

Breonna Martin

Microbiology

September 27th, 2019

Dr. Hawker

Lab Report Five

Purposes: This lab was to test our hypothesis that bacteria should be sensitive to UV light exposure and they should grow at an optimal temperature.

Materials:

- Agar Plates
- Test tubes
- Pipette
- Q-tips
- Bacteria
- Ultraviolet light
- Refrigerator
- Room temp incubator
- 37-degree incubator
- 55-degree incubator
- Marker

Methods:

Growth

1. Each lab table will take 5 agar plates.
2. Each person will remove a drop of bacterial culture from the tube cultures and pipette on an agar plate.
3. Spread the culture evenly over the plate with a sterile Q tip swab. Allow the liquid time to absorb into the agar.
4. Invert and incubate (face-down) 4 of the plates at one of the following temperatures: 1) 4 °C (refrigerator), 2) 23°C (Room temp incubator), 3) 37°C (incubator), and 4) 55°C (incubator) incubate until the next lab period (48 hrs).
5. The 5th plate will be exposed to uv light as described below.

UV Light

1. Each table will take one agar plate and spread on it a lawn of bacteria as described above.

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Single-Molecule Enzymology: Nanomechanical Manipulation and Hybrid Methods ,2017-01-03 Single Molecule Enzymology Part B the latest volume in the Methods in Enzymology series continues the legacy of this premier serial with quality chapters authored by leaders in the field This volume covers research methods in single molecule enzymology and includes sections on such topics as force based and hybrid approaches fluorescence high throughput sm enzymology and nanopore and tethered particle motion Continues the legacy of this premier serial with quality chapters authored by leaders in the field Covers research methods in single molecule enzymology Contains sections on such topics as force based and hybrid approaches fluorescence high throughput sm enzymology and nanopore and tethered particle motion **Assembly of the Photosystem II Membrane-Protein Complex of Oxygenic Photosynthesis** Julian J. Eaton-Rye,Roman Sobotka,2017-08-08 Photosystem II is a 700 kDa membrane protein super complex responsible for the light driven splitting of water in oxygenic photosynthesis The photosystem is comprised of two 350 kDa complexes each made of 20 different polypeptides and over 80 co factors While there have been major advances in understanding the mature structure of this photosystem many key protein factors involved in the assembly of the complex do not appear in the holoenzyme The mechanism for assembling this super complex is a very active area of research with newly discovered assembly factors and subcomplexes requiring characterization Additionally the ability to split water is inseparable from light induced photodamage that arises from radicals and reactive O₂ species generated by Photosystem II chemistry Consequently to sustain water splitting a self repair cycle has evolved whereby damaged protein is removed and replaced so as to extend the working life of the complex Understanding how the biogenesis and repair processes are coordinated is among several important questions that remain to be answered Other questions include how and when are the inorganic cofactors inserted during the assembly and repair processes and how are the subcomplexes protected from photodamage during assembly Evidence has also been obtained for Photosystem II biogenesis centers in cyanobacteria but do these also exist in plants Do the molecular mechanisms associated with Photosystem II assembly shed fresh light on the assembly of other major energy transducing complexes such as Photosystem I or the cytochrome b₆ f complex or indeed other respiratory complexes The contributions to this Frontiers in Plant Science Research Topic are likely to reveal new details applicable to the assembly of a range of membrane protein complexes including aspects of self assembly and solar energy conversion that may be applied to artificial photosynthetic systems In addition a deeper understanding of Photosystem II assembly particularly in response to changing environmental conditions will provide new knowledge underpinning photosynthetic yields which may contribute to improved food production and long term food security **Proteomics, Multi-Omics and Systems Biology in Optic Nerve Regeneration** Sanjoy K. Bhattacharya,2025-01-28 Proteomics Multi Omics and Systems Biology in Optic Nerve Regeneration is a comprehensive reference that covers all vistas of standardization of axon regeneration as well as all multi

omics and system level data and integration tools By adopting a translational approach the book bridges current research in the field to clinical applications and readers can expect to learn standardization approaches for axon regeneration multi omics datasets different databases search engines multiple dataset integrative tools pathway convergence approaches and tools outcome and outcome measures that unify bench research with clinical outcome The axon regeneration from existing neurons in central nervous system CNS have become a potential possibility in the last decade The potential possibility of long distance axon growth has opened the possibility of re connectivity of axons of retinal ganglion cell neurons within the lateral geniculate nucleus in the brain The long distance axon regeneration and re connectivity is a promise to restore lost vision in the optic nerve Further long distance regeneration and re innervation is equally helpful for other fields such as spinal cord injuries Includes updates on the use of multi omics datasets for selecting molecules for axon regeneration Bridges the preclinical and clinical world from selection of the molecules to outcome leading to IND filing and their use Includes system level knowledge needed for central nervous system axon and dendrite regeneration and standardizes the system level biology for axon regeneration Explores the current state of multi omics in axon and dendrite regeneration in the optic nerve and its comparison to other CNS regeneration Fish Molecular Innate Immunity and Innate Immune responses against pathogens

Chunsheng Liu,2023-09-06 Soil Survey Manual (U.S. Department of Agriculture Handbook No. 18) U.S. Department of Agriculture,2019-04-06 The Soil Survey Manual USDA Handbook No 18 provides the major principles and practices needed for making and using soil surveys and for assembling and using related data The term soil survey is used here to encompass the process of mapping describing classifying and interpreting natural three dimensional bodies of soil on the landscape This work is performed by the National Cooperative Soil Survey in the United States and by other similar organizations worldwide The Manual provides guidance methodology and terminology for conducting a soil survey but does not necessarily convey policies and protocols required to administer soil survey operations The soil bodies contain a sequence of identifiable horizons and layers that occur in repeating patterns in the landscape as a result of the factors of soil formation as described by Dokuchaev 1883 and Jenny 1941 **Structural aspects of peroxisome biogenesis and functions** Marek

Skoneczny,Ralf Erdmann,Tânia Francisco,Christos Gatsogiannis,2023-01-19 **Andrology** Eberhard Nieschlag,Hermann M. Behre,Sabine Kliesch,Susan Nieschlag,2023-10-26 The successful book of andrology now in a new edition This book gives a complete interdisciplinary overview of the central topics of andrology infertility hypogonadism contraception and erectile dysfunction It contains detailed information on the clinical practice of couple treatment andrology relevant gynecology and modern methods of assisted fertilization psychological factors of infertility endocrinology and reproductive functions of the aging man as well as on an important sub area of andrology the male contribution to contraception In addition the relevant scientific foundations including molecular biology and genetics are also covered Completely revised and updated according to the latest scientific research the new edition represents a reference for andrology which no doctor who deals with the

topic can miss For andrologists practitioners and residents urologists dermatologists and internists who deal with the area of andrology and male reproductive medicine **Soil Survey Manual** United States. Bureau of Plant Industry, Soils, and Agricultural Engineering, 1951 *Functional and Comparative Genomics of Saccharomyces and non-Saccharomyces Yeasts: Potential for Industrial and Food Biotechnology* Isabel Sá-Correia, Ed Louis, 2020-02-25 Since 1996 when the first *Saccharomyces cerevisiae* genome sequence was released a wealth of genomic data has been made available for numerous *S. cerevisiae* strains its close relatives and non conventional yeast species isolates of diverse origins Several annotated genomes of interspecific hybrids both within the *Saccharomyces* clade and outside are now also available This genomic information together with functional genomics and genome engineering tools is providing a holistic assessment of the complex cellular responses to environmental challenges elucidating the processes underlying evolution speciation hybridization domestication and uncovering crucial aspects of yeasts physiological genomics to guide their biotechnological exploitation *S. cerevisiae* has been used for millennia in the production of food and beverages and research over the last century and a half has generated a great deal of knowledge of this species Despite all this *S. cerevisiae* is not the best for all uses and many non conventional yeast species have highly desirable traits that *S. cerevisiae* does not have These include tolerance to different stresses e g acetic acid tolerance in *Zygosaccharomyces bailii* osmotolerance in *Z. rouxii* and thermotolerance in *Kluyveromyces marxianus* and *Ogataea Hansenula polymorpha* the capacity of assimilation of diverse carbon sources e g high native capacity to metabolize xylose and potential for the valorization of agroforest residues by *Scheffersomyces Pichia stipites* as well as high protein secretion fermentation efficiency and production of desirable flavors capacity to favor respiration over fermentation high lipid biosynthesis and accumulation and efficient production of chemicals other than ethanol amongst many Several non *Saccharomyces* species have already been developed as eukaryotic hosts and cell factories Others are highly relevant as food spoilers or for desirable flavor producers Therefore non conventional yeasts are now attracting increasing attention with their diversity and complexity being tackled by basic research for biotechnological applications The interest in the exploitation of non conventional yeasts is very high and a number of tools such as cloning vectors promoters terminators and efficient genome editing tools have been developed to facilitate their genetic engineering Functional and Comparative Genomics of non conventional yeasts is elucidating the evolution of genome functions and metabolic and ecological diversity relating their physiology to genomic features and opening the door to the application of metabolic engineering and synthetic biology to yeasts of biotechnological potential We are entering the era of the non conventional yeasts increasing the exploitation of yeast biodiversity and metabolic capabilities in science and industry In this collection the industrial properties of *S. cerevisiae* in particular uses are explored along with its closely related species and interspecific hybrids This is followed by comparisons between *S. cerevisiae* and non conventional yeasts in specific applications and then the properties of various non conventional yeasts and their hybrids *Computational Prediction of Protein Complexes from*

Protein Interaction Networks Sriganesh Srihari, Chern Han Yong, Limsoon Wong, 2017-05-30 Complexes of physically interacting proteins constitute fundamental functional units that drive almost all biological processes within cells A faithful reconstruction of the entire set of protein complexes the complexosome is therefore important not only to understand the composition of complexes but also the higher level functional organization within cells Advances over the last several years particularly through the use of high throughput proteomics techniques have made it possible to map substantial fractions of protein interactions the interactomes from model organisms including *Arabidopsis thaliana* a flowering plant *Caenorhabditis elegans* a nematode *Drosophila melanogaster* fruit fly and *Saccharomyces cerevisiae* budding yeast These interaction datasets have enabled systematic inquiry into the identification and study of protein complexes from organisms Computational methods have played a significant role in this context by contributing accurate efficient and exhaustive ways to analyze the enormous amounts of data These methods have helped to compensate for some of the limitations in experimental datasets including the presence of biological and technical noise and the relative paucity of credible interactions In this book we systematically walk through computational methods devised to date approximately between 2000 and 2016 for identifying protein complexes from the network of protein interactions the protein protein interaction PPI network We present a detailed taxonomy of these methods and comprehensively evaluate them for protein complex identification across a variety of scenarios including the absence of many true interactions and the presence of false positive interactions noise in PPI networks Based on this evaluation we highlight challenges faced by the methods for instance in identifying sparse sub or small complexes and in discerning overlapping complexes and reveal how a combination of strategies is necessary to accurately reconstruct the entire complexosome

Novel Insights into Sperm Function and Selection: from Basic Research to Clinical Application Kun Li, Tao Luo, Rossella Cannarella, 2023-10-25 *Heritage, Culture and Society* Salleh Mohd Radzi, Mohd Hafiz Mohd Hanafiah, Norzuwana Sumarjan, Zurinawati Mohi, Didi Sukyadi, Karim Suryadi, Pupung Purnawarman, 2016-10-26 *Heritage Culture and Society* contains the papers presented at the 3rd International Hospitality and Tourism Conference IHTC2016 2nd International Seminar on Tourism ISOT 2016 Bandung Indonesia 10 12 October 2016 The book covers 7 themes i Hospitality and tourism management ii Hospitality and tourism marketing iii Current trends in hospitality and tourism management iv Technology and innovation in hospitality and tourism v Sustainable tourism vi Gastronomy foodservice and food safety and vii Relevant areas in hospitality and tourism *Heritage Culture and Society* is a significant contribution to the literature on Hospitality and Tourism and will be of interest to professionals and academia in both areas

Mapping of salt-affected soils - Technical manual Food and Agriculture Organization of the United Nations, 2020-08-01 Salt affected soils such as saline or sodic soils are distributed in all continents at various levels of problem intensity They are soils with high amounts of soluble salts and or sodium ions An updated information of their distribution and drivers is a first step towards their sustainable management This book provides

technical guidelines and approach for developing a harmonized multiscale soil information of salt affected soils The book is organized into three sections covering seven chapters The sections are sequentially arranged but independently designed to benefit focused readership who may want to go straight to any section Section 1 gives the background information It has three chapters covering existing literature on the characteristics and mapping methods for salt problems in the soil It is intended to illustrate the basic concepts linkage of the characteristics of salt affected soils with input data requirements for their mapping existing classification methods and global distribution of these soils Section 2 covers the methodological procedures for developing multiscale spatial information of salt affected soils It has two chapters describing requirements input data preparation and the procedural steps for developing spatial information of salt affected soils It outlines how data from different sources and characteristics are harmonized and integrated to produce information of salt affected soils Section 3 covers information sharing and resources mobilization when developing information on salt affected soils It gives the guidelines for preparing spatial maps and steps for value addition to benefit end users of the information It also contains a generic training program for building technical capacity for mapping salt affected

Peroxisome Biology: Breakthroughs, Challenges and Future Directions Maya Schuldiner,Einat Zalckvar,Peter Kijun Kim,Sigrun

Reumann,Michael Sattler,2021-08-31 **Theoretical Aspects of Computing - ICTAC 2018** Bernd Fischer,Tarmo

Uustalu,2018-10-13 This book constitutes the refereed proceedings of the 15th International Colloquium on Theoretical Aspects of Computing ICTAC 2018 held in Stellenbosch South Africa in October 2018 The 25 revised full papers presented together with two short and two long invited talks were carefully reviewed and selected from 59 submissions The ICTAC conference aims at bringing together researchers and practitioners from academia industry and government to present research and exchange ideas and experience addressing challenges in both theoretical aspects of computing and the exploitation of theory through methods and tools for system development ICTAC also specifically aims to promote research cooperation between developing and industrial countries Xenopus Models of Organogenesis and Disease John Noel

Griffin,Emily Sempou,Karen Liu,2020-07-09 *Genome Instability: Old Problem, New Solutions* Vivian Kahl,Nicolas

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