## ZOOLOGY

## 6<sup>TH</sup> SEM (CC-XIII) UNIT - 6 (principles of genetics)

Dr.C. Chatterjee

#### **Polygenic Inheritance**

Many traits and phenotypic characters present in plants and animals such as height, skin pigmentation, hair and eye colour, milk and egg production are inherited through many alleles present in different loci. This is known as **polygenic inheritance**.

#### Definition

**Polygenic inheritance** is defined as **quantitative inheritance**, where multiple independent genes have an additive or similar effect on a single quantitative trait. Polygenic inheritance is also known as **multiple gene inheritance** or multiple factor inheritance.

#### characteristics of Polygenic Inheritance

- **Polygene** refers to a gene that exerts a slight effect on a phenotype along with other genes
- Effect of a single gene is too small so it is difficult to detect
- Multiple genes produce an equal effect
- Each allele have a cumulative or additive effect
- Polygenic inheritance differs from multiple alleles, as in multiple alleles, three or more alleles are present in the same locus of which any two alleles are present in an organism, e.g. ABO blood group system, which is controlled by three alleles
- There is no epistasis involved, i.e. masking of the expression of an allele of the different locus
- There is no linkage or dominance, rather there exist contributing and non-contributing alleles, which are known as active or null alleles respectively
- Polygenic inheritance is characterised by the **continuous variation** of the phenotype of a trait

#### Examples

## **Polygenic Inheritance in Humans**

There are many traits in humans, which show polygenic inheritance, e.g. skin and hair colour, height, eye colour, the risk for diseases and resistance, intelligence, blood pressure, bipolar disorder, autism, longevity, etc.

Brief description of some of the traits:

## Skin pigmentation:

1. The pigment melanin is responsible for dark coloration in the skin and there are at least three genes, which control for human skin color. Using a hypothetical example where the production of melanin is controlled by *contributing alleles* (denoted here as A, B and C), resulting in dark skin color, and therefore light skin color is produced by *non contributing alleles* (denoted here as a, b and c), it is possible to see how the spectrum of different skin colors can result in the offspring.

- 2. In polygenic inheritance, alleles do not display dominance over others, rather, each contributing allele gives an additive effect rather than a masking effect, and so the way that the alleles interact is different to those in Mendelian genetics. The additive effect means that each contributing allele produces one unit of color.
- 3. In an example using two parents, <u>heterozygous</u> for each of the melanin-producing genes (AaBbCc x AaBbCc), it is possible to see how the additive effects and combinations of alleles results in all the possible *genotypes*.
- 4. In this simplified example, there are 64 possible allele combinations, which result in the production of 7 different colored skin tones.
- 5. The skin tones which are least likely to occur are those resulting from entirely *homozygous* genotypes. The lightest skin tone, 0 (aabbcc), which lacks any alleles contributing melanin pigment, or the darkest skin tone, 6 (AABBCC), which contains all possible contributing alleles; each of these phenotypes occurs at a probability of 1/64.
- 6. As the number of contributing alleles changes within the allele combinations, the units of melanin pigment increases and decreases; the probability of the second lightest or darkest skin tones (1 or 5) is 6/64, the third lightest or darkest skin tones (2 or 4), is 15/64 and an entirely intermediate skin tone (3) is the most common at 20/64. As shown in the histogram above, this pattern fits the normal distribution.



#### Punnett square showing F2 generation offsprings continuous variation

#### From light to dark $\rightarrow$

- 1. **Height:** There are around 400 genes responsible for the phenotype and environment greatly influences the expression of genes.
- 2. **Eye colour:** The colour of the eye is determined by polygenes. At least 9 colours of eye colour are recognised in humans. There are two major eye colour genes and 14 more genes that determine the expression of the phenotype. A different number of alleles contribute to each colour. These are found to be X-linked.

#### **Polygenic Inheritance in Plants**

Polygenic inheritance in plants includes the colour and shape of the stem, pollen, flower, yield, oil content, size of a seed, time to mature or flower, etc.

Brief description of some of the traits:

1. **Kernel colour of the wheat:** The three independent pairs of alleles are involved in the expression of kernel colour of wheat. They show independent assortment. When dark red wheat kernel (AABBCC) is crossed with the white wheat kernel (aabbcc) the F<sub>1</sub> generation has an intermediate red colour kernel (AaBbCc). When F<sub>1</sub> generation is crossbred, F<sub>2</sub> generation has 63 red kernel plants having different shades of red and 1 white kernel.

 $\mathbf{F}_2$ 

1	6	15	20	15	6	1
Dark red	Moderate Red	Red	Intermediate red	Light red	Very light red	White

#### 63 Red (many shades):1 (white)

1. **Length of the corolla in tobacco:** There are around 5 genes involved in the expression of phenotype for corolla length of tobacco. There is a wide variety in the length of the corolla in tobacco due to polygenic inheritance.

### Effect of environment on Polygenic Inheritance

The expression of polygenes is greatly influenced by environmental conditions. The genotype sets the range for a quantitative trait but the environmental conditions decide the phenotype within its genetic limits. Genes function differently in different environmental conditions. Environment regulates the activity of certain genes and sets them on or off.

The range of phenotype possible under the different environmental conditions from the same genotype is termed as '**norm of reaction'.** The norm of the reaction is narrow for certain genotypes and broad for some genotypes, e.g. genotypes involved in human height have a very broad norm of reaction.

Identical twins raised in two different environments show that individuals may have genetic potential or vulnerability but environmental conditions influence the expression of genotype. Human characters such as intelligence, depression, height, skin colour, schizophrenia show the effect of the environment on gene expression. Phenotypic expression is dependent on both nature and nurture.

### **Examples:**

- 1. Diet and general health greatly influences height
- 2. Flower colour of a shrub, Hydrangeas, depends on the level of aluminium present in the soil
- 3. Effect of temperature on the skin of Himalayan rabbits.

# (FOR BETTER UNDERSTANDING please go through these examples)

#### Example :Color of wheat caryopsis

Color of wheat caryopsis may be of various range of red - from white to a dark-red. All first-generation offspring from crosses between the white and light-red sorts had intermediate color, while in the second generation, the ratio of phenotypes of white, intermediate, and light-red was 1:2:1. In the first offspring generation from crosses of white and red sorts was light-red, while in the second generation could be identify 5 different types coloring of caryopsis - from white to red. The proportion of white caryopsis was approximately equal to 1/16. Hybrids of first-generation from crosses between the white and dark-red sorts had intermediate color of caryopsis, in contrast with their parents, while in the second generation could be identify 7 different types coloring of caryopsis - from white to dark-red. The proportion of white caryopsis was approximately equal to 1/64 from the total amount. So we can conclude that the color of wheat ears is controlled by three genes, each of which has a small effect. Each gene is represented by two alleles, one of which determines the red color and the other white. Let's mark the alleles of these three loci as "Aa", "Bb" and "Cc". Then the genotypes of tese sorts will be as follows: white - "aabbcc", light-red - "AAbbcc", red - "AABBcc" and dark-red - "AABBCC". However, it's necessary to say that the red color of caryopsis will be not only in plants with the genotype "AABBcc", but also in plants with genotypes "AAbbCC", "aaBBCC", "AaBbCC", "AaBBCC", "AABbCc". It is also will be right for light-red plants and plants with intermediate coloration of caryopsis. Let's write the traits file, which will include all the possible variants:

A A B B C C:dark-red wheat

A A B B C:mid dark-red wheat

A A B C C:mid dark-red wheat

A B B C C:mid dark-red wheat

A A B B:red wheat

A A C C:red wheat

A A B C:red wheat

A B B C:red wheat

A B C C:red wheat

- B B C C:red wheat
- A A B:mid red wheat
- A A C:mid red wheat
- A B B:mid red wheat
- A B C:mid red wheat
- A C C:mid red wheat
- B B C:mid red wheat
- B C C:mid red wheat
- A A:light-red wheat
- A B:light-red wheat
- A C:light-red wheat
- B B:light-red wheat
- B C:light-red wheat
- C C:light-red wheat
- A:mid light-red wheat
- B:mid light-red wheat
- C:mid light-red wheat
- \*:white wheat

Parental genotypes for crosses between the white and light-red will be - "aabbcc" for white, and "AAbbcc" or "aaBBcc" or "aabbCC" for a light-red. All first-generation offspring will be mid light-red wheat (for example "Aabbcc"). As a result of crossing first-generation hybrids, we obtain the Traits phenotypes ratio 1:2:1.

Parental genotypes for crosses between the white and red will be - "aabbcc" for white, and "AABBcc" or "aaBBCC" or "AAbbCC" for a light-red. All first-generation offspring will be light-red wheat (for example "AaBbcc"). As a result of crossing first-generation hybrids, we obtain the Traits phenotypes ratio 1:4:6:4:1.

Parental genotypes for crosses between the white and dark-red will be - "aabbcc" for white, and "AABBCC" for dark-red. All first- generation offspring will be mid red wheat ("AaBbÑc"). As aresult of crossing first-generation hybrids, we obtain the Traits phenotypes ratio 1:6:15:20:15:6:1. Traits file in this case look like plenty bulky and complicated. But we can simplify it. Since each dominant allele has the same effect in the exprression of red color, then the color is caused only by the number of dominant alleles and is independent of

the locus to which they belong. So we can mark all the polygenes by the same letters, for example "Aa". Then the parental genotypes of wheat with white caryopsis will be "aaaaaaa", with a light-red "AAaaaa" or "aaAAaa" or "aaAAAA", with red "AAAAAaa" or "aaAAAA" or "AAaaAA", and with dark-red "AAAAAA". And the traits file will look much simpler:

A A A A A A:dark-red wheat

- A A A A A:mid dark-red wheat
- A A A A:red wheat
- A A A:mid red wheat
- A A:lighte-red wheat
- A:mid lighte-red wheat
- \*: white wheat

Example: The length of the ears of rabbits

Suppose, that the length of the ears of rabbits is controlled by two pairs of polygenes. Dominant alleles of these loci we mark as "D", and the recessive alleles as "d". The length of the ears of dominant homozygous rabbits with genotype "DDDD" is equal to 28 centimeters, and the length of the ears of recessive homozygous rabbits with genotype "dddd" is equal to 12 centimeters. If four recessive alleles gives us 12 centimeters of length, then one allele gives us 3 centimeters (12/4 = 3). And one dominant allele gives us 7 centimeters (28/4 = 7). Thus we can say that each dominant allele increases the length of the ears by 4 centimeters (7 - 3 = 4). Then the length of the ears of rabbits with three dominant alleles will be equal to 24 centimeters (28 - 4 = 24), with two - 20 centimeters (24 - 4 = 20), and with one will be equal to 16 centimeters (20 - 4 = 16). And we can write our traits file like this:

- D D D D:length28
- D D D:length24
- D D:length20
- D:length16

\*:length12