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A Biotechnology Technique for Crop Enhancement and Its Use in the Industry

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Editorial

A sharp decline in the availability of arable land and sufficient supply of irrigation water along with a continuous steep increase in food demands have exerted a pressure on farmers to produce more with fewer resources. A viable solution to release this pressure is to speed up the plant breeding process by employing biotechnology in breeding programs. The majority of biotechnological applications rely on information generated from various -omic technologies. The latest outstanding improvements in proteomic platforms and many other but related advances in plant biotechnology techniques offer various new ways to encourage the usage of these technologies by plant scientists for crop improvement programs. Farmers have been under pressure to produce more with fewer resources due to a significant drop in the quantity of arable land and an adequate supply of irrigation water, as well as a continuing steep growth in food consumption. A feasible way to alleviate this pressure is to use biotechnology in breeding projects to speed up the plant breeding process. The information supplied by various -omic technologies is used in the majority of biotechnological applications. The most recent breakthroughs in proteomic platforms, as well as a slew of other but related innovations in plant biotechnology approaches, have opened up a slew of new opportunities for plant scientists to use these technologies in crop improvement initiatives.

Knowledge of important proteins that play vital functions in a plant's normal growth and development is critical for crop plant biotechnology advancement. These proteins influence physiological and biochemical pathways to maintain cellular homeostasis in a particular environment. According to a review of the scientific literature, genomics and proteomics are the two key wheels that keep the discovery of novel genes moving forward, with the goal of eventually putting them into the pipeline for crop enhancement projects. Two of the most extensively used proteomics technologies, two-dimensional electrophoresis (2-DE) and mass spectroscopy (MS), are used to catalogue and identify proteins in various proteome states or settings. Due to some of the drawbacks and disadvantages associated with gel-based proteomics, such as labour intensiveness, insensitivity to low-copy number proteins, low reproducibility, and the inability to characterise complete proteomes, many gel-free proteomic techniques have become a valuable tool for scientists.

In recent years, world agriculture has been subjected to increased climate unpredictability, as well as a decrease in the amount of arable land available per person, adding to the burden on producer groups. In the current situation, plant breeders and plant biologists are under increasing pressure to develop "smart crop varieties" that are better suited genotypes with the ability to withstand a wider range of climatic variability in order to address future generations' food insecurity while maintaining/exceeding quality parameters. Traditional plant breeding methods, which were critical during the 20th century's green revolution, are now handicapped in the 21st century because current plant breeders demand precise gene changes with a gene monitoring system for the changed feature. Integration has become increasingly important in the post-genomic age.

In this post-genomic era, the integration of proteomics into the field of crop science will certainly enrich genome annotation efforts and accelerate the development of crop models for the elucidation of gene functions influencing phenotypes for the success of field crops. The sole stipulation for using proteomics in biotechnology is that the genetic alteration be expressed at the protein level. Progress made with the help of various -omics approaches along with the creation of a wider gene pool by utilizing modern biotechnological tools is the best approach to improve crop productivity for meeting food production goals [1-6].

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Conflict of Interest

The authors declare that they are no conflict of interest

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