RAMA UNIVERSITY

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FACULTY OF AGRICULTURAL SCIENCES

AND ALLIED INDUSTRIES

MULTIPLE FACTOR HYPOTHESIS

Polygenic inheritance quantitative characters

It shows more or less continous variation and are governed by a large number of genes called ' multiple gene' or 'multiple factor' or 'polymeric genes' or 'polygenes'.

Nilson -Ehle's studies on kernel colour in wheat

The Swedish geneticist Nilson - Ehle (1908) effected crosses between different true breeding strains of wheat with red kernels and those with white kernels. Careful examinations however revealed that, a red colour of the F1 was not so intense as the red colour of the parent and that in the F2. Some red grains wree as dark as those of parent and others only as dark as those of the F1. It was possible to separate the F2 in to the following;

Dark red	1	-	R1 R2 R2 R2 - 4 contributing genes.
Meidum dark red	4	-	3 contributing genes
Medium red	6	-	"
Light red	4	-	"
White	1	-	No "

	Red			White
Parents	R1 R1	R2 R2	x	r1 r1 r2 r2
F1	R1 r1	R2 r2	Medium red.	
F2	1	: 4 :	6 :	4 : 1

It is evident that, red colour is due to two pairs of alleles. Each gene is capable of producing red colour. Each is in completely dominant over white and in cumulative in its effect. The intensity of red colour depends upon the number of colour producing gene present.

From these studies, Nilson-Ehle proposed the multiple factor hypothesis for the inheritance of quantitative characters. This assumes that there is a series of independent genes for a given quantitative trait. Dominance is usually in complete, but these genes are cumulative or additive in their effect. Each gene adds something

to the strength of expression of the character, whereas its allele does not posses any effect.

Transgressive segregation

The appearance of individuals in the F2 or a subsequent generation which exceed the parental limits withrespect to one or more characters.

e.g. Skin colour in human beings

White x Negro Mariages -

By Daven port (1913) by multiple factor hypothesis.

Hypothetical example,

Plant height (cm)

200 cm tall 100 cm tall

T1 T1 T2 T2 x t1 t1 t2 t2

F1 T1 t1 T2 t2 150 cm

T1 T2 - Active contributing genes

T1 t2 neutral or inert alleles F2 1 : 4 : 6 : 4 : 1

Cm 200 175 150 125 100 cm.

Fine structure of Gene

Benzer in 1955 divided the gene in to recon, muton and cistron. He worked on rII locus of baceriophage. Recon is the recombinational unit, muton is the mutational unit and cistron is the functional unit.