

Use of monosomic analysis to locate recessive genes to chromosomes

- ✓ Cross as female a set of 21 monosomic stocks that have the dominant allele with the homozygous recessive stock (aa).

Noncritical

$2n-1 (AA) \times 2n (aa)$
↓
 Aa

Critical monosomic

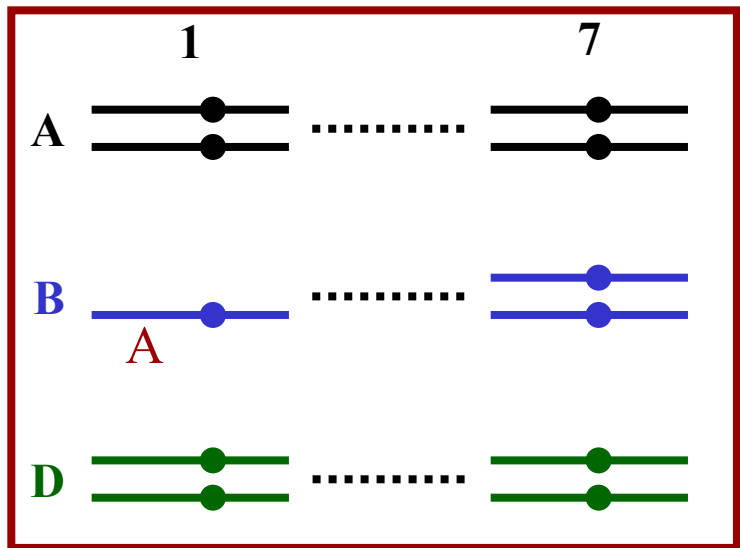
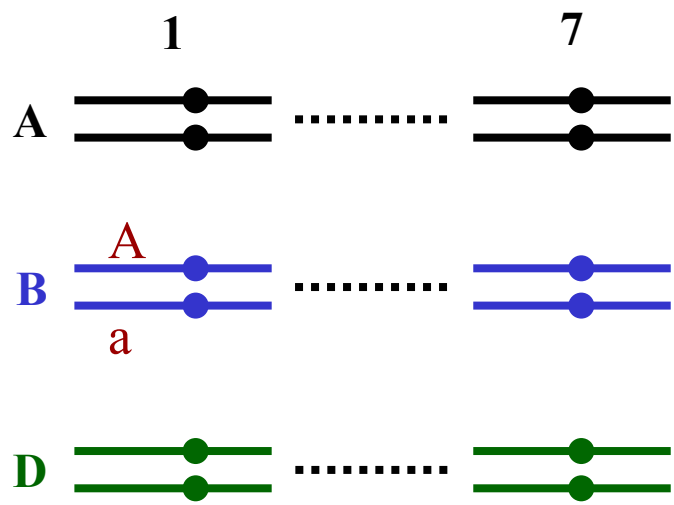
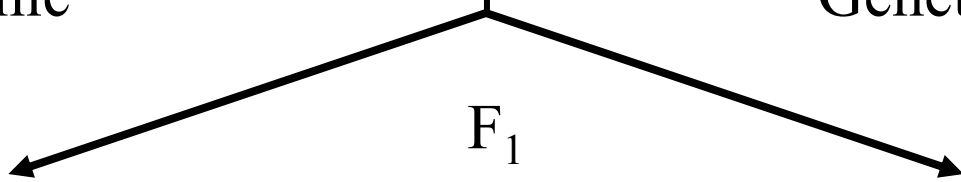
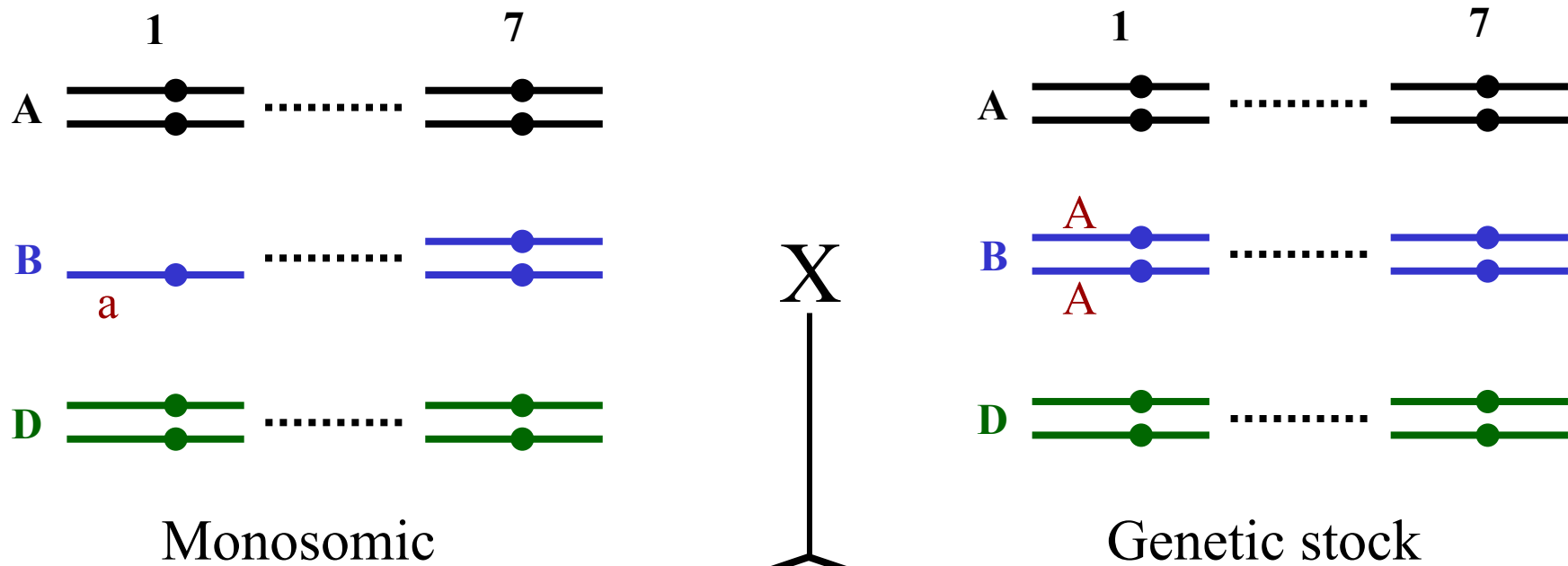
$2n-1 (A_) \times 2n (aa)$
↓
 $2n (Aa) \quad 30\%$
 $2n-1 (a_) \quad 70\%$

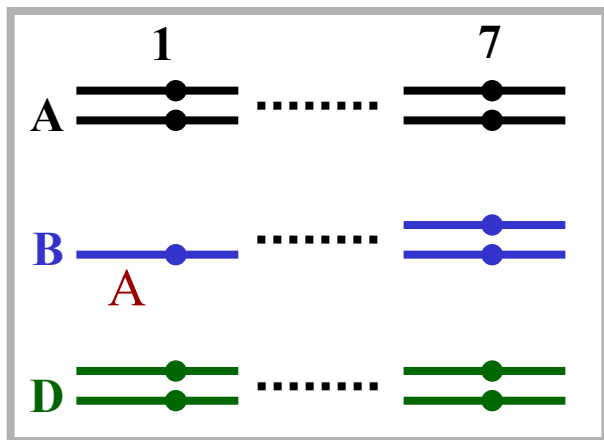
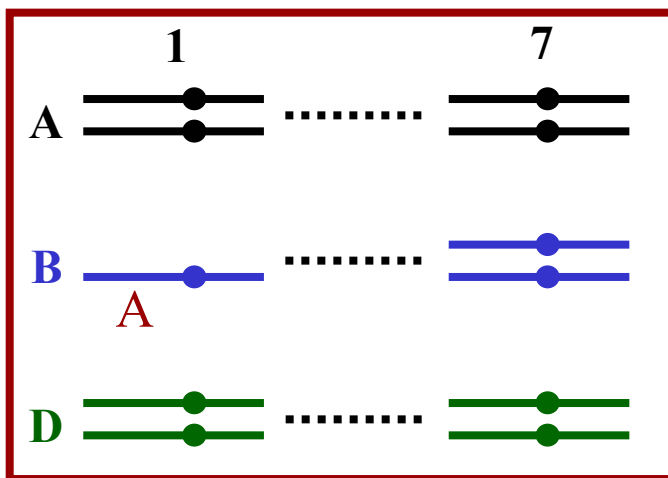
Use of monosomic analysis to locate recessive genes to chromosomes

- ✓ **Cross as female a set of 21 monosomic stocks that have the dominant allele with the homozygous recessive stock (aa).**
- ✓ **If a recessive gene is not associated with a monosomic chromosome, all of the progeny will express the dominant phenotype.**
- ✓ **If the gene is associated with the monosomic chromosome, the monosomic progeny will express the recessive phenotype due to the absence of the dominant allele.**

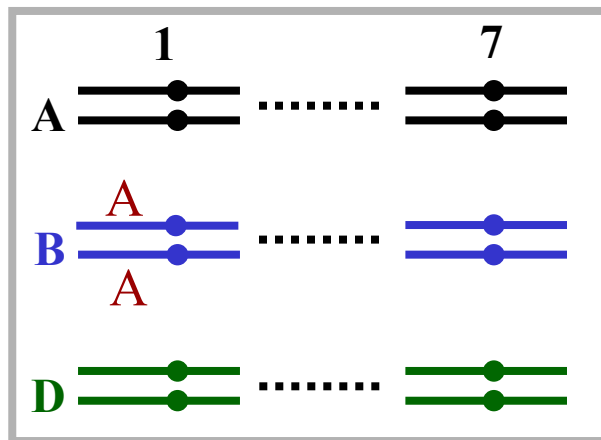
Use of monosomic analysis to locate dominant genes to chromosomes

- ✓ Cross as female a set of 21 monosomic stocks that have the recessive allele with the homozygous dominant stock (AA).
 - All F_1 progeny will express the dominant phenotype.
- ✓ Identify monosomic F_1 plant cytologically.
- ✓ Grow F_2 populations from monosomic F_1 plants.
 - Populations from disomic plants may be grown as control

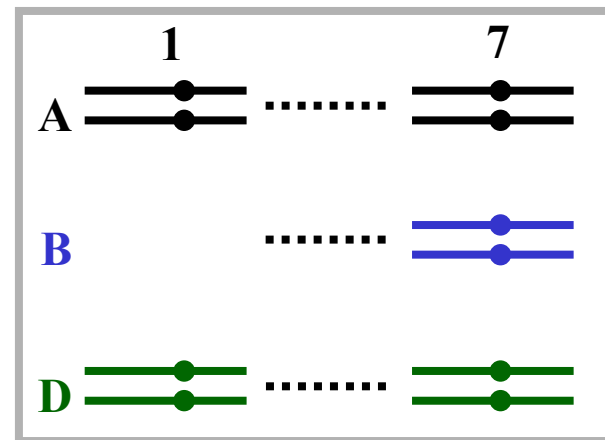




25%



70%



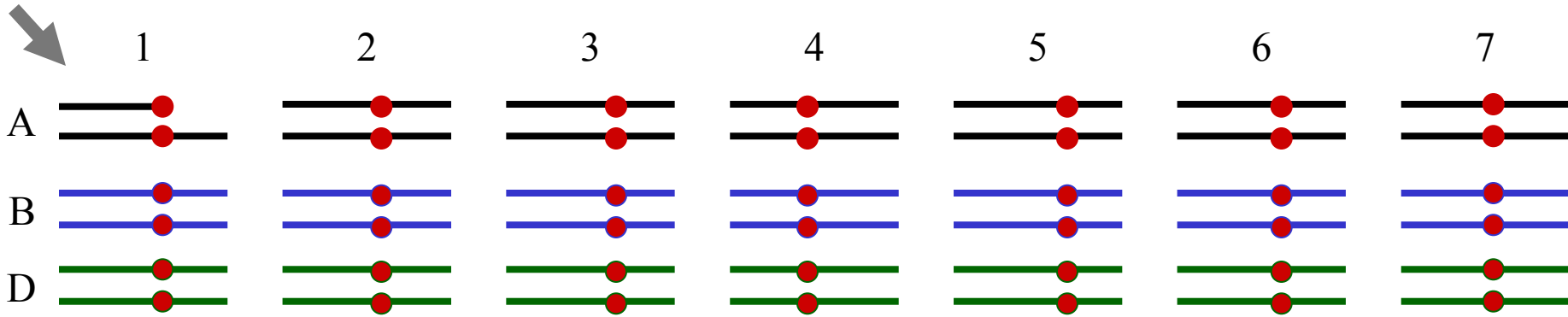
5%

Use of monosomic analysis to locate dominant genes to chromosomes

Expected Outcome:

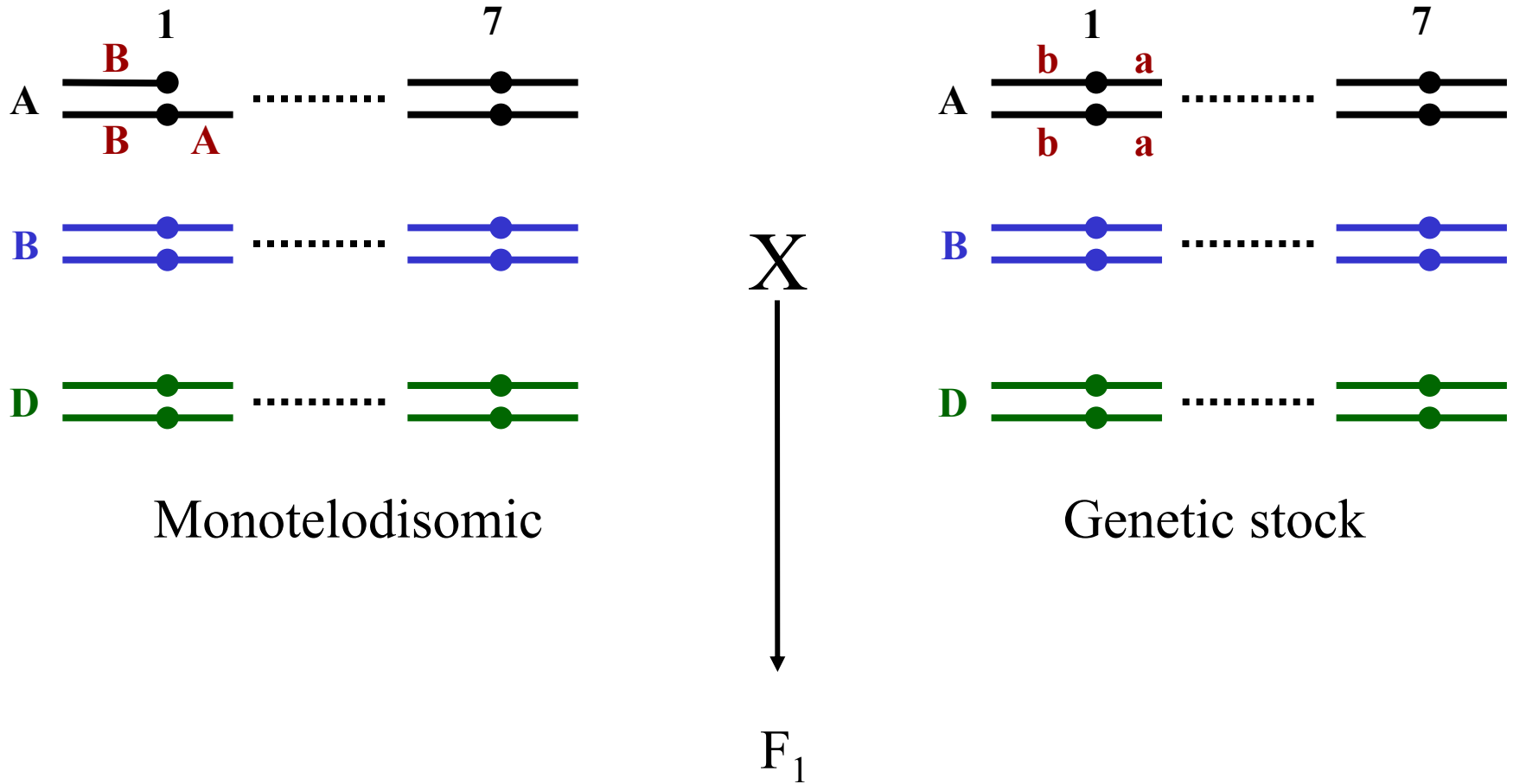
- ✓ Noncritical F2 families segregate 3 dominant : 1 recessive phenotypes and will fit a 3:1 ratio when tested with a chi square test.
- ✓ The critical F2 family will produce no recessive phenotypes except for nullisomics that result from the transmission of an n-1 gamete transmitted through the pollen uniting with a female n-1 gamete.
 - The segregation of critical F2 family will deviate from the expected 3:1 ratio indicated by the chi square test.
- ✓ Recessive individuals in the critical family indicate the frequency of nullisomics

Monotelodisomics ($2n=20''+1t''$)

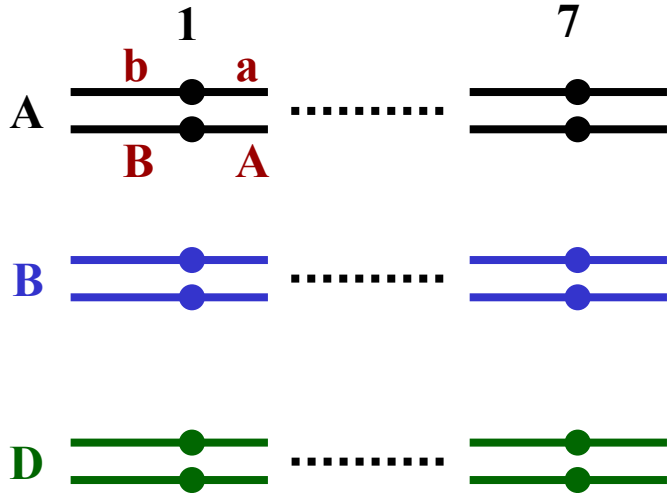


After a gene has been located to a specific chromosome, its arm location can be determined by the use of monotelodisomics for either of the two arms.

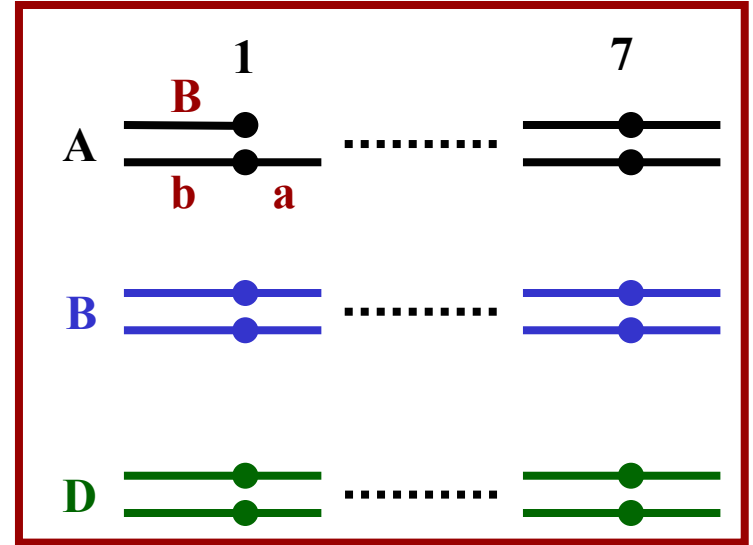
Use of monotelodisomics to locate recessive genes to chromosome arms



F₁

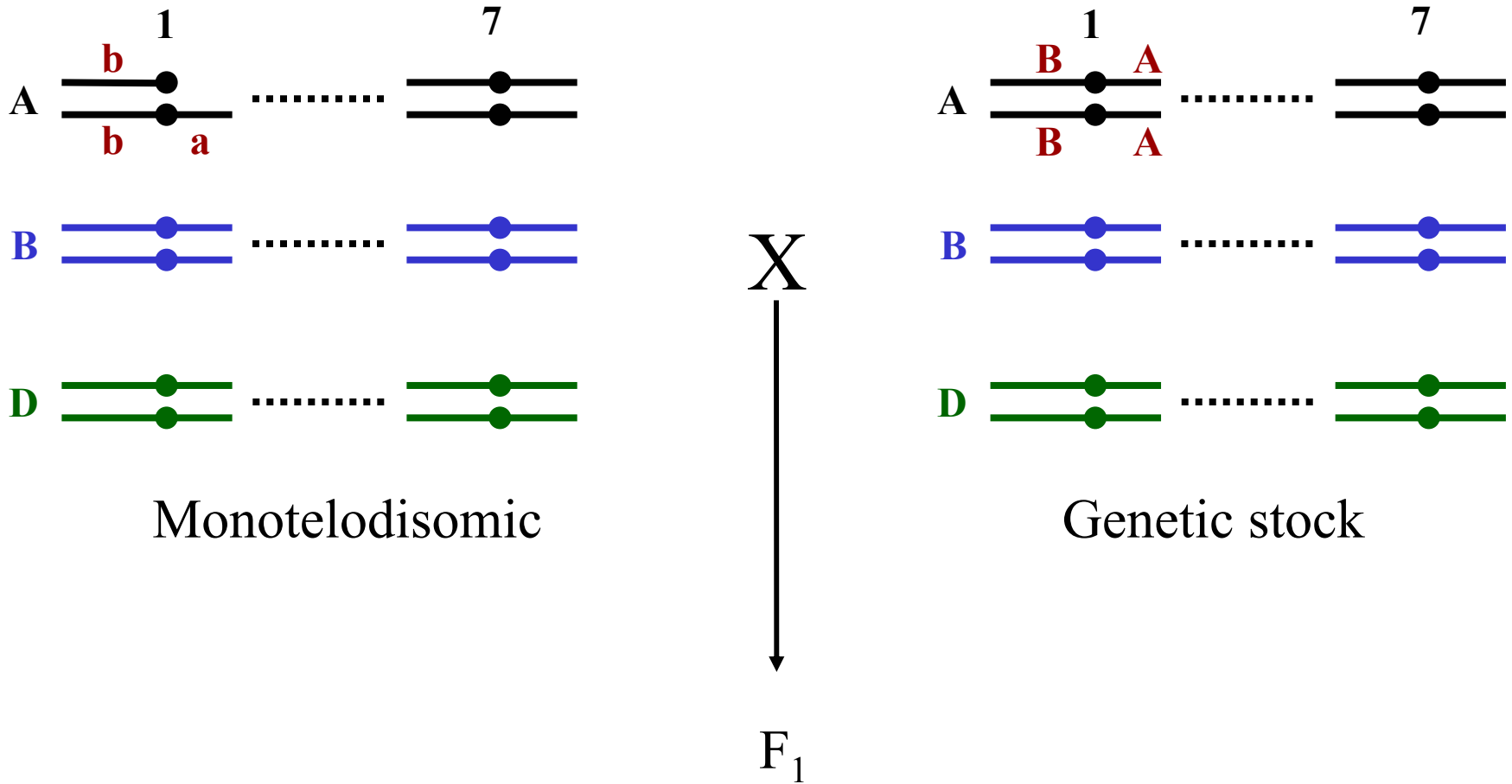


Dominant phenotype for both loci in disomic plants

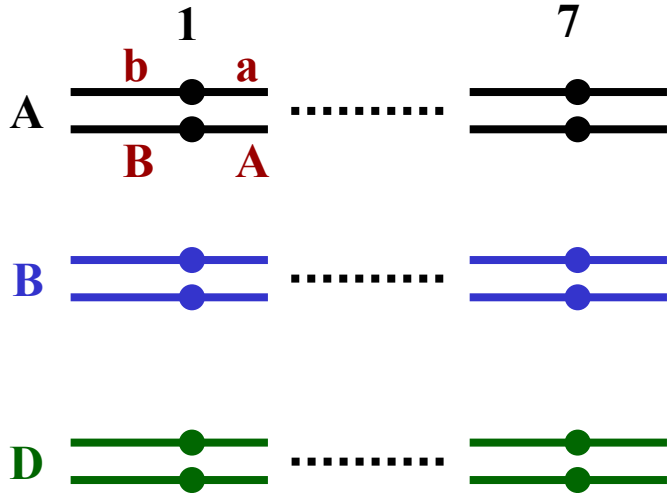


Monotelodisomic will express dominant phenotype for genes in the telosomic chromosome and recessive phenotype for genes located in the arm that is missing

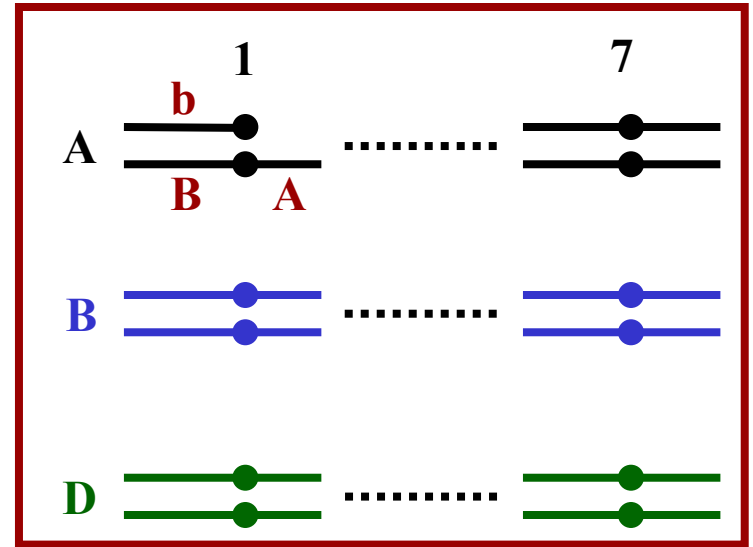
Use of monotelodisomics to locate dominant genes to chromosome arms



F₁

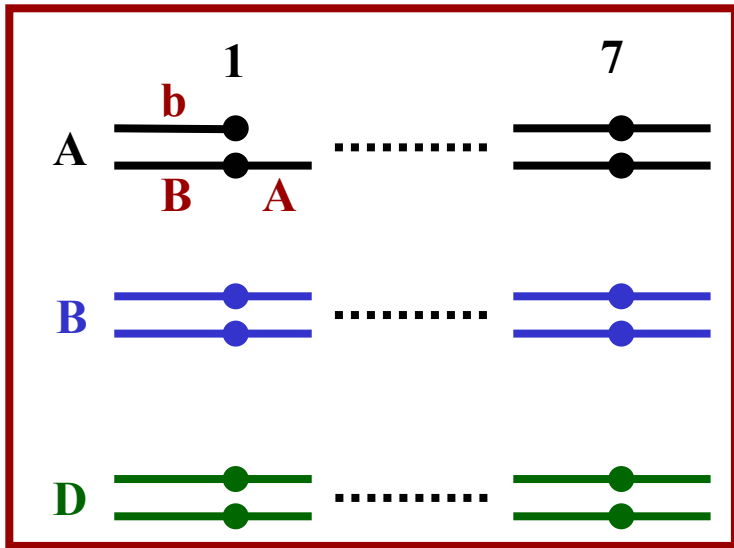


- ✓ Dominant phenotype for both loci in disomic plants.
- ✓ F₂ will segregate 3:1.



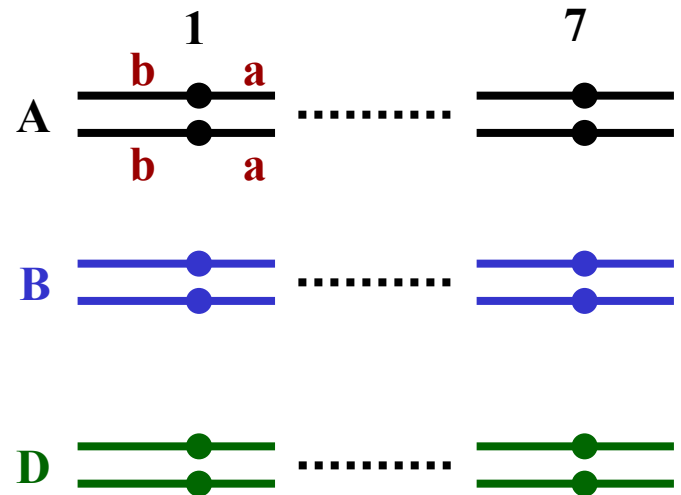
- ✓ Dominant phenotype for both loci in monotelodisomic plants.
- ✓ F₂ will not segregate for the gene located on the missing arm.

Gene-centromere distance determination using monotelodisomics



Heterozygous monotelodisomic

X



Homozygous recessive stock

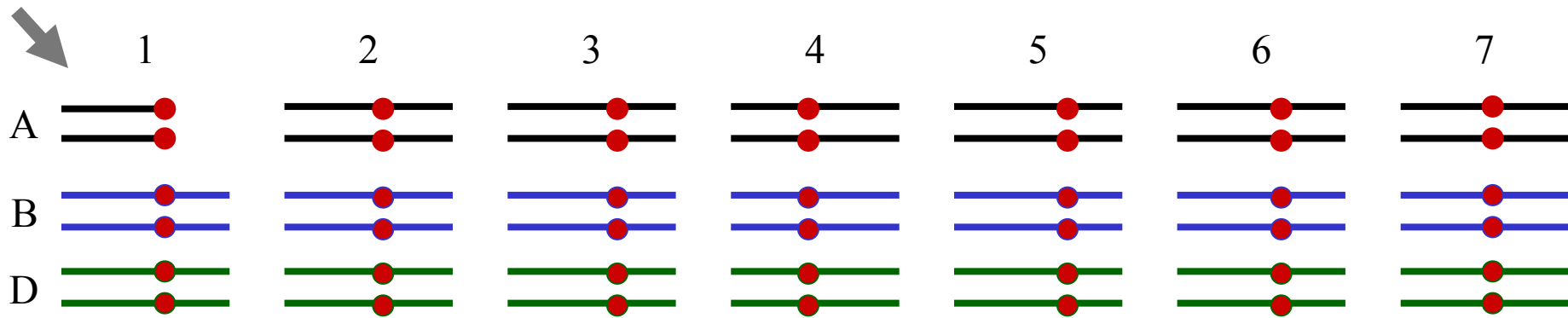


Parental class at 1:1



Recombinant class

Ditelosomics ($2n=20''+t''$)

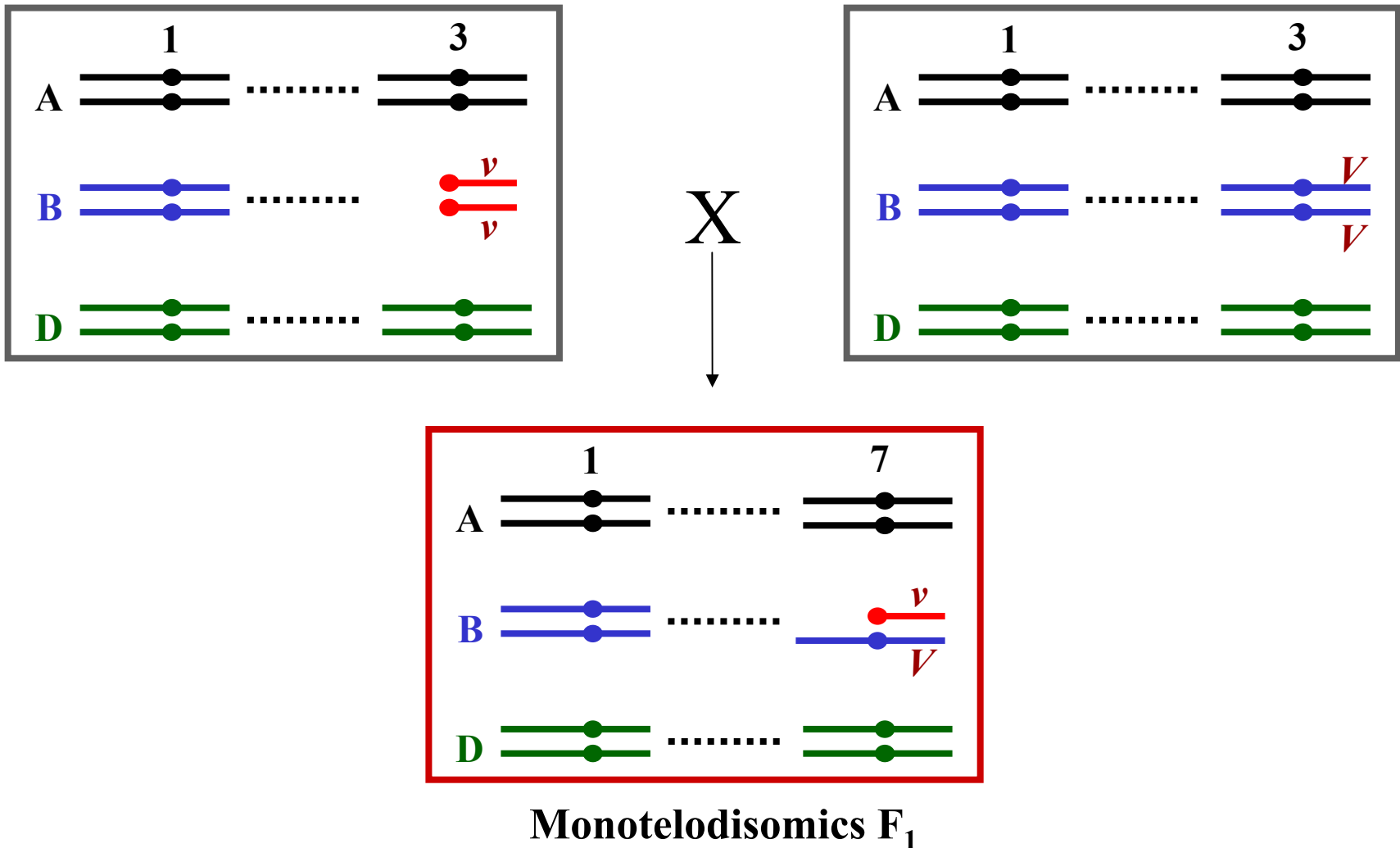


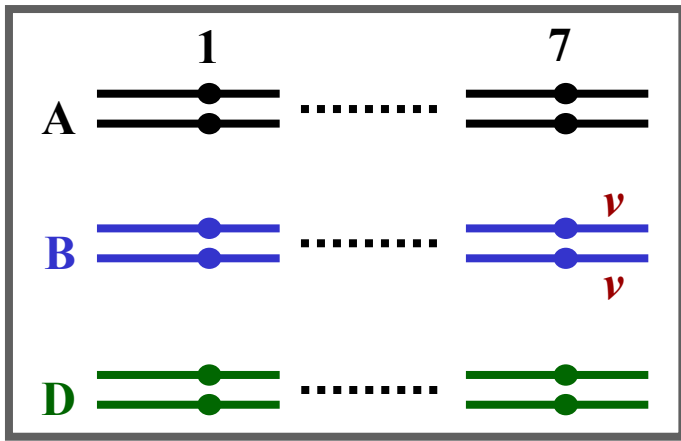
Use of telocentrics to determine the distance of a gene from the centromere

Sears, E.R. 1966. 2nd Intl. Wheat Genet. Symp. Pp. 370-381.

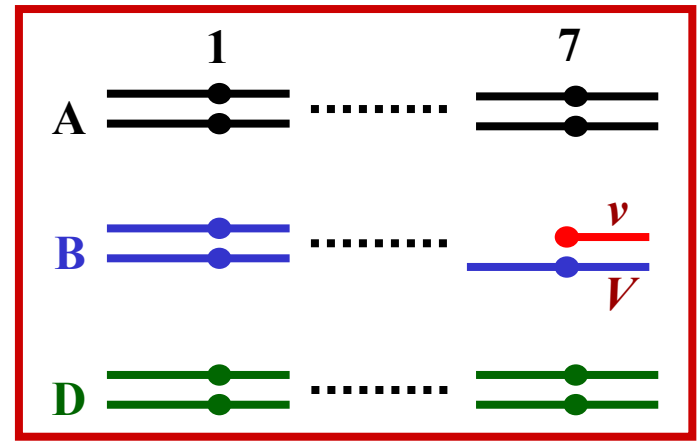
Use of telocentrics to determine the distance of a gene from the centromere

Sears, E.R. 1966. 2nd Intl. Wheat Genet. Symp. Pp. 370-381. (Neatby's virescens on 3B)





X



Monotelodisomics F_1

- ✓ Transmission of the telocentric through the pollen is expected to be low, resulting in very few virescent progeny if v is close to the centromere
- ✓ Assuming no transmission of the telocentric and/or no crossing over between the gene and the centromere, there would be no virescent progeny

Progeny of the monotelosomic backcross to *vv*

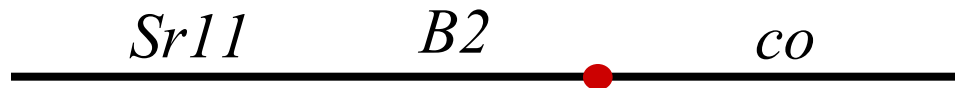
# of Progeny	Phenotype	Male Gametes		
		Genotype	Chromosome Type	Crossover
333	Green	<i>V</i> (or $_$)	Entire or none	No
16	Virescent	<i>v</i>	Telocentric	No
9	Virescent	<i>Vv</i>	Entire + Telo.	No
1	Virescent	<i>v</i>	Entire	Yes

359

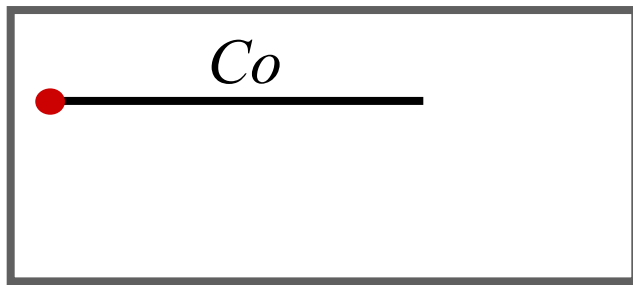
- ✓ 9 virescent plants received both the telocentric v and the normal chromosome V through the pollen resulting in Vvv genotype that produces virescent phenotype
- ✓ 16 virescent telocentrics which must be omitted because if crossover telocentrics were transmitted, they would be green plants and overlooked ($359-16 = 343$)
- ✓ Only one plant produced a virescent phenotype and received the normal chromosome through the pollen indicating crossing over between the gene and the centromere

$1/343 = 0.29\%$ recombination between the gene and the centromere

Linkage studies using telocentrics (Chromosome 6B)

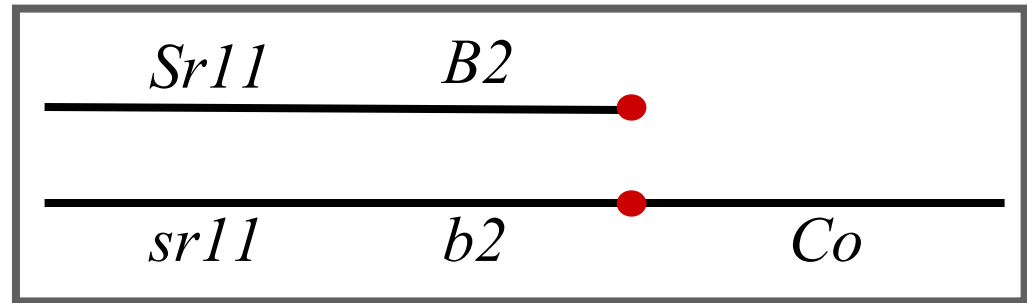


- ✓ *co* (corroded) located on 6BS and produces necrotic patches on the leaves
- ✓ *B2* located on 6BL and is a major awn inhibitor
- ✓ *Sr11* located on 6BL and confers stem rust resistance



Monotelosomic

X



Monotelodisomic

- ✓ All female gametes are deficient for 6BL, and are effectively *b2* and *sr11*
- ✓ About 75% of the female gametes are completely deficient for 6BS and are effectively *co*
- ✓ Pollen carrying 6BL would give rise to corroded plants except for the 25% that receive *Co* from the female

Progeny from the monotelosomic X monotelodisomic cross

# of plants	Constitution of male gamete	Region of crossover
126	<i>sr b2 Co</i>	None
99	<i>Sr b2 Co</i>	<i>Sr – B2</i>
1	<i>Sr B2 _</i>	None
1	<i>sr B2 _</i>	<i>Sr – B2</i>
3	<i>Sr B2 _/sr b2 Co</i>	None
1	<i>Sr B2 Co</i>	<i>B2 – Centromere</i>

- ✓ Six awnless segregants (*B2*) were observed
 - Two of these had the corroded phenotype and thus carry the parental telocentric
 - Three of the remaining four had both parental chromosomes and were considered noncrossovers
 - One plant had the normal chromosome and was a crossover

Crossover value: $B2 - \text{Centromere} = 1/231 = 0.44\%$

$Sr11 - \text{Centromere} = 101/231 = 43.7\%$