Suppression subtractive hybridization versus next-generation sequencing in plant genetic engineering: challenges and perspectives

ABSTRACT

Suppression subtractive hybridization (SSH) is an effective method to identify different genes with different expression levels involved in a variety of biological processes. This method has often been used to study molecular mechanisms of plants in complex relationships with different pathogens and a variety of biotic stresses. Compared to other techniques used in gene expression profiling, SSH needs relatively smaller amounts of the initial materials, with lower costs, and fewer false positives present within the results. Extraction of total RNA from plant species rich in phenolic compounds, carbohydrates, and polysaccharides that easily bind to nucleic acids through cellular mechanisms is difficult and needs to be considered. Remarkable advancement has been achieved in the next-generation sequencing (NGS) field. As a result of progress within fields related to molecular chemistry and biology as well as specialized engineering, parallelization in the sequencing reaction has exceptionally enhanced the overall read number of generated sequences per run. Currently available sequencing platforms support an earlier unparalleled view directly into complex mixes associated with RNA in addition to DNA samples. NGS technology has demonstrated the ability to sequence DNA with remarkable swiftness, therefore allowing previously unthinkable scientific accomplishments along with novel biological purposes. However, the massive amounts of data generated by NGS impose a substantial challenge with regard to data safe-keeping and analysis. This review examines some simple but vital points involved in preparing the initial material for SSH and introduces this method as well as its associated applications to detect different novel genes from different plant species. This review evaluates general concepts, basic applications, plus the probable results of NGS technology in genomics, with unique mention of feasible potential tools as well as bioinformatics.