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Review Article

Various Omics Techniques Used for Authentication and Standardization of Herbal Medicines

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ABSTRACT

Herbal remedies have been used for many years to diagnose and treat various diseases. The quality of research procedures pertaining to the safety and effectiveness of herbal products depends on the standardisation of herbal plants. The most popular method for the standardisation of medicinal plants is to evaluate the physical and chemical characteristics of the plants. Many standardisation methods are currently in use, however they are not adequate for all plants on the planet. We can readily gain a thorough understanding of the pharmacodyanamics, pharmacokinetics, and toxicological characterisation of any herbal plant's active ingredient by employing more recent methods, such as omics techniques. Omics technique involves various technologies such as metabolomics, proteomics, lipidomics, genomics, transcriptomics, etc. Multi-omics integration has been used in recent years to explore the mechanism of action of herbal medications. New platforms linked to "-omic" technologies have emerged, making it easier to analyse and characterise biological systems in-depth and uncovering aspects that were previously unknown.

INTRODUCTION

Background: -

Herbal medicine involves the application of medicinal plant for prevention and treatment of diseases. This practice encompasses a wide spectrum, from traditional and folk remedies found in various cultures to the utilization of standardized and processed herbal extracts.[1] The historical use of herbal remedies for both prevention and treatment of diseases is well documented, reflecting a longstanding tradition across different societies.[2] For over 5000 years, medicinal plants have been employed to address a variety of health issues in regions such as China, India, and Egypt and they continue to be utilized

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today, even in the presence of modern pharmaceuticals.[3] The standardisation of herbal plants is crucial for guaranteeing the quality of research processes concerning the safety and efficacy of herbal products. This is particularly important for scientist and regulators who aim to maintain the quality and interoperability of this products.[4] Authenticating plant materials and examining metabolic pathways are the two main responsibilities of medicinal plant research. Numerous omics methods, such as proteome profiling, transcriptome sequencing, genome sequencing, and phenotyping, have been widely used to accomplish these goals.[5]. There is a tendency towards evaluating hundreds of possible biomarkers rather than just a few since analytical chemists have recently developed techniques that can analyse a wide variety of analytes from a single sample. This method leads to contemporary "omics" experiments.[6] The Latin suffix "ome," meaning mass or many, is where the word "omics" comes from. The simultaneous study of the molecular effects of chemical mixtures has been made possible by the development of information-reach methodologies such as transcriptomics, proteomics, and genomics as well as a variety of profiling techniques like metabolomics, a non-targeted analytical method primarily focused on low molecular weight molecules.[7] Omics technique facilitate the concurrent evaluation of different classes of molecules, serving as a primary experimental framework for this approach.[8] Omics technology includes a variety of research approaches, including transcriptomics, proteomics, metabolomics, and genomics, that make use of high-throughput analysis and detection methods in contemporary biological research systems. Instead of focussing on a single target or route, this technique evaluates thousands of them, enabling the analysis of global alterations in genes, proteins, metabolites, and other components involved in biological signalling transduction processes.[9] Although proteomics focuses on many proteins, metabolomics looks at different metabolites, while transcriptomics analyses a broad range of transcripts. Large-scale methods for the purification, identification, and characterisation of proteins, RNA, DNA, and other bio molecules are included in high-throughput technologies. Since these techniques are typically automated, a large number of samples may be analysed quickly.[10] By looking at all biological processes to identify different components, like genes, RNA, proteins, and metabolites, rather than analysing each part separately, "omic" approaches aim to provide a comprehensive and integrated understanding of biological systems. Nowadays, "omics" methods concentrate on answering specific biological queries, frequently without necessitating a fundamental comprehension of the biology at play. As technology continues to advance, “omic” research may evolve to tackle more intricate systemic questions and serve as a valuable resource in diagnostics and drug development. However, we remain significantly distant from realizing these ambitious objectives due to the inherent complexity of the task.[6] It is imperative to emphasise the need for multi-omics technologies to address both basic and applied issues in medicinal plants, as this can aid in the creation of improved medicinal plant resources and the discovery of novel therapeutic molecules. Thus far, multi-omics techniques have helped to build large datasets that include the genome, transcriptome, proteome, metabolome, and phytochemical profiles of individual or several species of medicinal plants.[11] In this article we focused on various omics technique used for authentication and standardization of herbal medicines. Here we are discussing omics techniques like metabolomics, proteomics, transcriptomics, genomics and lipidomics.

Application of omics technique:-New platforms linked to "-omic" technologies have emerged, making it easier to analyse and characterise biological systems in-depth and uncovering aspects that were previously unknown. Tens of thousands of genes and proteins can be detected at the same time because to this.[12] The main use of omic techniques is the identification of biomedical resources, including DNA microarrays, fingerprinting, and genomic procedures in DNA sequencing. Studies pertaining to herbal plants and their pharmacological characteristics are increasingly using omic approaches as pharmacological research gains more attention.[13] The capacity of proteomics to differentiate between species is one of its most important applications in herbal therapy. For quality assurance, toxicity evaluations, and the standardisation of herbal products, this capacity is an invaluable asset.[14] The genome, transcriptome (the entire collection of transcripts, or mRNA molecules), proteome (the entire collection of proteins inside a particular cell or tissue), metabolome (all metabolic products and intermediates within a cell or tissue), interactome (the network of molecules, including biologically active metabolites, that interact with a particular protein), and phenome (the entirety of observable traits of an organism) are among the levels of data collected by omics technologies.[12]

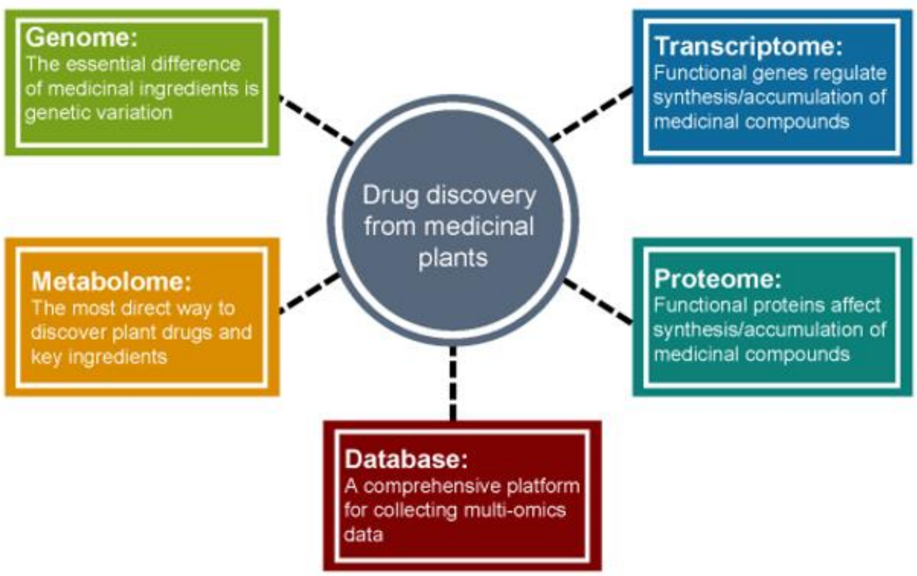

Figure1: - Medicinal plant multi-omics research to facilitate drug discovery[11]

Various omic techniques: -

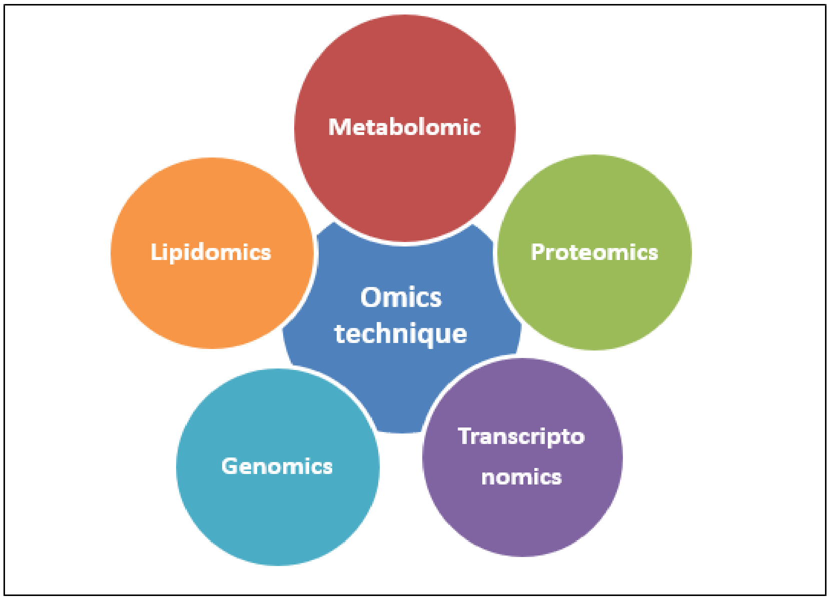

Figure2: Various omics techniques used in authentication and standardization of herbal medicines.

Metabolomics: -

The methodical study of distinct chemical fingerprints connected to particular biological functions is known as metabolomics. The study of small-molecule metabolite profiles is included in this field. The entire collection of metabolites found in a biological organism, mostly as a result of gene expression, is referred to as the metabolome.[15] The term "metabolomics" refers mainly to comprehensive, objective, high-throughput analysis of complex metabolite mixtures, especially those derived from plant extracts. When used on a variety of herbal plants, the chromatographic fingerprinting approach has proven to be an efficient and all-encompassing way to assess the quality of herbal remedies. Metabolomic profiling analyses extracts using Fourier transform ion cyclotron mass spectrometry (FTMS) with the goal of identifying the best phytochemical profiles.[16] Metabolomics is a new method that emerged after proteomics and transcriptomics. It performs both quantitative and qualitative evaluations of metabolites found in organisms or cells using advanced detection techniques, analytical procedures, and statistical algorithms.[17] Metabolomics provides a more suitable degree of biological organisation for study as a downstream method from transcriptomics and proteomics.[18] Systems biology, biomarker discovery, and functional genomics all benefit greatly from this approach.[19] As a rapid, sensitive, and non-invasive tool, metabolomics explores metabolic alterations within biological systems and generates profiles of small molecules associated with diseases.[20] Research in metabolomics focused on medicinal plants aims to deliver a thorough analysis of metabolite profiles and assess the quality of these plants.[21] The phenotypic traits of phytochemical ingredients in medicinal plants and the differences in the concentration of active components may be directly correlated, according to metabolomics. This approach is also instrumental in identifying quality markers (Qmarkers) that differentiate bioactivity related to function and aid in the discovery of active compounds.[22] Target compound analysis, which involves measuring particular metabolites; metabolic profiling, which focuses on the quantitative and qualitative evaluation of related compounds or specific metabolic pathways; metabolomics, which includes the qualitative and quantitative evaluation of all metabolites; and metabolomic fingerprinting, which classifies samples through rapid global analysis, are the four different categories into which metabolic analysis can be divided.[12] Research in metabolomics is currently focused on untargeted, widely targeted, and targeted strategies. In traditional medicine formulations, the targeted metabolome is especially useful for distinguishing unrefined therapeutic ingredients from closely related species.[23] Additionally, studies on widely targeted metabolomes indicate that the medicinal quality of plants can be evaluated based on the levels of secondary metabolites.[24] By identifying particular metabolites produced under the influence of target genes, metabolite profiling of mutagenesis lines with either gain- or loss-of-function genes successfully establishes the link between genes and metabolites. Moreover, the genes that contribute to the diversity of secondary metabolite chemical structures can be examined using a reverse genetic approach with a metabolomics focus.[25] As a result, metabolomics-based research has been the main driving force behind the investigation of biosynthetic regulatory pathways that produce active metabolites in medicinal plants, which is a prerequisite for molecular breeding and synthetic biology.[26] Spatial metabolomics addresses the shortcomings of bulk metabolomics by enabling precise identification of metabolite types, concentrations, and their spatial distributions. This technique allows for a detailed characterization of the chemical composition of tissues or organs with high spatial resolution.[27] The ability to produce detailed geographical distribution profiles of metabolites and enable "real-time reporting" of the metabolome in living organisms are thus made possible by spatial metabolomics.[28] It is widely recognized that relying on a single analytical method is insufficient for a thorough visualization of the metabolome; thus, a combination of various technologies is essential for a complete understanding.[29] Consequently, a variety of analytical methods have been used to profile the metabolome.. These include methods such as infrared spectroscopy (IR)[30], nuclear magnetic resonance (NMR)[31], thin layer chromatography (TLC)[32], high-performance liquid chromatography with ultraviolet and photodiode array detection (HPLC/UV/PDA)[33], capillary electrophoresis with ultraviolet absorbance detection (CE/UV)[34], capillary electrophoresis with laser-induced fluorescence detection (CE/LIF)[35], capillary electrophoresis coupled with mass spectrometry (CE/MS)[36], gas chromatography-mass spectrometry (GC/MS), liquid chromatography-mass spectrometry (LC/MS), liquid chromatography tandem mass spectrometry (LC/MS/MS)[37], Fourier transform ion cyclotron mass spectrometry (FTMS)[38], and high-performance liquid chromatography combined with both mass spectrometry and nuclear magnetic resonance detection (LC/NMR/MS)[39], as well as LC/NMR/MS/MS.[40] Selectivity, sensitivity, and speed are frequently traded off while selecting the best technology. Techniques like NMR, for example, are renowned for their speed and selectivity, but their sensitivity is very low. In contrast, methods such as capillary electrophoresis with laser-induced fluorescence (CE/LIF) detection demonstrate high sensitivity but fall short in selectivity. Hyphenated mass spectrometry techniques, including GC/MS and LC/MS, strike a balance between sensitivity and selectivity, although they require longer analysis times.[41] Metabolomics presents several advantages over other '-omic' approaches, with its primary benefit being its close biological relevance to the phenotype of the system, allowing for quick detection of perturbations within the metabolome.[42] This field emphasizes the intricate interactions among system components, focusing on the entire system rather than isolated elements, thereby offering a unique insight into cellular homeostasis.[43,44]

Limitation to metabolomics: A more detailed characterization of the human metabolome and its subsequent therapeutic implications can enhance outcomes. Moreover, this technique presents challenges regarding reproducibility. It remains uncertain how contemporary clinicians will utilize this data, as even minor physiological changes, such as dietary intake or ascending a flight of stairs, can significantly affect the metabolome. Integrating pharmacometabolomics with pharmacogenomics may facilitate the screening of more clinically pertinent information.[45]

Proteomics: -

The thorough investigation of the proteome linked to particular cells, tissues, or body fluids utilising large-scale, high-throughput, and methodical techniques with an emphasis on their structures and activities is known as proteomics.[46, 47] Clarifying the expression and functional dynamics of every protein found in the cells of different organisms is the goal of this field. Protein expression, types of modifications, structures, functions, and interactions are all included in this investigation.[48] Proteomics has recently expanded its definition to include not just gene products but also post-translational modifications, which are structural modifications of these products that affect cellular turnover and metabolism.[49] Australian researchers Wilkins and Williams coined the term "proteome" in 1994 refers to the entire collection of proteins that are expressed by a cell, tissue, or organism's genome.[50] Proteomics builds upon this concept by examining the composition and activity of proteins that dynamically change within cells.[51] Proteomics has grown to be a crucial part of multi-omics research as a potent method for improving our comprehension of molecular processes and discovering novel therapeutic targets.[52] Today, proteomics is increasingly recognized as an advantageous method for exploring the effects of a complex herbal combination on multiple targets, discovering individual bioactive compounds, developing active fractions, characterizing safe herbal prescriptions, and ultimately refining molecular diagnostics.[53] The proteomics techniques evaluate the types, levels, modifications, interactions, functions, and structures of proteins in various samples, offering high throughput, sensitivity, linear range, and accuracy. Additionally, proteomics can detect variations in protein levels between physiological and pathological states, identifying dysregulated proteins before and after traditional Chinese medicine treatments.[54] Two-dimensional electrophoresis (2DE), followed by staining, selection, and identification through mass spectrometry, and the use of isotope tags for protein labelling, coupled with separation via multidimensional liquid chromatography and subsequent mass spectrometry analysis, are currently the two main mass spectrometry-based techniques that are most frequently used for global quantitative protein profiling. Both of these basic proteomic methods can be improved by using insightful information from molecular imaging.[55] The majority of proteome studies on medicinal plants focus on analysing changes in protein abundance in various environmental conditions. Important variables affecting the concentrations of regulators or enzymes involved in metabolite biosynthesis in medicinal plants include light exposure,[56] temperature, drought,[57,58] flooding, salinity,[59] application of exogenous hormones,[60] air composition, and cultivation methods. Proteomics is essential for clarifying the regulatory mechanisms that control the growth and secondary metabolism of medicinal plants because proteins are essential for carrying out and controlling almost all biological processes.[61]

Proteomic technologies enable the simultaneous investigation of the function, organization, diversity, and dynamic changes within a cell or entire tissue.[53] The ability of proteomics to distinguish between different species, as shown in the case of Panax (P. ginseng versus P. quinquefolium), is one of its most convincing applications in the study of herbal plants.[62] For quality assurance, toxicity evaluations, and standardisation of herbal preparations and decoctions, proteomics is a crucial tool. In contrast to transcriptomic and genomic approaches, proteomic investigations have successfully clarified the mechanisms of action for several herbal compositions.[63] The advancement of proteomics technology is among the fastest in the scientific field, enhancing our comprehension of biological processes. Additionally, proteomics is instrumental in the chemical and pharmacological standardization of plant extracts, as well as in evaluating their toxicological properties.[64] Currently, proteomics is primarily utilized for (1) identifying and validating action targets, (2) analyzing the composition and variations among them, and (3) elucidating the mechanisms of activity and toxicity in Traditional Chinese Medicine. The top-down and bottom-up approaches are the two complementary techniques used in proteomics to determine protein sequences using mass spectrometry.[65] A mass spectrometer, such as ESI or MALDI, is used to analyse the peptides that are produced when proteins of interest are enzymatically digested, usually with trypsin, in the bottom-up process. After the masses of the intact enzymatic peptides are recorded, low-energy collision-induced dissociation (CID) is used in tandem mass spectrometry (TMS) to get information about the sequences and, in certain cases, posttranslational changes of the peptides. On the other hand, the top-down method can directly generate fragment ions from a big intact protein that are sufficiently informative, exposing the protein's whole amino acid sequence and all of its modification. However, a number of obstacles prevent the top-down strategy from being widely used in the majority of biomedical labs. To date, the bottom-up proteomics approach has been the exclusive source of proteomics data pertaining to TCM research.[66] Large-scale proteome analysis makes use of modern mass spectrometry's comprehensive analytical capabilities, which can be combined with a variety of offline or online separation methods. Proteomics now uses two main types of separation techniques: liquid chromatography (LC)-based techniques and electrodriven techniques. Isoelectric focussing, one-dimensional polyacrylamide gel electrophoresis (PAGE), two-dimensional electrophoresis (2DE), nondenaturing 2DE, and two-dimensional blue native/sodium dodecyl sulphate PAGE (2D BN/SDS-PAGE) are among the electrodriven methods frequently used in proteomic research. The 2D BN/SDS-PAGE method is particularly effective for analyzing hydrophobic membrane complexes, as it first separates native protein complexes in a nondenaturing PAGE based on their apparent molecular weight and structure, followed by a denaturing SDS-PAGE in the second dimension.[67] The development of mass spectrometry and high-throughput analytical technology has greatly speeded up proteomics research in a variety of fields. In proteomic research, two-dimensional gel electrophoresis (2DE) is still a fundamental method that is frequently used. Improving 2DE's sensitivity, resolution, capacity, and detection accuracy is essential to its advancement. A more efficient approach to proteomics is provided by a sophisticated technology called 2D Fluorescence Difference Gel Electrophoresis (2-D DIGE), which uses very sensitive protein labelling methods in conjunction with narrow pH gradient gel separation.[68,69]

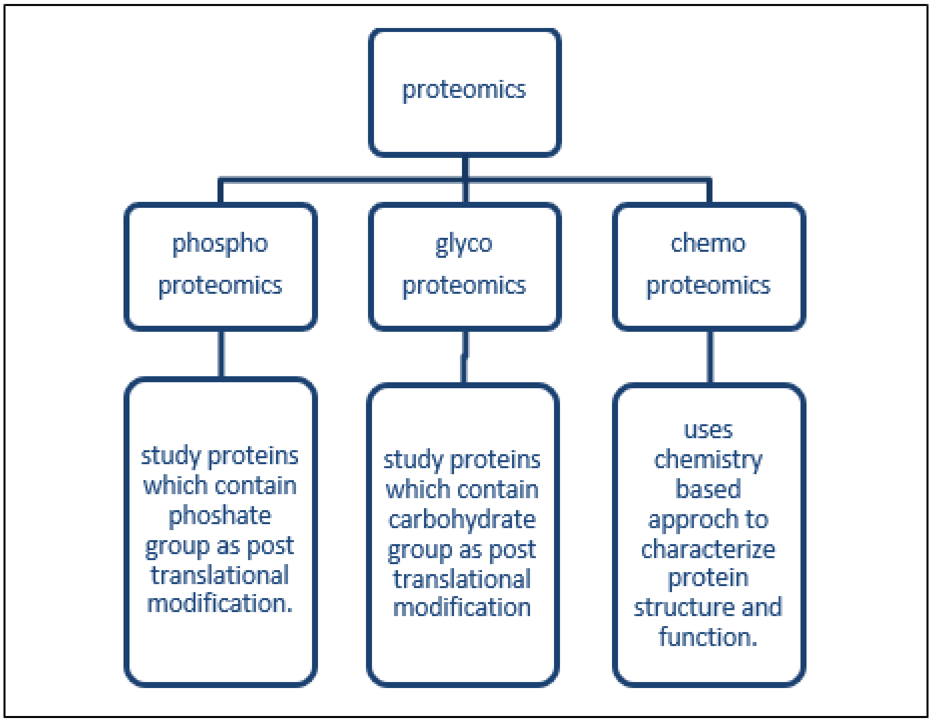

Figure 3: Types of proteomics technique.

Phosphoproteomics focuses on the study of proteins that undergo phosphorylation as a form of post-translational modification. In order to advance phosphoproteomics research, the main methods used in this discipline are the identification and detection of phosphorylated proteins.[70,71] In contrast, the field of glycoproteomics focuses on identifying, classifying, and characterising proteins that include carbohydrates as post-translational modifications.[72] Identification of glycoproteins, identification of glycosylation sites, and analysis of the structural and functional features of these proteins are all included in glycoproteomics research. Glycoproteins and glycopeptides are usually separated and enriched as part of current glycoproteomics techniques.[73,74] Chemoproteomics examines the structures and functions of proteins using a chemistry-focused methodology. This field often utilizes functional small molecules to modulate specific elements of the proteome, allowing for the detection and isolation of target proteins through chemical interactions with proteins.[75]

Limitation to proteomics:

Proteomics' sensitivity to certain tissues is its main limitation. For proteome analysis, getting tissue samples from organs such as the lung, kidney, heart, or brain presents substantial challenges compared to blood-based targets or established tumour tissues, which are generally accessible for accessing the relevant biological matrix.[76]

Transcriptomics: -

The entire collection of RNA molecules that are transcribed from a particular tissue or cell at a given functional or developmental stage is referred to as the transcriptome. This includes non-coding RNA (nc-RNA) as well as messenger RNA (mRNA). While non-coding RNA is essential for controlling gene expression, protein synthesis, and other cellular processes on numerous levels, certain RNA types are sometimes referred to be "bridges" due to their ability to efficiently transport genetic information from DNA to protein.[77,78] Research on the functions of cells, organs, and organisms benefits greatly from a fuller comprehension of transcriptomics. The study of transcriptomic profiles is made easier by RNA-Seq, a relatively new technology that measures the transcriptome's whole biological content.[79] Transcriptomics is a technique that examines gene expression levels through the analysis of the transcriptome. To assess mRNA expression, this method uses high-density or high-throughput techniques.[80] As a fundamental platform for translational medicine, transcriptomics uses DNA microarray technology to examine the biological effects that different herbal formulations cause in order to evaluate the safety and effectiveness of their treatments. This method makes it possible to find significant parallels between expression signatures.[81] The study of the transcriptome lies at the core of transcriptomics. Because of their high throughput, improved accuracy, and cost-effectiveness, genomic sequencing technologies have significantly expanded the number of genomic sequence databases during the last 20 years.[82–84] Total RNAs generated after transcription are the main focus of transcriptomics. Compared to genomics, transcriptomics generates a relatively lesser volume of data, making analysis simpler.[85] This field has been extensively explored across various organisms, yielding essential insights into gene structure, expression, and regulation.[86] Recently, transcriptomics research has experienced remarkable growth, driven by rapid advancements in sequencing technologies.[87,88] There are significant differences between transcriptomics and genomics in the context of plant study. First off, compared to transcriptomics (RNA-Seq), genome assembly in plant research is more complex and costly. The transcriptome is a useful tool for assessing an organism's or plant's total transcriptional activity when a reference genome is not available. Second, because it contains data on secondary metabolic pathways and variances in gene expression, the transcriptome is dynamic, reflecting changes over time and across various spatial locations.[89] Because of continuous improvements in sequencing techniques, the methods for examining transcriptomes have changed from simple DNA microarray platforms to RNA-Seq technologies.[90] Transcriptomics is a potent technology that offers trustworthy and easily comprehensible insights into changes in gene expression, which might shed light on complex drug action mechanisms.[91–93] Transcriptomics overcomes the constraints on the number of genes that can be measured, allowing for the simultaneous analysis of thousands of genes at different levels, such as organ, tissue, and cell types, in contrast to conventional transcriptional techniques like northern blotting and quantitative real-time polymerase chain reaction.[94,95] Many areas of biomedical research have made extensive use of transcriptomic techniques, especially in the diagnosis and profiling of diseases.[96] The identification of genes and pathways that respond to and minimise biotic and abiotic environmental stressors is made easier by this research. Transcriptomics' untargeted feature makes it possible to investigate new transcriptional networks in complex biological systems.[97] Additionally, transcriptomic profiling is essential for understanding the mechanisms underlying drug resistance.[98] These techniques have proven invaluable in elucidating gene functions and pinpointing those associated with specific phenotypes. For instance, transcriptomic studies of Arabidopsis ecotypes that exhibit hyperaccumulation of metals have linked genes related to metal uptake, tolerance, and homeostasis to the observed phenotypic traits.[99]

Limitation to transcriptomics:

In the clinical setting, transcriptomic analysis has not yet shown any promise. There have been few attempts to use the approach in translational research, and this field is mainly based in basic science. Transcriptomic tests have a significant obstacle in their capacity to accurately anticipate clinical implications because mRNAs serve as intermediate products of disease rather than the main results.[100]

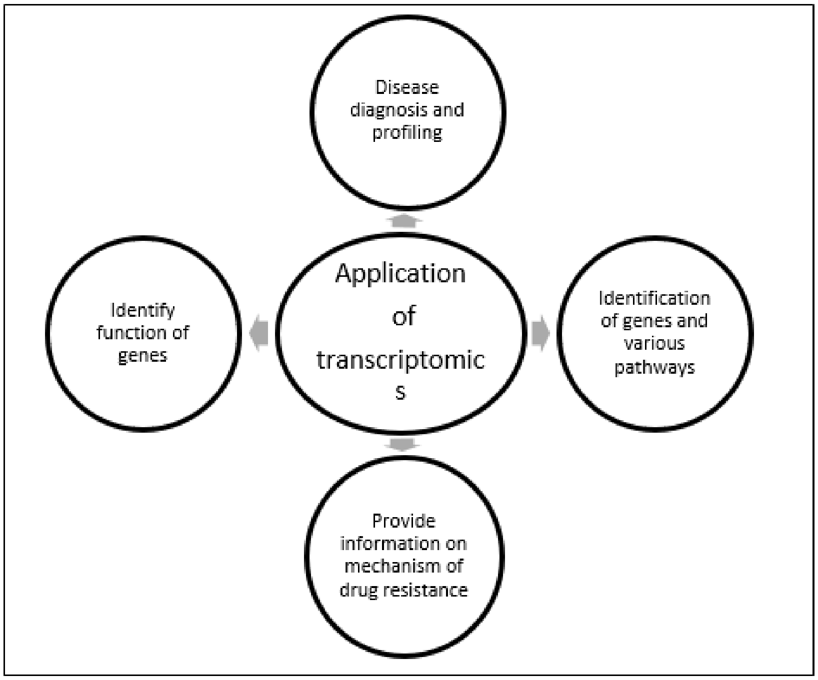

Figure 4: Applications of transcriptomics.

Genomics and modified techniques: -

Genomics is an advanced omics technology that can evaluate extensive genomic changes both before and after medication intervention.[85] When Tom Roderick coined the term "genomics," it originally meant the study of the complete genome. Today, a broader definition of it includes extensive, high-throughput molecular investigations of several genes, their byproducts, or certain gene sections.[101] The field of genomics includes the study of the human genome and the detection of DNA variations. Pharmacogenomics specifically examines the interactions between pharmaceutical agents and genetic outputs, marking one of the initial challenges effectively tackled by omics techniques in herbal research.[102] New, revolutionary automatic assays and specialised tools for DNA analysis, such as mini sequencing technologies, microsphere-based suspension arrays, and nanoscale DNA sequencing, are being developed on a regular basis. The next generation of genomic technology stands to benefit greatly from this developments.[103] With an emphasis on the examination of base sequence composition, DNA methylation, and chromatin changes, genomics includes the study of genetic variation, gene expression, and their roles. Research on Traditional Chinese Medicine (TCM) has made considerable use of genetics from its inception. High-throughput sequencing methods like whole-exome capture and sequencing, quantitative approaches like real-time fluorescence-based quantitative PCR, and single-cell sequencing—which has witnessed notable technological breakthroughs recently—are examples of key genomic technologies. With significant advantages like high-throughput capabilities, thorough and accurate results, and the capacity to perform investigations at the microscopic level, these genomic technologies enable the simultaneous examination of tens of thousands of genes. As a result, they are essential tools for developing precision medicine in modern medicine.[104] Several DNA polymorphism-based assay methods have been developed for the extraction and identification of herbal products. The development of DNA chips featuring specific DNA sequences has enabled the identification of plant materials, particularly in herbal samples.[105] Microarray analysis is another genomic technology that uses an advanced gene chip methodology to quickly and completely evaluate thousands of transcripts. The microarray falls within the category of transcriptomic technologies when used in this way.[106] Genomics represents a genome-scale approach applicable across all biological research domains. Generally, there are two types of genomic studies: structural genomics and functional genomics. By using a high-throughput approach that blends modelling and experimental methods, structural genomics seeks to clarify the three-dimensional structures of proteins encoded by particular genomes. Even now, there is still a lot of interest in sequencing the genomes of different creatures, especially looking at how genes express themselves in different environments. The goal of functional genomics is to clarify the functions of genes and proteins as well as how they interact. Microarrays and bioinformatics are important tools in this discipline, and methods like sequence-tagged fragment displays, cDNA microarrays, DNA chips, and serial analysis of gene expression (SAGE) are all very important. Genomics encompasses a wide range of topics, particularly in areas like pharmacogenomics, metagenomics, and epigenomics.[107]

Limitations to genomics:

The high expense of pharmacogenomic screening methods has prevented their widespread use. Depending on the number of necessary polymorphisms and vendor pricing, a genomic screen can cost anywhere from hundred dollars to several thousand dollars.[108] However, commercialisation, the use of microarray technologies, and an increase in clinical applications have made single screens more accessible.[109]

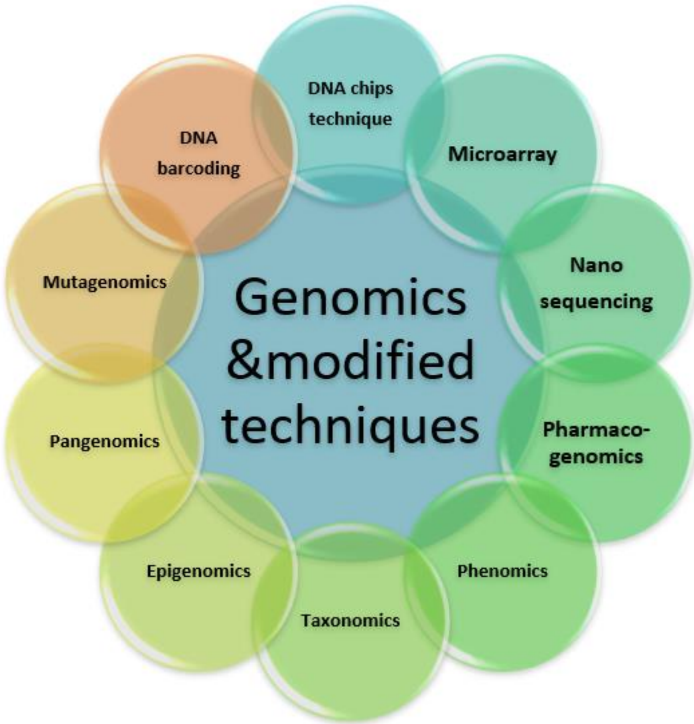

Figure 5: various modified techniques of genomic.

Lipidomics: -

As the building blocks of cell membranes, lipids serve as reserves of energy and are involved in many critical cellular functions. Lipidomics refers to the extensive examination of lipid pathways and networks within biological systems. [110-112] By analysing different lipid species, their amounts, biological roles, subcellular locations, and tissue distribution, this field offers a comprehensive understanding of lipid profiles. One subfield of metabolomics is lipidomics.[113] The kinds, distribution, and functions of lipids in animals, tissues, or cells as well as their interactions with other bio molecules are examined using sophisticated analytical techniques. A more thorough and methodical investigation of the molecular activities and regulatory roles of biological lipids is made possible by lipidomics, which emphasises the important contributions of lipids to cellular processes and disease mechanisms in contrast to other omics fields like proteomics and genomics. It also aims to comprehend how physiological processes are impacted by changes in lipid profiles and associated metabolites.[114] The objective evaluation of general lipid alterations in samples, identifying patterns and variances in lipid composition, is the main goal of non-targeted lipidomics. Finding differential markers that can offer insightful information for more study into lipid activities and processes is its main goal.115 Targeted lipidomics, on the other hand, includes in-depth qualitative and quantitative examinations of a single lipid or a small subset of lipids. Because of its great sensitivity and specificity, this method is especially helpful for monitoring metabolic pathways and low-abundance lipids. Targeted lipidomics is frequently used to examine or confirm important metabolic targets or pathways. Because lipids have variable structural properties, such as varying sizes and polarities, it is crucial to distinguish between these two approaches in lipidomics. This is because different lipid species require distinct procedures.[116] Immunoassays, shotgun lipidomics, and mass spectrometry approaches that employ chromatographic separation are currently the most common lipidomics analysis methods.[117] The sensitivity and dependability of lipidomic investigations are greatly impacted by the crucial stages of analytical sample extraction and preparation. Extracting lipid molecules from a complex matrix in order to exclude interfering components such as proteins, carbohydrates, and other polar metabolites is usually the initial step in lipidomic analysis. To guarantee the success of the ensuing analysis, this stage is crucial.[118] Although lipidomics frequently uses a number of reliable approaches, new approaches have emerged in recent years. Three main goals are being pursued by the development of these new techniques: 1. to focus on target molecules, where the optimal approach would be highly sensitive, fast, and specific; 2. to collect extensive data, where the optimal approach would be able to identify almost all lipid species at once; and 3. to investigate dynamic biological processes, which would enable direct cell visualisation. It is evident that these three objectives cannot be accomplished simultaneously with a single method. Consequently, various techniques are employed to create suitable methods tailored for different lipidomics applications. Lipidomic research has been greatly advanced by recent developments in analytical technologies for lipidomics, such as two-dimensional (2D) NMR, new mass spectrometry ionisation techniques, improvements in mass spectrometry imaging, and the use of two-dimensional liquid chromatography (2D LC).[119]

Limitation to lipidomics:

One of the primary concerns is ion suppression, which can influence ion formation, thereby impacting dynamic range and detection limits, as well as precision and accuracy in quantification. The presence of ion suppression can restrict the analysis of certain lipid classes, particularly those that are less abundant or have lower ionization potential. Another challenge in traditional shotgun lipidomics is the difficulty in distinguishing between isobaric and isomeric mass overlaps among individual lipid species, which hinders clear identification of lipids, even within specific classes or subclasses.[120]

Challenges to omics technique: -

Significant obstacles stand in the way of the omics technique, especially when it comes to data collection, multi-omics data analysis, and modelling. Managing the complex multi-omics datasets is one of the main challenges. Omics-based analysis has become a common practice within the last 20 years, and acquiring large-scale omics datasets through high-throughput analytical methods is now feasible. Looking ahead, the integration of various omics techniques will become increasingly prevalent to comprehensively characterize biological processes, resulting in extensive and intricate datasets. Online databases or experimental results are the usual sources of omics data. However, a number of issues, including the diversity of data formats, database redundancy, and the lack of standardised data description methods, make processing this data difficult. The most difficult task in omics research is still managing the large amount of data, especially multi-omics data from many sources.[121] Conducting dynamic analysis presents a significant challenge in omics research. Researchers increasingly recognize that the subjects of omics studies such as the lipidome, proteome, metabolome, and genome, are dynamic and can change even within the same sample that is examined under the same circumstances. To address this issue, it is essential to take time factors into account, necessitating sampling at various time points.[122] Additionally, there is a need for innovative analytical techniques, as multi-omics, particularly dynamic omics, demands more sophisticated methods.[107]

CONCLUSION: -

Omics methods were created to collect accurate molecular and genetic data on herbal plants. Nowadays, varieties of omics techniques are being used globally to characterise, identify, standardise, and control the quality of herbal formulas. They are also being used to identify the mechanism of action and molecular mechanisms that predict adverse drug reactions, side effects, and interactions between drugs and food. Numerous fields of biological science, agriculture, medicine, and research make use of omics methodologies. However, there are still issues in the field of omics, including with modelling, data gathering, and multi-omics data analysis. Reducing the number of factors assessed in each sample while increasing the number of repetitions is a clear way to improve omics research. This strategy fits in nicely with the limitations of measurement technologies as they stand right now. Researchers may collect vast amounts of data using platforms like genomics, proteomics, and metabolomics. These data can then be analysed using bioinformatics and mathematical techniques to reveal important patterns and insights about organisms. Additionally, the advancement of translational research aimed at engineering plant systems to satisfy changing societal demands depends on the integration of distinct omics datasets from various plant species.

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