

– Genetics Honors Course Code 2000440Revised 201516

	Quarter 1 August–October (45 Sessions)	Quarter 2 October–December (45 Sessions)	Quarter 3and part of 4 January–
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Students will identify differences between Mendelian and nonMendelian inheritance patterns; provide examples of codominance and incomplete dominance; using the ABO Blood Group system, determine inheritance patterns in families and the use of ABO Blood groups for paternal and maternal determination; identify and evaluate differences between the X and Y chromosome in relation to inheritance of alleles through sexual reproduction and homozygosity; sex chromosomes; perform sexlinked Punnett squares for the inheritance of alleles on the X chromosome; identify patterns of sexlinked inheritance in pedigree analysis; construct a sexlinked pedigree using appropriate symbols and lines; identify abnormal karyotypes and describe issues of nondisjunction in chromosomal aberrations;

Students will provide a detailed understanding of the discovery of DNA as the mechanism of heredity, including the Griffith, AveryMacCloudMcCarty, and HersheyChase experiments; chemical understanding of DNA structure, the bonds that bond each component of a nucleotide; identify purine and pyrimidine structures and differentiate between A, T, G, C, and U; describe and create the WatsonCrick model of DNA; perform calculations for Chargaff's distribution of bases; pairing rule; outline the events of DNA replicationtranscription, and translation; identify the chemical structure of all 20 biologically needed amino acids; perform protein folding based on the chemical composition of each amino acid and how a mutation from one amino acid to another can impact the threedimensional shape of the resulting protein; describe the mutations that result in the mutations that lead to cancer development in the organism;perform laboratory skills in bacterial transformation, gel electrophoresis, and analysis of gel bands; culture of C. elegansas a model organism

Students willdescribe natural selection as the major force driving allele frequency changes; use the

