Degree Applicable

Glendale Community College
November 2014

COURSE OUTLINE

Biology 103
Molecular Biology and Genetics

I. Catalog Statement

Biology 103 is an extension of the study of molecular biology, cell biology and genetics introduced in Biology 101. The course examines the structure and function of nucleic acids and proteins in the living cell, how they are studied and manipulated in the laboratory, and how the study of entire genomes and proteomes has given unprecedented insight into the workings of cells and organisms. Topics include regulation of gene expression, tissue culture, protein purification and analysis, antibodies, recombinant DNA technology, extensions of Mendel, linkage mapping, pedigree analysis, genomics, genome-wide association studies, and proteomics, all with a strong emphasis on data analysis and problem-solving.

Total Lecture Units: 4.0
Total Course Units: 4.0

Total Lecture Hours: 64.0
Total Faculty Contact Hours: 64

Prerequisites: Biology 101 and Chemistry 105 (Chemistry 105 may be taken concurrently)

II. Course Entry Expectations

Prior to enrolling in the course, the student should be able to:

1. identify the properties of lipids, carbohydrates, proteins, and nucleic acids;
2. describe the structure of prokaryotic and eukaryotic cells;
3. explain cell respiration and photosynthesis;
4. describe the relationships between meiosis and Mendelian genetics;
5. solve Mendelian genetics and pedigree problems;
6. describe the processes of deoxyribonucleic acid (DNA) replication, transcription, and translation;
7. describe techniques and applications of biotechnology;
8. explain the basic mechanisms of gene regulation in prokaryotes and eukaryotes;
9. demonstrate proper use of laboratory equipment including the microscope, spectrophotometer, and micropipettes;
10. demonstrate proficiency with data collection, analysis, and graphical representation;
11. summarize the main points of a scientific article;
12. be familiar with the system of classification of compounds by structure which is the framework of organic chemistry;
13. delineate the principles of organic chemical reactions;
14. be familiar with the laboratory methods and specialized instruments typically used in organic chemistry;
15. keep accurate laboratory records;
16. prepare themselves for pre-professional examinations that include organic chemistry, e.g. MCAT, DAT, pharmacy and dental hygiene aptitude examinations;
14. read and evaluate scientific material of significance to them as citizens.

III. Course Exit Standards

Upon successful completion of the required course work, the student will be able to:

1. describe in detail the structure of both DNA (deoxyribonucleic acid) and proteins, including the ultrastructure of chromatin, and epigenetic modifications and their significance;
2. describe in detail the steps involved in the expression of genes, in both prokaryotes and eukaryotes, as well as some of the control mechanisms that cells can apply at each step;
3. explain some of the methods used to purify and characterize proteins, grow cells in the lab, generate and use antibodies in the lab, and briefly describe stem cells (embryonic, adult, and induced pluripotent);
4. describe the methods employed in basic recombinant DNA technology, including the use of restriction enzymes, electrophoresis, library construction and screening, blotting and hybridization, DNA sequencing, PCR (polymerase chain reaction), and DNA microarrays;
5. explain the steps involved in producing transgenic and knockout organisms;
6. briefly describe genome editing with engineered sequence-specific nucleases, and explain how genome editing is combined with somatic cell nuclear transfer (SCNT) to produce transgenic and knockout animals;
7. describe RNA (ribonucleic acid) interference and the mechanisms involved in it, the utility of knockdown organisms, and other uses of RNAi to discern gene function;
8. describe the composition of the human genome, including transposable elements and various other classes of repetitive elements, as well as various types of DNA polymorphisms, including single nucleotide polymorphisms (SNPs), simple sequence polymorphisms, and copy number variations;
9. summarize Mendel's contributions and explain and solve problems involving various extensions of Mendel;
10. draw linkage maps using data from 3-point crosses and from human pedigrees;
11. describe various methods used in cytogenetics, including nomenclature for G-banded chromosomes, and how they are used to detect deletions and other chromosomal rearrangements;
12. explain how genomes are sequenced, assembled, and analyzed;
13. define haplotype, and explain how analysis of haplotype blocks is performed and used to carry out genome-wide association studies, as well as describe other computational methods for analyzing genomes;
14. describe some of the methods used in proteomics, including chromatin immunoprecipitation as a method for identifying transcription factor/enhancer interactions and histone modifications;
15. describe proto-oncogenes, oncogenes, tumor suppressor genes, transformation, and requirements for metastasis;
16. use online tools including BLAST and PubMed to identify, analyze, and research an unknown DNA sequence;
17. demonstrate proficiency with micropipets, and ability to perform restriction digests, agarose electrophoresis, and to purify genomic DNA from salmon sperm nuclei using organic extractions and ethanol precipitation;
18. solve problems in and out of class requiring detailed understanding of all of the above topics.

IV. Course Content **Total Faculty Contact Hours = 64 hours**

A. Structure and biosynthesis of nucleic acids 4 hours

B. Structure, biosynthesis, trafficking, and degradation of proteins 4 hours

C. Regulation of gene expression in prokaryotes and eukaryotes 6 hours
1. Transcriptional control and operons
2. Eukaryotic RNA processing, alternative splicing, and RNA editing
3. Enhancers and silencers
4. Chromatin structure and epigenetic modification

D. Growing cells in the lab, tissue culture, flow cytometry, and embryonic and induced pluripotent stem cells 2 hours

E. How macromolecules are manipulated and analyzed 4 hours
1. Centrifugation methods
2. Protein purification and analysis
3. Antibodies and their uses, immunogenetics, and VDJ (variable diversity joining) recombination
4. Electrophoresis of proteins and DNA

F. Recombinant DNA technology 6 hours
1. Restriction enzymes, electrophoresis, and restriction mapping
2. DNA libraries and their screening
3. DNA sequencing by the dideoxy and newer methods
4. The polymerase chain reaction, including quantitative and multiplex PCR
5. DNA microarrays, including tiling arrays and SNP arrays and their uses

G. RNA interference and micro-RNA's, including mechanisms and applications in cultured cells and transgenic knockdown organisms 2 hours

H. Transgenic and knockout organisms by traditional methods 2 hours

I. Genome editing with engineered, sequence-specific nucleases, and its application to transgenic and knockout organisms 2 hours

J. DNA polymorphisms 2 hours
1. Single nucleotide polymorphisms (SNP's) and simple-sequence polymorphisms, and their detection and applications as molecular markers
2. DNA typing using short tandem repeats (STR's)
3. Copy-number variations and their implications for phenotypic variation

K. Transposable elements 2 hours
1. DNA transposons and LTR (long terminal repeat) and non-LTR retrotransposons
2. How transposable elements facilitate gene duplication and chromosomal rearrangement

L. A review of Mendel and some extensions of Mendel — 2 hours
1. incomplete dominance and multiple allele systems, with emphasis that these are the norm, not the exceptions
2. penetrance and expressivity
3. polygenic traits, gene interaction, and epistasis

M. Linkage mapping using 3-point crosses, accounting for undetected double crossovers, and interference and coincidence — 2 hours

N. Creating genetic maps of molecular marker loci using pedigrees and Lod scores, and using them to localize phenotypic loci like disease genes — 4 hours

O. Positional cloning from an unsequenced genome by chromosome walking — 2 hours

P. Haplotype blocks and genome-wide association studies using SNP arrays — 2 hours

Q. Cytogenetics, including G-banding nomenclature, deletion mapping, detection of chromosomal rearrangements, and FISH (fluorescence *in situ* hybridization) — 2 hours

R. Genetics of cancer — 2 hours

S. Genomics — 4 hours
1. Genome sequencing and methods for assembling the sequence data
2. Identifying genes in a genome sequence computationally
3. Ascertaining function of identified genes experimentally and computationally
4. Bioinformatics
5. Comparative genomics

T. Proteomics, including chromatin immunoprecipitation (ChIP) and ChIP chips, the yeast two-hybrid system, and identification of proteins in a sample from mass spectrometry and genomic sequence — 2 hours

U. In-class laboratory work — 6 hours
1. Restriction digests of lambda phage DNA
2. Agarose electrophoresis of the digests, and analysis of the ethidium-stained gels
3. Purification of genomic DNA from salmon sperm nuclei, using organic extractions and ethanol precipitation

V. Methods of Instruction

The following instructional methodologies may be used in the course:
1. in-class completion of a lecture note "skeleton" that the students purchase;
2. black and/or white board presentation;
3. multimedia;
4. in-class laboratory work.

VI. Out of Class Assignments

The following out of class assignments may be used in the course:

1. challenging problem sets covering all lecture topics, adapted from end-of-chapter problems in various molecular biology and genetics texts;
2. identification and analysis of an "unknown" DNA sequence and its encoded protein using online tools (e.g. BLAST, PubMed, translation tools, open reading frame (ORF) search, calculation of isoelectric point and molecular weight, and prediction of intracellular location).

VII. Methods of Evaluation

The following methods of evaluation may be used in the course:

1. written examinations consisting primarily of short answer, data analysis, and problem solving questions;
2. quizzes on the structures of the amino acids and nitrogenous bases, and on restriction mapping problems and laboratory work;
3. evaluation of homework and online sequence analysis assignment.

VIII. Textbooks

Lodish, Harvey and Berk, Arnold. *Molecular Cell Biology*, 7th ed. New York: W.H. Freeman, 2012. Print.
13th grade textbook reading level. ISBN-13: 978-1429234139

Pierce, Benjamin A. *Genetics: A Conceptual Approach*, 5th edition. New York: W.H. Freeman, 2013. Print.
13th grade textbook reading level. ISBN-13: 978-1464109461

IX. Student Learning Outcomes

Upon successful completion of the required coursework, the student will be able to:

1. summarize the steps involved in gene expression in prokaryotic and eukaryotic organisms, and explain various methods by which cells regulate this expression;
2. explain several methods for purifying proteins, growing and manipulating cells, and to summarize the roles of antibody molecules in the body and in the lab;
3. explain various basic methods in recombinant DNA technology, and to interpret data and solve problems involving these methods;
4. analyze data and solve genetics problems involving linkage mapping, pedigree analysis, DNA polymorphisms, and genome characterization.