

**Unit
8:**

Genetics
Anchor 2

Module B

Assessment Anchors: Answer these questions in AT LEAST 2 Complete Sentences

MA.8.2.2.1 Describe and/or predict observed patterns of inheritance (i.e., dominant, recessive, codominance, incomplete dominance, sex-linked, polygenic, and multiple alleles).

Dominant- The trait that will show. **Recessive**- Must be copied for twice (less frequent). **Codominance** both show (like A+ blood type).

Incomplete dominance- when both red and white make pink. **Sex-linked** is related to gender. **Polygenic**- many traits. **Multiple alleles**- more than two alleles put make up the trait.

MA.8.2.2.2 Describe processes that can alter composition or number of chromosomes (i.e., crossing over, nondisjunction, duplication, translocation, deletion, insertion, and inversion).

Crossing over Where the ends of the chromosome switch.

Nondisjunction Chromosomes don't separate.

Duplication make an extra chromosome/segment.

Deletion Lose a chromosome/segment.

Insertion Add a section.

Inversion Flip a section (ABC -> CBA).

MA.8.2.2.3 Describe how genetic mutations alter the DNA sequence and how or they may affect phenotype (e.g., silent, nonsense, frameshift).

Silent mutation do not change phenotype.

Nonsense changes sequence that doesn't make sense.

Frameshift moves what is read to code.

MA.8.2.2.4 Explain how genetic engineering has impacted the fields of medicine, forensics, and agriculture (e.g., selective breeding, gene splicing, cloning, genetically modified organisms, gene therapy).

Genetics Module B Anchor 3 Answer Key

J Spring



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JAM IIT Biotechnology Question Bank MSc Entrance Mocktime Publication, This question bank for IIT JAM Biotechnology code BT is tailored for MSc entrance and includes full previous year papers topic wise question sets molecular biology genetics cell biology biochemistry microbial technology PDF downloads answer keys and explanatory solutions Additionally books linked to this bank offer concise revision notes aligned to the JAM Biotechnology syllabus model tests under exam like time constraints and analysis of previous paper trends The IIT JAM exam pattern for Biotechnology follows the standard JAM structure multiple sections objective questions specified marks per section Using this question bank enables aspirants to build conceptual clarity practice repeated questions effectively and simulate actual entrance exam conditions It is ideal for those targeting admission to MSc Biotechnology in IITs and other top institutes Environmental Health Perspectives ,1993 Marker-Assisted Selection (MAS) in Crop Plants, volume II Ting Peng,Baohua Wang,Muhammad Kashif Riaz Khan ,Peng Chee,2024-06-13 Global climate change reductions in arable land and food security demands that plant breeding will continue to play an imperative role in feeding 9 billion people sustainably by 2050 In order to face this challenge modern plant breeding will necessitate the adoption of new technologies and practices to boost production of cultivated plants by capturing or generating more favorable genetic diversity In crop plants the majority of agronomically important traits are quantitatively inherited controlled by multiple genes each with a small effect quantitative trait loci QTLs The most common approach to pre breeding is to use genetic mapping to identify QTLs for key phenotypic variation followed by introgressing those QTLs into the elite gene pool with marker assisted selection MAS which can enhance the selection criteria of phenotypes comparing to conventional breeding with the selection of genes As the cost of genotyping continues to decline the use of genotyping by sequencing GBS technologies or whole genome re sequencing coupled with the release of the genome sequences of plant species have permitted the development of dense arrays of single nucleotide polymorphisms SNPs covering the entire genome which have in turn paved the way to genome wide association studies GWAS Meanwhile fine mapping guided by genome sequences of many plant species have facilitated the exploration of functional genes in addition pan genomes constructed from various available resources such as the reference sequence and its variants raw reads and haplotype reference panels provide a new perspective on QTL locations and potential molecular targets for plant breeding Similarly new approaches to marker trait association analyses such as quantitative trait locus sequencing QTL seq and quantitative trait gene sequencing QTG seq that are based on bulked segregant analysis BSA and whole genome resequencing will help accelerate QTL fine mapping and identification of the causal genes In conclusion the tools and strategies for MAS in modern plant breeding have been expanding in recent years By embracing a broad array of conventional and new molecular techniques modern plant breeding has a bright future in delivering new crop cultivars to keep our food fiber and biobased economy diverse and safe Cytokines Anthony R. Mire-Sluis,Robin Thorpe,1998-04-15

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