

Unit
8:

Genetics

Anchor 2

Module B

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

MS.B.2.1.1 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 you always observe (brown hair, rooster feathers)
Recessive- The trait that you don't always observe (blue eyes, blood type)

Incomplete dominance- when both alleles make their own contribution to genetic
Polygenic- many genes
Multiple alleles- more than two alleles per locus on the trait

MS.B.2.1.2 Describe processes that can alter chromosome or number of chromosomes (i.e., crossing over, nondisjunction, duplication, translocation, deletion, insertion, and inversion)

Crossing over - where the ends of the chromosomes switch
Nondisjunction - chromosomes don't separate
Duplication - make an extra chromosome/segment

Deletion - remove a chromosome/segment

Translocation - transfer a chromosome/segment

Inversion - flip a section

Insertion - add a section

Amplification - flip a section (AMP) -> AMP

MS.B.2.1.3 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 coded to code

MS.B.2.1.4 Explain how genetic engineering has impacted the fields of medicine, forensics, and agriculture (e.g., selective breeding, gene editing, cloning, genetically modified organisms, gene therapy)

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M Mosston



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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 This book provides comprehensive coverage of the cytokines from a pharmacological approach The chapters are presented in a consistent format allowing easy cross reference with sample diagrams and a summary table of essential facts for each chapter at the end of the book Cytokines is unique in stressing cytokine biology and the application of research data to provide disease therapy With 33 detailed and up to date chapters about individual cytokines this comprehensive reference will provide both clinicians and researchers in immunology and pharmacology with invaluable information Genetic information and sequences Protein structure Cell sources and production Biological activity Cytokine receptor structure and signal transduction Discussion of the role of cytokines in disease and the potential for therapy Summary table of essential facts Comprehensive bibliography *Index Medicus*, 2001 **Environmental Health Perspectives**, 1993 **Agrindex**

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