

## Translational Research in Crops, Engineering Leader Alleles

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In the genomic era, the completion of the sequencing of several plant genomes has enabled the development of reverse genetics strategies, where one first identifies a target gene based on its sequence identity, and then proceeds with the phenotypic characterisation of mutant alleles. Chemical mutagenesis based on an alkylating agent like ethylmethane sulfonate (EMS); provides an easy and cost-effective way to saturate a genome with mutations. TILLING uses EMS mutagenesis coupled with a gene-specific detection of single-nucleotide mutations. We have constructed EMS-mutant populations under controlled conditions and developed a database, UTILLdb, which presents phenotypic data based on visual characterization of M2 plants. A hierarchical categorisation of mutant phenotypes was used to describe the mutant plants. In order to exploit the mutant population using reverse genetics, genomic DNA was prepared from the mutant lines and organized in pools for bulked screening. Genes and mutations were integrated in UTILLdb through a web interface, which allows for global analysis of TILLING mutants. This database also serves as a portal for users to request materials or TILLING experiments. We have selected, for each crop, a list of agronomic traits to be studied by TILLING. The identification and the characterization of mutant line affected in fruit related traits will be discussed.