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Review Article

Molecular Pharmacognosy and Nutrition: Unlocking Bioactive Compounds for Human Health

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Abstract

The application of molecular biological methods to pharmacognosy has broadened the field of pharmacognosical research and is crucial to the responsible and effective use of prescription medications. Therefore, authentication is needed for these raw medications. With its current explosive growth, pharmacognosy has emerged as an extensively multidisciplinary area of study. Molecular pharmacognosy is an emerging field that exists at the intersection of pharmacognosy and molecular biology. Molecular pharmacognosy leverages the techniques and tools of molecular biology to address a broad spectrum of difficult issues, including molecular marker assay-based drug population distinction between botanical and animal-derived compounds, genetic diversity-based resource conservation and utilization, influential compound accumulation procedure research, and genetic engineering-based resource augmentation. The primary investigation areas assigned to molecular pharmacognosy are as follows: studies regarding environmentally friendly disposal of crude drug supplies, preservation of curative plant and animal ecosystems, marker developing for medicinal plants, cultivating of freshly developed kinds, genome-wide regulation of metabolic pathways, directional monitoring of the quality of Chinese herbal remedies, the application of tissue culture and genetic modification to accomplish excellent expression and production of naturally occurring pharmaceutical ingredients or ingredients modified via genetic modification, and green in color, free of pollutants botanical medicine. From this review, the concept of Molecular Pharmacognosy and its responsibilities are described. It also includes applications of molecular pharmacognosy.

Keywords: Nutrition; Molecular Pharmacognosy; Molecular Makers; Chinese Medicinal Products

Introduction

The molecular pharmacognosy concept

Molecular pharmacognosy is the study of how to produce beneficial components at a molecular scale and how to classify, identify, cultivate, and safeguard crude pharmaceuticals. Molecular pharmacognosy is a potential and interesting cross-disciplinary field in pharmacognosy, grounded in the ideas and practices of both molecular biology and pharmacognosy. One may argue that molecular pharmacognosy adds novel possibilities along with difficulties to pharmacognosy while maintaining its traditional goals and contents.

Although some minerals are also regarded as crude pharmaceuticals, plants, and animals are the primary suppliers of these sub-

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stances. The origins of crude pharmaceuticals found in wildlife and plants are the only subjects to be investigated for molecular pharmacology. 6 fundamental biological stages can be distinguished in molecular pharmacognosy: genetic material, cells, organs, living things, populace, and society. These levels have their foundations in the progressive interaction linkage and various organism levels. The biological spectrum refers to the multiple stages of biological activity. A centuries-old method is found at every individual grade in the biological spectrum. In that instance with the initial identification of cells and genes, logically speaking, the advancement of organisms' stages in the micro- and macro-directions led to the progressive recognition of every degree. Numerous autonomous fields within life science have emerged as a result of research into the distinctive research concerns at every tier. Molecular biology and cytobiology are two examples of branches that could complement one another yet cannot replace one another. Pharmacognosy nowadays is primarily concerned with studies conducted at the tissue, organ, organism, and population divisions. Based on these investigations, separate and reasonably established hypotheses and techniques, including pharmacognosy histology and morphology, were developed. Molecular pharmacognosy, whose concepts and techniques have their foundation in molecular biology, encompasses crude pharmaceuticals at the level of gene expression [1].

Key issues and responsibilities in molecular pharmacognosy

- Molecular Pharmacognosy's primary responsibilities are as follows:
- A methodical collection of different types of botanicals and research on standardization of quality.
- Preservation of variety in therapeutic plants and animals, as well as studies on the environmentally friendly use of raw materials for drugs.
- Improved species development and marker breeding for therapeutic use.
- Targeted management of medicinal product grade and genetic modulation of metabolic pathways.
- The execution of gene therapy and cell culture techniques to tissue engineering to produce naturally occurring chemical compounds or ingredients that have been genetically altered at an elevated level of activity.
- Organic herbal remedies untainted by pollution and modified genes [2].

Applications of Molecular pharmacognosy

The recognition of cultivars:

Given that crude drug cultivars exhibit varying medicinal properties and vary in cost, it is imperative to identify them. Comparing molecular marker detection to morphological, microscopic, and chemical marker experiments, one can benefit from its excellent precision as well as high consistency. Certain molecular recognition techniques, including SNP and DNA barcoding, which depend on sequencing operations, and PCR and electrophoresis-based MARMS, PCR-RFLP, APAPD, RAPD, AR-PCR, and SSR, are being effectively applied to cultivar recognition. Thirteen species and three variations of trichosanthin and analogs were identified from 26 specimens using the RAPD technique [1]. 5 different Panax Ginseng-related species have been found using the APAPD and MARMS techniques, according to reports [4,5]. The nuclear ITS fragments, chloroplast trnH-psbA sequence, and mitochondrial COI (cytochrome c oxidase I) gene were viable options regarding this advancement, as DNA barcoding innovation offers great potential for cultivar recognition [6,7].

Resource safeguarding:

The creation and safeguarding of health-related assets, in particular those that are uncommon and threatened, may be guided by knowledge of genetic variation. By separating the process of evolution of relevant components, examining the interactions between organisms, choosing the marker of excellent DNA assets, and utilizing fertilization supported by molecular markers, molecular marker innovation has a benefit when assessing the genetic variation of organisms. An evaluation of the variation in genes and structure of two medicinal plants that are in danger of extinction, Cistanche deserticola and C. Tubulosa, revealed reasons to support the preservation of natural assets [8]. A novel framework and approach for the investigation of genetic variety were offered by molecular phylogeography, which serves to examine the genetic variance within a population [9,10].

The production method of high-quality therapeutic resources:

An environmentally friendly setting and a person's genetic background have a noteworthy effect on the caliber of therapeutic materials. The basis is genetic material, and ecological variables influence how inorganic substances are absorbed and distributed as well as how secondary compounds build up. Molecular breeding and the production of herbal products will benefit from research into the development process of high-quality therapeutic substances. Currently, it has been demonstrated that cloned genes from medicinal plants are crucial for the transmission of signals [14], controlling gene expression [13], and synthesizing secondary metabolites [11,12]. These will enhance research on the processes involved in the production of high-quality pharmaceutical components [15].

Synthesis of active components:

Transgenic technology is being effectively applied to produce transgenic medicinal herbs with greater yields of active chemicals or durability against disease, insects, drought, and salt. TMV and Bt coat protein genes were recently inserted into medicinal crops, giving them the ability to resist illness and attack by insects [16]. Salvia miltiorrhiza's hairy roots and suspension cells were used to produce tanshinone [17]. Scopolamine concentration in transgenic Hyoscyamus niger is approximately 9.6 times larger compared to that of the wild-type varieties [19]. A produced yeast species having a hundred milligrams per liter yield L may directly manufacture artemisinic acid, a precursor of artemisinin [20]. By genetically modifying tobacco, it is also possible to in to soar crease the amount of artemisinic acid present by altering the subcellular location of terpene synthase [21].

Methodical selection of Chinese herbal types and the investigation of quality standardization:

According to conventional taxonomy, a variety of Chinese botanical kinds can be used for organized selection, categorization, and verification; however, additionally, numerous human variables play a role, especially with established groups of Chinese medicinal herbs, where issues like genuine raw material verification still arise. Systems, the theory of evolution, categorization, and verification research now have a useful tool and foundation thanks to the advancements in molecular systematics and species biology. Technological advances in biological engineering and molecular systems theory have made it possible to analyze molecules and categorize and efficiently identify crude drugs. The approaches most frequently employed for the organized selection of Chinese herb forms and the investigation of quality standardization depend on a blend of PCR and electrophoresis approaches, including MARMS (multiplex amplification-refractory mutation system) allele-specific PCR, RFLP (restricted fragment length polymorphism) [22], APAPD (anchored primer amplification polymorphism DNA) SNP (single nucleotide polymorphism) and DNA barcoding technological innovations. Many botanical and veterinary medications, including Panax ginseng [23], Bupleurum chinese [24], Dendrobium officinale [25], Solegnathus hardwickii [26], and Saiga tatarica [27], were subjected to such procedures in the past decade. A number of the main goals of molecular pharmacognosy is to come up with an approach and framework for identifying crude drugs that utilize species biology, molecular systematics, Chinese beneficial assets, and medicinal plants. Another goal is to advance the advancement of Chinese herbal medicines' organized collection and quality standardization across one's personal, societal, as well as hereditary levels.

Investigation into the long-term management of raw pharmacological supplies and the preservation of the biodiversity of medicinal herbs and wildlife:

DNA variety is the foundation of biodiversity. DNA variation trends can be tested directly by molecular makers employing DNA polymorphism assessment and molecular systems theory focused on genome sequence analysis to identify the critical elements to safeguard. The extent of population extinction as well as growth status may be inferred from the molecular systematics investigation into therapeutic wildlife and plants. This means that novel operational techniques for measuring biodiversity and safeguarding uncommon therapeutic vegetative and animal assets are required. Phylogeographic inquiry into the genomic investigation of the solitary relictual species Cathaya argyrophylla was conducted, as reported by Wang et al. [28], to clarify its endangerment strategy. The historical development and regional distribution of Taxus wallichiana and the East Asian flora were examined by Gao., *et al*. [29]. The Qinghai-Tibet Plateau's uplift is responsible for the extremely varied phylogeography trend of the fragile plant Dipentodon sinicus, as reported by Yuan., *et al*. [30]. Pinus kwangtungensis's migration path and habitat during the glacial era were examined by Tian., *et al*. [31]. Furthermore, the utilization of discoveries in DNA polymorphism-based molecular systematics enhances the efficacy and efficiency of locating and expanding the range of therapeutic vegetative and animal supplies. Molecular systematics may be employed to discover and expand the range of crude drug supplies by elucidating the interactions between DNA molecules' genetic makeup, pharmaceutical components, and effectiveness when utilized with chemical taxonomy, as well as by acquiring the molecular genetic history of significant chemical components to figure out whether or not unidentified vegetation have the genes needed to generate particular chemical compositions.

Breeding markers for therapeutic plants and cultivating novel varieties:

It might be argued that molecular systematics and the molecular identification of genetic variability provide the groundwork for comprehending and altering the environment as one explores molecular concepts and applications. Our ability to comprehend and alter nature is based on our investigation and utilization of molecular markers exhibiting significant characteristics. Genomics and cellular synthesis help to render molecular pharmacognosy investigations more beneficial. The quantitative trait loci (QTL) approach offers data regarding the arrangement of the statistical trait loci, including the number of genes linked to the target trait, genetic consequences, gene-to-gene interactions, and breakdown of the quantitative characteristics, which would not have been delivered through conventional quantitative genetics. The QTL method incorporates breeding technological advances with a vital therapeutic agricultural and livestock inheritance map built with molecular genetic markers. The latest version of high-throughput sequencing equipment is being utilized to sequence vegetation through their genomes and produce abundant transcriptome information, which includes a significant amount of EST sequences [32]. This is due to the method's quick advancement and decline in sequencing prices. Gai., *et al*. [33], for instance, sequenced the de novo transcriptome of 8 L.-q. Huang., *et al.* Paeonia suffruticosa using the Roche 454 GS FLX technology. Following splicing, 23,652 sequence crossover groups (contigs) and single sequences (singletons) were recovered, of which 15,284 had been greater than 300 bp. Ultimately, 625,342 translated sequence tags (ESTs) with a typical length of 358.1 bp had been generated. From 454 ESTs, 2253 SSR loci were obtained in total. After that, 149 SSR loci were chosen to create the primers. 121 primer pairs in all were able to lengthen the bands effectively. Of them, the PCR results showed polymorphism in 73 primer pairs. The sequences in question offered genetic assets for researching P. suffruticosa's physiological significance.

Directed management of Chinese medicinal product quality and gene oversight of the metabolic pathway:

The fundamental study of secondary metabolite biosynthesis needs to receive greater scrutiny. Specifically, studies on The oversight of genomes of important enzymes will stand out and may end up being one of the most difficult and exciting areas of molecular pharmacognosy; secondary metabolites are the primary sources of medicinal substances found in Chinese herbs. The number and existence of secondary metabolites determine the quality of Chinese botanical treatment; therefore, Genetic transformation and increasing the number of active components in Chinese remedies using herbs would aid relieve some of the strain on their natural assets. Antisense technology inhibits the synthesis methods of other chemicals and increases the concentration of the intended substance. For instance, Mol., *et al*. [34]. were able to suppress the biosynthesis of lignin in the branching metabolism and effectively control the metabolic processes of cinnamyl alcohol dehydrogenase in the hairy roots of Linum flavum, thereby increasing the concentration of the anticancer chemical 5-methoxypodophyllotoxin. Furthermore, the determination of functional properties of genes in addition to the vetting and reproducing of novel genes has made extensive use of RNA interference (RNAi) research. Utilizing the RNA exclusion technique, Schweizer., *et al*. [35] effectively inhibited the dihydroxyflavonol 4-reductase gene encoding maize and barley at the individual at the cellular level, resulting in a reduction in the buildup of red anthocyanin about cells.

The use of cultured tissues and genetic engineering methods to produce naturally occurring chemical compounds or genetically modified ingredients at elevated levels of expression

One of the most alluring possibilities in genetic engineering is the application of organisms that have been biological reactors with altered genes to produce external gene-encoding products; for this reason, these bioreactors are referred to as "new-generation pharmaceutical factories." They are associated with several benefits, including the ability to express complex natural proteins in their native form, the ability to be continually derived from plant bodies and animal milk and blood, and the ability to pass across the digestive system. Furthermore, the sequence responsible for toxicity might be eliminated or its expression suppressed in plant or animal proteins that have potent active chemicals but also adverse consequences, such as trichosanthin, and scorpion venom, thereby enhancing the production of the drugs. Modern developments in plant genetic engineering and cell engineering, coupled with the discovery of hairy root and crown gall traditions, have created fresh possibilities for the study and advancement within active medicinal ingredient manufacturing. Biotechnology is expected to stimulate investigation into incorporating novel genetic features into conventional crude drugs through enhanced expression effectiveness and an expanded range of receptor plants. Simultaneously, new bioreactor methods and the setting up and refinement of effective cultivation methods will expedite the sale and economic growth of biotechnology in herbal medicine. After analyzing the hairy root cultivars of Salvia miltiorrhiza at various production stages using transcriptome sequencing in conjunction with metabolome examination, Gao [36]. found 20,972 genes, out of which 6358 displayed distinct expressions at various production stages. Seventy recordings in all parameters associated with the buildup and management of tanshinone were identified by concentrating on the investigation of genes associated with tanshinone production and management.

Non-polluting botanical medicines and genetic engineering

The public's anger has been sparked by the issue of pesticide contamination in botanical products, which harms the ecosystem, jeopardizes the safety of citizens, and restricts the worldwide shipment of Chinese herbal remedies. Therefore, encouraging the use of free of contaminants therapeutic plants developing pest management strategies for therapeutic herbs avoiding the use of industrial pesticides have grown into objectives for people to meet. One other use for molecular pharmacognosy is the genetic modification of medicinal herbs to increase their resistance to pests.

Conclusion

Molecular pharmacognosy is a scientific discipline that employs molecular biology technological advances to investigate crude drugs. Crude drugs are defined as unprocessed or minimally refined goods originating from animals, plants, and mineral content. They can be utilized as herbal medicines or as inputs for pharmaceutical manufacturing. In the past few decades, there has been significant advancement in the fields of molecular pharmacognosy, cultivar verification, safeguarding resources, quality construction processes, and active chemical manufacturing. In a short time, cultivar enhancement, a DNA barcoding database structure, and quality production techniques may all lead to significant advancements in molecular pharmacognosy.

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