

MONOSOMICS

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Nutshell

- Introduction
- Methods of production
- Identification of monosomics
- Meiotic behavior of monosomics
- Breeding behavior
- Checking identity of monosomics
- Locating genes on polyploid crops
- Human disorder

Introduction

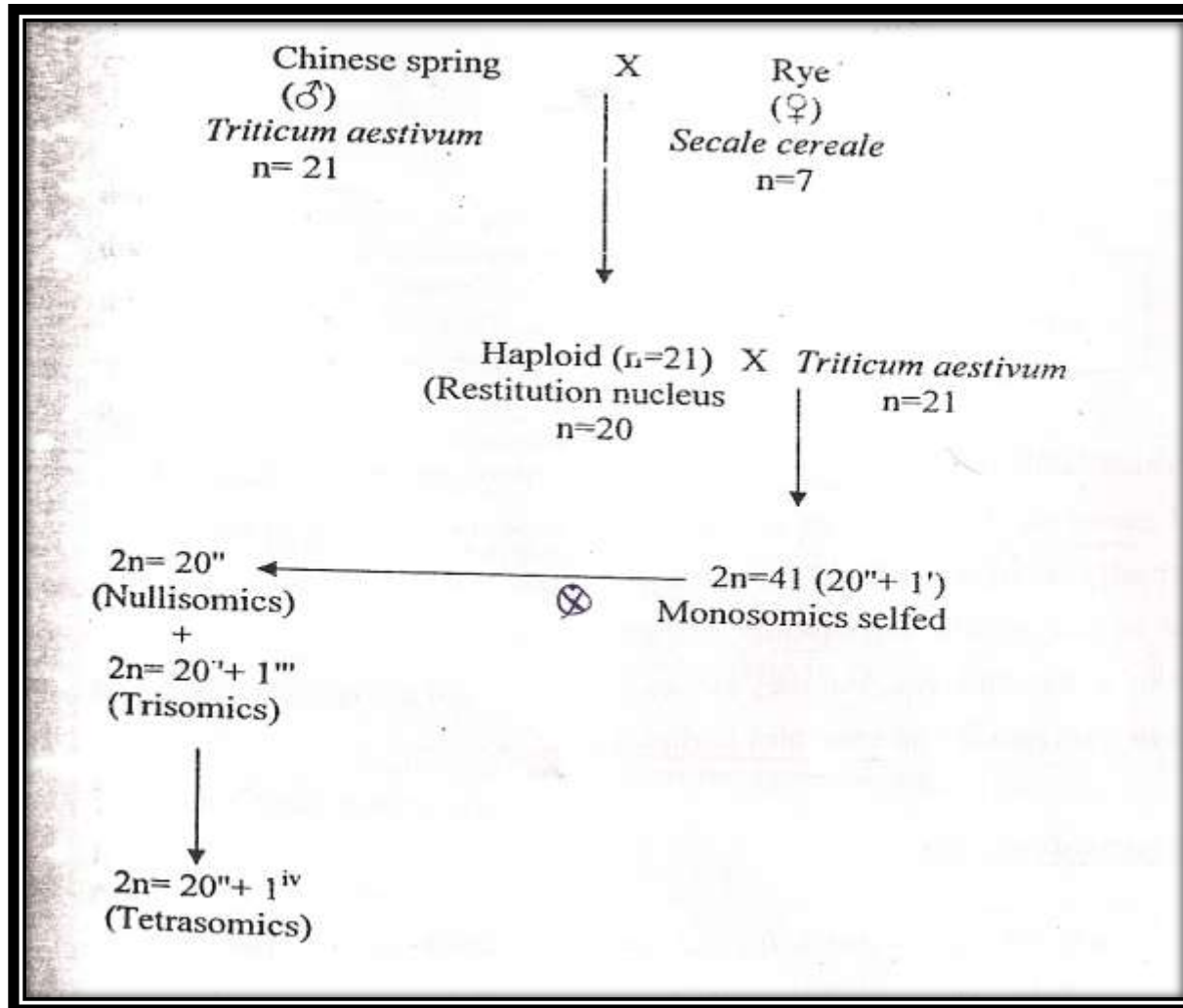
- Polyploids can tolerate not diploid (except Maize - diploid or segmental polyploid)

History:

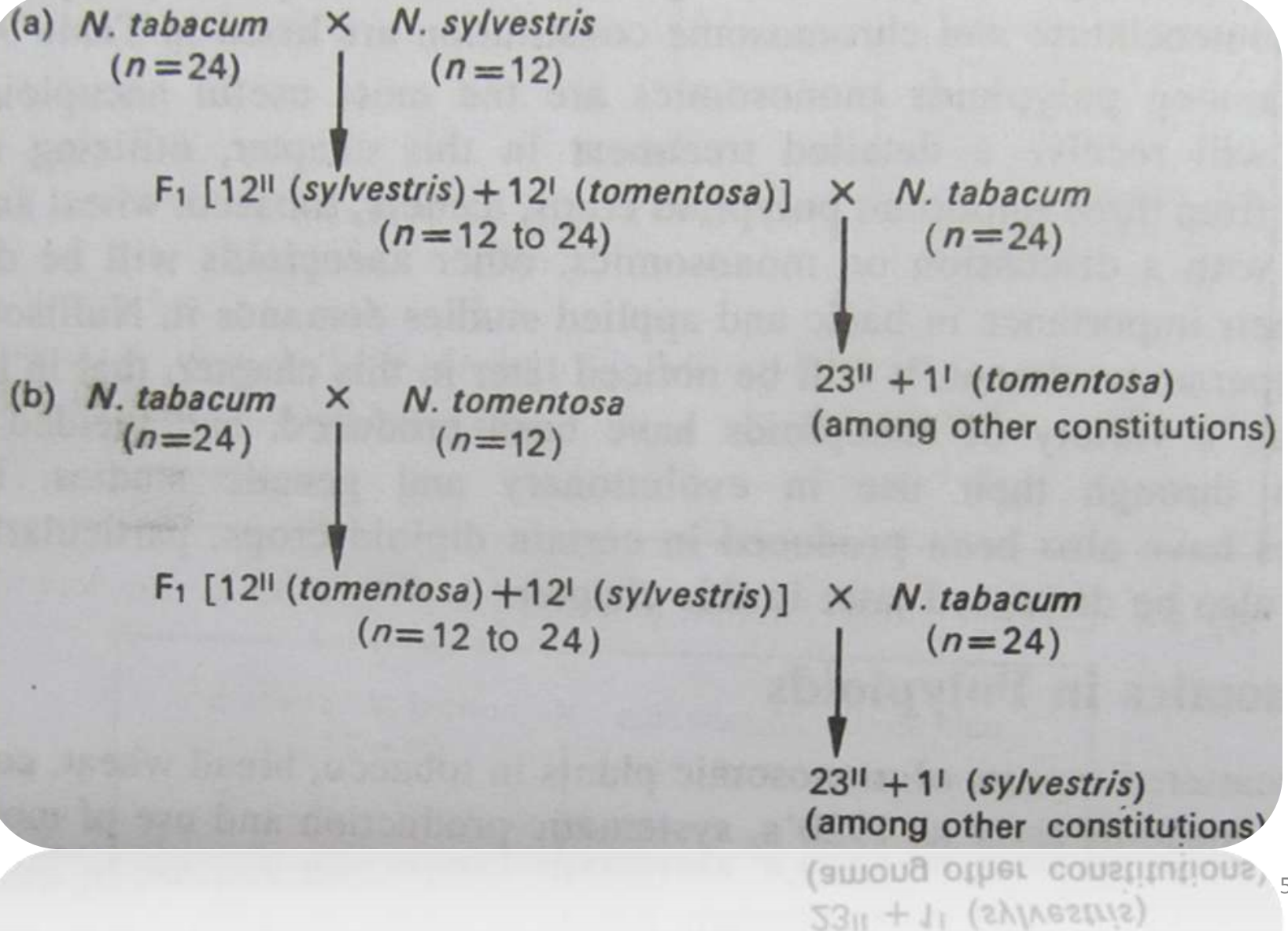
- Scattered work on monosomics initiated in early 1920's
- Systematic work started by-
- Clausen & Cameron (1944)- *Nicotiana tabacum*
- Sears (1954)- Hexaploid wheat
- Endrizzi et al. (1963, 84, 85)- *Gossypium hirsutum*

Methods of Monosomic Production

1. From haploids:

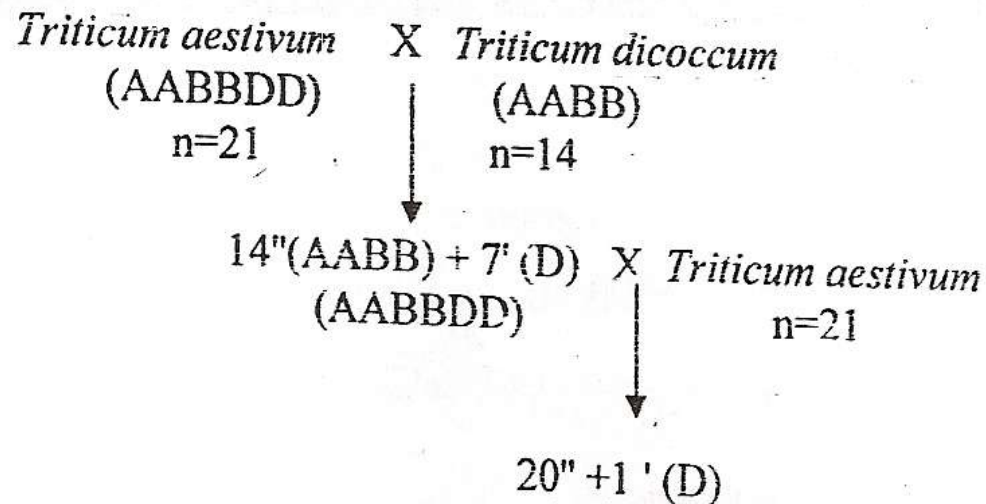


2. Backcrosses of interspecific hybrids

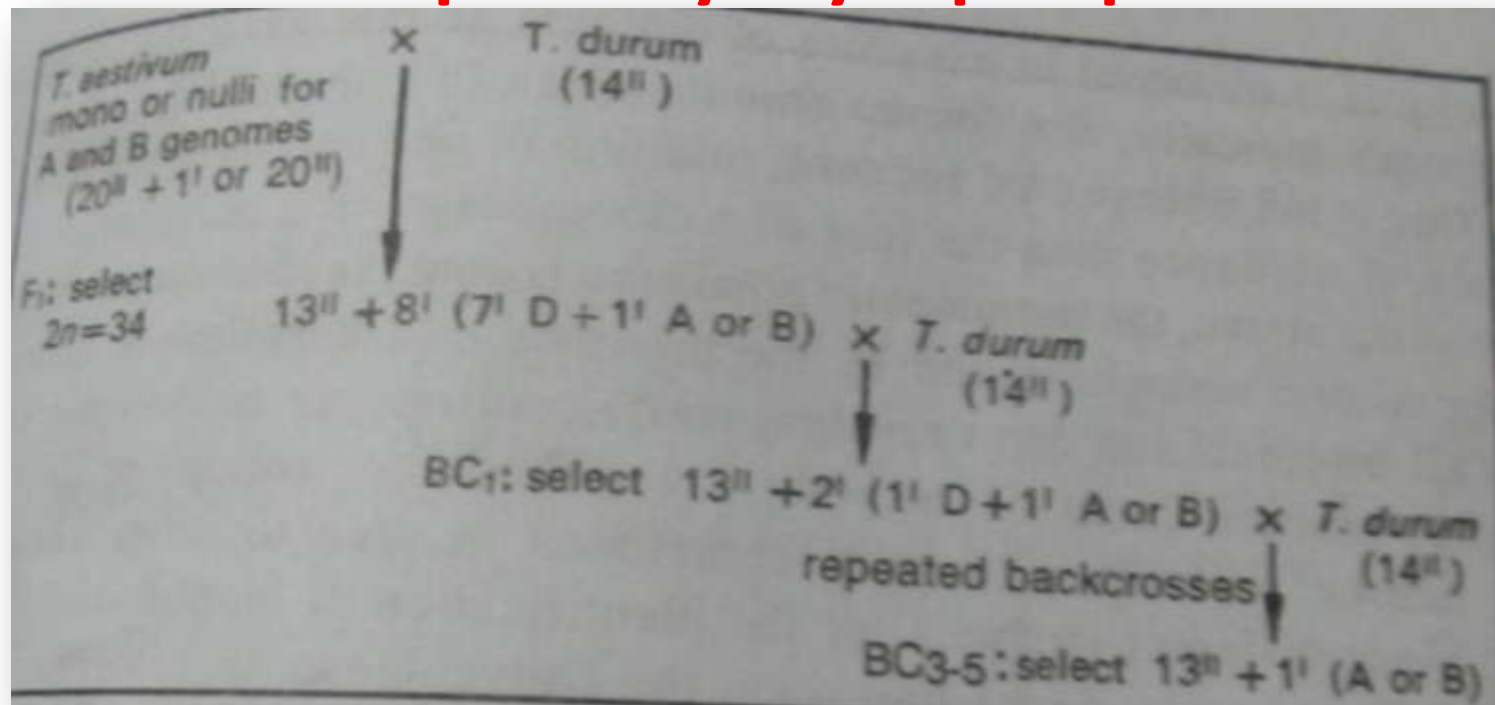


Production of monosomics of D genome in bread wheat

• In wheat Matsumura, 1940 gave a scheme for production of monosomics



3. From partially asynaptic plants



Pale sterile *N. tabacum* $n = \text{variable}$ X Normal *N. tabacum* $n = 24$

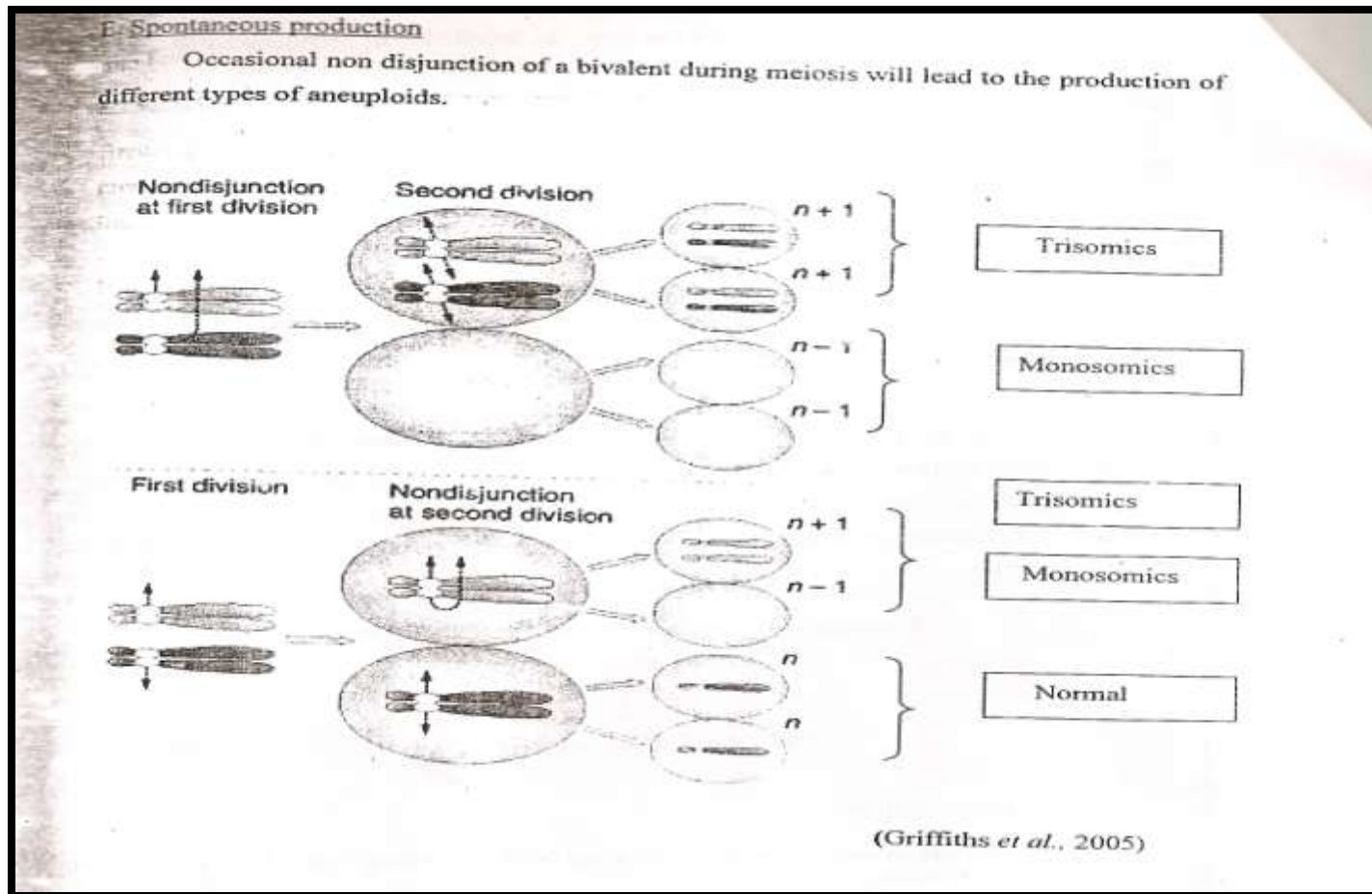
$2n = 23'' + 1'$ (Monosomic)

4. Irradiation treatment: Inflorescence is irradiated

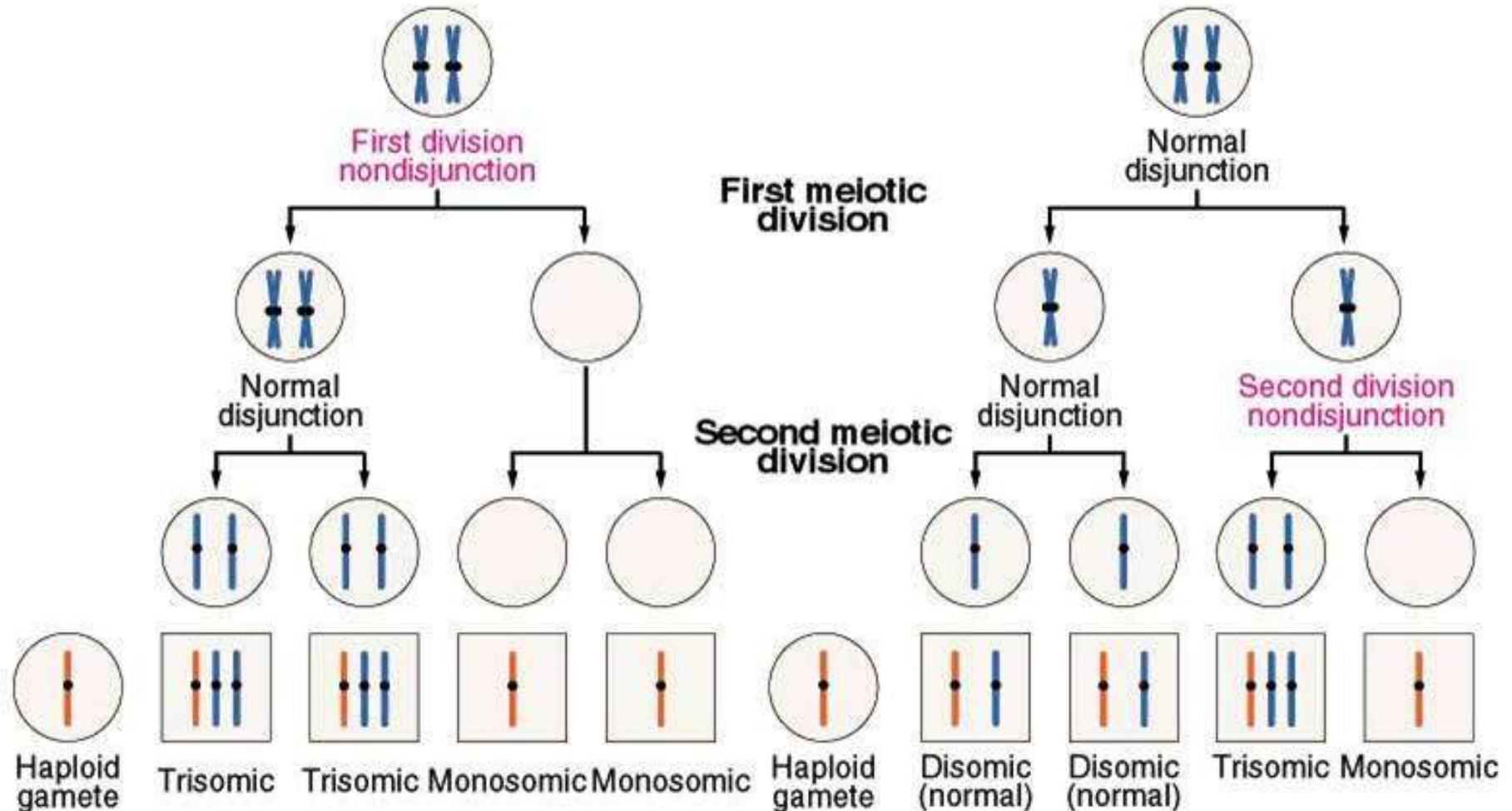
- Non-disjunction of normal bivalents- production of gametes with $2x+1$ and $2x-1$

5. Spontaneous production:

- Occasional non-disjunction of bivalents during meiosis

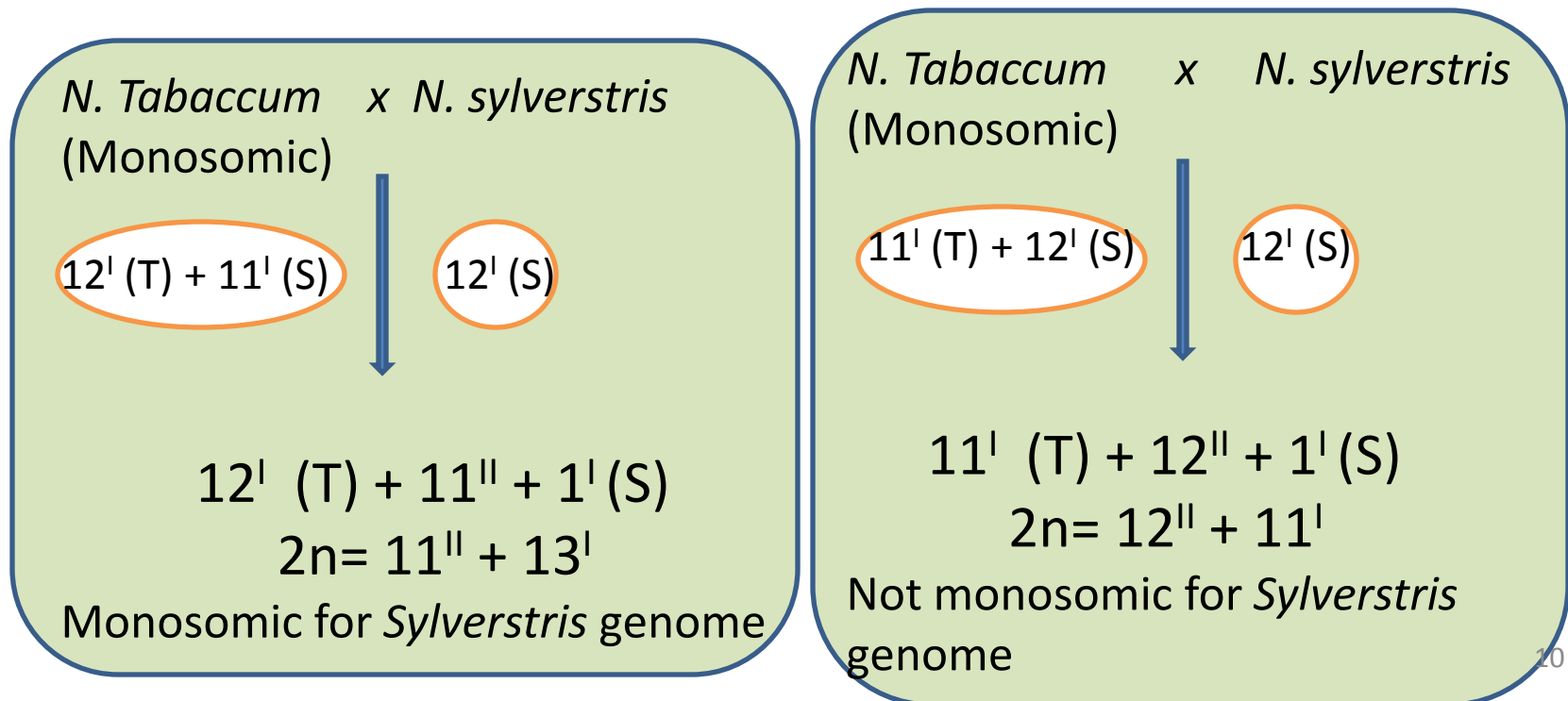


Meiotic Nondisjunction Generates Aneuploidies



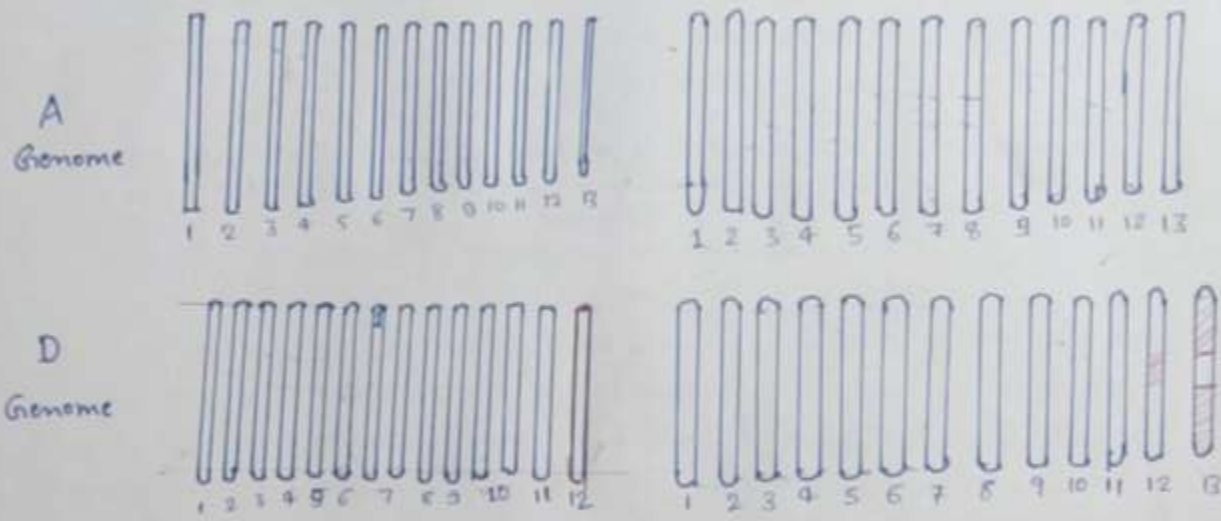
Description and identification of monosomics

- Generally polyploids don't show drastic alterations in morphology (bcz. addition of chromosome to diploid creates greater disturbance)
- Chromosome count in mitosis & univalents in meiosis



Identification in Cotton

1. Cross monosomic with progenitor
2. Study of meiosis in hybrids b/w monosomic and translocated testers that are available in cotton



Monosomic for

Translocation Testes

A Genome 13^{II}
+

F₁



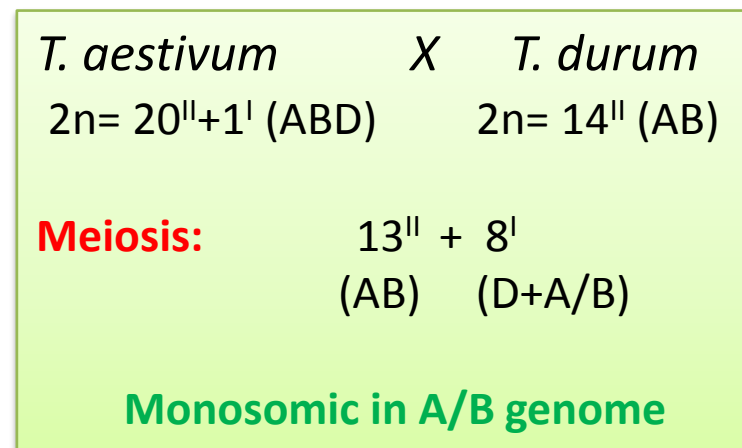
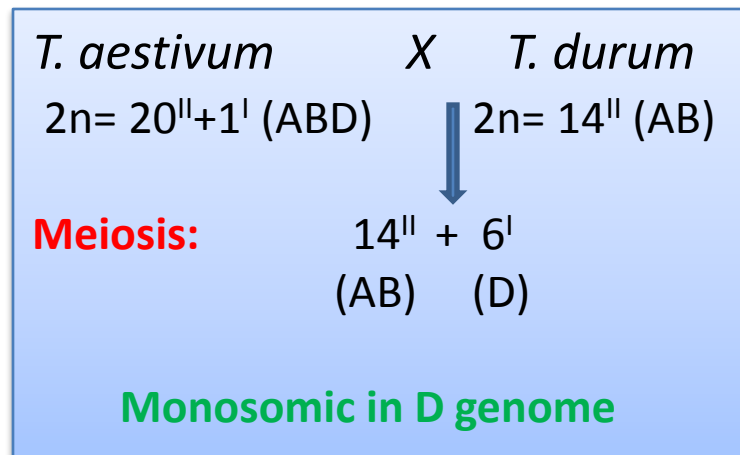
B Genome

$$2n = 51 (24^{\text{II}} + 1^{\text{III}})$$

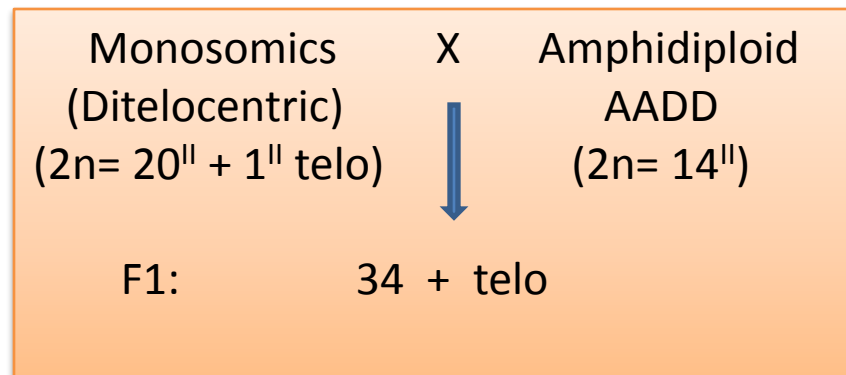
"Monosomic involved a chromosome, which is also involved in the translocation of the testes"

Identification of monosomics & related phenomena in wheat

- a) Classification of monosomics in durum group (A & B genome) & D genome



Distinction b/w monosomics of A & B genomes



- If telocentric chr. was involved in the formation of heteromorphic bivalent, then the monosomic belongs to A genome if not to B genome

C. Assessing chr. to homeologous groups in Wheat (compensating nullisomic-tetrasomic lines)

- It has been demo. that the presence of an extra chr. may separately compensate phenotypically for the absence of each of the other two chr. “This is an evidence of homeology among 3 chr.”
- **Confirmed by-**
 1. Study at gametophytic level; in a mixture of pollen derived from mono-trisomic plant, nulli-di pollen ($n=19+2$) function as normal wheat pollen ($n=21$) only when the missing chr. & extra chr. in nulli-di pollen were homeologous each other
 2. Loss of 5B Chr.; pairing b/w non-homologous chr.
 3. Genetic evidence of homeology by using genes on same chromosomes

Homology has extended to genera Triticae (Aegilops, Agropyron, Haynaldia, Hordium, Secale etc.)

“Homeology proved the common ancestry & Genome didn't differentiate very much after their initial divergence”

D. Diploidizing (5B) system in Bread wheat

- Due to presence of *Ph1* gene on long arm of 5B chr.
- Diploidizing system function even in hemizygous condition (monosomic), but hemizygous inefficient (in 6x *Festuca*) & hemizygous insufficient (in polyploid *Hordeum*)

Meiotic behavior

- Monosomics form bivalents and solitary univalents, rarely trivalents
- **Univalent shift**; formation of more than one univalents due to failure of association of one/more pairs homologous chr., which gives rise to other monosomics
- The solitary univalent either gets included in one of the two nuclei may lag/divide at AI consequently at AII it may divide of lag
- Behavior of univalent at meiosis determines the frequency of microspore with different chr. constitutions
- Eg: Wheat ($2x-1$) & tobacco ($3x-1$) – 75%
- Oat ($3x-1$) – 84-91%

Breeding behaviour of Monosomics

- Breeding behavior is studied by examining the progeny obtained by **selfing** them and **crossing them** separately as male and female parent with normal's. **This helps to calculate the frequency of functional deficient gamete relative to normal.**
- **Deficient gametes produced in higher frequency but function at low frequency in pollen**
- **Eg: fig.**

Fig. Monosomic selfing

If we assume that gametes are transmitted through male and female are 50% n and 50% $n-1$ then expected ratios will be $2n: 2n-1: 2n-2$.

♀ \ ♂		
	n	$n-1$
n	$2n$ (0.25)	$2n-1$ (0.25)
$n-1$	$2n-1$ (0.25)	$2n-2$ (0.25)

Expected:
 $1 (2n): 2 (2n-1): 1 (2n-2)$

Although functional deficient gametes are produced at a frequency higher than 75% they function in pollen in a very low frequency (4%) and through female it will be 75%. So the ratio of disomics: monosomics: nullisomics will be 24: 73: 3.

Expected ratios of $2n:2n-1:2n-2$ progeny from selfing a monosomic

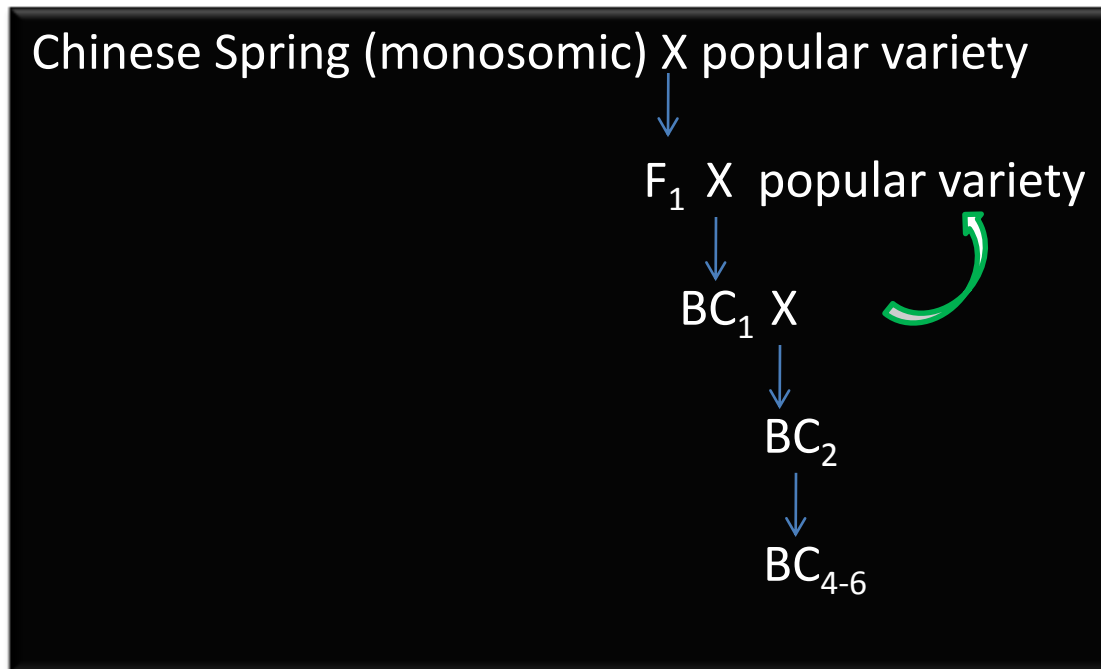
Assumptions: 96% n and 4% $n-1$ through the male
25% n and 75% $n-1$ through the female

♀ \ ♂		
	n (96%)	$n-1$ (4%)
n (25%)	$2n$ (24%)	$2n-1$ (1%)
$n-1$ (75%)	$2n-1$ (72%)	$2n-2$ (3%)

73% ($2n-1$) : 24% ($2n$) : 3% ($2n-2$)

Production of monosomic series in a new variety

- Wheat; monosomic series was initially produced in the variety Chinese Spring
- For convenient use, one may like to use monosomic series in a popular variety of his country



Checking the identity of monosomics

Monosomic X nullisomic



True identity: F1 20II

Mistaken identity: 19II + 1II

Monosomic X ditelocentric



True identity: F1 20II + 1 telo

Mistaken identity: 19II + 1^{heteromorph}

Uses of Monosomics

- The preparation of linkage map in polyploid species has been difficult due to the presence of duplicate genes or due to polygenic inheritance. So a technique known as **monosomic analysis** has been successfully used.
- Based on nature of gene, different types of monosomic analysis are possible.

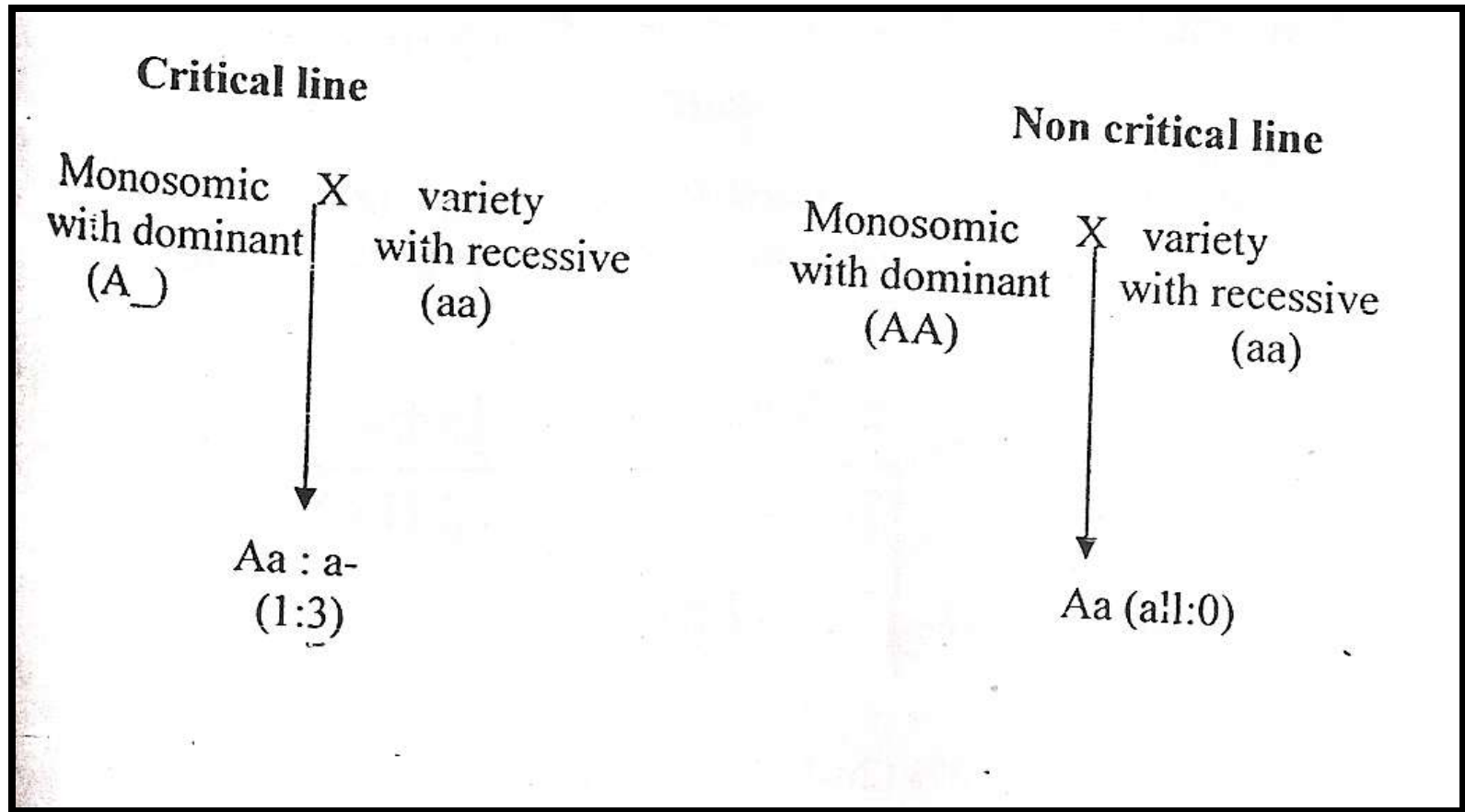
Different types of Monosomic analysis

1. Use of monosomic analysis to locate dominant genes to chromosomes
1. Use of monosomic analysis to locate recessive genes to chromosomes
2. Use of monosomic analysis in locating genes to chromosomes for digenic trait
3. Use of monosomic analysis in locating genes through intervarietal chromosomal substitutions
4. Use of monosomic analysis in locating genes on chromosome arms

Locating dominant gene by absence of expression in the nullisomic

- Nullisomic for the chr. carrying the gene should express the effect of absence
- Self each of 21 monosomics & observe for the absence of gene expression
- Eg: 3D- Red kernel
4B- awn suppression

Locate dominant genes to chromosomes through F_1 analysis



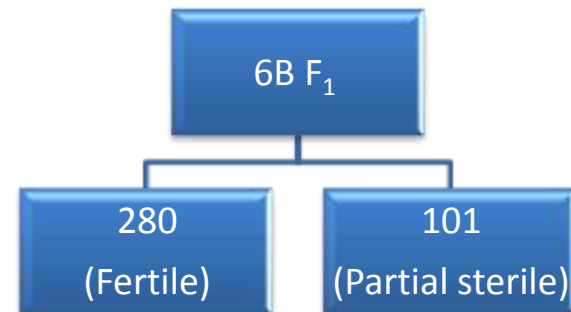
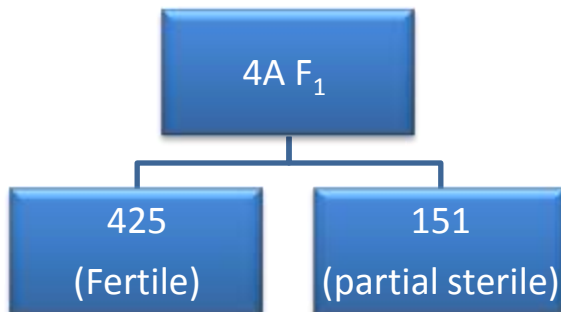
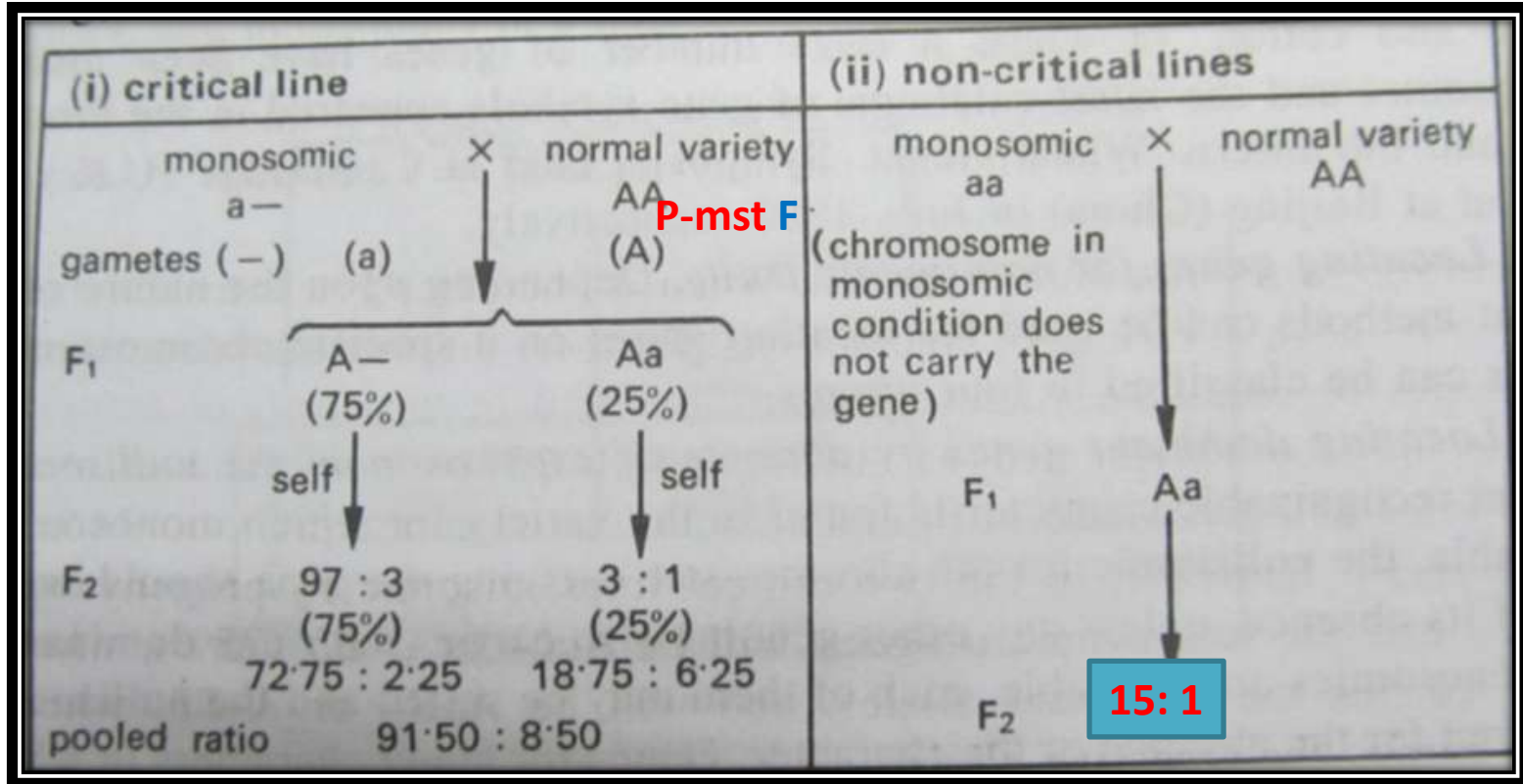
Locating recessive genes through analysis of F₂

(i) critical line	(ii) non-critical lines
<p>monosomic $a-$ × normal variety AA</p> <p>gametes $(-)$ (a) (A)</p> <p>F_1</p> <p>$A-$ (75%) Aa (25%)</p> <p>self ↓ self ↓</p> <p>F_2</p> <p>97 : 3 (75%) 3 : 1 (25%)</p> <p>72.75 : 2.25 18.75 : 6.25</p> <p>pooled ratio 91.50 : 8.50</p>	<p>monosomic aa × normal variety AA</p> <p>(chromosome in monosomic condition does not carry the gene)</p> <p>F_1 Aa</p> <p>F_2 3:1</p>

Monosomic analysis of genic male-sterility in hexaploid wheat

- In most of the crops male sterility is controlled by recessive nuclear gene *ms*
- Recently a novel genic male-sterility was reported by Singh (2002) where the male-sterility was incomplete, therefore, it was designated as p-mst (partial genic male sterility)
- In the present study, an attempt has been made to locate *ms* gene on specific chromosome of partial genic male sterile (p-mst) strain.
- **Material & methods**
- The partial genic male-sterility strain of *T. aestivum* (2n=42) from the Department of Genetics, IARI, New Delhi (full awning, single gene dwarf, late maturing, resistant to stem and leaf rusts of wheat. It produces 10 to 12% selfed seeds)
- The 21 aneuploid lines of cv. Chinese Spring used were originally produced by Sears (1954) (awnless and susceptible to rusts)

Contd..



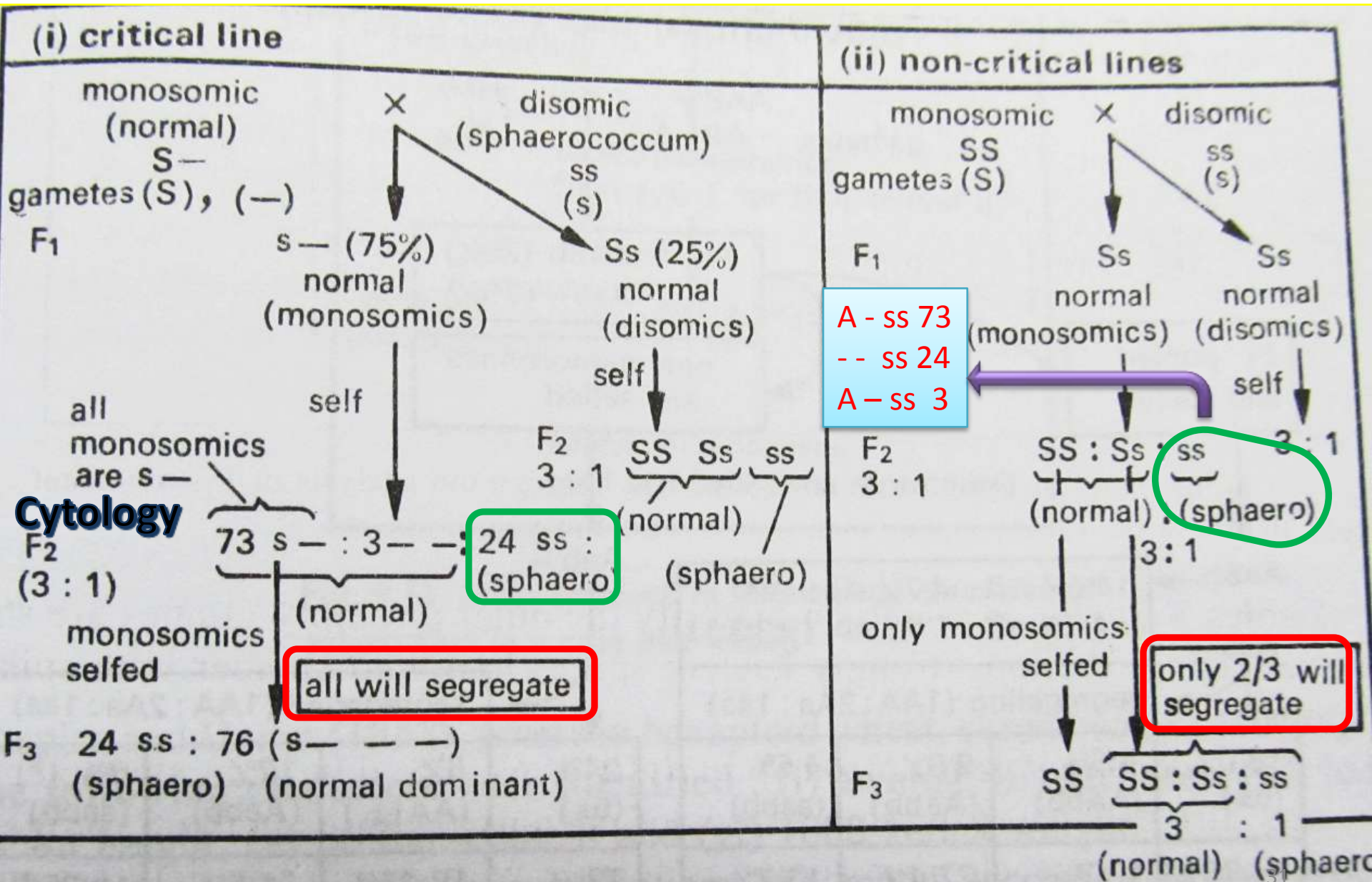
Result

- All the 21 monosomic F_1 hybrids produced less number of seeds per spikelet than disomic F_1 hybrid
- A good fit to a ratio of 15 fertile: 1 sterile was obtained in the F_2 's of the disomic cross (control) as well as in the 19 families of the monosomic F_2 's. In crosses involving chromosomes 4A and 6B expected digenic segregation was not observed.

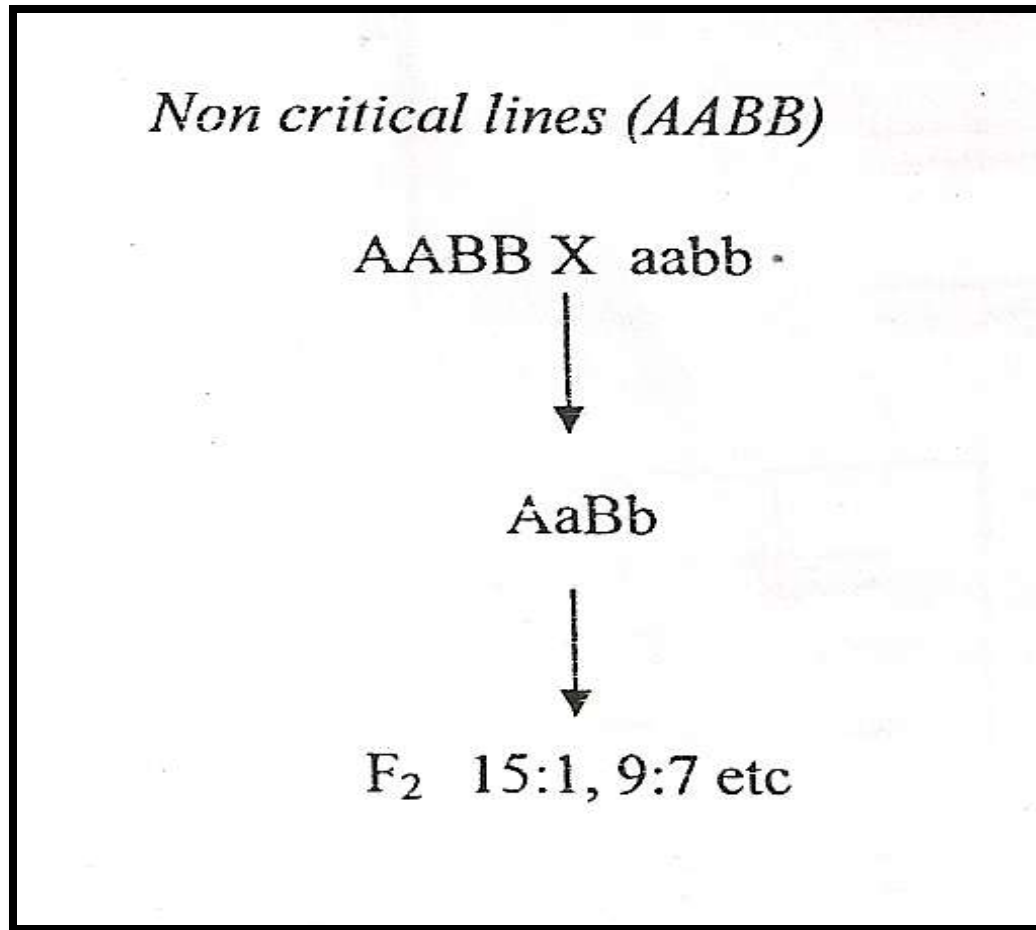
conclusion

- Location of gene for mst trait on chromosome 4A confirms the finding of Driscoll (1975) and Kleijer and Fossati (1976) where *ms* genes of Pugsley and Probus mutants were located, on chromosome 4A.
- Location of another gene for mst trait on chromosome 6B, is in support of the findings reported by Sears (1954)

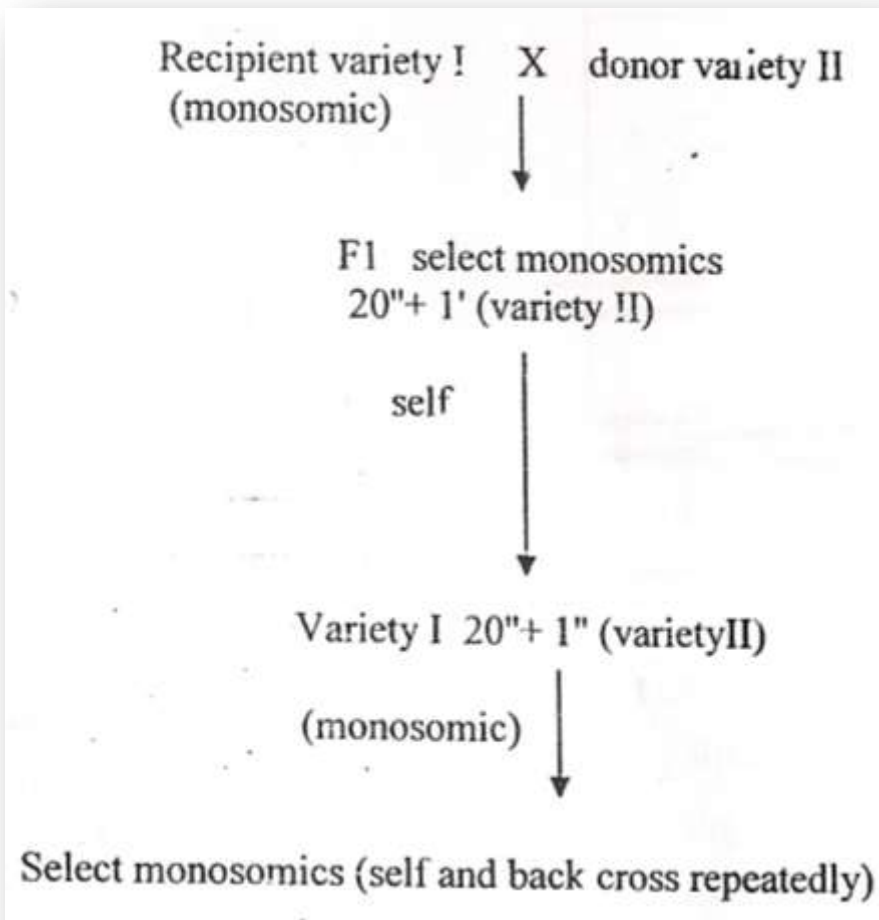
Locating hemizygous ineffective genes through analysis of F₃



Use of monosomic analysis in locating genes to chromosomes for digenic trait

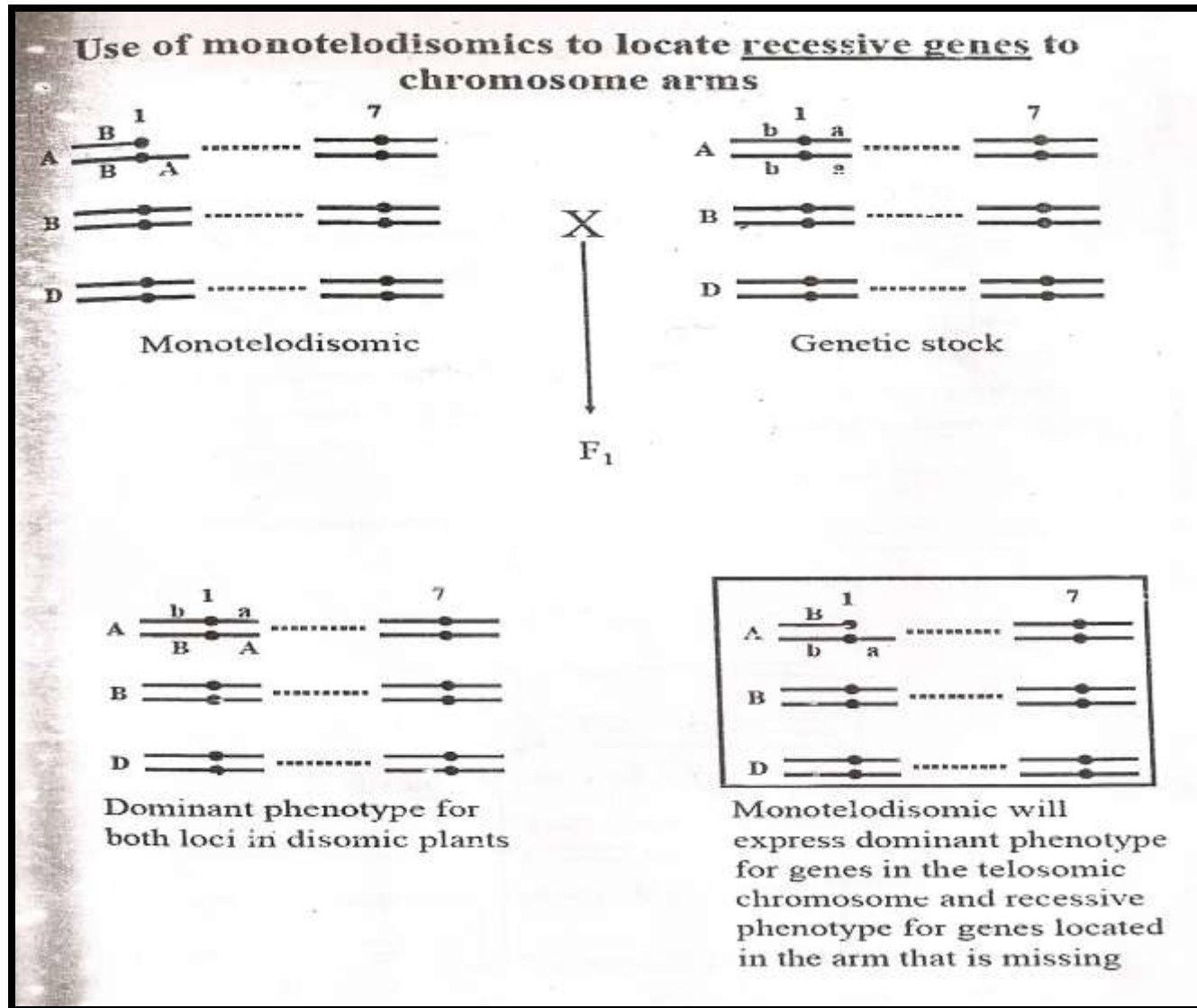


locating genes through inter-variatal chromosomal substitutions

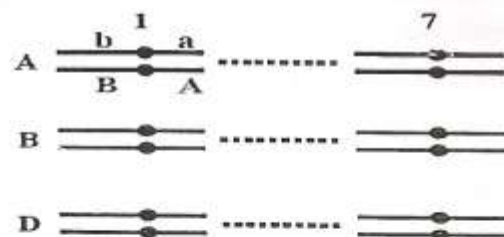
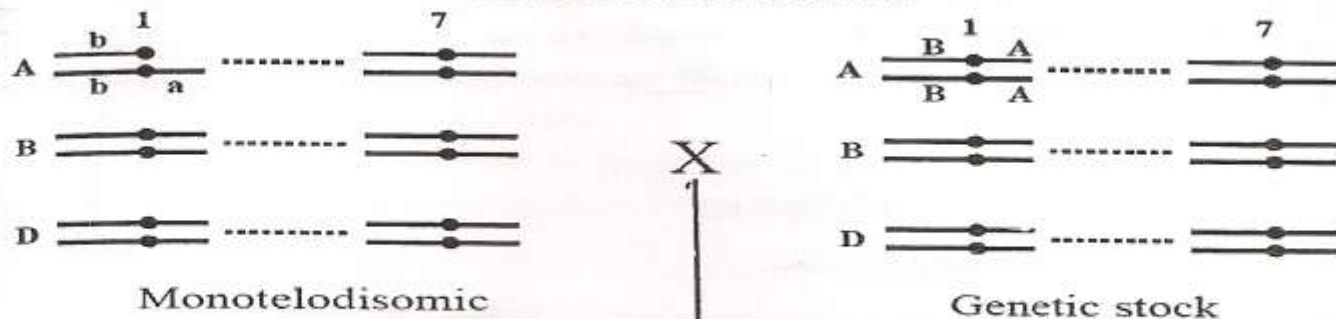


- If substitution leads to major change in the morphology for the character under investigation, gene(s) for these characters are present on these chr.
- Kuspira and Unrau (1957); identified genes for awning, earliness, lodging, plant height, protein content and 1000 kernel wt.

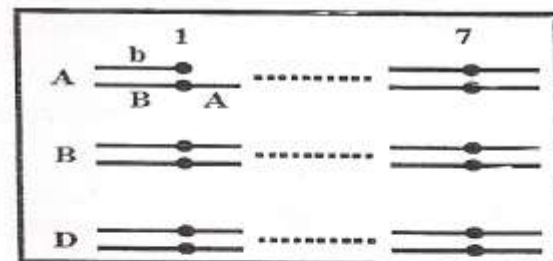
Locating genes on chromosome arms



Use of monotelodisomics to locate dominant genes to chromosome arms



- ✓ Dominant phenotype for both loci in disomic plants.
- ✓ F_2 will segregate 3:1.



- ✓ Dominant phenotype for both loci in monotelodisomic plants.
- ✓ F_2 will not segregate for the gene located on the missing arm.

Monosomics in diploids

- Chr. 4- *Drosophila melanogaster*
- X - human being
- *Datura stramonium*
- *Nicotiana glauca*
- *N. longsdorfii*
- *Solanum lycopersicon*
- *Zea mays*

Most of the cases, monosomic condition was not transmitted to progeny

Monosomics in diploid obtained by-

- Rare monosomics in the progeny of normal diploid
- Mutation treatment
- Progeny of aneuploids, haploid and polyploids
- Interspecific cross
- Progeny of specific genetic system (Maize)

Monosomics in human

Monosomy X (Turner Syndrome) (

Monosomy X (Turner Syndrome) is a karyotypic condition caused by non-disjunction of **X** chromosomes at **Meiosis I or II**. Frequency is 1 in 5000 female births

Symptoms

Short stature

Fold of skin

Shield shaped thorax

Constriction of aorta

Widely shaped nipples

Poor breast development

Elbow deformity

Rudimentary ovaries

Brown spots

Small finger nails

Monosomics for all human autosomes die in utero

Thank you