TEST BIOTECH
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Testbiotech Factsheet 02-05-2018

Differences: Genome editing and mutagenesis

There are some fundamental differences between genome editing and mutagenesis applied in conventional plant breeding that are important for risk assessment and traceability resp. identification (traceability) of the genetically engineered plants. For example, genome editing methods generally leave a specific fingerprint in the genome that can be used to identify the plants and is relevant for risk assessment. The following table lists some of the differences between genome editing and mutagenesis.

Since genome editing, especially CRISPR-Cas, is a very recent development with very little experience in practical application, these new genetic engineering techniques and the plants and animals they can create should be carefully risk assessed in each case before any decisions are made on using them in agriculture, or releasing them into the environment.

Table: Some differences between breeding resp. mutagenesis and new methods of genetic engineering

Criteria	Breeding/Mutagenesis	New genetic engineering methods / genome editing
Aims	Random mutagenesis or mutation-based breeding increases the range of genetic variations in the genome of plants within shorter periods of time than would normally be the case. The increase in genetic variation is then the starting point for selection and further crossing and selection.	Genome editing is not aiming increase the range of genetic variations in the genome. It is supposed meant to only introduce specific changes in the genome.
Depth of intervention	Methods of conventional breeding always start with the whole cell or organism and do not directly intervene in the DNA in the cell nucleus. This also applies to mutation-based breeding (mutagenesis). The plants and plant cells are exposed to stimulants that are effective from the outside.	Genetic engineering intervenes directly in plant DNA. In each case, material synthesised in the laboratory is physically inserted into the cells (DNA, RNA, enzymes).
Natural gene regulation	The results of mutagenesis are dependent on various factors. These include the kind of stimulant used to trigger the mutations, as well as cell mechanisms such as gene location, repair mechanisms and other elements of gene regulation.	The desired effects can be achieved through bypassing natural gene regulation and rules of inheritance.

Criteria	Breeding/Mutagenesis	New genetic engineering methods / genome editing
Patterns of genetic change in the genome	Plants in particular often have a redundant genome i.e. genetic information that is repeated. Methods of conventional and mutation-based breeding do not generally change all gene sequences with the same genetic information at the same time.	Sequences / gene clusters with the same genetic information are all changed at the same time.
Epigenetics	There are some specially preserved areas in the genome in which there is either no, or rarely, any natural mutation, and which are only slightly affected by evolutionary processes. This applies to genes that are crucial for the survival of the organism and the stability of the species.	Even the specially preserved areas in the genome can be accessed and changed by using CRISPR-Cas. Whereby efficacy can be variable in each case.
Repair mechanisms in the genome	Original gene sequences often still exist alongside the newly mutated versions. These can serve as templates for repair processes.	If DNA changed by CRISPR-Cas technology is changed back to its original status by cell repair mechanisms, the nuclease will again recognise its target region and stay active until all the original DNA structure has been destroyed.
Multiple genetic changes	Mutagenesis generally leads to changes at several gene locations. The result of the change is not specific for each method.	Gene editing makes it possible to change several of the same or different genes at the same time. These changes create specific new combinations of genetic information. Even when the individual changes only affect a small sequence of DNA, in combination, the changes can cause substantial changes in the biological characteristics of the organism.
Traceability	In general, the plants are identifiable by one or several specific gene locations.	The plants are often identifiable through a specific pattern (fingerprint) of the genetically engineered changes. In addition, there are often further desired or undesired changes that can be documented in the approval procedure.