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Biotechnological Advancements of Medicinal and Aromatic Plants

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INTRODUCTION

Throughout history, individuals have been exploring the natural world, particularly plants, in their quest for novel pharmaceuticals. This has facilitated the utilization of numerous medicinal and aromatic plants (MAPs) possessing therapeutic characteristics for the treatment of diverse ailments. However, it is important to note that over 80% of the global population depends on plants or plant-derived substances to fulfil their primary healthcare needs. Surprisingly, about 25% of the medications currently prescribed consist of at least one chemical derived from plants. Thus, the significance of MAPs is repeatedly upheld.

The utilization of omics methodologies, including as genomes, transcriptomics, and metabolomics, in the study of medicinal and aromatic plants (MAPs) has contributed to the advancement of phytomedicine. These have contributed to the understanding of the genes and proteins responsible for the production of important secondary metabolites (SMs).

Exploring plants for their potential medicinal compounds is a captivating endeavor, Scientists are currently performing genome-level investigations to identify the specific genes that are responsible for producing a diverse range of bioactive chemicals. Comprehending these networks of genes, proteins, and metabolites can provide improved prospects for enhancing the synthesis of crucial specialized metabolites using both traditional and modern techniques in plant biotechnology.

Biotechnological methods used in Medicinal and Aromatic Plants (MAPs)

Secondary metabolite generation is a crucial method with significant economic applications. Nevertheless, there are still substantial barriers impeding the industrial production of valuable compounds derived from these sources. Plant cell, tissue, or organ culture is a valuable and promising approach for the mass production of key secondary metabolites from plants, according to specific needs and market demand.

The ultimate result of cell/tissue cultures is the accelerated growth rate and synthesis of targeted medicinal phytochemicals, surpassing or matching the quantity found in the entire plant cultivated in natural environments. Alternatively, other methods such as strain generation, use of diverse cell lines, and optimization of media can be employed to enhance the concentration of secondary metabolites. Plant tissue culture techniques provide an effective and productive method for producing plants. These metabolites can be produced at the commercial level without being affected by external influences such as geographical and seasonal fluctuations.

Hence, it is feasible to modify the concentration of the secondary metabolite and acquire distinct molecules from the original plant, a feat that cannot be achieved using conventional methods. The conventional methods of plant tissue culture encompass organ culture, callus culture, hairy root culture, and bioreactors. Alternatively, the potential of SMs can be controlled using innovative methods such as the utilization of precursors, in vitro elicitation, endophytes, and metabolite engineering.

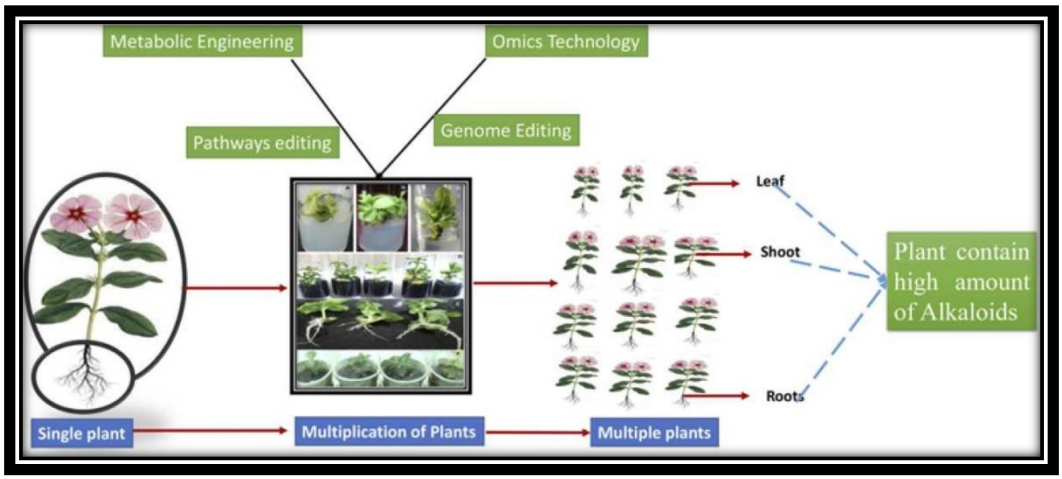
Genetic engineering:

Prior to boosting metabolite production or editing genes in homologous or heterologous systems, it is essential to identify and characterize the genes that are responsible for metabolite synthesis and modification. Due to advancements in sequencing technologies, it is now feasible to simultaneously profile a large number of genes. Typically, the goal is to enhance the production of particular molecules in medicinal and aromatic plants (MAPs) or to transfer a biochemical route to different organisms.

Two broad techniques have been employed to enhance the synthesis of one or more chemical substances. Initially, techniques have been employed to modify the gene expression, thereby overcoming particular stages that restrict the rate of metabolic route, deactivating competing metabolic pathways, and decreasing the breakdown of the desired product. Furthermore, there have been modifications to regulatory genes that govern many biosynthetic genes. Several research studies have been conducted to overexpress certain genes in pathways, aiming to generate novel floral colours. As an illustration, RNA interference technology was employed to produce decaffeinated coffee by suppressing the expression of the theobromine synthase gene. The transgenic plants exhibited a 70% reduction in their caffeine content. Under certain conditions, a metabolite can pose a risk to people in one state, but under different conditions, it may be found in lower quantities in its original form. By employing genetic engineering techniques, it is possible to convert these metabolites into a chemical derivative that is either nonhazardous or more potent.

Medicinal plant in OMICS era

Omics refers to the use of various branches of biology, including genomes, transcriptomics, proteomics, metabolomics, and ionomics, to examine a wide range of molecules using high-throughput methods . These methods are automated, enabling rapid, precise, and comprehensive examination of large quantities of materials within a brief timeframe . Genomic and transcriptomic sequencing can be efficiently achieved utilising cost-effective bioinformatic methods. In addition to aiding in the identification of genes that control metabolites, they have also enabled us to study their inherent effects inside cell lines. Omics refers to the application of interdisciplinary domains of biology, including genomes, transcriptomics, proteomics, metabolomics, and ion omics, to analyse various types of molecules on a massive scale using high-throughput technology. These technologies are automated, enabling rapid, precise, and comprehensive examination of large quantities of samples within a brief timeframe. Genome and transcriptome sequencing can be achieved efficiently and cost-effectively through the utilisation of bioinformatic methodologies. In addition to aiding in the identification of genes that control metabolites, they have also enabled us to study their necessary effects inside cell lines.



Genome editing

It refers to the process of making precise changes to the DNA sequence of an organism. Recently, genome editing has provided plant breeders and biotechnologists with a novel method to make accurate and extensive modifications to plants, which cannot be achieved using conventional genetic engineering methods. Currently, only a limited number of research have demonstrated the potential of genome editing in MAPs for the purpose of secondary metabolic engineering. CRISPR/Cas, TALENs, and ZFNs are now being artificially designed for this purpose. The CRISPR/Cas9 system is a cutting-edge gene modification technique that shows great potential. It enables plant metabolic engineering by modifying several genes in a specific region of the chromosome, resulting in intelligent alterations in the plants.

Genomics of Medicinal and Aromatic Plants (MAPs)

The genetic characterization of each crop species facilitates plant breeding activities. In the past, molecular markers like as RAPD, AFLP, and ISSR were commonly used for breeding purposes. In addition to morphological, anatomical, and chemical indicators, the genetic variability of medicinal plant species can be accurately verified using modern techniques such as SCAR, Loop-mediated isothermal amplification (LAMP), and DNA barcoding. Furthermore, DNA sequences and fingerprints have the potential to be utilized for the creation of a comprehensive reference library in the future. Next-generation sequencing (NGS) and third-generation sequencing (TGS) are more cost-effective and efficient compared to older sequencing techniques such as Maxam-Gilbert sequencing and Chain-termination. Additionally, NGS and TGS offer shorter turnaround times.

CONCLUSION

The comprehension of the biochemical processes involved in the formation of secondary metabolites based on MAPs has been enhanced in recent years through the use of omics methodologies. The emergence of DNA markers has facilitated the identification of QTLs located on the chromosomes that regulate these biomolecules, representing a significant advancement in this field. In addition, the progress of MAPs faces other challenges, such as gene knockdown, irregular gene expression caused by a complex gene network, and a restricted or nonexistent increase in the concentration of desired secondary metabolites up to the point of commercialization. Hence, the future of Medicinal and Aromatic Plants (MAPs) in relation to human health relies on the implementation of interdisciplinary methodologies encompassing fundamental aspects of biology, ethnobotany, conservation biology, and the latest omics technologies. These multidisciplinary approaches involve

the integration of classical methodology, omics, marker assisted selection, and artificial intelligence technologies in the design and manufacture of compounds.

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