RAMA UNIVERSITY

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FACULTY OF AGRICULTURAL SCIENCES

AND ALLIED INDUSTRIES

Changing Concept of Gene

(1) A Genetic View:

The genetic view or perspective of gene is based mainly on the Mendelian inheritance, chromosomal theory of inheritance and linkage studies. Mendel used the term factors for genes and reported that factors were responsible for transmission of characters from parents to their offspring. Sutton and Boveri (1903) based on the study of mitosis and meiosis in higher plants established parallel behaviour of chromosomes and genes. They reported that both chromosomes and genes segregate and exhibit random assortment, which clearly demonstrated that genes are located on chromosomes. The Sutton- Boveri hypothesis is known as chromosome theory of inheritance. Morgan based on linkage studies in Drosophila reported that genes are located on the chromosome in a linear fashion. Some genes do not assort independently because of linkage between them. He suggested that recombinants are the result of crossing over. The crossing over increases if the distance between two genes is more. The number of linkage group is the same as the number of chromosomes. The chromosome theory and linkage studies reveal that genes are located on the chromosomes. This view is sometimes called as bead theory. The important points about the bead theory are given below: 1. The gene is viewed as a fundamental unit of structure, indivisible by crossing over. Crossing over occurs between genes but not within a gene. 2. The gene is considered as a basic unit of change or mutation. It changes from one allelic form to another, but there are no smaller components within a gene that can change. 3. The gene is viewed as a basic unit of function. Parts of a gene, if they exist, cannot function. The chromosome has been viewed merely as a vector or transporter of genes and exists simply to permit their orderly segregation and to shuffle them in recombination. The bead theory is no more valid for any of the above three points. Now evidences are available which indicate that: (1) a gene is divisible (2) part of a gene can mutate, and (3) part of a gene can function. The Gene is Divisible Earlier it was believed that gene is a basic unit of structure which is indivisible by crossing over. In other words, crossing over occurs between genes but not within a gene. Now intragenic recombination has been observed in many organisms which indicates that a gene is divisible. The intragenic recombination has following two main features. 1. It occurs with rare frequency so that a very large test cross progeny is required for its detection. Benzer expected to detect a recombination frequency as low as 10-6 , the lowest he actually found was 10-4 (0.01 x 2 = 0.02%). 2. The alleles in which intragenic recombination occurs are separated by small distances within a gene and are functionally related. Examples of intragenic recombination include bar eye, star asteroid eye and lozenge eye in Drosophila. The bar locus is briefly described below. Lozenge eye and star asteroid have been discussed under pseudoalleles. Bar Eye in Drosophila The first case of intragenic recombination was recorded in Drosophila for bar locus which controls size of eye. The bar locus contains more than one unit of

function. The dominant bar gene in Drosophila produces slit like eye instead of normal oval eye. Bar phenotype is caused by tandem duplication of 16A region in X chromosome, which results due to unequal crossing over. The flies with different dose of 16A region have different types of eye as follows: 1. Single 16A region → Wild type oval eye 2. Double 16A region → Bar eye small in size 3. Triple 16A region → Double bar or ultrabar eye very small in size The homozygous bar eye (B/B) produced both wild and ultra bar types though at a low frequency which indicated intragenic recombination in the bar locus but the frequency was much higher than that expected due to spontaneous mutations. Part of a Gene Can Function It was considered earlier that gene is the basic unit of function and parts of gene, if exist, cannot function. But this concept has been outdated now. Based on studies on rll locus of T4 phage, Banzer (1955) concluded that there are three sub divisions of a gene, viz., recon, muton and cistron. These are briefly described below: Recon Recons are the regions (units) within a gene between which recombinations can occur, but the recombination cannot occur within a recon. There is a minimum recombination distance within a gene which separates recons. The map of a gene is completely linear sequence of recons. Muton It is the smallest element within a gene, which can give rise to a mutant phenotype or mutation. This indicates that part of a gene can mutate or change. This disproved the bead theory according to which the entire gene was a mutant or change. Cistron It is the largest element within a gene which is the unit of function. This also nocked down the bead theory according to which entire gene was the unit of function. The name cistron has been derived from the test which is performed to know whether two mutants are within the same cistron on in different cistrons.

(2) A Biochemical View: It is now generally believed that a gene is a sequence of nucleotides in DNA which controls a single polypeptide chain. The different mutations of a gene may be due to change in single nucleotide at more than one location in the gene. Crossing over can take place between the altered nucleotides within a gene. Since the mutant nucleotides are placed so close together, crossing over is expected within very low frequency. When several different genes which affect the same trait are present so close that crossing over is rare between them, the term complex locus is applied to them. Within the nucleotide sequence of DNA, which represents a gene, multiple alleles are due to mutations at different points within the gene.

Fine Structure of Gene

Benzer, in 1955, divided the gene into recon, muton and cistron which are the units of recombination, mutation and function within a gene. Several units of this type exist in a gene. In order words, each gene consists of several units of function, mutation and recombination. The fine structure of gene deals with mapping of individual gene locus. This is parallel to the mapping of chromosomes. In chromosome mapping, various genes are assigned on a chromosome, whereas in case of a gene several alleles are assigned to the same locus. The individual gene maps are prepared with the help of intragenic recombination. Since the frequency of

intragenic recombination is extremely low, very large population has to be grown to obtain such rare combination.

CLASSIFICATION OF GENES

Genes can be classified in various ways. The classification of genes is generally done on the basis of (1) dominance, (2) interaction, (3) character controlled, (4) effect on survival, (5) location, (6) movement, (7) nucleotide sequence, (8) sex linkage, (9) operon model, and (10) role in mutation.

1. Based on Dominance

- Dominant genes: Genes that express in the F1
- Recessive genes: Genes whose effect is suppressed in F1

2.Based on Interaction

- Epistatic gene: A gene that has masking effect on the other gene controlling the same trait.
- Hypostatic gene: A gene whose expression is masked by another gene governing the same trait

3.Based on Character Controlled

- Major gene: A gene that governs qualitative trait. Such genes have distinct phenotypic effects.
- Minor gene: A gene which is involved in the expression of quantitative trait. Effect of such genes cannot be easily detected.

4.Based on Effect on Survival

- Lethal gene: A gene which leads to death of its carrier when in homozygous condition. It may be dominant or recessive.
- Semi lethal gene: A gene that causes mortality of more than 50% of its carriers.
- Sub-vital gene: A gene that causes mortality of less than 50% of its carriers.
- Vital gene: A gene that does not have lethal effect on its carriers.

5.Based on Location

- Nuclear genes: Genes that are found in nuclear genome in the chromosomes.
- Plasma genes: Genes that are found in the cytoplasm in mitochondria and chloroplasts. Also called cytoplasmic or extranuclear genes.

6. Based on Position

- Normal genes: Genes that have a fixed position on the chromosomes. Most of the genes belong to this category.
- Jumping genes: Genes which keep on changing their position on the chromosome of a genome. Such genes have been reported in maize.

7. Based on Nucleotide sequence

- Normal genes: Genes having continuous sequence of nucleotides which code for a single polypeptide chain.
- Split gene: A gene having discontinuous sequence of nucleotides. Such genes have been reported in some eukaryotes. The intervening sequences do not code for amino acids.
- Pseudo genes: Genes having defective nucleotides which are nonfunctional. These genes are defective copies of some normal genes.

8. Based on Sex Linkage

- Sex linked genes: Genes which are located on sex or X chromosomes.
- Sex limited genes: Genes which express in one sex only
- Sex influenced genes: Genes whose expression depends on the sex of individual e.g., gene for baldness in humans.

9. Based on Operon Model

- Regulator gene : A gene found in lac operon of E.Coli which directs synthesis of a repressor In lac operon.
- Operator gene: a gene which control the function of structural genes.
- Promotor gene: A gene in lac operon of E.Coli which initiates mRNA synthesis
- Structural genes: The genes in lac operon of E.Coli which control the synthesis of protein through mRNA.

10. Based on role in Mutation

- Mutable genes: Genes which exhibit higher mutation rate than others e.g., which eye gene is Drosophila.
- Mutator genes : Genes which enhance the natural mutation rate of other genes in the same genome e.g., dotted gene in maize.
- Antimutator genes: Genes which decrease the frequency of natural mutation of other genes in the same genome. Such genes are found in bacteria and bacteriophages.

Jumping Genes

Generally, a gene occupies a specific position on the chromosome called locus. However in some cases a gene keeps on changing its position within the chromosome and also between the chromosomes of the same genome. Such genes are known as jumping genes or transposons or transposable elements. The first

case of jumping gene was reported by Barbara Mc-Clintock in maize as early as in 1950. However, her work did not get recognition for a long time like that of Mendel. Because she was much ahead of time and this was an unusual finding, people did not appreciate it for a long time. This concept was recognized in early seventies and McClintock was awarded Nobel Prize for this work in 1983. Later on transposable elements were reported in the chromosome of E. coli and other prokaryotes. In E.coli, some DNA segments were found moving from one location to other location. Such DNA segments are detected by their presence at such a position in the nucleotide sequence, where they were not present earlier. The transposable elements are of two types, viz, insertion sequence and transposons.