

Meiosis I

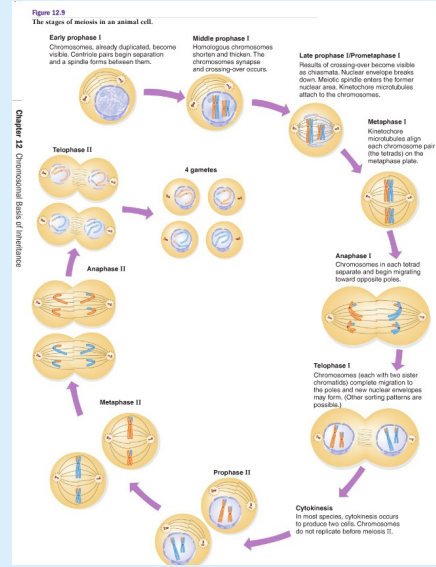
Prophase I Chromosomes condense, 2N
homologous pairs align, **synapsis** (precise alignment, ensures 1 copy of each gene in a daughter cell). Synapsed set called a **tetrad** (4 chromatids). Then, **crossing-over** occurs (exchange of chromosome segments between pairs of *homologous* chromosomes, or *nonsister chromatids*). **Chiasma** forms, visible structure from crossover. X and Y chromosomes pair and synapse thru terminal ends (**PARs**).

Metaphase I Nucleoli and envelope 2N
broken down, centrioles w/ spindle enternuclear area, *kinetochore microtubules* attach to sister kinetochores, tetrads align at *metaphase plate*.

Anaphase I Chromosomes of tetrad 2N-
separate (now **dyads**). N
Sister chromatids remain attached at centromeres. *DNA content is halved.*

Telophase I Spindles disassemble, N
cytokinesis forms two **haploid** cells.

Meiosis



Meiosis II

Prophase II Chromosomes condense and spindles form, kinetochores attach to tubules..

Metaphase II Alignment on metaphase plate.

Anaphase II Centromeres separate, daughter chromosomes (still haploid) pulled to opposite sides.

Telophase II Chromosomes decondense, nuclear envelope forms, cytokinesis. *Four haploid cells produced, each with one chromosome from each homologous pair.*

Meiosis Results

♥ Generates *haploid* nuclei with *half* the number of chromosomes found in diploid cell. (2N -> N) Diploid number restored in fertilization.

♥ **Independent assortment of genes**
paternal and maternal chromosomes have an equal chance of aligning on one side of metaphase plate.

♥ Number of chromosome arrangements is 2^{n-1} , n = # chromosomes pairs (haploid number).

♥ Number of chromosome combinations resulting from *independent assortment* is 2^n (number of different *gametes*).

♥ Number of *kinds* of genotypes is 3^n .

Ploidy

Haploid ONE copy of each chromosome. (N)

Diploid TWO copies (homologues) of each chromosome. (2N)

Homologous pairs Same gene loci, structure, and pair during meiosis.

Genes

Allele Alternative forms of a single gene on the same locus that determine the same trait, but can produce different phenotypes.