

# The Wheat Genome Reference Sequence

## — HOW BREEDERS USE IT —

The availability of a reference genome for a crop helps plant breeders to speed up the development of new improved varieties

### Gene discovery

CTGCA  
TCTGA  
CTCCT  
GAGAA  
GT TCA

Plant scientists use the information provided in a reference genome sequence to identify and locate genes responsible for desirable agronomic traits (such as high yield, stress tolerance and disease resistance), isolate those genes and study how they function.

Once a gene is known, this information can – for example – be utilized to tap into the natural diversity of the crop to discover new versions of the gene with more favorable features than those found in the variety used to produce the reference sequence and use those to introduce improved traits into commercial varieties.

### Gene improvement

TGGCC  
ATTCTT  
CCCATT

The information provided in a reference genome sequence can also be used to look for modified and improved versions of the genes into mutant collections and /or create modified and improved versions by genetic engineering.

### Marker-assisted breeding



Molecular markers are easily identifiable fragments of DNA sequence that are located close to a specific gene. With a reference sequence in hands, breeders have an unlimited source of molecular markers close to or within the genes of interest.

They can use these markers to identify suitable parents containing the traits of interest for new crosses and track down the presence of the genes of interest in the descendants during the selection process.

### New varieties breeding



Ultimately, breeders use markers and genes to speed up the development of new varieties with specific characteristics such as higher yield, tolerance to a stress (heat, water scarcity, high salt content in soil) or resistant to a specific disease (such as rust diseases and Fusarium head blight disease).

