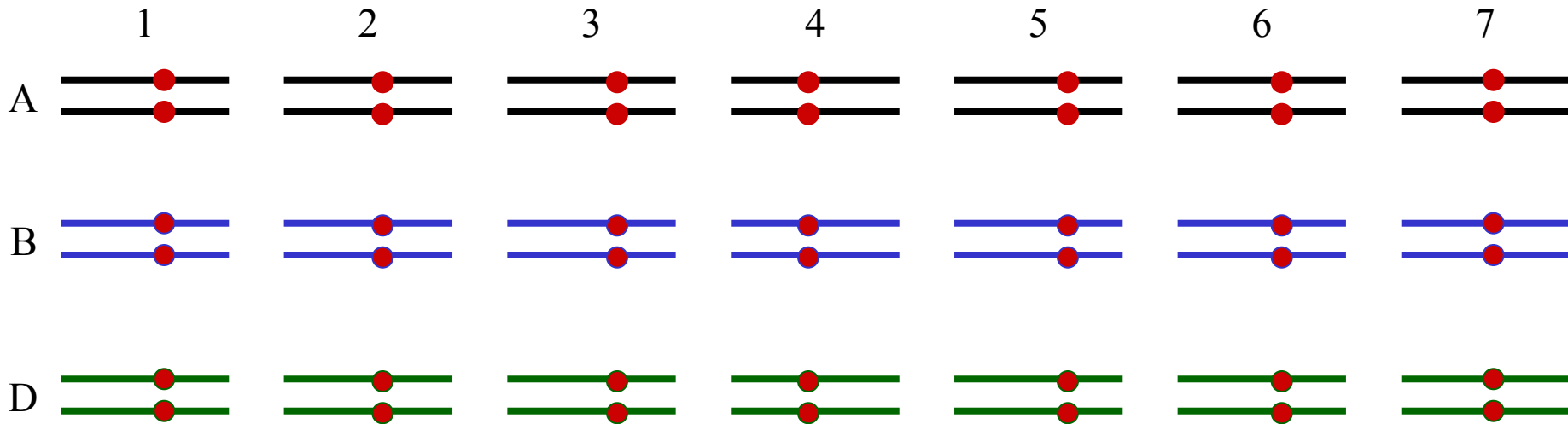


Aneuploids of Allopolyploids

- *Triticum aestivum* (bread wheat) is an allohexaploid ($x=7$, $2n=42$) and its three genomes are designated A, B, and D.
- Each genome contains 7 chromosomes.
- The evolution of the three genomes has been traced to specific wild diploid species:

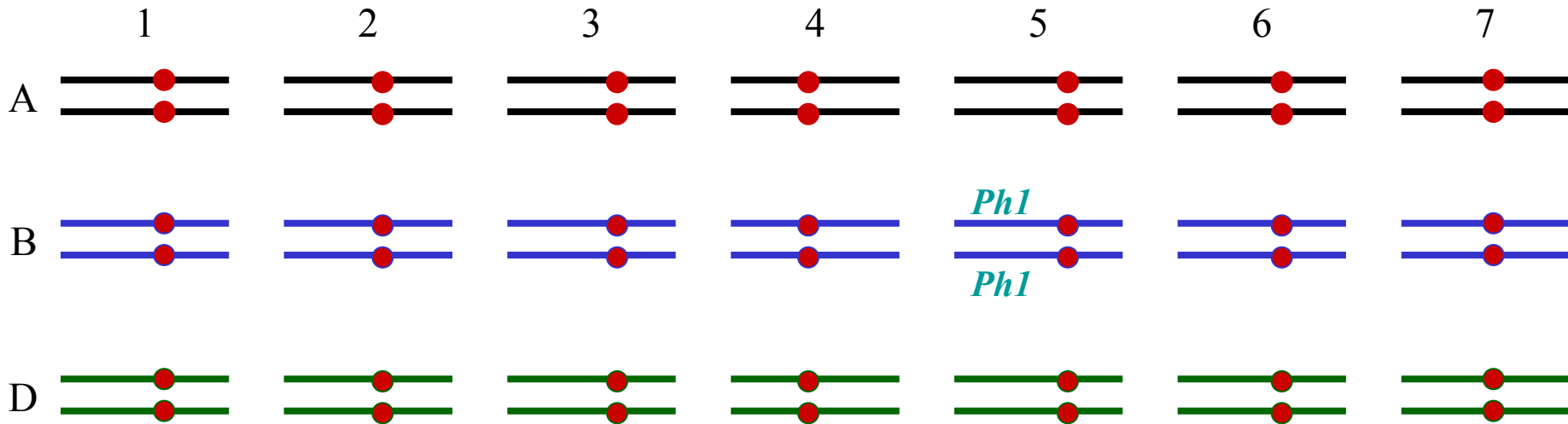
A	→	<i>T. monococcum</i>
B	→	<i>T. speltoides</i> (??)
D	→	<i>T. tauschii</i>

Aneuploids of Allopolyploids



- Only bivalent pairing occurs with no homoeologous pairing even though the homoeologous groups have considerable homology.
- Gametes with 21 chromosomes are regularly produced.

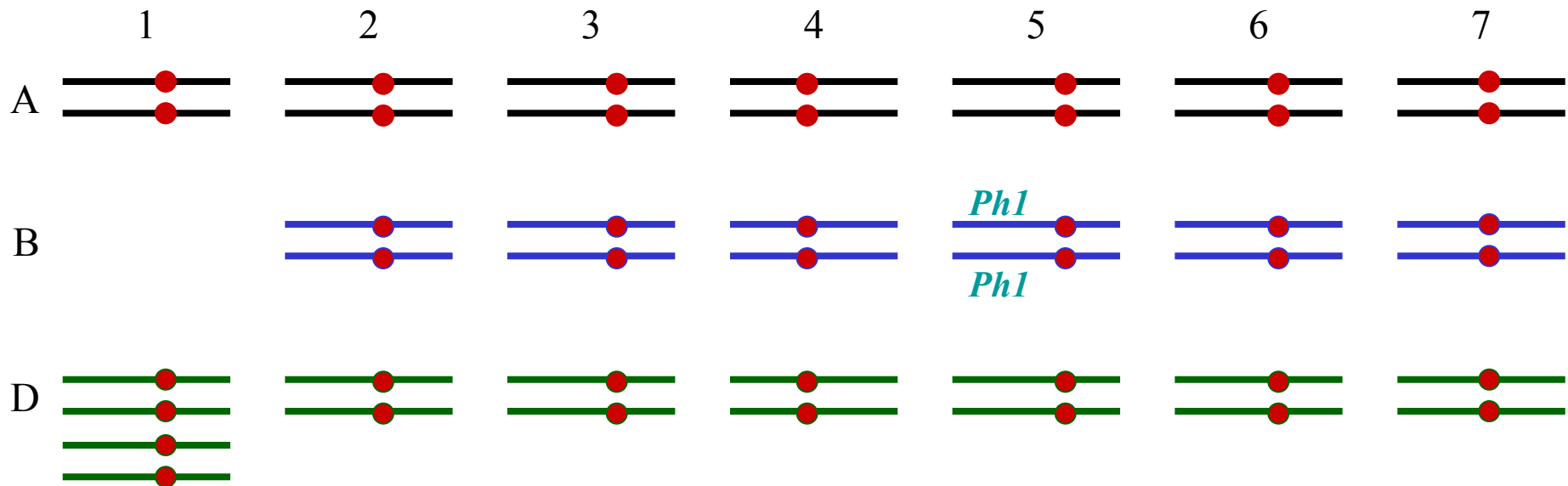
Aneuploids of Allopolyploids



- Only bivalent pairing occurs with no homoeologous pairing even though the homoeologous groups have considerable homology.
- Gametes with 21 chromosomes are regularly produced.

Aneuploids of Allopolyploids

- Polyploid buffering- Homoalleles of one genome compensate for a deficiency of another genome as Sears (1939) demonstrated by nullisomic-tetrasomic compensation.



Nullisomic 1B- Tetrasomic 1D (N1B-T1D)

Aneuploids of Allopolyploids

- Monosomic plants and other types of aneuploids were identified among the progeny of wheat haploids crossed with normal bread wheat.
- The haploids occurred in the progeny of a cross between rye and a variety of wheat known as 'Chinese Spring' that was recognized as producing a higher percentage of wheat-rye hybrids than most other wheat lines.
- Nullisomics and trisomics appeared among progeny from selfed monosomics.
- Telosomics and isomics were identified in the progeny of monosomics.

Sources of aneuploids

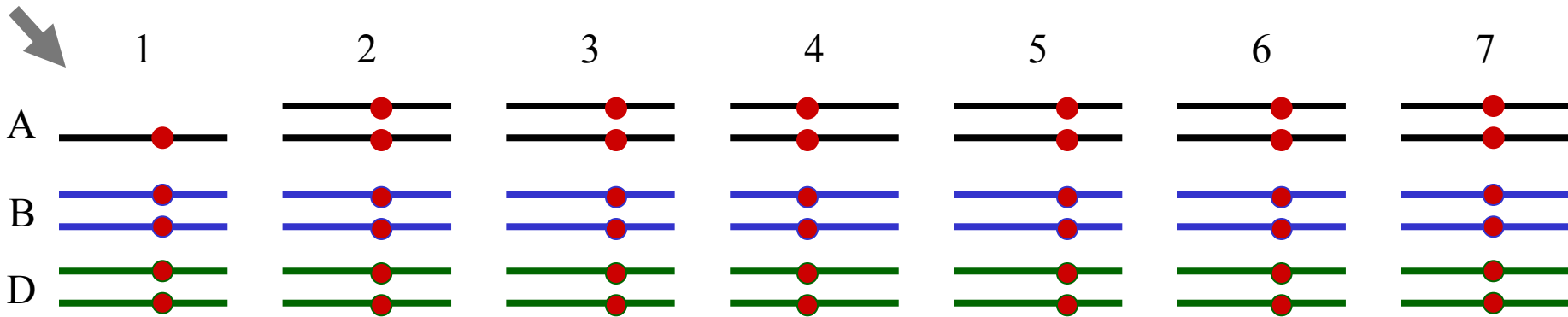
1. Spontaneous occurrence from normal $2n$ plants, usually from random segregation of a univalent.
2. From asynaptic disomics and aneuploids – meiotic mutants.
3. Haploids and other polyploids – Unequal segregation from autopolyploids ($2x \times 4x$).
4. Numerical nondisjunction from multivalent configurations may generate trisomics and monosomics – Interchange heterozygotes.

Univalent behavior

The behavior of a univalent during meiosis is of particular interest due to its effect on the rate of transmission of n vs. $n-1$ gametes.

1. Pass to one of the poles at anaphase I undivided and divide normally at the second division.
2. Lag and fail to be included in either of the anaphase I nuclei.
3. Divide equationally and sister chromatids pass to opposite poles or one or both may lag and fail to be included in telophase I nuclei.
4. Misdivide and give rise to telocentrics and isochromosomes which may also lag or become included in one of the sister halves.

Monosomics ($2n-1$)



Expected ratios of $2n:2n-1:2n-2$ progeny from selfing a monosomic if gametes are transmitted through male and female are 50% n and 50% $n-1$

	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 ($2n-2$)

Monosomics (2n-1)

% n vs. n-1 spores produced by wheat monosomics

n	n-1	other	Authority
30.0	62.0	8.0	Morrison (20 monos)
35.6	64.4		Bhowal (mono 3D)

Monosomics ($2n-1$)

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% ($2n-2$)

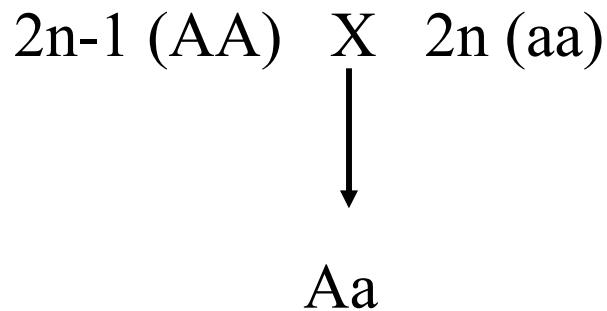
Monosomics ($2n-1$)

- Most wheat monosomics produce $<10\%$ nullisomic F_2
- Wheat (AABBDD) produces 57.3 to 81.9% $n-1$ spores
- Oat (AACCCDD) produces 85 to 100% $n-1$ spores

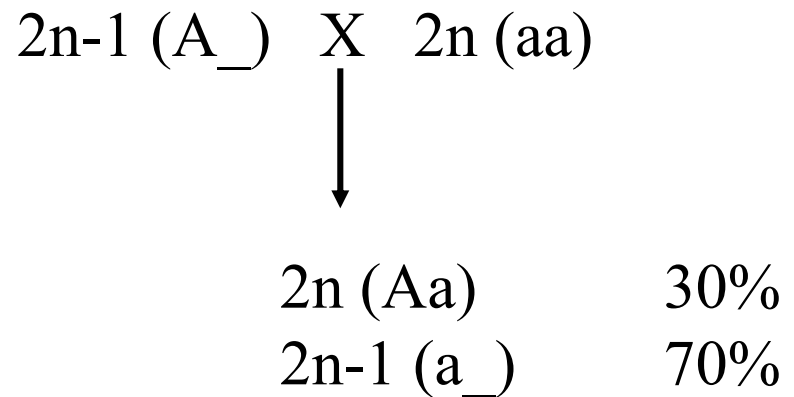
Use of monosomic analysis to locate recessive genes to chromosomes

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

Noncritical



Critical monosomic



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 populations

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

