Homeotic gene (Arabidopsis MADS box) :—

Homeosis or homeotic transformation is the development of one body part with the phenotype of another.

Expression of ~~homoe~~ homeotic genes determines which adult structures will be formed by each body segment. Three classes of floral homeotic genes control the development of the following organs. Class A genes specify sepals, class A and class B genes specify petals, and class B and class C genes control stamen formation. Class C genes alone specify carpels. Class A genes are active in whorls 1 and 2 (sepals and petals), class B genes are expressed in whorls 2 and 3 (petals and stamens), class C genes are expressed in whorls 3 and 4 (stamens and carpels). Each organs formation depends on the expression pattern of different genes. Expression of class A genes in whorl 1 causes sepals to form. Expression of class A and class B genes in whorl 2 leads to petal formation. Expression of class B and class C genes in whorl 3 leads to stamen formation. In whorl 4, expression of class C genes causes carpel formation.

Mutation in homeotic genes causes organs to form in abnormal locations. For example, in AP2 ~~mutats~~ mutants (caused by mutation of a class A gene), the order of outer to inner organ is carpel, stamen, stamen & carpel. In B loss-of-function mutants, petals become sepals and stamens are transformed in carpels & the ~~org~~ order of organs becomes sepal, sepal, carpel, carpel. Plants carrying a mutation for the class C gene AGAMOUS will have ~~pat~~ petals in whorl 3 (instead of stamens) & sepals in whorl 4 (instead of carpels), and the orders of organs will be sepal, petal, petal & sepal.

Homeotic selector Genes in Arabidopsis

Class A	APETALA 1 (AP1). APETALA 2 (AP2).
Class B	APETALA 3 (AP3) PISTILLATA (P1)
Class C	AGAMOUS (AG)

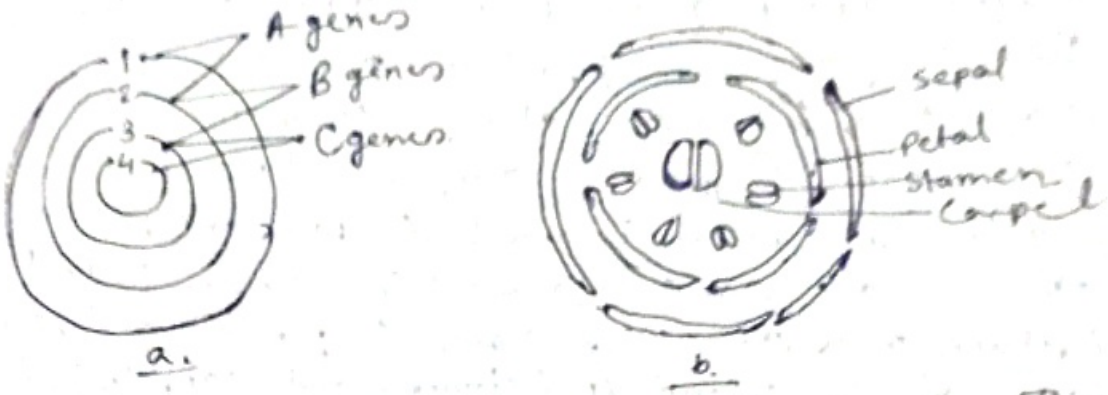

Fig:- Cell arrangement in floral meristem. a. The four concentric rings, on whorls labeled 1–4, influenced by genes A, B and C in the manner shown, give rise to the sepals, petals, stamens & carpels respectively. b. The arrangement of these organs in the mature flower.

Sequencing of floral organ-identity gene or homeotic genes has revealed that many encode proteins belonging to the MADS-family of transcription factors. MADS-box proteins are members of a different family of transcription factors. Each member of this family contains a common sequence of 58 amino acids.

Transposons :-

Transposons are DNA elements that can hop, or transpose from one place in DNA to another. It is a type of nonhomologous recombination. Transposable DNA elements were first discovered in corn by Barbara McClintock in early 1950s and about 20 years later in bacteria by others. Transposons are now known to exist in all organisms on Earth, including humans. The movement by a transposon is called transposition, and the enzymes that promote transposition are called transposases. The transposon itself usually encodes its own transposases, so that it carries with it the ability to hop each time it moves. For this reason, transposons have been called "Jumping genes".

McClintock discovered the Ac and Ds elements by studying chromosome breakage. She used genetic markers like maize kernel-pigmentation (anthocyanin gene activity loci) to detect the breakage events. When a particular marker was lost, Mc. clintock inferred that the chromosome segment on which it was located had been lost, an indication that a breakage event had occurred. The loss of the marker was detected by a change in the colour of the aleurone of maize kernels.

McClintock found that, in one strain of maize, chromosome 9 broke very frequently and at one particular site. Breakage of the chromosome at this locus was due to the presence of two genetic factors.

One factor that she called Ds (for Dissociation) was located at the site of the break. Another, unlinked genetic factor was required to "activate" the breakage of chromosome 9 at the Ds locus which is called factor Ac (for Activator).

McClintock hypothesized that Ds had moved from a site near the centromere into the C-gene located close to the telomeric end. (In this location, Ds produced very unusual changes in the expression of the C-gene. The spotted kernel is an example of an unstable phenotype. McClintock concluded that such unstable phenotypes resulted from the movement or transposition of Ds away from the C-gene.)

She explain the interactions between Ds, Ac & the pigment gene C by the following figure. Here Ds is shown as a piece of DNA that has inactivated the C-gene [the allele is called c-mutable (Ds) or c-m (Ds)] by inserting into its coding region. A strain with c-m (Ds) and no Ac has colourless kernels because Ds can not move; it is stuck in the C-gene. A strain with c-m (Ds) and Ac has spotted kernels because Ac activates Ds, in some cells, to leave (called excise or transpose) the C gene, thereby restoring gene function.

Other strains were isolated in which the Ac element itself had inserted into the C-gene [called c-m (Ac)]. Unlike the c-m (Ds) allele, which is unstable only when Ac is in the genome, c-m (Ac) is always unstable. Furthermore, Ac-type could be transformed into Ds type concluding that