Meden School Curriculum Planning							
Subject	Biology	**Year Group**	12	**Sequence No.**		**Topic**	3.4 Genetic Information etc

Retrieval	Core Knowledge	Student Thinking
What do teachers need **retrieve** from students before they start teaching **new content**?	What **specific ambitious knowledge** do teachers need teach students in this sequence of learning?	What real life examples can be applied to this sequence of learning to **development of our students thinking, encouraging them to see the inequalities around them** and 'do something about them!'
AQA GCSE B1 Cells, eukaryotic and prokaryotic cells B6 Inheritance DNA, DNA and protein synthesis, Variation, Natural selection and evolution, antibiotic-resistant bacteria AQA GCSE Biology B7 Ecology, random sampling, maintaining	**3.4.1 DNA, Genes and Chromosomes** In prokaryotic cells, DNA molecules are short, circular and not associated with proteins. In the nucleus of eukaryotic cells, DNA molecules are very long, linear and associated with proteins, called histones. Together a DNA molecule and its associated proteins form a chromosome. The mitochondria and chloroplasts of eukaryotic cells also contain DNA which, like the DNA of prokaryotes, is short, circular and not associated with protein. A gene is a base sequence of DNA that codes for: • the amino acid sequence of a polypeptide • a functional RNA (including ribosomal RNA and tRNAs). A gene occupies a fixed position, called a locus, on a particular DNA molecule. A sequence of three DNA bases, called a triplet, codes for a specific amino acid. The genetic code is universal, non-overlapping and degenerate. In eukaryotes, much of the nuclear DNA does not code for polypeptides. There are, for example, non-	

ecosystems and biodiversity, food security and farming A level Biology 3.2.1 Cell structure. 3.1.5 Nucleic Acids A level Biology 3.2.2 Mitosis	coding multiple repeats of base sequences between genes. Even within a gene only some sequences, called exons, code for amino acid sequences. Within the gene, these exons are separated by one or more non-coding sequences, called introns. **3.4.2 DNA and Protein Synthesis** The concept of the genome as the complete set of genes in a cell and of the proteome as the full range of proteins that a cell is able to produce. The structure of molecules of messenger RNA (mRNA) and of transfer RNA (tRNA). Transcription as the production of mRNA from DNA. The role of RNA polymerase in joining mRNA nucleotides. • In prokaryotes, transcription results directly in the production of mRNA from DNA. • In eukaryotes, transcription results in the production of pre- mRNA; this is then spliced to form mRNA. Translation as the production of polypeptides from the sequence of codons carried by mRNA. The roles of ribosomes, tRNA and ATP. **Students should be able to:** • relate the base sequence of nucleic acids to the amino acid sequence of polypeptides, when provided with suitable data about the genetic code • interpret data from experimental work investigating the role of nucleic acids. Students will **not** be required to recall in written papers specific codons and the amino acids for which they code. **3.4.3 Genetic diversity can arise as a result of mutation or during meiosis** Gene mutations involve a change in the base sequence of chromosomes. They can arise spontaneously during DNA replication and include base deletion and base substitution. Due to the degenerate nature of	

the genetic code, not all base substitutions cause a change in the sequence of encoded amino acids. Mutagenic agents can increase the rate of gene mutation.

Mutations in the number of chromosomes can arise spontaneously by chromosome non-disjunction during meiosis.

Meiosis produces daughter cells that are genetically different from each other.

The process of meiosis only in sufficient detail to show how:

- two nuclear divisions result usually in the formation of four haploid daughter cells from a single diploid parent cell
- genetically different daughter cells result from the independent segregation of homologous chromosomes
- crossing over between homologous chromosomes results in further genetic variation among daughter cells.

Students should be able to:

- complete diagrams showing the chromosome content of cells after the first and second meiotic division, when given the chromosome content of the parent cell
- explain the different outcome of mitosis and meiosis
- recognise where meiosis occurs when given information about an unfamiliar life cycle
- explain how random fertilisation of haploid gametes further increases genetic variation within a species.

3.4.4 Genetic diversity and adaptation

Genetic diversity as the number of different alleles of genes in a population.

Genetic diversity is a factor enabling natural selection to occur. The principles of natural selection in the evolution of populations.

	Random mutation can result in new alleles of a gene. Many mutations are harmful but, in certain environments, the new allele of a gene might benefit its possessor, leading to increased reproductive success. The advantageous allele is inherited by members of the next generation. As a result, over many generations, the new allele increases in frequency in the population. Directional selection, exemplified by antibiotic resistance in bacteria, and stabilising selection, exemplified by human birth weights. Natural selection results in species that are better adapted to their environment. These adaptations may be anatomical, physiological or behavioural. **Students should be able to:** use unfamiliar information to explain how selection produces changes within a population of a species interpret data relating to the effect of selection in producing change within populations show understanding that adaptation and selection are major factors in evolution and contribute to the diversity of living organisms. **Required practical 6:** Use of aseptic techniques to investigate the effect of antimicrobial substances on microbial growth. **3.4.5 Species and Taxonomy** Two organisms belong to the same species if they are able to produce fertile offspring. Courtship behaviour as a necessary precursor to successful mating. The role of courtship in species recognition. A phylogenetic classification system attempts to arrange species into groups based on their evolutionary origins and relationships. It uses a hierarchy in which smaller groups are placed within larger groups, with no overlap between groups. Each group is called a taxon (plural taxa). One hierarchy comprises the taxa: domain, kingdom, phylum, class, order, family, genus and species.	Over use of certain antibiotics has allowed the development of superbugs which are resistant to all antibiotics. According to the 2019 Antibiotic Resistance Threat ReportTrusted Source, published by the Centers for Disease Control and Prevention (CDC), more than 2.8 million drug-resistant infections happen every year in the United States, and more than 35,000 of them are fatal. What can the science community do to help reduce the development of these suprbugs?

Each species is universally identified by a binomial consisting of the name of its genus and species, eg, *Homo sapiens*.

Recall of different taxonomic systems, such as the three domain or five kingdom systems, will **not** be required.

Students should be able to appreciate that advances in immunology and genome sequencing help to clarify evolutionary relationships between organisms.

3.4.6 Biodiversity and Community

Biodiversity can relate to a range of habitats, from a small local habitat to the Earth.

Species richness is a measure of the number of different species in a community.

An index of diversity describes the relationship between the number of species in a community and the number of individuals in each species.

Calculation of an index of diversity (d) from the formula

$d = N N - 1 \Sigma n n - 1$

where N = total number of organisms of all species

and n = total number of organisms of each species.

Farming techniques reduce biodiversity. The balance between conservation and farming.

3.4.7 Investigating diversity

Genetic diversity within, or between species, can be made by comparing:

the frequency of measurable or observable characteristics
the base sequence of DNA
the base sequence of mRNA
the amino acid sequence of the proteins encoded by DNA and mRNA.

	Students should be able to: interpret data relating to similarities and differences in the base sequences of DNA and in the amino acid sequences of proteins to suggest relationships between different organisms within a species and between species appreciate that gene technology has caused a change in the methods of investigating genetic diversity; inferring DNA differences from measurable or observable characteristics has been replaced by direct investigation of DNA sequences. Knowledge of gene technologies will **not** be tested. Quantitative investigations of variation within a species involve: collecting data from random samples calculating a mean value of the collected data and the standard deviation of that mean interpreting mean values and their standard deviations.	What will farming look like in the future, how can farming and biodiversity co-exist. What is regenerative farming and could it help Regenerative farming shift could reduce UK climate emissions, say experts | Farming | The Guardian