INTRODUCTION TO THE FINE STRUCTURE OF PLANT CELLS pdf

1: Online Introduction to Biology - Cells - Cell Functions

The Healthy Mind Cookbook By Rebecca Katz & Mat Edelson. Release Date: Genre: Special Diet A collection of more than recipes formulated to optimize brain health, boost memory, improve mood, sharpen the central nervous system, and more.

In this article we will discuss about Gene: Introduction to Gene 2. The Changing Concept of Gene 3. Thus on the basis of these classical observations, a gene was considered in the early days as a single, small and indivisible hereditary unit that occurred at a definite point on the chromosome and was responsible for a specific phenotypic character. As the knowledge of gene increased day by day in the subsequent studies, the classical concept about gene was changed and modified accordingly. The Changing Concept of Gene: The discovery of many phenomena like crossing over, gene-recombination and gene mutation have provided another set of information about gene. But recombination was not believed to occur only between the beads or genes. Hence the gene was not considered sub-divisible. Thus a gene is considered to control the inheritance of one character, to be indivisible by recombination and to be the smallest unit capable of mutation. It was soon realised that a gene, in true sense, is not responsible for the expression of one trait by itself, although it may exercise the major control on its development. Tatum due to their discovery of biochemical mutations in Neurospora. Thus it became evident that a gene controlled a biochemical reaction by directing the production of a single enzyme. But it was also realised that one gene produces a single polypeptide and not one enzyme as the latter may consist of more than one polypeptide. Thus, the gene may now be defined as a segment of DNA which contains the information for a single polypeptide the functional unit. But it is shown that a change in as little as one nucleotide of the polypeptide specifying gene may mutate and produce a variant of the wild type chain that differs in one amino acid residue. So the functional gene or unit is not the same as the mutational gene, but appears to consist of many mutable sites. The gene must also be considered from the standpoint of the nature of the sites of which recombination may occur. The functional gene, therefore, appears to be composed of many mutational as well as re-combinational sub-units. The first evidence that the gene was sub-divisible by mutation and recombination came from studies of the X- linked lozenge locus of Drosophila melanogaster by C. According to classical concept a gene is not sub-divisible in that crossing over does not occur within a gene; it always occurs between two separate genes. They were first steps towards the present concept of the gene as a long sequence of nucleotide pairs that is capable of mutating and recombining at many different sites along its length. This is an indirect experimental evidence to prove that a gene is sub-divisible. The standard phenotype, i. Before going to discuss the cis-trans test, it is reasonable to understand the meaning of cis and trans arrangement of gene. Cis arrangement means the condition in which a double heterozygote has received two linked mutations from one parent and their wild type alleles from the other parent, e. In a cis-trans test the phenotypes produced in cis and trans heterozygotes for two mutant alleles are compared with each other. Thus it is expected to produce the wild type phenotype unless the mutant alleles are dominant or co-dominant irrespective of whether the two mutant, alleles are located in the same gene or in two different genes. On the other hand, in case of trans heterozygotes one, mutant alleles are located in the homologous chromosomeâ€”they are linked in the repulsion phase. Hence, in trans heterozygotes, it is expected to produce the mutant phenotype if the two alleles are located in the same gene. But if they are located in two different genes, the wild type phenotype would be produced. Hence simply by comparing the phenotypes for any two mutant alleles it is possible to determine if they are located in the same gene or in two different genes. They are located in the same gene if their cis heterozygotes produce the wild type phenotype, while their trans heterozygotes have the mutant phenotype. But if both their cis and trans-heterozygotes have the wild type phenotype they are considered to be located in two different genes. The production of wild type phenotype in a trans-heterozygote for two mutant alleles is termed as complementation and such a study is known as complementation test. Actually, this concept is generally true in prokaryotes but in eukaryotes several noteworthy exceptions are known. The basis of complementation test Fig. A gene produces its effect primarily by directing the production of an active enzyme or polypeptide. On the other hand, a mutant allele of

this gene directs the production of an inactive form of the enzyme as a result of which it produces the mutant phenotype. In the cis heterozygote, one of the two homologous chromosomes has the wild type allele s of the gene s. But if two mutant alleles are located in two different genes, one chromosome of trans heterozygote will have the wild type allele of the other gene. Therefore, the trans heterozygote will have functional product of both the genes and the wild type phenotype will be produced by complementation. The complementation test has proven to be useful in delimiting genes. But, in many cases, this test does not provide evidences to delimit gene. Dominant or co-dominant mutation. Genes in which mutations occur that show intragenic complementation. The gene in question does not produce a diffusible gene product, e. Some other genesâ€”such as operator and promotor genes which generally occur in the operonâ€”do not code for a polypeptide or an enzyme. Therefore, a gene is neither a functional nor a re-combinational unit but is a complex locus whose fine structure should be studied. The most extensive study on the fine structure of gene was undertaken by Seymour Benzer for a locus in T4 bacteriophage infecting E. T4 bacteriophage contains a linear molecule of DNA of about , base pair long which is packed within its head Fig. When T4 bacteriophage infects E. When the inoculum of E. This leads to the development of a clear area in the bacterial lawn. The clear areas are called plaques which indicate the areas of infection and lysis of bacterial cell due to infection by phage and is characteristic of phage. The plaques are surrounded by a fuzzy or turbid margin called halos which are produced due to a phenomenon called lysis inhibition [Fig. The mutants can be recognised to some extent on the basis of the morphology of plaques, the ability of mutants to cause lysis of bacterial cell. Mutants in the rII locus are easily recognised due to their inability to multiply in E. These distinguishable properties enabled Benzer to distinguish mutants and wild type phage with high efficiency. Each plaque to be tested left side of Fig. If plaques develop on the E. Benzer placed all rII mutants in two arbitrary groups named be A and B. The rII A region appears to consist of about 2, deoxyribonucleotide pairs. B polypeptides are needed for lysis of K type E. A mutant produces normal B polypeptide but not A, and vice versa. Hence infection only by identical rII A mutants or by identical rII B mutant alone can cause lysis of the host cells, because none of the phages can produce both A and B polypeptide Fig. On the other hand, infection by two different mutants one an rII A mutant and the other an r II B mutant on the same host cell does result in lysis Fig. It indicates that regions A and B are functionally different and show complementation. But the lysis did not occur when the mutation A or B were in the trans configuration. Thus, it was clear that mutation in one functional region A or B Eire complementary only to mutations in the other region and complementation is detectable by cis-trans test. Each functional region is responsible for the production of a given polypeptide chain. This cistron, therefore, may be thought of as the gene at the functional level. There can be over a hundred points within a functional unit wherein a mutation can take place and cause a detectable phenotypic effect. This means that a cistron is over hundred nucleotide pairs in length and there is some evidence that some cistrons may be as long as 30, nucleotide pairs. A cistron also includes initiating, terminating and any un-transcribed nucleotides. It is the smallest unit of DNA which, when altered, can give rise to a mutation. Study of the genetic code makes it clear that an alteration of a single nucleotide pair in DNA may result in a missense codon in transcribed mRNA e. So a cistron may be expected to consist of many mutable units or mutons. The term muton was given by Benzer. A recon may occur within a cistron. Thus a gene of classical concept is made up of a number of functional unitsâ€”the cistronsâ€” which consist of a number of recons and mutons Fig. The complementation test shows that all the rII mutants were located within A and B cistrons. If the crossing occurs between two chromosomes of mutant strain it yields one wild type and one double mutant type for each crossing over event Fig. Therefore, some of the progeny phage present in the lysate of the B strain infected by a mixture of two rII mutant would be of wild type. Each wild type phage would produce a plaque on this lawn. A equal number of phage would have the double mutant produced due to recombination. Thus, the frequency of recombination may be measured as follows: Hence Benzer was able to avoid such a laborious undertaking by developing a shortcut method of mapping that used overlapping deletion mutation. This technique is known as deletion mapping. It permits the deletion of recombination value of 0. Benzer first mapped a number of rII mutants using the data of recombination test. Benzer classified these non-reverting, non-recombining rII mutations as deletion mutation. Benzer also proposed that these deletion mutations multisite mutations

resulted from the deletion or loss of segments of DNA. These deletions were arranged in sets of overlapping deletions representing segments of different sizes in rII regions as shown in Fig. The principle involved in this method was that if a particular mutation presents in the region of a deletion represented by a rII mutant, then, on mixed infection with this deletion mutant, the point mutation will not be able to give rise to wild type, but if it falls outside the deletion regions it will be able to give rise to wild type and recombinant type. The extents of the deleted segments can be analysed by crossing the deletion mutants to a set of reference point mutations which are previously mapped. When an unknown new mutant carrying a point mutation is isolated, the mutant can immediately be mapped to a defined interval by crossing the mutant with each of the overlapping deletion mutants. A mutant in interval D will not produce any wild type recombinant progeny in any of the four crosses. A mutation in interval C will recombine with deletion IV Fig.

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2: Gene: Introduction, Concepts and Structure | Cell Biology

It is appro pi ate to the contents of this book to recall a few highlights in the history of plant cytology from its inception over three centuries ago. Robert Hooke in presented his observations of what he called Â«cells" in cork and other plant parts and beautifully illustrated and described.

An ameba crawling across a pebble, a photosynthesizing leaf cell, a skin cell rising to the surface, are all in interphase. If a particular cell is going to divide, its interphase can be subdivided into an early working stage, called the G1 Stage. If the cell is going to divide, certain critical RNAs and enzymes are made in this stage. If the cell is not going to divide, it stays in this stage until it dies. But in dividing cells, there is an S Stage, when DNA is replicated, followed by a G2 Stage, another active stage that also includes preparation for the division. The division of a eukaryote cell requires the division of the nucleus first, a process called mitosis. At the "ends" of the cell away from the equator, the cell poles, microtubule-organizing centers called centrioles, inside a complex known as a centrosome, have moved into position the cell had started with one from the last division, and a copy has been made during interphase and begin to grow microtubules, called spindle fibers, in all directions. Some of the spindle will attach to the cell membrane and hold the centrioles in place - others will attach to structures on the chromosomes centromeres called kinetochores. But there is something in the way - the nuclear envelope is between the microtubules and the chromosomes, and nuclear structures such as the nucleolus and the nuclear matrix surround them. All of these structures will "disappear" during prophase, although what exactly happens to them isnt clear - are they broken into bits and dispersed within the cell or broken down entirely? Probably both, to varying degrees in different cells. But once these obstructions are removed, the microtubules attach to the chromosomes and start to pull on them - the longer the microtubule, the stronger the pull, and the ensuing "tug of war" will go on until each chromosome has equal-length microtubules on each side, putting the chromosomes on the equator of the cell. This phase lasts until the cell signals the chromatids to separate. In plant cells, the beginnings of the cell wall that will separate the two new cells, the cell plate, begins to form. The spindle detaches from the chromosomes and disassembles. The nuclear envelope reforms around the chromosomes, which loosen up into chromatin and seem under a light microscope to disappear, while the nucleolus reappears. Eventually, conditions are back in interphase. Some cells use mitosis, which is technically just production of new nuclei, to produce a multi-nucleated cell that may or may not divide at some point. When cells divide, microfilaments usually pinch the membrane until separate cells are made. The last two are also forms of asexual reproduction in multicelled organisms, producing multicelled offspring but following the same patterns. DNA is replicated, producing two separate looped chromosomes, but each then attaches to the cell membrane well away from where the cell will divide by binary fission. After division, the chromosome releases into the new daughter cell. This is one of the reasons that eukaryotes are diploid , carrying two sets of matched chromosomes. One set can be separated out to mix with one set from the other source note that the word is "source" rather than "parent," as this can be done with just one parental individual. Whether this is done with the mixing of nuclei directly, as happens with some protozoans or fungi, or done with cells to carry nuclei, as in animals and plants, the process requires nuclei that are haploid also called monoploid , with just one set of chromosomes rather than two. The process to make these is called meiosis , sometimes called a reduction division. Meiosis begins like mitosis , with an interphase that, among other things, replicates DNA. This means that the cell undergoing meiosis starts with its two sets of chromosomes doubled - its going to have to make four nuclei if each will have only one set each. Meiosis gets to four nuclei by going through two division stages - one to two cells, then another to four - that are called Meiosis I and Meiosis II. Both divisions go through the prophase, metaphase, anaphase, telophase order, but there are some differences compared to mitosis. Crossing over separates linked alleles. The odds that two linked alleles will separate depends on how far apart they are - separation rates can be used to map locations of genes on chromosomes. During metaphase, the chromosomes do not separate into single strands - homologous chromosomes are pulled away from each other and eventually wind up in different nuclei. These nuclei are haploid one set , but the chromosomes are double-stranded. A short interphase

follows, just a bridge to the next division. Four nuclei usually in 4 cells , each with a single set of single-stranded chromosomes, are produced. This can happen when nuclei are exchanged between protozoans, when non-gendered cells cross fungal bridging fibers, or when sperm cells enter egg cells. But what makes males male and females female is not what you probably think it is. Remember, maleness and femaleness are terms that have to apply not just to people and dogs but to trees, and flower parts, and organ systems in animals that are male and female simultaneously monoecious, what used to be called hermaphroditic, as opposed to separate-gendered dioecious species. And dont assume it always involves "X" and "Y" chromosomes, which is just one way of several to set up gender. Simply put, male and female are defined by the gametes , the sex cells, that are made - everything else is peripheral to that. Many of the "regular" differences between males and females can easily be traced to the differences in their gametes.

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