

# **Lesson 03: Haploid genetics**

# **1. Haploid organism**

A biological cell is haploid when the chromosomes it contains are each in a single copy (n chromosomes). These definitions only apply to eukaryotic organisms (protists, animals, plants and fungi), which have real chromosomes.

Most haploids are lower eukaryotic species, so there are several advantages to studying them:

- The genotype is expressed directly as a phenotype (set of genetic materials)
- All the products of a single meiosis can be studied
- These organisms are easy to grow, and a large number of offspring can be produced from a single cross.
- The aim of studying these organisms is to determine the distance between two genes or between a gene and a centromere.

# **Examples of haploid organisms**

- *Sordaria macrospora* is a species of ascomycete fungus. The mycelium of this fungus is haploid. The mycelial filaments produced by spore germination are made up of rows of cells with n=7 chromosomes in the nucleus.
- The ascomycete fungus *Neurospora crassa*, with spores arranged in asci.
- The ascomycete fungus, the yeast *Saccharomyces cerevisiae*, whose spores are not aligned in the asci.
- *Chlamydomonas reinhardtii*  unicellular algae

# **2. The vital development cycle**

The 2 organisms have two different ways of reproducing:

- **Asexual reproduction**: occurs through the cell division mechanism known as **mitosis.**
- **Sexual** reproduction**:** this requires the fusion of two cell types of opposite sign

These haploid organisms therefore have a haplobiontic or haplodiplobiontic development cycle.



Tetrad analysis is used to locate genes in fungi and unicellular algae.

In haploid organisms, the **gametes** are the **ascospores** and the **haploid mycelia**  derived from them. Their morphological or biochemical characteristics are directly observable:

The haploid phase (ascospores + mycelium) can be observed using the tetrad analysis technique, which identifies the characteristics of each of the four gametes (tetrad) resulting from an individual meiosis.

# **3. Segregation of a monogenic trait in haploid organisms**

# **a. Tetrad analysis**

The order of the spores in the ascus corresponds to the position of the chromatids at

meiosis.

- A distinction can be made between the segregation of alleles at the first or second division of meiosis
- Crossing over between the gene and the centromere leads to segregation at the second division of meiosis.
- The number of post-reduced asci is a function of the centromere gene distance
- In haploid organisms, it is only possible to calculate the distance between a gene and a centromere by analysing ordered tetrads in N. Crassa, but this is impossible in the case of non-ordered tetrads in yeast.

### **b. Example**

A strain of Sordaria with white spores is crossed with a strain of Sordaria with black spores. Observe the results of the cross by classifying the different types of asci present in the perithecia according to the arrangement of the spores. The spores contained in the asci are ordered. (Only asci containing 8 spores are taken into account).

### **c. Determining the distance (gene-centromere)**

The experiments show that the greater the distance between the centromere and the gene, the more frequent the crossovers:

#### If there is no crossing over

- The half-tetrades are homogeneous with a or A
- Asci are pre-reduced (segregation at 1st division of meiosis)

#### **If there was a crossing over**

-The half-tethers are heterogeneous with A and a

Asci are post-reduced (segregation at the second division of meiosis)

To determine the centromere gene distance, a mathematical formula can be used to calculate this distance, which depends mainly on the Crossing-Over frequency  $(C.0)$ :

#### Frequency  $(C.O)$  = [Number of post-reduced asci/total asci ] X 100

Gene-Centromere distance= [(No. of post-reduced asci / 2) / total asci ] X100 We divide by two because we have two chromatids.

#### **4. Segregation of two characteristics (two genes) in haploid organisms**

In the case of 2 genetic traits, transmission is associated with the behaviour of 2 homologous or non-homologous chromosomes.

If a gene  $(A/a)$  occupies a locus on a given chromosome and a gene  $(B/b)$  occupies another locus on the same chromosome, the 2 genes are said to be linked. If a gene  $(A/a)$  occupies a locus on a given chromosome and a gene  $(B/b)$  occupies another locus on another non-homologous chromosome, the 2 genes are said to be independent.

#### **4.1 Tetrad analysis**

For the two genetic characters (2 genes), meiotic analysis in haploids has made it possible to classify the asci into 3 classes, regardless of whether the genes are linked or independent:

- **1st type of ascus:** all the products with the same phenotype as the parents are products of meiosis without crossover, they are called **(Parental Ditypes) (PD).**
- **2nd type of ascus**: half of the products of meiosis have the same phenotype as that of the parents, but the other half is recombined, i.e. the result of a crossover; this type is called **(Tetra types) (T).**
- **3rd type of ascus:** No parental phenotype is observed in the products of meiosis. They have undergone two or more Crossing-Over events. They are called: **Recombinant Ditypes (RD)**

#### **4.2 Examples**







 $D<sub>2</sub>$ 

 $a<sup>1</sup>$ 

 $h<sup>+</sup>$ 



Ségrégation de deux couples d'allèles localisés sur le même chromosome au cours de la méiose.

#### · 2 crossing-over

 $b<sup>1</sup>$ 

 $a<sup>1</sup>$ 

· 2 chromatides sur 4 sont remaniées



#### **4.3 Determining the distance (gene-centromere)**

The study of the transmission of two traits in haploids has made it possible to find mathematical relationships that make it possible to determine whether the two genes are linked or not.

**1st case:** the genes (A/a) and (B/b) are on 2 different chromosomes, **the frequency of PD equals that of DR**, so the two genes are independent.

**2nd case**: the genes (A/a) and (B/b) are on the same chromosome, **the frequency of DP is too great for that of DR**, so the genes are linked.

In this case, the distance between gene and gene can be calculated using the following relationship:

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Distance Gene - Gene = [(\sum DR+\sum T/2) /total (DR+DP+T)] \times 100
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