**5.1.U1 Evolution occurs when heritable characteristics of species change.**

**5.1.U2 The fossil record provides evidence for evolution.**

**5.1.U3 Selective breeding of domesticated animals shows that artificial selection can cause evolution.**

**5.1.U4 Evolution of homologous structures by adaptive radiation explains similarities in structure when there are differences in function.**

**5.1.U5 Populations of a species can gradually diverge into separate species by evolution.**

**5.1.U6 Continuous variation across the geographical range of related populations matches the concept of gradual divergence.**

**5.1.A1 Development of melanistic insects in polluted areas.**

**5.1.A2 Comparison of the pentadactyl limb of mammals, birds, amphibians, and reptiles with different methods of locomotion.**

**5.1. NOS Looking for patterns, trends and discrepancies- there are common features in the bone structure of vertebrate limbs despite their varied use.**

**5.2.U1 Natural selection can only occur if there is variation among members of the same species.**

**5.2.U2 Mutation, meiosis and sexual reproduction cause variation between individuals in a species.**

**5.2.U3 Adaptations are characteristics that make an individual suited to its environment and way of life.**

**5.2.U4 Species tend to produce more offspring than the environment can support.**

**5.2.U5 Individuals that are better adapted tend to survive and produce more offspring while the less well adapted tend to die or produce fewer offspring.**

**5.2.U6 Individuals that reproduce pass on characteristics to their offspring.**

**5.2.U7 Natural selection increases the frequency of characteristics that make individuals better adapted and decreases the frequency of other characteristics leading to changes within the species.**

**5.2.A1 Changes in beaks of finches on Daphne Major.**

**5.2.A2 Evolution of antibiotic resistance in bacteria.**

**5.2. NOS Use theories to explain natural phenomena- the theory of evolution by natural selection can explain the development of antibiotic resistance in bacteria.**

**5.3.U1 The binomial system of names for species is universal among biologists and has been agreed and developed at a series of congresses.**

**5.3.U2 When species are discovered they are given scientific names using the binomial system.**

**5.3.U3 Taxonomists classify species using a hierarchy of taxa.**

**5.3.U4 All organisms are classified into three domains.**

**5.3.U5 The principal taxa for classifying eukaryotes are kingdom, phylum, class, order, family and genus and species.**

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| **5.3.U6** | **In a natural classification, the genus and accompanying higher taxa consist of all the species that have evolved from one common ancestral species.** |
| **5.3.U7** | **Taxonomists sometimes reclassify groups of species when new evidence shows that a previous taxon contains species that have evolved from different ancestral species.** |
| **5.3.U8** | **Natural classification helps in identification of species and allows the prediction of characteristics shared by species within a group.** |
| **5.3.A1** | **Classification of one plant and one animal species from domain to species level.** |
| **5.3.A2** | **Recognition features of bryophyte, filicinophyta, coniferophyta, and angiospermophyta.** |
| **5.3.A3** | **Recognition features of porifera, cnidarian pletyhelmintha, annelida, Mollusca, arthropda and chordata.** |
| **5.3.A4** | **Recognition of features of birds, mammals, amphibians, reptiles and fish.** |
| **5.3.S1** | **Construction of dichotomous keys for use in identifying specimens.** |
| **5.3. NOS** | **Cooperation and collaboration between groups of scientists- scientists use the binomial system to identify a species rather than the many different local names.** |
| **5.4.U1** | **A clade is a group of organisms that have evolved from a common ancestor.** |
| **5.4.U2** | **Evidence for which species are part of a clade can be obtained from the base sequences of a gene or the corresponding amino acid sequence of a protein.** |
| **5.4.U3** | **Sequence differences accumulate gradually so there is a positive correlation between the number of differences between two species and the time since they diverged from a common ancestor.** |
| **5.4.U4** | **Traits can be analogous or homologous.** |
| **5.4.U5** | **Cladograms are tree diagrams that show the most probable sequence of divergence in clades.** |
| **5.4.U6** | **Evidence from cladistics has shown that classifications of some groups based on structure did not correspond with the evolutionary origins of a group or species.** |
| **5.4A1** | **Cladograms including human and other primates.** |
| **5.4.A2** | **Reclassification of the figwort family using evidence from cladistics.** |
| **5.4.S1** | **Analysis of cladograms to deduce evolutionary relationships.** |
| **5.4. NOS** | **Falsification of theories with one** |
| **10.1.U1** | **Chromosomes replicate in interphase before meiosis.**<br>● Identify tetrad, bivalent, sister chromatids and non-sister chromatids in diagrams of replicated chromosomes. |
| **10.1.U2** | **Crossing over is the exchange of DNA material between non-sister homologous chromatids.**<br>● State that crossing over occurs during prophase I.<br>● Define chiasmata. |
| **10.1.U3** | **Crossing over produces new combinations of alleles on the chromosomes of the haploid cells.**<br>● State two consequences of chiasmata formation between non-sister chromatids. |
| **10.1.U4** | **Chiasmata formation between non-sister chromatids can results in an exchange of alleles.**<br>● Draw a diagram to illustrate the formation of new allele combinations as a results of crossing over. |

- Explain how crossing over between linked genes can lead to genetic recombinants.

**Homologous chromosomes spate in meiosis I.**

**10.1.U5**

- Contrast meiosis I with meiosis II.

**Independent assortment of genes in due to random orientation of homologous chromosomes pairs in meiosis I.**

**10.1U6**

- Describe random orientation and independent assortment.
- Given a parent cell genotype, determine the allele combinations that are possible in the gametes due to independent assortment and random orientation.

**Sister chromatids separate in meiosis II.**

**10.1.U7**

- Compare meiosis II with mitosis.

**Drawing diagrams to show chiasmata formed by crossing over.**

**10.1.S1**

- Draw a diagram to illustrate the process and result of crossing over.

**Making careful observations- careful observations and record keeping turned up anomalous data that Mendel's law of independent assortment could not account for. Thomas Hunt Morgan developed the notion of linked genes to account for the anomalies.**

**10.1 NOS**

- Describe the experiment of Bateson and Punnett that lead to results that did not support Mendel's law of independent assortment.
- Describe the trends and discrepancies that led Morgan to propose the idea of linked genes.

**Unlinked genes segregate independently as a result of meiosis.**

**10.2.U1**

- State the difference between independent assortment of genes and segregation of alleles.
- Describe segregation of alleles and independent assortment of unlinked genes in meiosis.

**Gene loci are said to be linked if on the same chromosome.**

**10.2.U2**

- Define autosome and sex chromosome.
- Describe what makes genes "linked."

**10.2.U3** **Variations can be discrete or continuous.**
**The phenotypes of polygenic characteristics tend to show continuous variation.**

**10.2.U4**

- Explain polygenetic inheritance using an example of a two gene cross with codominant alleles.
- Outline the use of Pascal's triangle to determine phenotype frequencies that results from polygenic crosses.
- State that a normal distribution of variation is often the result of polygenic inheritance.
- State example human characteristics that are associated with polygenic inheritance.

**Chi-squared tests are used to determine whether the difference between an observed and expected frequency distribution is statistically significant.**

**10.2.U5**

- State the two possible hypotheses of a statistical test.
- Calculate the chi square value to determine the significance of differences between the observed and expected results of a genetic cross.

- Determine the degrees of freedom and critical value for the chi-square test.
- Draw a conclusion of significance by comparing the calculated and critical chi-square values.

**10.2.A1** **Completion and analysis of Punnett squares for dihybrid traits.**

- Determine possible allele combinations in gametes for crosses involving two genes.
- Use correct notation to depict a dihybrid cross between two unlinked genes.
- Construct a Punnett square to show the possible genotype and phenotype outcomes in a dihybrid cross.

**10.2.A2** **Morgans's discovery of non-Mendellian ratios in Drosophilia.**

- Describe how Morgan discovered relationship between eye color and sex in Drosophila.

**10.2.A3** **Polygenic traits such as human height may be influenced by environmental factors.**

- Outline two example environmental factors that can influence phenotypes.
- Compare continuous to discrete variation.

**10.2.S1** **Calculation of the predicted genotypic and phenotypic ratio of offspring of dihybrid crosses involving unlinked autosomal genes.**

- Determine the predicted genotype and phenotype ratios of F1 and F2 offspring of dihybrid crosses.

**10.2.S2** **Identification of recombinants in crosses involving two linked genes.**

- Use correct notation to show alleles of linked genes.
- Construct a Punnett square to show the possible genotype and phenotype outcomes in a dihybrid cross involving linked genes.
- Explain how crossing over between linked genes can lead to genetic recombinants.

**10.2.S3** **Use of chi-squared test on data from dihybrid crosses.**

- Calculate a chi-square value to compare observed and expected results of a dihybrid genetic cross.
- Using the df and critical chi-square value, determine if there is a significant difference between observed and expected results of a dihybrid cross.

**10.2. NOS** **Looking for patterns, trends and discrepancies- Mendel used observations of the natural world to find and explain patterns and tends, Since then, scientists have looked for discrepancies and asked questions based on further observations to show exceptions to the rules. For example, Morgan discovered non-Mendellian ratios in his experiments with Drosophilia.**

- Describe the trends and discrepancies that led Morgan to propose the idea of linked genes.

**10.3.U1** **A gene pool consists of all the genes, and their different alleles, present in an interbreeding population.**

**10.3.U2** **Evolution required that allele frequencies change with time in populations.**

**10.3.U3** **Reproductive isolation of populations can be temporal, behavioral or geographic.**

**10.3.U4** **Speciation due to divergence of isolated populations can be gradual.**

**10.3.U5** **Speciation can occur abruptly.**

**10.3.A1** **Identifying examples of directional, stabilizing and disruptive selection.**

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| **10.3.A2** | **Speciation in the genus Allium by polyploidy.** |
| **10.3.S1** | **Comparison of allele frequencies of geographically isolated populations.** |
| **10.3 NOS** | **Looking for patterns, trends and discrepancies- patterns of chromosome number in some genera can be explained by speciation due to polyploidy.** |