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Genome wide identification of important DNA sequences in plant genomes and its application in plant biotechnology

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Advent of next generation sequencing (NGS) has been dramatically altered the fields of omics technologies including genomics, transcriptomics, proteomics and metabolomics. NGS provides mass analysis for genome and transcriptome of organisms including plants. This advanced technique accelerates identification of genes, regulatory sequences and biomarkers found in plant genomes. Although many draft plant genome sequences have been published over the past decade, all genes in genomes have not been completely detected. Therefore, gene family identification studies have been still continued. Gene families are often spread in the genome through tandem and segmental arrangements. Orthologous-paralogous genes, transcription factor family genes, some simple sequence repeats, microsatellites, microRNAs and long intergenic noncoding RNAs are in great demand for genome survey researchers. Development of new bioinformatics tools has caused detection of these important sequences in plant genomes. Transcriptome, molecular breeding, genetic transformation and genome editing studies can be considered as samples for this application in plant biotechnology. RNA-sequencing technology has been widely used for both measurement of gene expression levels and discovery of new genes and new alternative splicing isoforms. Aim of modern plant breeding programs is to improve and increase some agronomically important traits. The most significant contribution of genome wide investigation studies has provided precious source for functional genomics and plant breeding programs. Genome editing strategies including genetic transformation, RNA interference and CRISPR/Cas9 have a great potential to obtain new plant phenotypes with desirable characteristics. In the future, new omics analysis tools will be emerged and will provide deep investigation for plant genomes.

Biography

Mehmet Cengiz Baloglu is an Associate Professor of Department of Genetic and Bioengineering at Kastamonu University. He has received his PhD from Middle East Technical University (METU). He has established molecular biology, transcriptomics and bioinformatics research laboratories at the Kastamonu University. He has also published over 50 peer-reviewed manuscripts on topics concerning with gene identification in plants, transcriptome and miRNA analysis using NGS and abiotic stress in plants. He is serving as an Associate editor and Editorial Board member for International journals with high impact factors.

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