

Abstract

Use of transgenic plants in functional analysis of plant genes

Functional genomics makes it possible to detect the functions of uncharacterized genes. It allows you to understand not only the functions of individual genes, but also the relationships between them. The acquired knowledge can also be used in improving the properties of various cultivated plants. With decreasing cost and increasing sequencing efficiency, many plant genomes are sequenced, but without the associated function of individual genes. Reverse genetics approaches are used to characterize these genes. In the first place, these include approaches that include the analysis of insertional mutants or the use of RNA interference that inactivates or reduces the expression of the individual genes studied. We can also inactivate whether to specifically modify the function of a particular selected gene using site-specific endonucleases, which include meganucleases, zinc finger nucleases, TALEN (transcription activator-like effector nucleases) and CRISPR (clustered regularly interspaced short palindromic repeats). In contrast to inactivation approaches, there are approaches such as activating mutagenesis and ectopic expression, through which we increase the expression. In addition, gene expression and protein localization can be analyzed using reporter genes in translational and transcriptional fusion. In this work I summarize the methods of reverse genetics based on the creation of transgenic plants, but I will also mention those that are based on other approaches.

KEYWORDS: functional genomics, reverse genetics, gene identification, mutant plants, transgenic plants