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HOW MUTATIONS AFFECT CHROMOSOME NUMBERS.

Q33

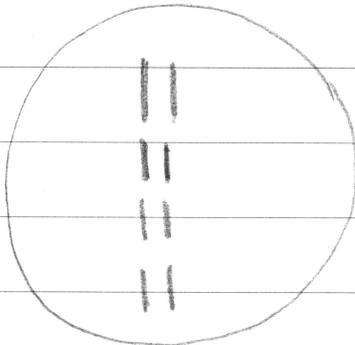
(a)

| TYPE OF MUTATION | HOW IT EFFECTS THE CHROMOSOME: |
|-------------------|---|
| Trisomy | A trisomy ^{mutation} basically when, a pair of chromosomes don't segregate into each cell during the division of meiosis. The pair together goes into one cell. This means the gamete is lacking a whole chromosome. |
| Polyploidy | A polyploidy mutation is when, all the pairs of chromosomes during meiosis don't segregate into different cells during meiosis. This results in one gamete having no chromosomes. And the other gamete cell having a diploid number, when ^{should be} haploid. |
| Base Substitution | Base substitution means during the replication of the strands of DNA, the one base is substituted for another. For example (A instead of T) this results in the incorrect combination of bases, which can lead to incorrect protein produced. |

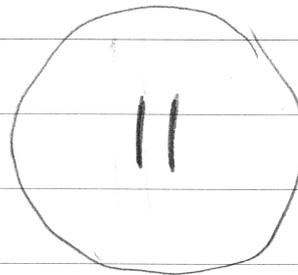
* Note: all three ~~the~~ types of mutations can lead to things such as death or genetic disease if the DNA does not repair itself, one mutation taken place.

(b) The similarities and differences between:

Diploid cell (4) (somatic cell)



Haploid cell (2) (gametic cell)



Similarity: Both have (as shown) chromosomes.

Both are cells, and a product of cell division

Differences: The Diploid cell has full number of chromosomes (4) and Haploid has half the number of chromosomes.

There are two different types of cells, the diploid cell is a somatic cell,

Key
|| = pair of chromosomes

but the other cell in order for it to be Haploid, has to be a gamatic cell or (germ cell) therefore ~~the~~ two different types of cells.

(c) (i) Both are recessive genes.

(ii) phenotypes & Ratios of vision defect & Limb defect
Normal vision is dominant (N) over vision defect (n) Normal limb dominant (L) over limb defect (e)

NOT LINKED, Individual both 9 and 10 don't have the vision disease, but could have carrier. Individual 9 has limb defect so carries the gene, but individual 10, could have the defective, gene this is unknown. DUE to Mendel's laws and Dihybrid

~~the~~ crosses we know if the genes are not linked, the ratio would be 9:3:3:1.

But if they are linked they could be any possible combination, but they aren't predictable due to the possible variation there is. In Mendel's law of segregation, he recognises that there are circumstances where genes are linked and if these genes are linked. ~~then they~~ Then ~~the~~ we know that the recombinant DNA will be less ~~than~~ ~~the~~ ~~parental~~, in the offspring so they will be more

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parental DNA showing. ~~But~~ So therefore we can conclude that the ratios for linked will be less than 50% for the RECOMBINANT DNA, but stronger for the parental DNA. The ratio could be anything ~~at~~ depending on how far away or close the linkage is. But if linked the recombinant DNA would be smaller ratio.

For example:

Parental DNA (7) : Recombinant DNA (3)
∴ (7:3)

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33 (continued)

(d)

(i) To determine linked genes, we can use Recombinant DNA technology, we can die a section of DNA by extracting a section of a gene ^{via restriction enzymes.} Put it back into a cell and watch ~~the transcription and translation.~~ ^{transcript} to help us identify how close the genes are ^{and compare it with many secondary sources and other results.} actually together. We can do this many times ^{under a microscope,} to try to hypothesise, the position of the linked gene and how close they are together.

(ii) Firstly the ^{gene} linkage maps, do show the relative position and how close the genes are together on the chromosome but they do not reveal them what each gene, actually does and what ~~is~~ the gene's trait is. ^{which defeats their aim in the project of identifying the 30,000 genes.}

(2) Secondly gene linkage does not actually reveal the base sequence of DNA which is what the Humane genome project was aiming to do. So therefore can't be used.

(3) Thirdly gene linkage maps don't deal with the ethncal side of the human genome project. They donated \$3-5% of their budget in facting their issue. The gene linkage simply shows how close the genes are it does not deal with the wider issue.

(e) Gene cloning, is the cloning of one particular gene, many times to form an organism of life. Gene cascade on the other hand, is the role of the HOX genes in producing ~~an~~ organism and how they develop the genes ~~one~~, ~~by~~ ^{and} limbs in proportion and in a specific linear order. The discoveries of these new techniques have resulted in the development of New Artificial life. With the knowledge of ~~gene~~ ^{cascades} and HOX genes, we have been able to study the way in which the organism grows and transforms. This knowledge has allowed us to monitor our new life that we have created to make sure that what we ~~have~~ ^{are} creating is producing properly and efficiently. What this does effectively is that it allows us to produce ~~new~~ ^{new} technologies to replicate this process. What ~~we~~ we can also do now is take the HOX genes from other organisms and place that into the bacterium. We are able to do this, because with the knowledge that in some organisms. (ie mouse and fruit fly) These HOX genes are ~~in fact~~ 100% identical.

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With this knowledge and these ~~new~~ new technologies as a result we are artificially able to replicate the process's ~~of~~ that are needed to start life. For example 'gene cloning' has been used for many different things such as to produce BT cotton and ~~the~~ insulin for the human body. We are also able to produce sheep such as Dolly, through a different form of cloning rather than whole organism cloning. The most important thing is that gene cloning and the understanding of gene cascades go hand in hand together. It is because of one that we are able to create the other.

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