

The genetic information is stored on chromosomes - long, densely packed molecules of DNA. Most of our cells contain two homologous sets of chromosomes - one set inherited from each parent. Because the parents themselves also have two such sets, during a meiotic cell division, gametes - either sperm or egg cells, obtain only one version of a given chromosome. This process alone leads to large genetic variability between gametes, and consequently - in the offspring, however, there's another mechanism that gets it even higher. Before being randomly segregated to the gametes, the homologous chromosomes exchange parts of their arms in an event called "crossing over". This process leads to the emergence of completely new versions of chromosomes, which carry unique sets of alleles - that is versions of genes.

Crossing over is one of the main mechanisms shaping genetic diversity, however, we still are not completely sure what determines its precise chromosomal localization. We know that the chromosomal regions where the exchange happens are not random, and some regions experience disproportionately high, or low crossing-over frequency. This phenomenon is especially important in the field of plant breeding. The frequency and localization of crossovers influence our ability to achieve and maintain favorable combinations of alleles which determine the plant's performance in terms of, for example, yield or resistance to environmental stresses. This, in turn, directly translates to the amount of food or other resources that the cultivation of such plants can provide.

In our study, we want to assess what genomic factors are associated with a variable crossing-over frequency throughout a genome of rapeseed - an important resource for oil and proteins. Using long-read DNA sequencing, we want to check whether regions that accumulate many crossing overs differ in their DNA sequence from non-recombining regions. Moreover, we aim to build a machine learning model that would allow us to predict a region's crossing-over potential, basing on its DNA sequence alone.

The results of this study may help us understand more about the crossing-over in rapeseed, and plants in general. Particularly, we hope to gain new knowledge regarding the determinants of the localization of the crossovers, which could move us closer towards more controllable use of this process in the development of new plant varieties.