Class - Part II

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Linkage

In a dihybrid cross in plants and animals the phenotypic ratio is 9:3:3:1. But there are some exceptions. Mendel mere on chance selected 7 pairs of characters in garden pea Pisum sativum which were located on seven chromosomes and no two genes were present in the same pair of chromosomes. Now it is an established fact that genes which are responsible for the expression of characters are situated on chromosomes and on one chromosome there may be more than one or more than a hundred genes present. Genes located on a chromosome are tied or linked with one another in such a way that they are passed together during gamete formation. The number of gene pairs in two homologous chromosomes forms a linkage group. This linking of genes on a chromosome is known as linkage. The genes which show linkage are also called linked genes. Before this phenomenon of linkage came to light many geneticists found in their experiment a deviation from 9:3:3:1 ratio in a dihybrid cross in F_2 generation.

Bateson and Punnet In 1906 found an exceptional result in F_2 generation in dihybrid cross of a sweet pea. They considered the two pairs of characters. These were flower colours purple (P) and red (p) and shape of pollen grain - Long (L) and round (l). They crossed the purple long with red round and obtained in F_1 all purple long as purple and long were dominant characters. When the F_1 dihybrids were crossed together in the F_2, they observed the following result which was different from the expected 9:3:3:1 ratio. The result was

Purple long = 4831
purple round = 390
Red long = 393
Red round = 1338
Total = 6952

Bateson and Punnet explained the above result as follows.
Sometimes two dominant characters from the same parent take part in the formation of offspring and these pairs of characters from the same gamete and are transmitted together to the next generation. This phenomenon is called coupling. This takes place when one dominant and one recessive character (gene) form F_1 dihybrid and they come from each parent in place of two dominant genes from one parent and two recessive genes from the other.

There is a tendency of two unlike pairs like one dominant and one recessive to combine together and to avoid their own type dominant with dominant and recessive with recessive. This phenomenon is called repulsi This above explanation was not satisfactory for the devi- ation of phenotype ratio in a dihybrid cross. The results obtained by Bateson and Punnet were also obtained by Morganin 1910 in Drosophila.

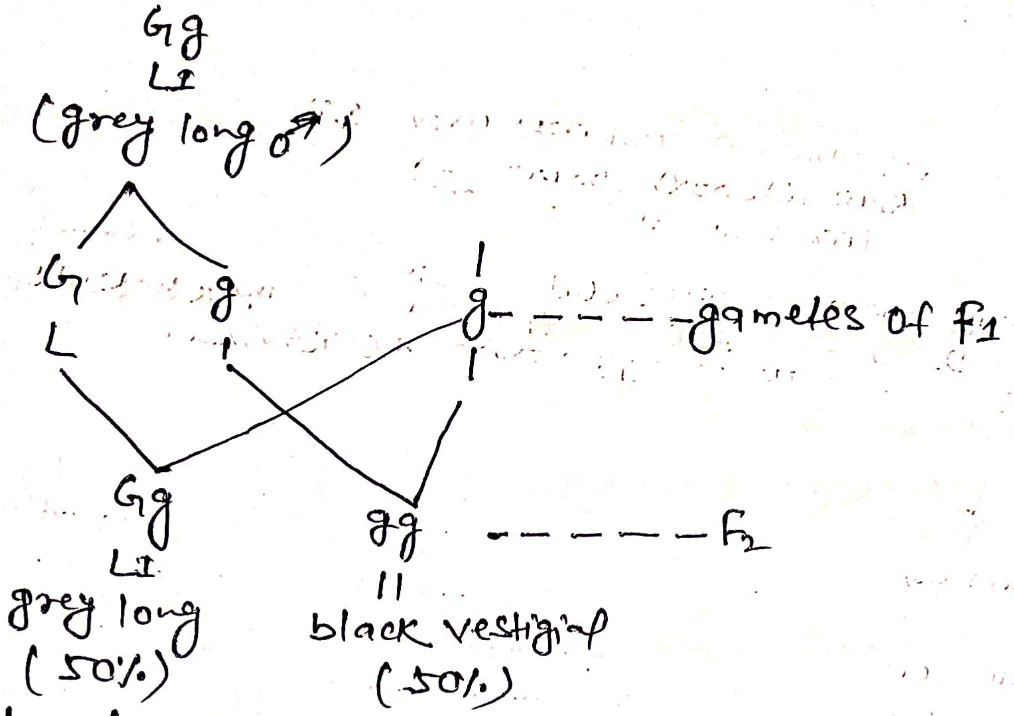
* **Complete Linkage** :- Mendel crossed a black and vestigial winged Drosophila with a grey and long winged one. In F_1 all were with grey body and long wing. So, grey and long were dominant characters. Next a male with grey and long was crossed with black and vestigial female. It was expected due to independent assortment that new types of insects will be formed. But this

GG LL (grey long ♀) ✕ gg ll (black vestigial ♂) ------ P

↓ G L ↓ g l

Gg Ll (grey long) ------ F_1

✕



did not occur. In F2 the characters remained like grandparents 50% of these were black and vestigial and the other 50% were grey with long wings. This shows that grey body and long wing characters are such that both were on the same chromosome and were not separated even when transferred from one generation to the next one but were linked together. From this study Morgan could forward his theory as "coupling and repulsion are two aspects of linkage."

Explanation

(i) As in F1 all were grey and long type, so these were dominant factors and were represented by GLgl.

(ii) In F1 the males produced two types of gametes one with gl and the other with GL in equal number but the female produces only one type of eggs with gl.

Now sperm gl with ovum gl produced black vestigial, sperm GL with ovum gl produced grey long (GLgl) offspring, This indicates the presence of G and L in one chromatid and g and l in another chromatid and so whenever there is a union b/w sperm and ovum only two types of individuals are formed either black vestigial or grey long. Further these show that grey with long and black with vestigial are linked together and pass on from one generation to another two genes show complete linkage.