

Mendelian Genetics Worksheet

Names: Adrienne Mekelle B. Alcantara

Directions: In your groups of 2, complete the worksheet below. Each question should be answered by a different partner (i.e. you should not answer multiple questions in a row). Initial by the questions you complete.

1. A male and female bird have 4 unhatched eggs. The female is on the left heterozygous; the male on the right is homozygous recessive. Use B or b for your genotypes.

- a. Write the genotype of the female (left) below:

Answer: Bb

- b. Write the genotype of the male (right) below:

Answer: bb



- c. Which color is dominant, gray or black? How do you know?

Answer: It is gray, because the female's genotype has one dominant allele while the male has none.

- d. Write the phenotype of the female and the phenotype of the male below:

Answer: The female is gray and the male is black.

- e. Complete the Punnett Square below for this couple:

	b	b
B	Bb	Bb
b	bb	bb

- f. If they follow the Punnett Square ratios, what will the babies in the eggs look like when they hatch?

Answer: There are two grays

- g. Will all four offspring adhere exactly to the ratios predicted by the Punnett Square? Explain:

Answer: It is likely because the Punnett square only gave us a predicted probability.

Genetics Statistics Worksheet

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Genetics Statistics Worksheet:

Omics and Systems Approaches to Study the Biology and Applications of Lactic Acid Bacteria

Konstantinos Papadimitriou, Jan Kok, Pierre Renault, Kimberly Kline, 2020-10-13 The economic importance of lactic acid bacteria LAB for the food industry and their implication in health and disease has rendered them attractive models for research in many laboratories around the world. Over the past three decades molecular and genetic analysis of LAB species provided important insights into the biology and application of starter and probiotic LAB and in the virulence of LAB pathogens. The knowledge obtained prepared LAB researchers for the forthcoming opportunities provided by the advent of microbial genomics. Today developments in next generation sequencing technologies have rocketed LAB genome research and the sequences of several hundreds of strains are available. This flood of information has revolutionized our view of LAB. First of all a detailed picture has emerged about the evolutionary mechanisms allowing LAB to inhabit the very diverse ecological niches in which they can be found. Adaptation of LAB to nutrient rich environments has led to degenerative evolution processes that resulted in shortening of chromosomes and simplified metabolic potential. Gene acquisition through horizontal transfer on the other hand is also important in shaping LAB gene pools. Horizontally acquired genes have been shown to be essential in technological properties of starters and in probiosis or virulence of commensals. Progress in bioinformatics tools has allowed rapid annotation of LAB genomes and the direct assignment of genetic traits among species strains through comparative genomics. In this way the molecular basis of many important traits of LAB has been elucidated including aspects of sugar fermentation flavor and odor formation production of textural substances stress responses colonization of and survival in the host cell to cell interactions and pathogenicity. Functional genomics and proteomics have been employed in a number of instances to support *in silico* predictions. Given that the costs of advanced next generation methodologies like RNA seq are dropping fast bottlenecks in the *in silico* characterization of LAB genomes will be rapidly overcome. Another crucial advancement in LAB research is the application of systems biology approaches by which the properties and interactions of components or parts of a biological system are investigated to accurately understand or predict LAB behavior. Practically systems biology involves the mathematical modeling of complex biological systems that can be refined iteratively with wet lab experiments. High throughput experimentation generating huge amounts of data on the properties and quantities of many components such as transcripts enzymes and metabolites has resulted in several systems models of LAB. Novel techniques allow modelling of additional levels of complexity including the function of small RNAs structural features of RNA molecules and post translational modifications. In addition researchers have started to apply systems approaches in the framework of LAB multispecies ecosystems in which each species or strain is considered as a part of the system. Metatranscriptomics, metaproteomics and metametabolomics offer the means to combine cellular behavior with population dynamics in microbial consortia.

Plant Pathology Concepts and Laboratory Exercises Bonnie H. Ownley, Robert N. Trigiano, 2016-11-03

Continuing in the tradition of its predecessors this new edition combines an informal easy to read style with a thorough introduction to concepts and terminology of plant pathology After reviewing fundamental concepts the book discusses groups of plant pathogens and molecular tools for studying them pathogen interactions epidemiology and disease control and special topics in plant pathology The book details various disease causing organisms including viruses fungi prokaryotics nematodes and various biotic agents It also examines various plant pathogen interactions molecular attack strategies extracellular enzymes host defenses and disruption of plant function New in the Third Edition Molecular plant fungal interactions Expanded treatment of molecular tools Advanced biocontrol concepts How to use and care for microscopes

Multi-omic

Data Integration Paolo Tieri,Christine Nardini,Jennifer Elizabeth Dent,2015-09-17 Stable predictive biomarkers and interpretable disease signatures are seen as a significant step towards personalized medicine In this perspective integration of multi omic data coming from genomics transcriptomics glycomics proteomics metabolomics is a powerful strategy to reconstruct and analyse complex multi dimensional interactions enabling deeper mechanistic and medical insight At the same time there is a rising concern that much of such different omic data although often publicly and freely available lie in databases and repositories underutilised or not used at all Issues coming from lack of standardisation and shared biological identities are also well known From these considerations a novel pressing request arises from the life sciences to design methodologies and approaches that allow for these data to be interpreted as a whole i e as intertwined molecular signatures containing genes proteins mRNAs and miRNAs able to capture inter layers connections and complexity Papers discuss data integration approaches and methods of several types and extents their application in understanding the pathogenesis of specific diseases or in identifying candidate biomarkers to exploit the full benefit of multi omic datasets and their intrinsic information content Topics of interest include but are not limited to Methods for the integration of layered data including but not limited to genomics transcriptomics glycomics proteomics metabolomics Application of multi omic data integration approaches for diagnostic biomarker discovery in any field of the life sciences Innovative approaches for the analysis and the visualization of multi omic datasets Methods and applications for systematic measurements from single undivided samples comprising genomic transcriptomic proteomic metabolomic measurements among others Multi scale approaches for integrated dynamic modelling and simulation Implementation of applications computational resources and repositories devoted to data integration including but not limited to data warehousing database federation semantic integration service oriented and or wiki integration Issues related to the definition and implementation of standards shared identities and semantics with particular focus on the integration problem Research papers reviews and short communications on all topics related to the above issues were welcomed

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