

Science Media Centre Fact Sheet

Genome editing

Genome editing comprises a range of molecular techniques that allow targeted changes to be made to the genomes of organisms.

Also referred to as genome engineering or site-directed mutagenesis, genome editing can:

- modify genetic information within genomes to create new traits
- remove specific regions from genomes
- add transgenes (genes from other organisms) to specific locations in genomes

Genome editing is more precise than conventional crop breeding methods, as well as many standard genetic engineering (transgenic) methods, for introducing desirable traits in crops.

Standard genetic engineering techniques include using the naturally occurring plant pathogen *Agrobacterium* to insert genes in the genome of an organism, typically at a random position.

It is unclear how existing regulations for GMOs apply to plants modified by genome editing methods.

Genome editing precisely modifies nucleotides (A, T, G, C) in the genetic code, and is performed by:

1. Using specifically engineered 'molecular scissors' to create precise breaks in the genome
2. Repairing and editing the genome by harnessing the DNA repair mechanisms of cells

1. Techniques for creating breaks in the genome: sequence-specific nucleases

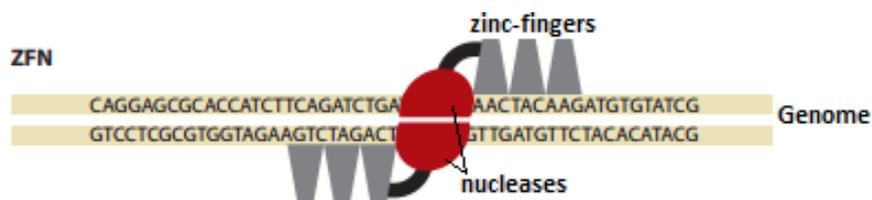
Nucleases are enzymes that sever nucleic acids (DNA, RNA), hence 'molecular scissors'. They can be engineered to target specific sites within genes and create breaks in the genome.

Four kinds of **sequence-specific nucleases (SSNs)** are currently used in genome editing:

Zinc-Finger Nucleases (ZFNs)

Zinc-fingers, protein structures containing zinc molecules, can be designed to recognise and bind to unique sequences in a genome.

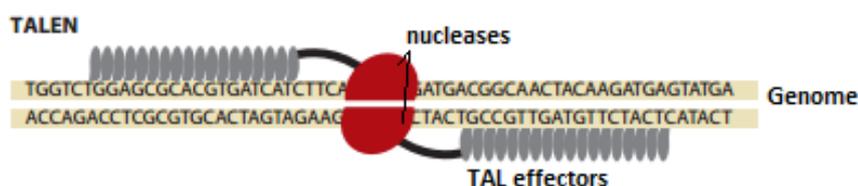
Two combinations of zinc-fingers are then fused to nucleases that create a break when they meet.



Transcription Activator-Like Effector Nucleases (TALENs)

Transcription activator-like (TAL) effectors are proteins produced by *Xanthomonas* bacteria, a family of plant pathogens, which bind to specific sections of a plant's genome.

TAL effectors can be engineered to target desired DNA sequences and when fused to nucleases can be used to create breaks in a similar way to ZFNs.



Meganucleases

Unlike ZFNs and TALENs which have separate DNA recognition and nuclease components, meganucleases (also called homing endonucleases) have DNA recognition built in.

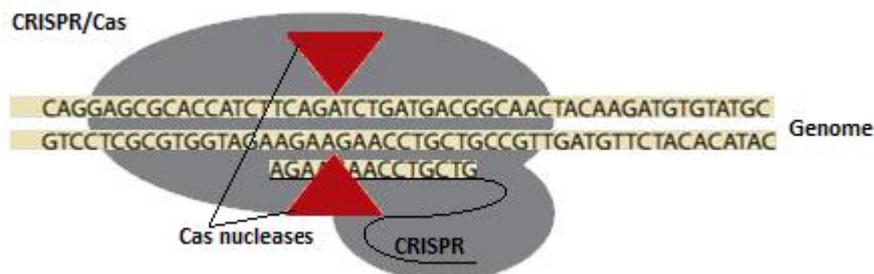
Meganucleases occur naturally and can be engineered, to some extent, to target specific sequences.



Clustered Regularly Interspersed Short Palindromic Repeats (CRISPRs)

CRISPRs are an immune defence system found in bacteria to protect against viruses; the system exploits short stretches of viral DNA that, when matched to the DNA sequence of an invading virus, trigger CRISPR associated (Cas) nucleases to make a break.

CRISPRs can be easily engineered to specify where a break should be made on the genome: the target DNA sequence is provided by a short RNA making it easier to implement than the three systems above.



2. Techniques for repairing and adjusting the genome

Once a break is made in the genome at the desired position the DNA repair mechanisms of a cell are triggered which can be harnessed to make the desired changes via two mechanisms:

Homologous Recombination involves introducing a DNA fragment as a template for repair which contains the desired genetic sequence and can be used to replace or insert nucleotides or full genes.

Non-Homologous End Joining (NHEJ) doesn't require a template and simply repairs the break, in general precisely but occasionally with small deletions or insertions.

Slight changes made to the genome will often stop a gene from functioning, creating a 'knock out', but NHEJ can also be purposefully used to make insertions and deletions of full genes.

Sources / further information

[Precision Genome Engineering and Agriculture: Opportunities and Regulatory Challenges](#) (PLOS Biology)

[Plant Genome Engineering with Sequence-Specific Nucleases](#) (Annual Review of Plant Biology)

[Genome engineering using the CRISPR-Cas9 system](#) (Nature Protocols)

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