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Highly selective modification and detection of epigenetic target nucleobases via tailored TALEs

Field of application

Epigenetic analyses close the gap between genetic predisposition (genotype) and appearance (phenotype). For the fine regulation of gene expression, there are different chemical switching elements that are located directly on the DNA. They can deactivate parts thereof, but do not change its structure. The actual expression of a genotype therefore depends on these regulation mechanisms and makes a specialization of cells possible in the first place. In times of personalized medicine, individual considerations of the genome are becoming more and more important, but epigenetics is also playing an increasingly significant role in medical prevention. It allows us to identify cancer, for instance, at a very early stage by detecting specific DNA methylation patterns.

State of the art

Detection methods for epigenetic nucleobases have already been established. However, their procedures still need to be optimized, as the technologies available today require multiple steps and/or workarounds.
Transcription-activator-like effectors (TALEs) are modularly structured proteins from chains of repetitive sequences that can be combined arbitrarily and selectively bind to DNA sequences. This allows for the generation of very specific binding proteins. Today, these are mainly used in genome engineering, but have not yet been considered for the in-vitro detection of epigenetic modifications.

Innovation

The invention developed at the University of Konstanz allows for the highly selective detection of epigenetic nucleobases in freely selectable sequences. For the first time, the nucleobases selective, chemical modification of DNA is directly combined with TALEs or tailored TALE repeats (mutants). The modification leads to the enlargement of the structural difference between the target nucleobase type and other, non-modified nucleobases. This enables a selective discrimination of a specific, freely selectable target sequence. The procedure harnesses the different affinity of the specifically designed TALE regarding its binding to DNA double strands and enables a simple, high-resolution and selective analysis of epigenetic cytosine derivatives. The technology can be combined with conventional biotechnological methods such as PCR, gel electrophoresis, micro-arrays or NGS and can be easily integrated into existing processes.

Patent portfolio

An EP application (EP3214183A1) is pending.

Your benefits at a glance

- ✓ Highly selective detection of freely selectable epigenetic target sequence
- ✓ Nucleobase selective modification of DNA to enlarge structural differences
- ✓ Significant competitive advantage regarding sample integrity and instrumentation required
- ✓ Combinable with a variety of well-known detection methods for sequence and concentration of target nucleic acids
- ✓ Easy to integrate into existing processes

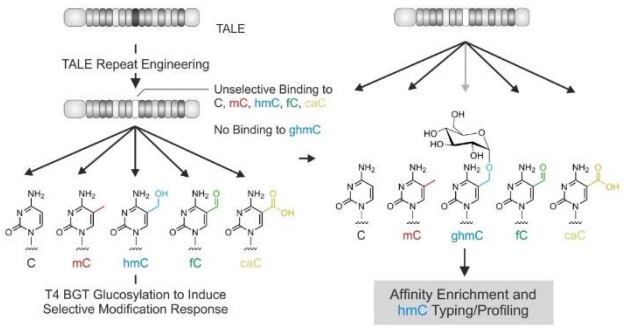

Figure: For the first time, a direct, programmable detection of nucleobases is enabled by using tailored TALEs.

Technology transfer

Technologie-Lizenz-Büro GmbH is responsible for the exploitation of this technology and assists companies in obtaining licenses.

Contact

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