Sample for a research paper

A MUTANT HOMEOBOX GENE CREATED SIX-ROWED SPIKE IN BARLEY DOMESTICATION

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Abstract

Increased seed production has been a common goal during the domestication of cereal crops. Early cultivators of barley (*Hordeum vulgare* ssp. *vulgare*) selected a phenotype with a six-rowed spike that stably produced three times the usual grain number during domestication. We isolated the six-rowed spike 1 (Vrs1) from barley by chromosome walking. We discovered that Vrs1 encodes a homeodomain leucine zipper I–class protein (HD-ZIP I), a potential transcription factor. RNA in situ hybridization revealed that the Vrs1 is expressed only in lateral spikelet primordia. Sequencing alleles of 54 six-rowed mutant lines revealed a single amino acid substitution in 22 lines, creation of a new stop codon in 12 lines, a nucleotide substitution in the conserved splicing site in 3 lines, a frameshift mutation by a deletion in 5 lines, complete deletion of the gene region in 7 lines, and no DNA changes throughout the coding region with no gene expression detected in the remaining 5 lines. We found three haplotypes among six-rowed barley revealing loss-of-function mutation of the homeobox gene Vrs1. We found that two of them independently originated from two different types of two-rowed barley, but the origin of the remaining one six-rowed allele remained unclear.

Sample for a review paper

PLANT MOLECULAR MUTATION BREEDING

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Abstract

The advance in molecular biology and DNA technologies has brought plant breeding into a molecular era. The paper discusses the concept, context and perspective of molecular mutation breeding. Molecular mutation breeding is defined as mutation breeding in which molecular or genomic information is used in breeding strategy development, and/or molecular genetic techniques are used in mutant gene screening, characterization, selection and utilization. First, the accumulating knowledge of DNA damage, repair and mutagenesis will lead to knowledge-based design of mutation induction techniques; second, molecular genetic understanding of genes controlling various traits and their linkage relationship is of great help in developing a proper mutation breeding strategy; third, molecular markers are useful for tagging mutated genes, and for marker assisted selection when they are further used in cross breeding including pyramiding several mutated genes into breeding lines; fourth, with the disclosure of genes controlling various traits, it becomes possible to screen mutations using high throughput DNA techniques, for example, TILLING (Targeting Induced Limited Lesions IN Genomes). For traits where the underpinning gene(s) in a target crop species are not known exactly, bioinformatics tools such as comparative genomics can be used to identify a candidate gene for mutation. Molecular mutation breeding will overcome to a great extent the disadvantages and limitations of conventional mutation breeding, hence significantly increasing both the efficiency and efficacy of mutation techniques in crop breeding. Indeed, molecular mutation breeding can directly tap the benefit of rapid advances in molecular genetics and genomics, and is providing a non-transgenic approach for plant improvement.

Note: For authors whose ‘given’ names are not abbreviated (e.g. Chinese names), these names have an initial capital only.