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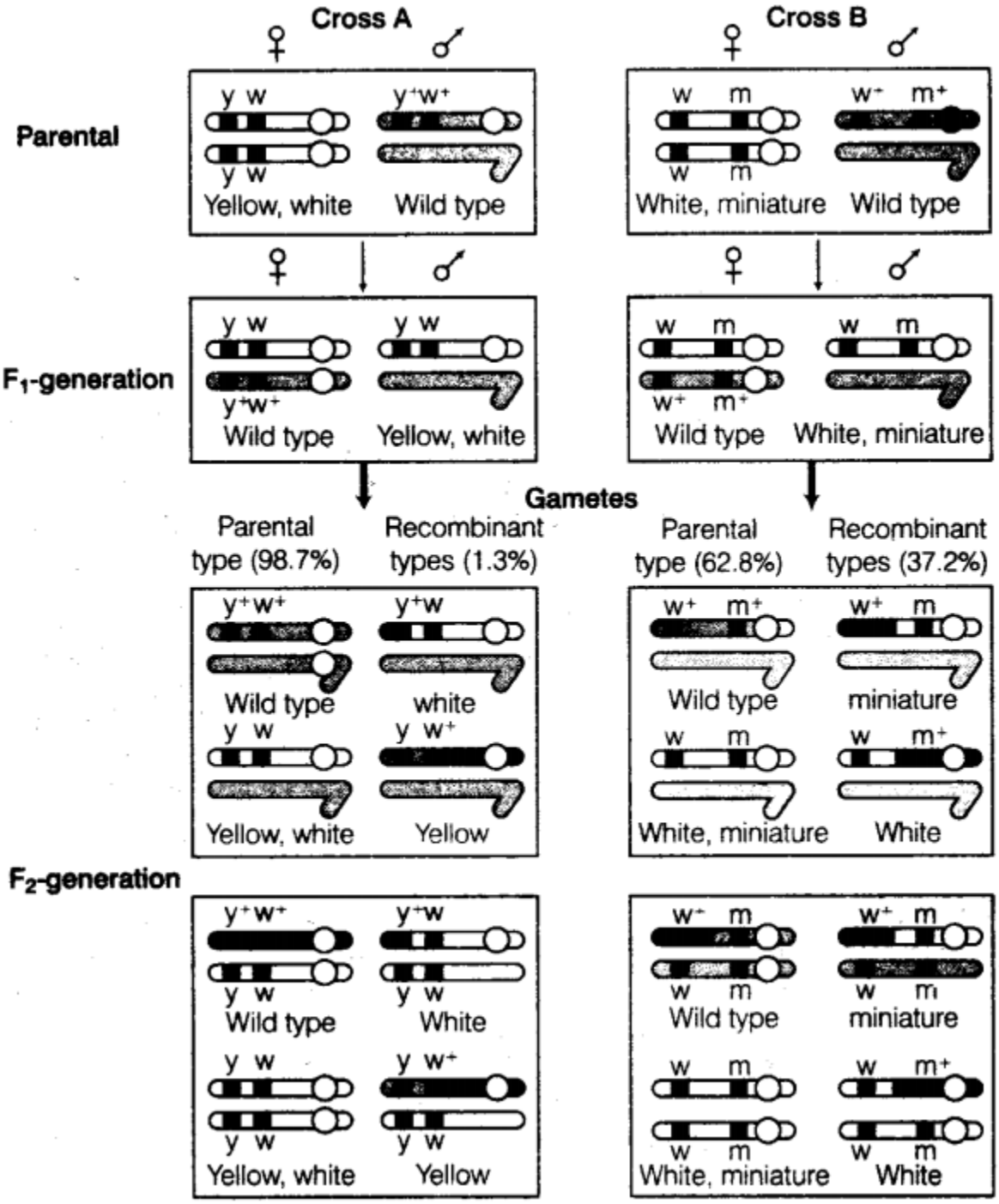
Principles of Inheritance and Variation –

20. Experimental verification of the chromosomal theory of inheritance was done by Thomas Hunt Morgan and his colleagues.
(i) Morgan selected fruit fly, Drosophila melanogaster for his experiments because:
(a) They could be grown on simple artificial medium in the laboratory.
(b) Their life cycle is only about two weeks.
(c) A single mating could produce a large number of flies.
(d) There was a clear differentiation of the sexes, i.e. male (smaller) and female (bigger).
(e) It has many types of hereditary variation that can be easily seen through low power microscopes.
(ii) Linkage and Recombination
(a) The physical association of two genes on a chromosome is called linkage.
(b) Recombination explains the generation of non-parental gene combinations.
(c) To explain the phenomena of linkage and recombination, Morgan carried out several dihybrid crosses in Drosophila to study genes that were sex-linked, i.e. the genes are located on X-chromosome. He observed that two genes did not segregate independently of each other.
(d) He observed that the proportion of parental gene combinations were much higher than the non-parental type, when two genes in a dihybrid cross were situated on the same chromosome. Morgan concluded this as a physical association or linkage.
(e) Morgan and his group also found that even when genes were grouped on the same chromosome, some genes were very tightly linked (very low recombination), while others were loosely linked (higher recombination).
(f) Recombination of linked genes is by crossing over (exchange of corresponding parts between the chromatids of homologous chromosomes).



Linkage results of two dihybrid crosses conducted by Morgan. Cross 'A' shows crossing between genes y and w. Cross 'B1 shows crossing between genes w and m. Here, dominant wild type alleles are represented with (+) sign.

(g) Alfred Sturtevant (Morgan's student) used the frequency of recombination between gene pairs on the same chromosome as a measure of the distance between genes and 'mapped' their position on the chromosome. Genetic maps are now used as a starting point in the sequencing of whole genomes as done in case of Human Genome Sequencing Project.