MULTIPLE FACTOR HYPOTHESIS

Multiple factor

It is quite natural that small differences exist among individuals of similar genotype due to the effect of environment on genotype. On the other hand, there are some heritable differences also exist with continuous variation. Most of the economical traits show continuous variation and they are measurable or quantifiable.

Quantitative characters

Quantitative characters are traits which show continuous variation and governed by a large number of genes called multiple genes or multiple factors or polymeric genes or polygenes. Their inheritance follows same mendelian principles.

Quantitative characters

Qualitative characters show

- discontinuous variation and
- are governed by one or two major genes or oligognes.

Multiple factor Hypothesis (Nilson – Ehle)

Nilson-Ehle studied Kernel colour in wheat concluded that is a quantitative character He crossed true breeding red kernel whet (RR) with true breeding white (rr) and the F1 was red (Rr) and the F2 segregated for red and white in 3:1 ratio indicating the dominance of red over white. However, careful examination indicated the variation in red color among the red color progenies. F1 red was not as intense as one of the parents. In F2 he could observe two grades of red ie. one was red as that of one of its parent, two were higher red as that of F1 individuals. In some crosses, a ratio of 15 red : 1 white was found in F2 indicating that there are **two pairs of genes** for red colour that either or both of these can produce red kernels. Finally he observed different shades of red in F2 for red kernel types. The F2 showed **red shades** and white as follows;

Dark red	:	1	
Medium dark red	:	4	
Medium red	:	6	15
Light red	:	4	
White	:	1	
Total	:	16	

- It was concluded two duplicate dominant alleles R1 and R2 **cumulatively decide** the intensity of red colour
- and both R1 and R2 are in completely dominant over white.
- **The high intensity of red colour depends on the number**.

The F2 ratio in wheat

Genotype	Genotypic ratio	Phenotype
$R_1R_1\ R_2R_2$	1	Dark red
$R_1R_1\ R_2r_2$	2	Medium dark red
$R_1r_1\ R_2R_2$	2	Medium dark red
$R_1r_1\ R_2r_2$	4	Medium red
$R_1R_1\ r_2r_2$	1	Medium red
$r_1r_1\ R_2R_2$	1	Medium red
$R_1r_1\ r_2r_2$	2	light red
$r_1r_1\ R_2r_2$	2	light red
$r_1r_2\ r_2r_2$	1	white

Hence, if two parents differ for the two genes the segregation was 1:4:6:4:1 provided both R1 and R2 contribute equally to the colour. If three genes are involved in F2 segregation showed 1:6:15:20:15:6:1 for red shades and 1 for white.

Thus, Nilson-Ehle's multiple factor states that

i) For a given quantitative trait there could be several genes, which were independent in their segregation, but had cumulative effect on phenotype

ii) Dominance is usually incomplete

iii) **Each gene contributes something** to the strength of expression of character whereas its recessive allele does not of genes present dominance gene.

Causes of Genetic Variation: The Multiple-factor Hypothesis

We are used to thinking about the genetics of discrete plant phenotypes, for example tall versus short peas in Mendel's experiments. In this example, variation (different alleles) at a single gene contributes to a major phenotypic difference. However, for many traits of interest (such as yield), it is often the case that a large number of genes, each of modest effect, collectively contribute to the genetic variation. This is the **multiple-factor hypothesis.**

Early support for this multiple-factor hypothesis came from H. Nilsson-Ehle (1909), a Swedish geneticist working on various cereal crops. Many of the characters that he examined yielded 3:1 ratios in the F2 generation following the cross of two parental strains, consistent with expectations for a single segregating locus with one allele completely dominant over the other. However, there were some striking exceptions. For example, when red-seeded and white-seeded wheat strains were crossed, the F1 progeny were identical in color (light red), but in some of the F2 crosses, a ratio of 63 red:1 white seeds was observed. Nilsson-Ehle interpreted this to be the result of the segregation of three independent factors, the initial parents being *AABBCC* and *aabbcc*, all members of the F1 being *AaBbCc* and hence uniform in color, and the F2 consisting of all possible genotypes, only one of which (*aabbcc*) gives rise to white seed. The probability of obtaining an *aabbcc* offspring from an *AaBbCc* £ *AaBbCc* cross is (1=4)3 = 1=64*:* From these results, Nilsson-Ehle arrived at two general conclusions. First, *sexual reproduction can produce a huge diversity of genotypes.* For example, since a locus with two alleles *A* and *a* can produce three genotypes (*AA, Aa,* and *aa*), ten diallelic loci can produce 310 ' 60*;* 000 genotypes. Second, given this huge potential diversity of genotypes, *apparently new types appearing within a population may be the result of rare segregants rather than new mutations.* Subsequent studies quickly confirmed these ideas. East (1911, 1916) and Emerson (1910; Emerson and East 1913) examined quantitative variation in a large number of plants. Typically, strains differing widely in some character were crossed and the variance of the resulting F1 and F2 generations recorded. In most of these crosses, especially when the parental populations were formed by repeated self-fertilizations, an **outbreak of variation** was seen in the F2 (Figure 1.2). Such outbreaks of variation, resulting from the segregation of multiple genotypes from the F1 heterozygotes, are consistent with the multiple-factor hypothesis. For example, if the two parents being crossed are inbred lines with genotypes *AABBCC* and *aabbcc*, then the resulting F1 also has a single genotype *AaBbCc*. However, in the F2, all of the F1 heterozygotes can segregate, so that an *Aa* parent can have *AA*, *Aa*, or *aa* offspring. Thus, the F2 consists of a large collection of different genotypes, and hence is more variable (having both genetic and

environmental contributions to variation) than either of the parental or F1 lines (which have only environmental contributions to the variance).

Figure 1.2 The distribution of ear size in the F1 and F2 generations formed by crossing two inbred lines of corn differing in ear length. The observed number of ears is given below each size class. The variation seen in the P1, P2 and F1 populations is due entirely to environmental factors, as all individuals in each population have the same genotype. These three populations show roughly similar amounts of variation. In contrast, the F2 generation shows considerably more variation, reflecting the diversity of genotypes in this population generated by segregation of genes in the F1 parents. (Data from East 1911.).

P_1 / P_2

Length (cm)	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
# ears	4	21	24	8					3	11	12	15	26	15	10	7	2

F_1

Length (cm)	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
# ears					1	12	12	14	17	9	4						

F_2

Length (cm)	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
# ears			4	5	22	56	80	145	129	91	63	27	17	6	1		