



Molecular concepts of gene; Cis-Trans complementation test; Structure of Phage T4, rII Locus.

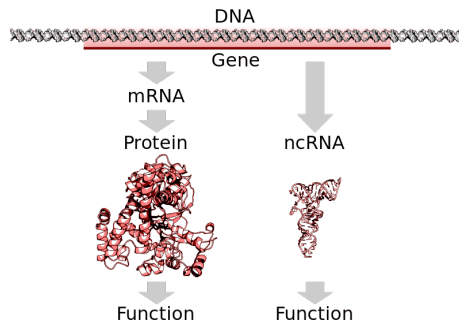
Modern concept of gene (Cistron, muton, recon, viral genes). After the discovery of DNA, the gene has been defined as cistron, recon and muton. The classical gene is the smallest unit that could undergo a mutational change. A gene further divided into smaller units of function, mutation and recombination. Seymour Benzer coined the terms cistron, recon, and muton to explain the relationship between DNA and genetic phenomena.

(a) Cistron: It is the unit of function. Cistron represents a segment of the DNA molecule and consists of a linear sequence of nucleotides, which controls some cellular function. In *E. Coli* cistron may contain about 1500 base pairs. Some cistrons may contain as many as 30,000 base pairs. The cistron begin with initiation codon and ends with a terminating codon. Each cistron is responsible for coding one m-RNA molecule which in turn controls the formation of one polypeptide chain. Each cistron consists of hundreds of mutons and recons.

(b) Recon: It is a unit of recombination. It is the smallest unit capable of recombining genetically. Recombination studies on microbes indicate that structurally the recon consists of one or two pairs of nucleotides, possibly only one pair.

(c) Muton: It is a unit of mutation. The shortest chromosomal unit capable of undergoing mutation has been called the muton. The muton consists of one or many pairs of nucleotides within the DNA molecule.

A gene is defined as the fundamental, physical, and functional unit of heredity since a gene is comprised of nucleotides (on a specific site on a chromosome) that is responsible for the physical



and heritable characteristics or phenotype of an organism.

It, therefore, specifies the structure of a protein, and an RNA molecule.

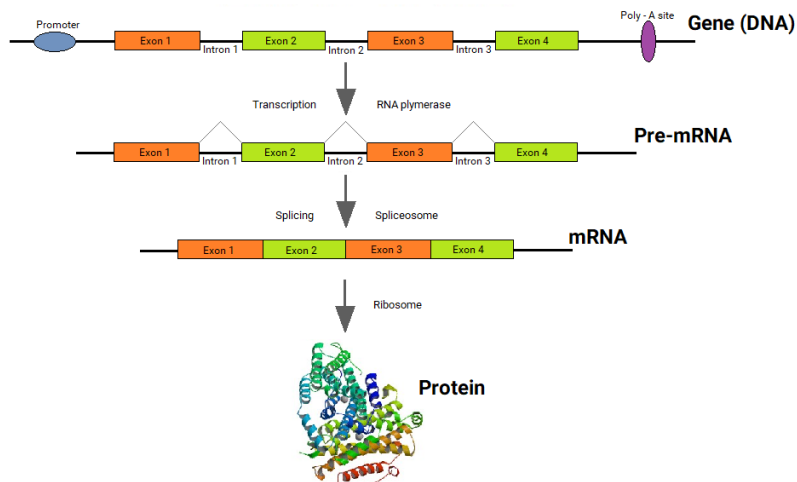
House Keeping Genes (Constitutive Genes):

They are those genes which are constantly expressing themselves in a cell because their products are required for the normal cellular activities, e.g., genes for glycolysis, ATP-ase.

Pseudogenes:

They are genes which have homology to functional genes but are unable to produce functional products due to intervening nonsense codons, insertions, deletions and inactivation of promoter regions, e.g., several of snRNA genes

Split Genes:



They were discovered in 1977 by many workers but credit is given to Sharp and Roberts (1977). Split genes are those genes which possess extra or nonessential regions interspersed with essential or

coding parts. The nonessential parts are called introns, spacer DNA or intervening sequences



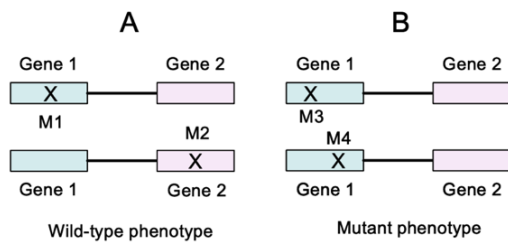
(IVS). Essential or coding parts are called exons. Transcribed intronic regions are removed before RNA passes out into cytoplasm. Split genes are characteristic of eukaryotes.

However, certain eukaryotic genes are completely exonic or non-split e.g., histone genes, interferon genes. Split genes have also been recorded in prokaryotes, thymidylate synthase gene and ribonucleotide reductase gene in T4. A gene that produces calcitonin in thyroid forms a neuropeptide in hypothalamus by removing an exon. Adenovirus has also a mechanism to produce 15—20 different proteins from a single transcriptional unit by differential splicing.

Fine structure of *rII* locus in T4 phage Distinction between wild type and *rII* mutants using K strain of *E. coli*.

The most refined analysis of a single gene ever conducted is the one undertaken by **Seymour Benzer** for a locus in T4 bacteriophage infecting *E. coli*. This locus is known as *rII* locus and a mutant at this locus is responsible for the formation of rough plaques or colonies. This locus had largest number of rapid lysing (*r*) mutants and is called *rII* locus. It can be distinguished from other *r* loci, by the inability of *rII* mutants to produce plaques on lysogenic 'K' strain of *E. coli*, which carries *X* prophage. The *rII* mutants, may though infect 'K' strain, but cannot cause lysis **and are, therefore, unable to produce any plaques (plaque is a clear space on petri dish formed due to destruction of bacterial cells due to infection by phage and is characteristic of a phage)**. In contrast, these *rII* mutants make large sharp plaques on *E. coli*, strain B. The wild type phage T4(*rII*⁺) will make *small* and *fuzzy plaques*, both on B and K strains. Further, when 'K' was infected simultaneously by *rII*⁺ and *rII*, large plaques were formed, since *rII*⁺ helps in lysis so that *rII* may express. These distinguishing features enabled Benzer to identify mutants and wild type phages with high efficiency.

Principle of complementation analysis.



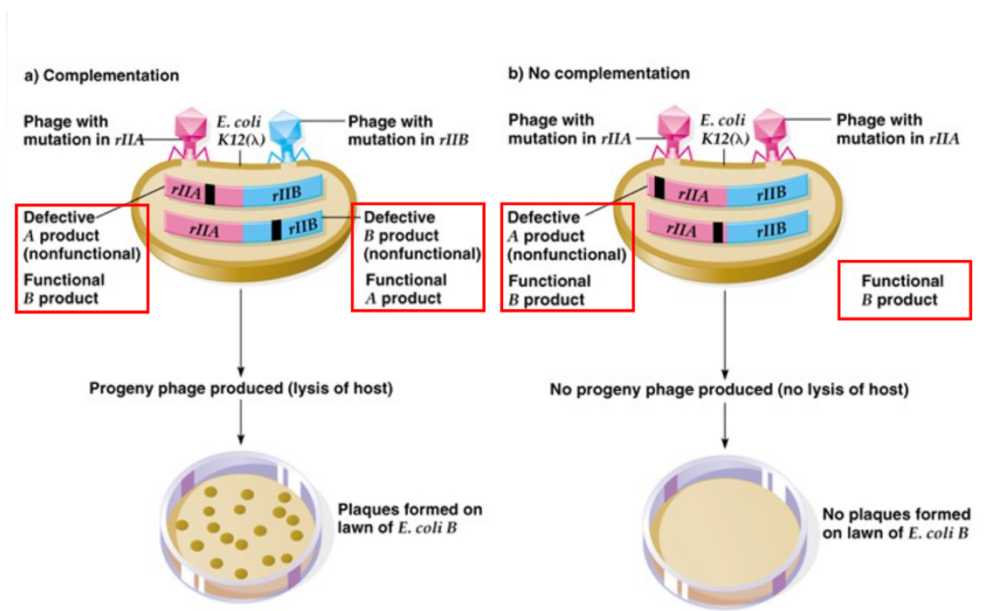
If the recessive mutations M1 and M2 are located on different genes on the homologous chromosomes, the functional copies of the two genes present can give rise to wild-type phenotype (A). If the mutations M3

and M4 are located on the same gene on both chromosomes, wild-type Gene 1 function is missing, and the organism will show a mutant phenotype (B).

Seymour Benzer's cis-trans complementation test:

1. Used to determine the number of functional units (genes) defined by a given set of mutations, and whether two mutations occur on the same unit or different units.
2. If two mutants carrying a mutation of different genes combine to create a wild type function, two mutations compliment.
3. If two mutants carrying a mutation of the same gene create a mutant phenotype, mutations do not compliment.

Seymour Benzer's cis-trans complementation test:



References

- www.biologydiscussion.com
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[The information, including the figures, are collected from the above references and will be used solely for academic purpose.]