

Session-13

ALLOPOLYPLOIDY Allopolyploids have genomes from two or more species. Several of our crop plants are allopolyploids. The productions of allopolyploids involve two steps.

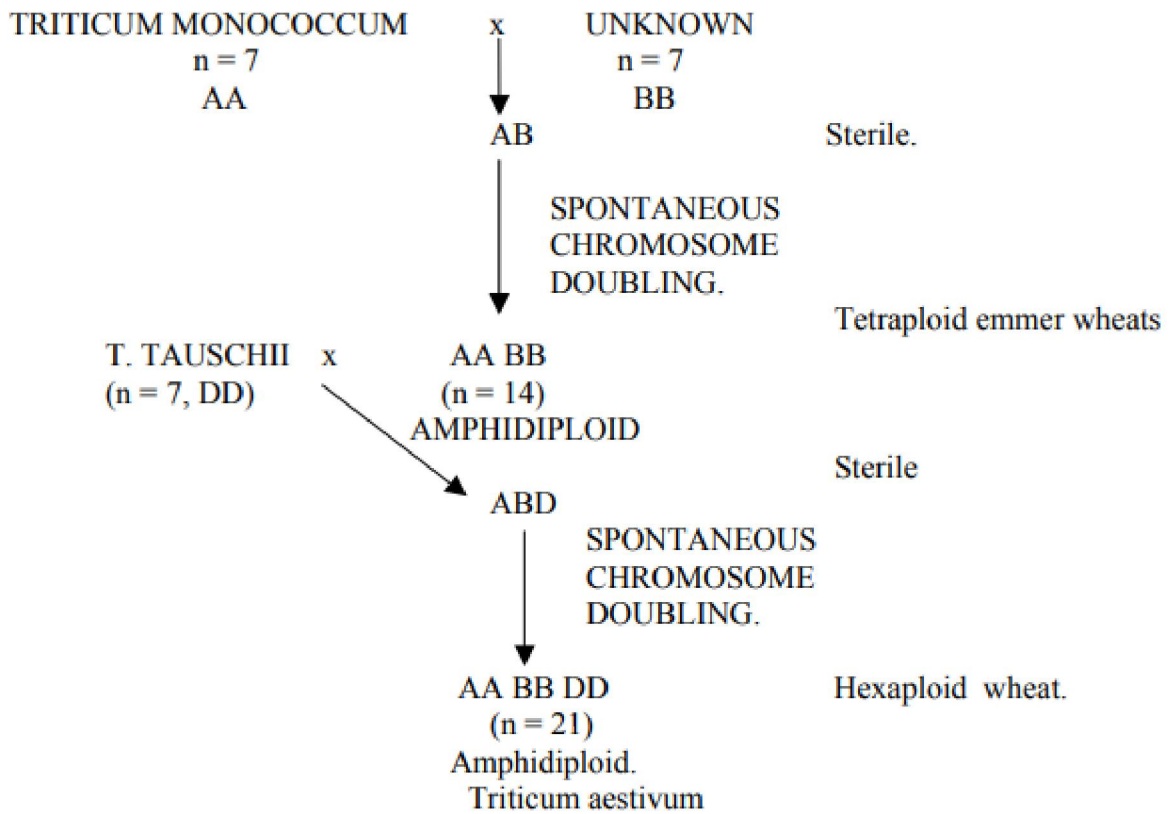
1. Production of F1 distant hybrid
2. Chromosome doubling

Production of allopolyploids has attracted considerable attention; the aim almost always was the creation of new species. Some success has been obtained as is evident from the emergence of Triticale as a new crop species in some areas, and the promise shown by some other allopolyploids, e.g., Raphanobrassica and some allopolyploids of forage grasses. Some genera, which contain allopolyploid species, and one or more crop species. The crop species themselves may be allopolyploid or diploid. Genera like Triticum, Brassica and Gossypium have both diploid and allopolyploid crop species.

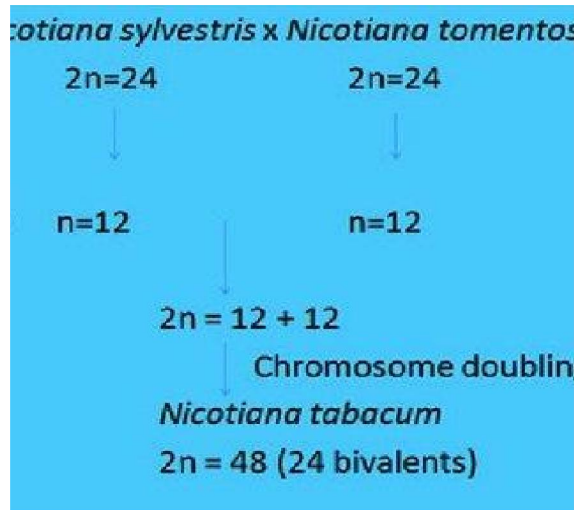
Role of polyploidy in evolution of crops – Wheat, Cotton, Tobacco and Brassica
Role of Allopolyploidy in Evolution: It is estimated that about one-third of the Angiosperms are polyploids, and by far the vast majority of them are allopolyploids. The identification of parental diploid species is primarily based on pairing between the chromosomes of the diploid and the allopolyploid species. When the chromosomes of a diploid species pair with some of those of the allopolyploid species, homology between chromosomes of the two species is apparent. This homology suggests that the diploid species may be one of the parental species of the allopolyploid. We shall briefly consider the possible evolutionary history of some important allopolyploid crop species, viz., wheat, tobacco, cotton and Brassica. Evolution of Bread Wheat (*Triticum aestivum*). Evolutionary history of wheat has been the most extensively investigated, and is perhaps the least understood. Identity of the diploid species contributing the three genomes (A, B, and D genomes) of *T. aestivum* has been investigated by many workers, more notably by Sears, Kihara and others.

Common cultivated wheat is another important example of allopolyploidy, although its allopolyploid nature has now been questioned. There are three different chromosome numbers in the genus *Triticum*, namely $2n = 14$, $2n = 28$ and $2n = 42$. The common wheat is hexaploid with $2n = 42$, and is derived from three diploid species : (i) AA = *Triticum aegilopoides* ($2n = 14$), (ii) BB = *Aegilops speltoides* ? ($2n = 14$) (in the past evidence was made available, showing that *Ae. speltoides* may not be the donor of B genome; it is also believed that the donor of B genome may never be discovered) and (iii) DD = *Aegilops squarrosq* ($2n = 14$). The hexaploid wheat, therefore, is designated as AABBDD, the tetraploid ($2n = 28$) as AABB and diploid ($2n = 14$) as AA. There is, however, evidence available now which suggests that A, B and D genomes from three diploid species mentioned above are not much different from one another, so that it is believed that the three diploid progenitors of common hexaploid wheat were derived from a

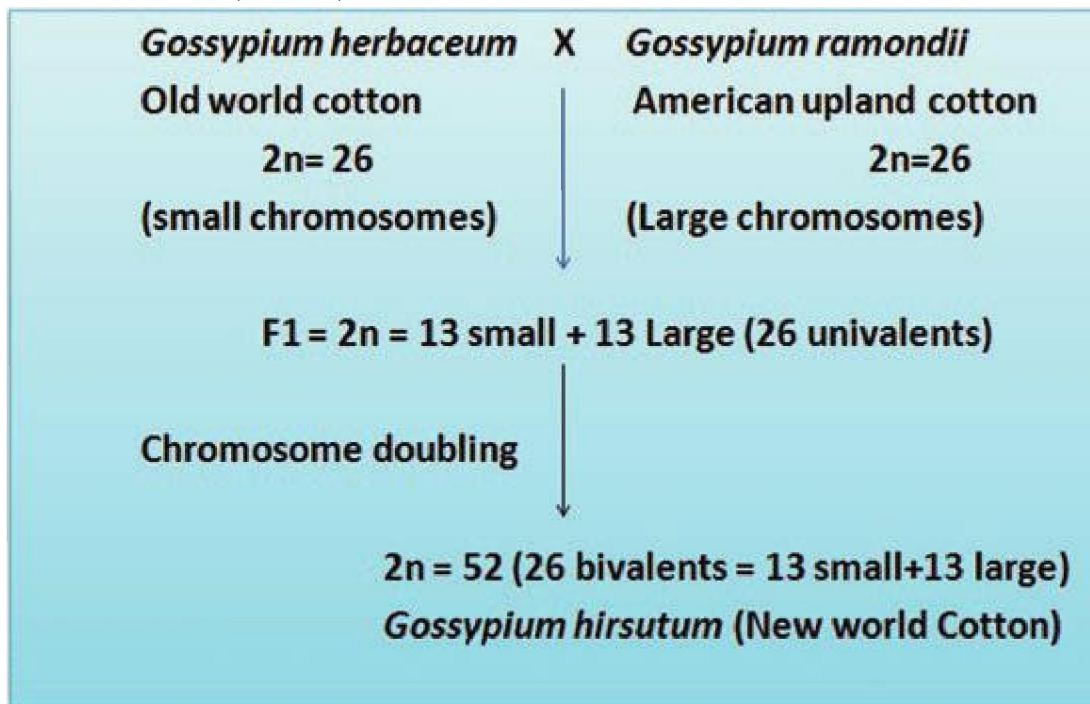
common ancestor. For this reason, the common hexaploid wheat is now considered an autopolyploid rather than an allopolyploid. At best, it may be a segmental allopolyploid.



Evolution of *Nicotiana tabacum*. *N. tabacum* ($n = 24$) is most likely an amphidiploid from the cross *N. sylvestris* x *N. tomentosa*; both the species are diploid with $n = 12$. The amphidiploid from the cross *N. sylvestris* x *N. tomentosa* is similar to *N. tabacum* in many characteristics, which further supports the above conclusion. The species *N. tabacum* has undergone considerable differentiation during its evolutionary history, mostly due to the accumulation of gene mutations and, to some extent, due to the loss of some duplicated segments of the two genomes.

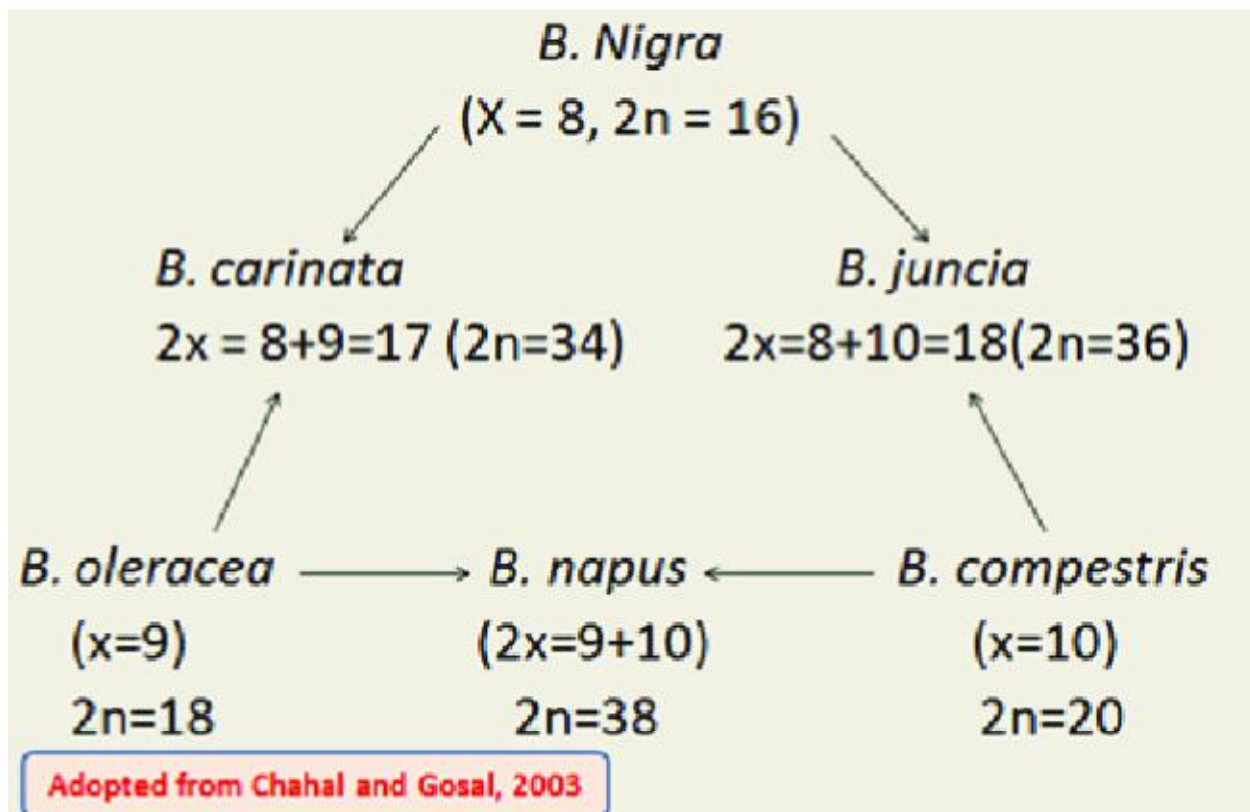


Evolution of *Gossypium hirsutum*: *Gossypium hirsutum*, popularly known as upland cotton, is another interesting example of amphidiploidy. **Old World cotton** has 13 pairs of large chromosomes, while American or **upland cotton** has 13 pairs of smaller chromosomes. The **New World cotton**, the cultivated long-staple type has 26 pairs of chromosomes, 13 large and 13 small. J.O. **Beasley** crossed the American and Old World cottons and doubled the chromosome number in the F₁ hybrids (Fig. 20.12). The amphidiploid thus produced resembled the cultivated New World cotton and when crossed with it gave fertile F₁ hybrids. The evidence presented in Figure 20.12, thus showed that New World cotton, the cultivated *Gossypium hirsutum* (tetraploid) originated from two diploid species, namely *G. herbaceum* ($2n = 26$) and *G. raimondii* ($2n = 26$).



Evolution of Amphidiploid Brassica Species: The origin of amphidiploid Brassica species is presented based on the famous U's Triangle proposed by N. U in 1935. According to this scheme, *B. juncea* ($n = 18$) is an amphidiploid from *B. nigra* ($n = 8$) x *B. campestris* ($n = 10$), *B. napus* ($n = 19$) is an amphidiploid from the cross *B. oleracea* ($n = 9$) x *B. campestris* ($n = 10$), and *B. carinata* ($n = 17$) is an amphidiploid from the cross *B. nigra* ($n = 8$) x *B. oleracea* ($n = 9$). The synthetic allopolyploids produced according to the above scheme resemble the natural amphidiploids, cross easily with them, and the hybrids between the synthetic and natural amphidiploids are reasonably fertile.

Brassica Triangle (Morinaga, 1934)



Segmental allopolyploids.

In some allopolyploids, the different genomes which are present are not quite different from one another. Consequently, in these polyploids chromosomes from different genomes do pair together to some extent and multivalents are formed. This means that segments of chromosomes and not the whole chromosomes are homologous. Therefore, such allopolyploids are called segmental allopolyploids according to **Stebbins** (1943, 1950). These segmental allopolyploids are intermediate between autopolyploids and allopolyploids and can be identified by their meiotic behaviour.

It is also believed that most of the naturally occurring polyploids are neither true autopolyploids nor true allopolyploids but are rather segmental allopolyploids. Our common hexaploid bread wheat is also regarded to be a segmental allopolyploid, because the three diploid genomes (A, B and D) are related (homoeologous) to each other.