the new methods developed since 1999. This second volume covers advances in forward and reverse genetic techniques, provides an update on the zebrafish genome and gene/mutant mapping technologies, examines the new systems for efficient transgenesis in the zebrafish, provides an in-depth view of informatics and the emerging field of comparative genomics, and considers the extensive infrastructure now available to the zebrafish community. * Details state-of-the art zebrafish protocols, delineating critical steps in the procedures as well as potential pitfalls * Illustrates many techiques in full-color * Summarizes the Zebrafish Genome Project

Analysis of Complex Disease Association Studies Springer Science & Business Media

Provides information on the molecular basis of human genetics and outlines the principles of other epigenetic processes which together create the phenotype of a human being. This work also discusses the

molecular basis for the concepts, methods and results in fields such as population genetics.
Garland Pub
There is a common misconception that our genomes - all unique, except for those in identical twins - have the upper hand in controlling our destiny. The latest genetic discoveries, however, do not support that view. Although genetic variation does influence differences in various human behaviours to a greater or lesser degree, most of the time this does not undermine our genuine free will. Genetic determinism comes into play only in various medical conditions, notably some psychiatric syndromes. Denis Alexander here demonstrates that we are not slaves to our genes. He shows how a predisposition to behave in certain ways is influenced at a molecular level by particular genes. Yet a far greater influence on our behaviours is our world-views that lie beyond science - and that have an impact on how we think the latest genetic discoveries should, or should not, be applied. Written in an engaging style, Alexander's book offers tools for understanding and assessing the latest genetic discoveries critically.
The Zebrafish John Wiley & Sons
This is the first of a planned two-volume work discussing the mathematical aspects of population genetics with an emphasis on evolutionary theory. This volume draws heavily

from the author's 1979 classic, but it has been revised and expanded to include recent topics which follow naturally from the treatment in the earlier edition, such as the theory of molecular population genetics.

Are We Slaves to our Genes? Cambridge University Press

Provides statistical information on the worldwide population of people 65 years old or older.

Principles of Plant Genetics and Breeding Cambridge University Press

Nuclear receptors (NRs) are ligand-sensitive transcription factors that regulate a wide array of biological processes including development, metabolism, and circadian rhythms. All NRs share a common protein structure, including highly conserved DNA binding domains and a highly variable N-terminal A/B domain, and are very popular drug targets. To better understand the role of alternative A/B domains between NR isoforms and the impact of genetic variation on gene expression in the liver, we employed two experimental approaches. The NR hepatocyte nuclear factor 4[alpha] (HNF4[alpha]), a master regulator of liver-specific gene expression, is regulated by two promoters (P1 and P2) in the liver resulting in proteins with different A/B domains. P1-HNF4[alpha] is expressed in fetal and normal adult liver while P2-HNF4[alpha] is expressed only in the fetal liver and in liver cancer. We compared wildtype

mice, which express only HNF4[alpha]1 (P1) in the adult liver, to exon-swap mice that express only HNF4[alpha]7 (P2) for global changes in gene expression (RNA-seq), chromatin binding (ChIP-seq), and unique protein interactions (RIME). The results show that P1- and P2-HNF4[alpha] isoforms differentially regulate hundreds of transcripts in the adult liver, including the NR CAR (Nr1i3), and may be recruited differentially to non-HNF4[alpha] binding sites by unique protein interactions. They also exhibit altered metabolic pathways, especially cytochrome P450 (Cyp) genes. All told, the results show that changes in just 16-30 amino acids in the AF-1 region of an NR can have profound effects on gene expression. Utilizing protein binding microarrays (PBM), we can measure the DNA binding affinity of a given NR against both alleles of 125,000 genetic variants in a single experiment to probe for affinity altering SNPs (aaSNPs). By mining SNPs from ChIP-seq peaks and eQTLs from the GTEx project, we have identified thousands of aaSNPs, hundreds of which show significant correlation to changes in gene expression within their regulatory network. Analysis of aaSNPs from GWAS studies associated with Alzheimer's disease identified a large number of genetic variants that can alter the DNA binding affinity of PPARy in the APOE locus. Additionally, we show the power of the PBMs to validate many aaSNPs derived from in vivo analysis and suggest

a role for the PBM technology in characterizing how genetic diversity may play a role in personalized medicine.

The Biology of Reproduction Academic Press

Principles of Nutrigenetics and Nutrigenomics: Fundamentals for Individualized Nutrition is the most comprehensive foundational text on the complex topics of nutrigenetics and nutrigenomics. Edited by three leaders in the field with contributions from the most well-cited researchers conducting groundbreaking research in the field, the book covers how the genetic makeup influences the response to foods and nutrients and how nutrients affect gene expression. Principles of Nutrigenetics and Nutrigenomics: Fundamentals for Individualized Nutrition is broken into four parts providing a valuable overview of genetics, nutrigenetics, and nutrigenomics, and a conclusion that helps to translate research into practice. With an overview of the background, evidence, challenges, and opportunities in the field, readers will come away with a strong understanding of how this new science is the frontier of medical nutrition. Principles of Nutrigenetics and Nutrigenomics: Fundamentals for Individualized Nutrition is a valuable reference for students and researchers studying nutrition, genetics, medicine, and related fields. Uniquely

foundational, comprehensive, and systematic approach with full evidence-based coverage of established and emerging topics in nutrigenetics and nutrigenomics Includes a valuable guide to ethics for genetic testing for nutritional advice Chapters include definitions, methods, summaries, figures, and tables to help students, researchers, and faculty grasp key concepts Companion website includes slide decks, images, questions, and other teaching and learning aids designed to facilitate communication and comprehension of the content presented in the book

Index Medicus Academic Press

Genetic diversity is one of the measures of biodiversity and has consequences in biological variation. It is crucial to understand the evolutionary and adaptative processes in all living species. This book is an interdisciplinary and integrated work that will contribute to the knowledge of academics from different areas of biological sciences. This collection of scientific papers was chosen and analyzed to offer readers a broad and integrated view of the importance of genetic diversity in the evolution and adaptation of living beings, as well as practical applications of the information needed to analyze this diversity in different organisms. This book was edited by geneticist researchers and provides academics with up-to-date and quality

information on the subject.

Genes, Behavior, and the Social Environment Springer Science & Business Media

Bears have fascinated people since ancient times. The relationship between bears and humans dates back thousands of years, during which time we have also competed with bears for shelter and food. In modern times, bears have come under pressure through encroachment on their habitats, climate change, and illegal trade in their body parts, including the Asian bear bile market. The IUCN lists six bears as vulnerable or endangered, and even the least concern species, such as the brown bear, are at risk of extirpation in certain countries. The poaching and international trade of these most threatened populations are prohibited, but still ongoing. Covering all bears species worldwide, this beautifully illustrated volume brings together the contributions of 200 international bear experts on the ecology, conservation status, and management of the Ursidae family. It reveals the fascinating long history of interactions between humans and bears and the threats affecting these charismatic species.

Investigation of Candidate Genes and HLA-Related Risk Factors in a Genetic Study of Autoimmune Disease Cambridge University Press

This text book, originally published in 1970, presents the field of population genetics,

starting with elementary concepts and leading the reader well into the field. It is concerned mainly with population genetics in a strict sense and deals primarily with natural populations and less fully with the rather similar problems that arise in breading live stock and cul t i vat ed plans . The emphasis is on the behavior of genes and population attributes under natural selection where the most important measure is Darwinian fitness. This text is intended for graduatestudents and advanced undergraduates in genetics and population biology. This book steers a middle course between completely verbal biological arguments and the rigor of the mathematician. The first two-thirds of the book do not require advanced mathematical background. An ordinary knowledge of calculus will suffice. The latter parts of the book, which deal with population stochastically, use more advanced methods.

Genetic Variation

Academic Press

Cultivated Beta vulgaris L. (beet) is a species complex composed of several distinct crop types developed for specific end uses. The crop types include sugar beet, fodder beet, table beet and leaf beet/chard. The evolution of each crop type appears to have resulted from interactions between selection, drift, gene flow, recombination, and the sorting of ancestral variation. Beets are generally heterozygous and contain self-incompatibility

mechanisms. Therefore, reproducing and maintaining the genetic constitution of a single individual for genetic and phenotypic analysis is a challenge. Beet populations are the fundamental unit of improvement and contain the evolutionary and adaptive potential of the species. This research used several approaches which explore the utility of pooled population genomic sequencing to survey the organization and distribution of genetic diversity within cultivated B. vulgaris lineages, and give context and clarity to the genetics underlying important agronomic characters.Whole genome sequence data was produced for important varieties and germplasm releases which represent the B. vulgaris crop type lineages. Using population genetic and statistical methods, relationships were determined between populations. Lineage-specific variation, or variation unique to specific crop types, was uncovered and used to quantify the level of support for these groups as discrete units. Allele frequency was able to differentiate between crop types using Principle Components Analysis (PCA), suggesting positive selection for end use was a major driver of crop type divergence. PCA carried out on a chromosome-by-chromosome basis showed the relative contributions of specific chromosomes to crop type diversification. Gene diversity (e.g., expected heterozygosity) and FST proved powerful

indicators of selection along the chromosome at nucleotide resolution. In total, 12.13% of loci within the genome were differentiated with respect to crop type. Interestingly, this corresponds to levels of divergence observed in studies of incipient speciation. Differentiated regions, indicated by FST outliers, contained 472 genes, or 1.6% of the 24,255 genes predicted in the reference genome assembly. Respectively, sugar beet, table beet, fodder beet, and chard genomes contained 16, 283, 2, and 171 genes characterized as differentiated between crop types. Cryptic relationships were observed between crop types due to a high degree of genetic variation shared between crop type lineages. Specific instances of common ancestry, sorting of ancestral variation, and admixture and introgression were identified, which explain the degree of substructure observed between specific crop types.The content and organization of diversity in beet genomes reflects a complex history related to B. vulgaris crop type diversification. With the exception of chard, much of the species' historical selection has focused on the improvement of root characters (e.g., root enlargement, biomass, dry matter content, and sucrose concentration). As a result, major differences in root morphology and physiology can be observed between these lineages. Measures of root development and physiology between crop

types were compared, and interestingly, much of the phenotypic variation partitioned between crop types corresponds to candidate genes identified from analyses of genome-wide variation using FST and 2pq. Admixture and introgression appear to have shared specific variation involved in the reduction of lateral roots (e.g., Root primordium defective 1), root enlargement (e.g., Brevis radix-like 4, putative NAC domain-containing protein 94, cytokinin dehydrogenase 3), and biomass accumulation (e.g., 6-phosphofructo-2-kinase). High relationship coefficients and high correlations in allele frequency for this variation were observed, indicating the genetic variation influencing these characters may have been derived from a single origin. The development of beet into an economically viable sugar crop required both an enlarged root and an increase sucrose concentration. Genes were identified that may explain these physiological changes within the root (e.g., decrease in water concentration, increase in dry matter content and increase in sucrose concentrations). These genes correspond to shared variation, distributed among crop types, as well as lineage-specific variation, restricted to sugar beet lineages. Integrating selection, drift, and admixture into a putative demographic history of beet provides evidence for the role of specific genes in the development

of beet crop types and the expression of novel phenotypic characters.

Genetic Management of Fragmented Animal and Plant Populations

Scientific Publishers

"Females and males have different sets of sex chromosomes and produce different levels of gonadal sex hormones. They also differ in many aspects of their anatomy and physiology, susceptibility to disease, drug metabolism, gene expression levels, and DNA methylation patterns. The liver is a sexually dimorphic organ showing major sex differences in steroid and drug metabolism profiles, as well as sex differences in gene expression and DNA methylation. We have recently generated a catalogue of sex-biased differentially methylated regions (sDMRs) for mouse liver and demonstrated that sex-chromosome complement and the sex phenotype influence autosomal DNA methylation. The mechanisms by which the Y chromosome and the sex phenotype influenced DNA methylation remained unclear. In this project, we had two aims: first, to understand how the Y chromosome influences DNA methylation, and second, how the sex phenotypes influence DNA methylation. For our first aim, we hypothesized that Y-chromosome dependent sDMRs were specific for the B6.TIR strain, and genetic variation in the Y chromosome between B6.TIR and C57BL/6J (B6) influenced DNA methylation. To test this hypothesis, we compared

the methylation levels of two Y-chromosome dependent sDMRs in B6 and B6.TIR animals. We also compared the expression of Y-linked genes that are expressed in the liver between the two strains.For our second aim, we hypothesized that androgen (testosterone) and estrogen (estradiol) signaling influenced DNA methylation through their receptors (androgen and estrogen receptors, respectively). To test this hypothesis, we examined the age dynamics of sex-biased methylation in B6 male and female mice, true hermaphrodites, and sex-reversed XY females. We also tested sex-biased methylation in the liver of androgen receptor knockout (ARKO) and estrogen receptor 1 knockout (ESR1KO) mice. Liver DNA samples were extracted from (1) B6 female and male mice at three different ages: embryonic day 14.5 (E14.5), 4 weeks, and 8 weeks after birth; (2) B6.TIR mice: XY males, hermaphrodites, and sex-reversed females, as well as XX females at 8 and 16 weeks of age; (3) XY ARKO and wild type littermates at 10-11 weeks of age; (4) homozygous and heterozygous ESR1KO mice and wild type littermates at 8 weeks of age. We examined DNA methylation levels using targeted pyrosequencing methylation assays at six sex-phenotype dependent sDMRs that were selected for their association with sex-biased expression: three with higher expression and lower methylation in male livers (male-biased sDMRs) and

three with higher expression and lower methylation in female livers (female-biased sDMRs). To test if the timing of sex-biased methylation coincides with sex-biased gene expression, we performed RT-qPCR for two male-biased and two female-biased genes.We show that Y-chromosome dependent sDMRs are specific to the B6.TIR strain and Y-linked genes may contribute to the TIR-specific sex-biased methylation. We show that sex bias in DNA methylation and gene expression varies with age. At eight weeks, hermaphrodites showed either intermediate or female-like methylation levels, and they established a male-like methylation level at 16 weeks. Our results suggest that the presence of an ovary and a testis in the same mouse affects DNA methylation in an age-dependent manner. AR loss in male mice leads to the feminization of DNA methylation at sDMRs. Loss of ESR1 changes methylation levels of both females and males at male-biased sDMRs, and only females at female-biased sDMRs.In summary, we demonstrate that signaling of both estrogen and testosterone through their receptors contributes to sex-biased methylation in the mouse liver"--

Bears of the World

Genetic Variation

Genetic VariationBoD – Books on Demand

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