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Review Article

Multi-Omics Integration in Personalized Medicine: Advancing Laboratory Diagnostics and Precision Therapeutics in the Era of Individualized Healthcare

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Abstract

Personalized medicine is revolutionizing healthcare by shifting from a one-size-fits-all model to a tailored approach that considers individual genetic, molecular, environmental, and lifestyle factors. This review comprehensively explores the role of personalized medicine in laboratory diagnostics and patient management through the lens of emerging omics technologies such as genomics, transcriptomics, proteomics, metabolomics, and pharmacogenomics. Each omics domain offers unique insights into disease mechanisms, drug response, and biomarker discovery, enabling more accurate diagnoses, targeted therapies, and improved treatment outcomes. While genomics and pharmacogenomics focus on the genetic basis of disease and therapeutic response, transcriptomics and proteomics bridge the functional gap between genotype and phenotype, revealing dynamic changes at the RNA and protein levels. Metabolomics adds another layer of complexity by capturing small-molecule metabolites that reflect cellular physiology in real time. Despite the promise of personalized medicine, its clinical implementation is hindered by technical limitations, high costs, data integration challenges, and concerns over reproducibility and data privacy. Moreover, optimizing transcriptomic study design, especially the balance between sequencing depth and biological replication, remains crucial for generating robust, reproducible data. The integration of multi-omics data holds the potential to drive breakthroughs in diagnosis and therapy, particularly in oncology, rare diseases, and complex disorders. This article highlights the critical role of personalized medicine in laboratory practice and advocates for continued investment in multi-omics technologies and data infrastructure to advance precision healthcare.

Keywords: Personalized medicine, Multi-omics, Pharmacogenomics, Metabolomics, Transcriptomics

Introduction

Personalized medicine is a healthcare approach that tailors disease prevention, diagnosis, and treatment to an individual's unique genetic, environmental, and lifestyle factors. By customizing medical interventions, it seeks to maximize treatment effectiveness while minimizing side effects. This approach leverages advanced diagnostic and therapeutic tools, including genomics, proteomics, and pharmacogenomics, to analyze a person's genetic makeup, molecular profile, and clinical data, enabling targeted and precise medical decisions. Precision medicine is a specialized subset of personalized medicine that emphasizes tailoring treatments to an individual's unique molecular characteristics[1]. While personalized medicine encompasses a broader approach, considering various factors that tailor healthcare to an individual's needs and circumstances, precision medicine specifically focuses on molecular-level interventions. The advancement of targeted therapies and companion diagnostics, tools that identify patients most likely to benefit from specific treatments, has been a key driver in the growing adoption of precision medicine[2]. The first successful application of precision medicine was the use of imatinib to treat chronic myelogenous leukemia

(CML) in 2001, which demonstrated the power of targeting specific genetic mutations to treat cancer[3]. Precision medicine represents a paradigm shift in the approach to healthcare[4]. While the completion of the Human Genome Project in 2003 significantly accelerated progress in this field, earlier medical breakthroughs had already demonstrated the potential of tailoring treatments based on individual patient characteristics.

The Human Genome Project, which aimed to map the entire human genome, played a crucial role in identifying genetic variations linked to various diseases, thereby laying the groundwork for the development of personalized medical interventions[5]. The revolutionary breakthroughs made by these scientists allowed researchers, for the first time in history, to connect diseases and human health to a wide range of individual genetic and environmental factors. The scientific discoveries helped researchers to gain a better understanding of what specific molecules within the human body determine a patient's individuality and, more importantly, their susceptibility to certain diseases. As a systematic survey recently concluded, whether called precision medicine or personalized medicine, the phrase has come to refer to the way personal data and biomarkers, particularly genetic biomarkers, might be used to tailor treatments for individual patients[6]. Precision medicine is not a new concept but has its roots in the early days of medicine, where physicians practiced personalized medicine by observing and treating individual patients based on their unique symptoms and characteristics[7]. The advent of next-generation sequencing and other high-throughput technologies has accelerated the pace of precision medicine research, enabling rapid identification of disease-causing mutations and personalized treatment options.

Precision medicine has many potential applications in healthcare, such as cancer treatment, where specific genetic mutations or biomarkers in cancer cells can be identified and targeted with drugs for more effective and personalized treatments[8]. In pharmacogenomics, precision medicine can identify genetic variations that affect an individual's response to medications, enabling doctors to prescribe the most effective treatment with minimal side effects. It can also identify the genetic causes of rare diseases and genetic disorders, allowing for earlier diagnosis and more targeted treatments. For infectious diseases, precision medicine can help identify genetic variations that make individuals more susceptible to certain diseases, leading to more targeted prevention and treatment[10]. Similarly, precision medicine can help identify the genetic variations that cause neurological disorders, such as Alzheimer's and Parkinson's diseases, enabling earlier diagnosis and more targeted treatments.

Personalized medicine is being revolutionized by the integration of multi-omics data, primarily genomics, transcriptomics, proteomics, and metabolomics[11]. This integrated approach provides a holistic view of individual health by capturing genetic, molecular, and biochemical information. The ability to generate and synthesize multi-omics data enables the development of highly specific and personalized therapeutic strategies, enhancing treatment efficacy and minimizing adverse reactions. Despite its promise, the full implementation of personalized medicine faces substantial barriers[11]. Chief among these is the complexity of integrating diverse omics datasets, the requirement for advanced bioinformatics and computational infrastructure, and the high costs associated with large-scale data generation. The challenges related to data privacy, lack of standardization across platforms, and limited validation in diverse populations continue to impede widespread clinical application.

History and Development

The evolution of personalized medicine has been driven by key breakthroughs in genetics, technology, and clinical practice, marking a clear departure from the traditional one-size-fits-all model toward a more precise, individualized approach that targets the molecular mechanisms underlying health, disease, and therapeutic response[12]. The origins of personalized medicine can be traced back to Hippocrates, who recognized that individual variability among patients could influence how they respond to treatment, an idea that laid the foundation for today's precision healthcare approaches. However, the scientific foundation of personalized medicine was solidified in the 20th century through the discovery of DNA and the elucidation of the genetic code[13], which provided the molecular basis for understanding individual variability in health and disease. The use of the term "personalized medicine" has gained momentum in recent years, driven by advances in diagnostic technologies and bioinformatics, particularly comparative genomics, which have deepened our understanding of the molecular basis of disease and enabled more precise patient stratification and targeted interventions.

Over the past six decades, extensive research has demonstrated that a substantial proportion of variability in drug response is influenced by genetic factors, alongside diet, health status, environmental exposures, and combination therapies[14]. Progress in pharmacogenomics and pharmacogenetics has been instrumental in uncovering the molecular mechanisms through which an individual's genetic makeup affects disease susceptibility and therapeutic efficacy, thereby advancing the principles of personalized medicine[15]. Consequently, drug therapies must be tailored to individual patient profiles to achieve more predictable and effective outcomes across geographically and ethnically diverse populations, accounting for genetic variability and other individual-specific factors that influence treatment response. Pharmacogenomics emerged from advances in molecular medicine aimed at understanding the molecular mechanisms that drive individual drug responses. This application of scientific research is what defines personalized medicine. While the concept remains largely unfamiliar to the average

patient, it holds the potential to transform the entire healthcare system by enabling more precise, effective, and patient-centered care[16]. Today, personalized medicine has significantly transformed cancer care. Advances in genomic sequencing and molecular diagnostics have enabled oncologists to classify cancers with greater precision, leading to more accurate diagnoses, improved prognostic assessments, and better prediction of treatment responses[17]. Targeted therapies such as HER2 inhibitors for breast cancer and EGFR inhibitors for lung cancer are developed based on specific genetic mutations identified within individual tumors[18], marking a shift toward more effective, individualized oncology treatment strategies.

Genomics and personalized medicine

Genomics has played a pivotal role in advancing personalized medicine, allowing for targeted therapies and precision medicine approaches to improve patient outcomes[19]. Genomics has been instrumental in advancing personalized medicine, and the field has rapidly evolved from sequencing a few genes to analyzing entire genomes, enabling tailored treatments based on an individual's genetic profile. Multi-omics integration techniques, particularly genomic data acquired from new sequencing technologies, have made a significant contribution to expanding and deepening understanding of the molecular mechanisms of diseases[20]. By analyzing an individual's genetic information, healthcare providers can gain insights into their unique risk factors for disease, drug response, and potential side effects. Genomics testing involves analyzing an individual's DNA to identify variations or mutations in specific genes or regions of the genome, and its purpose can vary depending on the type of test being performed[21]. The testing process involves collecting a sample of DNA, usually through a blood or saliva sample, and analyzing it in a laboratory setting. Different types of genetic tests can be performed, including sequencing, which determines the order of the nucleotides (A, C, G, T) that make up an individual's DNA, and genotyping, which identifies specific variations or mutations in the DNA sequence. Genomic testing is revolutionizing the field of personalized medicine, allowing for more precise diagnoses and targeted treatments. Genomics testing encompasses various types of testing that serve distinct purposes.

Cancer treatment, especially, benefits immensely from genomic analysis and precision medicine. Genomic analysis identifies specific genetic mutations that drive cancer progression[22]. By focusing on these mutations unique to each patient's cancer, targeted therapies can be developed to more effectively eradicate cancer cells while sparing healthy tissue. For instance, mutations in the BRCA1 and BRCA2 genes are crucial biomarkers for breast and ovarian cancers[23,24], enabling more tailored and effective treatment strategies. Gene therapy and gene-editing technologies like CRISPR allow for precise alterations to DNA[25]. These techniques involve introducing, removing, or modifying genetic material within a person's cells to treat or prevent diseases. They have the potential to correct genetic defects at their source, potentially offering cures for genetic disorders that were once deemed untreatable[26]. Overall, the convergence of genomics, biotechnology, and data analytics is propelling personalized medicine forward, offering transformative potential for healthcare systems. By enabling more precise, predictive, and preventive approaches, personalized medicine is set to improve patient outcomes and elevate public health on a broader scale.

Advantages and Limitations of Genetic Testing

Health information is increasingly recognized as a pivotal element in determining diagnosis and treatment within a patient's healthcare[27], with genetic data being a crucial component of this information. Genetic data can be obtained through various types of genetic testing, including molecular genetic tests that examine single genes or DNA strands, chromosomal tests that analyze long DNA strands and entire chromosomes, and biochemical tests that study protein behavior. Genetic testing plays an important role in healthcare as it offers valuable insights into an individual's genetic makeup and its potential impact on their health[28]. Critical to precision medicine, genetic testing informs various aspects of patient care, including risk assessment, prevention, diagnosis, treatment, and ongoing monitoring of genetic disorders like cancer. It provides patients and their families with important health risk information and tailored management plans.

The accuracy and reliability of genetic testing depend on factors such as the type of test, the quality of the sample, and the expertise of the laboratory performing the test. When conducted and interpreted by qualified professionals, genetic testing can be highly accurate and beneficial in guiding treatment decisions and identifying potential risks for family members. It is an invaluable tool for diagnosing and managing genetic disorders and conditions. However, genetic testing is not without limitations. Genetic testing has limitations and cannot provide definitive answers about a person's health status or future risks[29]. Even with its availability, genetic testing may not always be the most helpful option, as other medical tests may offer more direct benefits. For instance, in the case of hereditary hemochromatosis, an autosomal recessive disease common among Caucasians, genetic testing can identify carriers; however, current screening guidelines recommend measuring serum iron levels, total iron-binding capacity, and serum ferritin levels. These tests, which are less expensive than DNA-based testing, provide more relevant information about a patient's iron storage status. While genetic testing for hereditary hemochromatosis can reveal whether someone is a carrier or homozygous for the gene, it does not provide insight into the patient's current iron load[30]

Genetic testing cannot predict future health outcomes with absolute certainty[31]. It can also reveal unexpected or incidental findings, which may cause unnecessary anxiety and lead to unwarranted medical interventions. However, counseling services are now available to help

individuals understand these risks and benefits. It is crucial for individuals to carefully consider the potential risks before undergoing genetic testing, as it has limitations related to accuracy, predictive power, and clinical validity. Direct-to-consumer genetic testing allows individuals to access their genetic risk information without consulting healthcare providers, but it raises concerns over the accuracy and clinical validity of some tests. The absence of expert guidance and genetic counseling in these cases increases the risk of misinterpreting results. As a result, there is a call for greater regulation and oversight of direct-to-consumer genetic testing to ensure its responsible use and minimize potential harm to consumers[32].

Pharmacogenomics and personalized medicine

Pharmacogenomics investigates how an individual's genetic makeup affects their response to medications, combining principles from pharmacology, the study of drug action, with genomics, which focuses on genes and their functions. By aligning drug therapies with a patient's genetic profile, pharmacogenomics supports the development of personalized treatment plans that enhance efficacy and reduce adverse effects. As research advances and technological accessibility improves, the integration of pharmacogenomics into routine clinical practice is expected to expand, driving the shift toward more precise, individualized healthcare strategies[33,34]. Understanding how genetic variations affect individual responses to medications is essential, given the diversity in genetic profiles, lifestyles, and environmental exposures among patients. Differences in DNA sequences can alter drug metabolism, leading to significant variability in drug efficacy and the risk of adverse effects. This insight enables clinicians to select medications and dosages that are optimized for each individual's genetic makeup, resulting in more effective treatment outcomes and minimized side effects key principles at the core of personalized medicine[35].

Genome-wide association study approaches are now being successfully applied to pharmacogenomics research[36]. This is a powerful tool that has already produced some novel insights: HLAB5701 as a predisposing factor for flucloxacillin induced liver injury[37]; IL28B genotypes as predictors of hepatitis C treatment outcomes[38]; the ABO blood group genes as predictors of the antihypertensive efficacy of angiotensin-converting-enzyme inhibitors[39]; and several genotypes as tentative biomarkers for antipsychotic induced Parkinsonism[40]. Hopefully, many other genome-wide response studies will soon follow.

Advantages and Limitations of Pharmacogenomics

Pharmacogenomics plays a critical role in advancing precision medicine and its allied disciplines by enabling enhancements at every stage of the drug lifecycle from discovery to delivery. In drug research and development, pharmacogenomic data informs how candidate therapies are identified and refined for specific genetic profiles, improving the alignment between disease biology and therapeutic intervention[41]. Genome-wide association studies (GWAS) have been pivotal in identifying population subgroups that respond differently to specific medications, allowing for more stratified and effective therapeutic strategies[42]. In later stages of drug development, pharmacogenomic insights are increasingly embedded in the regulatory and manufacturing process. Drug labeling now frequently includes pharmacogenomic (PGx) data, guiding clinicians toward more precise prescribing based on genetic markers, with many labels containing clinically actionable information[41]. In clinical practice, PGx data also supports tailored prescribing decisions, enabling adjustments in drug type and dosage based on individual variations such as single nucleotide polymorphisms[43].

The application of pharmacogenomics in clinical trials is equally significant. Selecting genetically appropriate participants enables better assessment of pharmacokinetics and pharmacodynamics across genetically diverse populations, thereby supporting more population-specific dose optimization and enhancing trial efficiency[44]. This precision reduces the likelihood of adverse drug reactions while improving treatment efficacy[45]. Integrating pharmacogenomics into the drug development pipeline holds the potential to reduce R&D costs, shorten timelines, and improve healthcare outcomes by delivering more targeted therapies[46].

Nevertheless, the field faces substantial implementation challenges. These include the complexity of gene-drug and gene-environment interactions, limited availability of diverse genomic data, and high costs associated with genetic testing and data integration. Additionally, ethical, regulatory, and infrastructural barriers, along with the limited number of drugs with well-defined genetic targets, continue to restrict their clinical uptake[47]. However, as PGx testing becomes more widespread and cost-effective, it is expected to yield measurable improvements in clinical outcomes, mitigate adverse drug reactions, and contribute to more sustainable healthcare systems.

Proteomics and personalized medicine

Proteomics studies the complete set of proteins present in a biological sample, including their structures, functions, and interactions[48]. It is a large-scale approach to understanding the dynamic and complex nature of protein expression and its roles in biological processes. Proteomics techniques identify, quantify, and characterize proteins, their modifications, and interactions. The aim is to gain a comprehensive understanding of protein expression, regulation, and function, which can lead to the discovery of new biomarkers, drug targets, and therapeutic interventions[49]. Human phenotypes play a key role in biomedical research and clinical practice towards better diagnosis, patient stratification, and the selection of effective treatment strategies. Computational approaches developed for the integration of multiple omics data types allow for a more holistic understanding of molecular mechanisms in health and

disease-related processes[50]. Such combined approaches can lead to the discovery of biomarkers that enable personalized medicine approaches by representing personalized prognosis and treatment efficacy. The acquisition of data derived from genomic, transcriptomic, and proteomic personal phenotypes (among other types of omics techniques) holds implications for both personalized medicine and data privacy-related issues, considering technical, ethical, and legal aspects[51]. Through rapid proteomic screening of easily accessible tissue samples, early determination of the presence and/or severity of disease allows for quick response from medical personnel and improved patient outcome. The power of proteomics is in discovering the meaningful unknown in a bouillabaisse of unrelated molecules with high mass accuracy and sensitivity. For this reason, clinical proteomics will be most helpful for the diagnosis of diseases with rare or unknown etiology, monitoring the therapeutic effect and activity of drug regimens, improving treatment options for individual patients, and, as always, discovering a brave new world of medical possibilities.

Precision medicine aims to match patients with the best course of therapy to ensure optimal outcomes, and genetic profiling of HLA loci has reduced transplant rejection rates by matching donors and recipients. Despite this level of scrutiny, as many as 10% of transplants result in rejection or graft versus host disease (GVHD)[52,53]. Differential alteration of the self and transplant peptidome after infection has been implicated as a potential cause for these complications[54]. Personalized proteomic analysis of the HLA loci, minor antigen loci, and peptide repertoire of potential donor/recipient pairs could reduce this rate even further[54].

Molecular diagnosis is moving beyond genomics to proteomics[55]. To understand proteomics, understanding what the proteome is very necessary. According to the American Medical Association (AMA) and the Office of Cancer Clinical Proteomics Research at the National Cancer Institute, the term proteome was taken from two words: protein and genome, so “prote- “was taken from protein and “-ome” from genome. Therefore, proteomes are proteins that are expressed by different genomes and other cells[56]. Proteomics, the study of the proteome, is important because proteins represent the actual functional molecules in the cell. Importantly, proteomics provides important insights into our understanding of cell signaling; specifically, the quantitative identification of protein cargo and biological insights of extracellular vesicles[57].

Proteomics typically gives us a better understanding of an organism than genomics. The level of complexity resulting from co- and posttranslational modification events can only be dissected and understood through qualitative and quantitative studies at the level of the functional proteins themselves[55]. Proteins, not genes, are responsible for the phenotype of cells. Finally, protein degradation rate plays an important role in protein content[58]. Particularly, when interpretation of protein expression considers the dynamics of this expression in specific biological contexts. Chung et al. developed a method for analyzing serum potential biomarkers in patients with bronchial asthma[59]. Unlike other diseases (e.g., cancer), the goal of proteomics in patients with bronchial asthma is not to develop a new method for asthma diagnosis through analysis of body fluids; instead, it aims to determine the causal relationship between changes of proteins in body fluids and clinical phenotypes, to identify target molecules that play key roles in the pathogenesis of asthma, eventually leading to the development of new treatment protocols[55]. Proteomics can aid in the diagnosis and treatment of various medical conditions such as bronchial asthma, oncology, cancer, heart diseases, and neurodegenerative diseases such as Parkinson's and Alzheimer's. It also has applications in Met proteomics. These benefits make proteomics a valuable tool in medical laboratory diagnosis.

Advantages and Limitations of Proteomics

Proteomics has the potential to revolutionize lab management by providing more efficient and comprehensive analysis of biological samples[60]. It is a valuable tool for lab management, as it can improve the efficiency and reproducibility of experiments, facilitate quality control, and enable identification of novel biomarkers[61]. Proteomics has been noted to have significant benefits in lab management. Gromski and colleagues [62] suggest that the detection of protein markers specific to a disease through proteomic analysis may enhance diagnostic precision and expediency, thereby facilitating the development of customized treatment strategies.

Proteomics, despite its vast potential, continues to face significant technical and biological challenges. These include difficulties in the accurate identification and quantification of proteins, restricted dynamic range, and incomplete proteome coverage, primarily due to the inherent complexity of biological samples and current technological limitations[63]. Data analysis in proteomics remains particularly problematic, with persistent issues such as the inability to reliably detect low-abundance proteins and distinguish between true and false identifications, even with notable advancements in analytical methods[64]. Although technological progress has improved certain aspects, major hurdles persist related to sample heterogeneity, limited sensitivity, low throughput, and the dynamic nature of the proteome[65]. Additional complications stem from challenges in detecting specific proteins and post-translational modifications, ensuring reproducibility, and managing the high cost and complexity associated with proteomic data analysis.

Metabolomics and Personalized Medicine

Metabolomics emerged in the late 1990s as a progression from proteomics[66]. It focuses on the detection, identification, and quantification of low molecular weight compounds within a biological system. The metabolome encompasses all small

molecules typically less than 1000 to 1500 Daltons found in a biological sample, excluding macromolecules such as proteins and nucleic acids[67]. These metabolites include essential components of cellular energy metabolism, such as amino acids, sugars, nucleotides, and fatty acids. Additionally, some metabolites are species-specific and play specialized biological roles, for example, glucocorticoids and neurotransmitters in mammals or alkaloids in plants. Xenobiotics, which are chemicals present in living organisms but not naturally produced by them, such as drugs and environmental pollutants, are also considered part of the metabolome[68]. This inclusion is based on their presence in biological systems and their detectability using the analytical chemistry techniques employed in metabolomics.

Metabolomics presents a level of complexity that far exceeds the simplified metabolic pathways typically illustrated in biochemistry textbooks. Unlike theoretical proteomes, which can be relatively well predicted from genomic data, the total number of metabolites in living organisms remains undefined. This is due in part to the vast chemical diversity among metabolites, which range from polar, hydrophilic molecules like sugar derivatives to apolar, hydrophobic compounds such as lipids. As a result, there is no single analytical method capable of capturing the entire metabolome. Comprehensive metabolite detection, therefore, depends on the use of complementary analytical techniques in parallel[69]. The two primary technologies driving metabolomics data acquisition are nuclear magnetic resonance (NMR) spectroscopy and mass spectrometry (MS). MS can be used directly or in conjunction with separation techniques such as gas chromatography (GC-MS), liquid chromatography (LC-MS), or capillary electrophoresis (CE-MS). Since the early 2000s, metabolomics workflows encompassing sample preparation, analytical measurements, data pre-processing, statistical analysis, and visualization have evolved significantly and are now well-established. Today, metabolomics is recognized as a standalone analytical platform and is routinely applied in systems biology across diverse fields, including environmental science[70], plant biology[71,72], nutrition, and human and animal health[73].

In biomedical research, metabolomics plays a pivotal role within the broader framework of systems medicine, a holistic, data-driven approach to health and disease that underpins personalized medicine. Biomarker discovery has become a cornerstone of modern healthcare, essential for advancing precision diagnostics, prognosis, and therapeutic monitoring. Omics-based strategies, including metabolomics, are particularly valuable for identifying novel biomarkers or panels of biomarkers that reflect disease states or treatment responses. By enabling the comprehensive profiling of low molecular weight compounds in patient samples, metabolomics offers a promising avenue for uncovering biologically and clinically relevant molecular signatures. However, despite extensive research efforts over the past decade, the number of omics-derived biomarkers that have received regulatory approval and been integrated into clinical practice remains disappointingly low[74].

Advantages and Limitations of Metabolomics

The metabolome is highly responsive to both genetic and environmental influences[75]. As such, conducting a metabolomic study demands careful consideration of multiple variables to minimize confounding factors and maximize data integrity. Robust experimental design is critical for reducing interindividual variability, and selecting the most appropriate analytical platform, based on the specific objectives and capabilities of the laboratory, is a key decision that significantly impacts both the quality of results and the extent of data recovery. A persistent challenge, particularly in LC-MS-based metabolomics, lies in the accurate identification of biomarkers, which continues to be a major limitation in the field[76]. The metabolome is influenced by genetic, environmental, and gut microbiota pressures, thus, subtle variations between individuals can result in large perturbations to metabolite concentrations and flux.

Environmental factors, such as diet, stress, lifestyle, disease, and exposure to xenobiotics, along with genetic variations including gender differences, gene polymorphisms, and epigenetic modifications, significantly influence the metabolome[77]. Additionally, the gut microbiota plays a critical role in co-metabolizing dietary compounds, such as phenols and phenylalanine, as well as xenobiotics like prontosil, fostamatinib, and acetaminophen. Disruptions in the gut microbial environment have also been linked to conditions like obesity[78]. Collectively, these genetic, environmental, and microbiome-related factors contribute to substantial interindividual variability in metabolomic profiles. The complex interactions among them further complicate data interpretation, posing a challenge to achieving consistent and reliable results in metabolomic studies. To overcome the confounding effects of variation, the concept of a metabolic fingerprint or the metabotype was conceived to encompass and identify all the possible variations in an individual[79]. The most challenging part of a metabolomic study is confirmation of biomarker identity[80]. This is an essential step toward understanding the biological changes occurring within the system and remains a major bottleneck in metabolomics investigations.

Transcriptomics and Personalized Medicine

The transcriptome encompasses the complete set of RNA transcripts present within a cell or tissue[81]. This includes various alternative splice variants. A primary reason for studying the transcriptome is that the majority of human genes undergo alternative splicing. In eukaryotic genes, exons and introns are common structural components; however, only exons are ultimately translated into proteins. Introns are removed during RNA processing. The mechanism responsible for excising introns and joining exons to form a mature mRNA is known as splicing[82]. Transcriptomics is the study of the transcriptome and is involved in the

function of cells, tissues, or organisms, across a wide range of biological conditions[83]. The relationship between the transcriptome and the genome suggests that the information of an organism is stored in the DNA (the genome) and expressed by RNA (the transcriptome). The main focus of transcriptomics is to discover how transcripts of a cell, tissue, or living organism are influenced by disease or environmental factors (such as drugs, hormones, etc.)[84]. Non-coding RNA is another very important aspect of transcriptomics. These functional elements play an important role in the occurrence of a variety of diseases and their response to treatment. Transcriptomics encompasses the post-transcriptional phase of gene expression, enabling the detection of molecular alterations that may not be evident at the genomic level[85]. These transcript-level changes, if associated with pathogenic mechanisms, are critical to identify for the development of more effective and targeted therapeutic strategies. In essence, transcriptomics serves as a bridge between genomics and proteomics, complementing both and playing a pivotal role in advancing precision medicine[86]. Various techniques are employed in transcriptome analysis, depending on the scope of investigation, whether focused on a single gene or a limited set of genes, or aiming to profile the entire transcriptome of a cell, tissue, or organism.

Advantages and Limitations of Transcriptomics

One of the primary challenges in RNA-seq experiments is the extraction of sufficient quantities of high-quality RNA from the target tissue. RNA is highly unstable and degrades rapidly, making timely and precise tissue dissection essential, especially when working with small or delicate regions like specific brain areas. This is particularly demanding in small organisms such as zebrafish, where dissections must be completed within 2–3 minutes to preserve the integrity of the sample without compromising anatomical accuracy. Furthermore, obtaining adequate RNA yields is difficult due to the low abundance of messenger RNA (mRNA), which constitutes only 1–2% of total cellular RNA, the portion relevant for sequencing. In contrast, ribosomal RNA, which makes up approximately 90% of total RNA, must be selectively removed before analysis, adding another layer of complexity to the preparation process[87].

Pooling samples involves combining multiple individual biological samples into a single composite sample before transcriptomic analysis. This pooled sample is then processed as one library and represents a single biological replicate. In contrast, analyzing each sample individually involves constructing a separate library for each biological specimen, preserving the integrity of biological replicates. Pooling is often employed to reduce sequencing costs, address limitations in tissue availability, or compensate for low RNA yield. It may also be used to mitigate batch effects in sequencing runs[88]. Despite its practical benefits, pooling introduces significant limitations. Since each pool is treated as a single data point, it obscures individual biological variation and reduces the statistical power of downstream analyses. Therefore, results derived from pooled transcriptomic data must be interpreted with caution, and researchers must not mistake pooled samples for independent biological replicates.

In transcriptomic studies, researchers face a critical trade-off between sequencing depth and the number of biological replicates, both of which significantly influence the cost, statistical power, and reliability of the experiment[89]. This decision is particularly important in the context of ongoing concerns about reproducibility, especially in fields like psychology and neuroscience, where underpowered studies have led to questionable findings. In RNA-seq experiments, a common practice is to include a minimum of three biological replicates per condition. However, this threshold is largely arbitrary and may be insufficient. The appropriate number of replicates should be determined based on the specific research objective, the inherent biological variability of the system under investigation, and the level of statistical power required to detect meaningful biological differences. Balancing these factors is essential for producing robust, reproducible results that support genuine scientific discovery.

Future Interconnections Between Multi-Omics Data and Personalized Medicine

Modern advancements in personalized medicine are increasingly dependent on technologies that analyze a patient's fundamental biology, such as DNA, RNA, and protein profiling, which are crucial for accurate disease diagnosis[90]. As technological progress continues, the integration of DNA analysis with precision medicine is anticipated to broaden, offering new possibilities for disease prevention, treatment, and management. For example, personalized approaches like genome sequencing can identify DNA mutations that influence a wide range of diseases, from cystic fibrosis to cancer[91]. Omics sciences focus on the comprehensive characterization of biological molecules, offering valuable insights into an organism's structure, function, and dynamics. In precision medicine, multi-omics combines data from genomics, transcriptomics, proteomics, metabolomics, and other fields to understand how molecular variations impact disease development, progression, and treatment responses. This integrated approach provides a deeper understanding of complex biological processes and disease mechanisms, ultimately advancing personalized healthcare.

Several international networks and projects are currently dedicated to applying multi-omics approaches in precision medicine, including The Cancer Genome Atlas (TCGA), The Precision Medicine Initiative (PMI) Cohort Program, Pan-Cancer Analysis of Whole Genomes (PCAWG), and the Human Proteome Project (HPP)[92]. A notable example is the European Joint Programme on Rare Diseases (EJP RD), a Europe-wide initiative focused on accelerating the diagnosis and treatment of rare diseases by integrating multi-omics data to gain deeper insights into disease mechanisms and improve therapeutic precision[92]. In a 2018 study on

pancreatic ductal adenocarcinoma, researchers integrated genomics, transcriptomics, and proteomics data to identify distinct molecular subtypes with varying responses to treatment, thereby improving patient classification for personalized therapy[93]. Similarly, a 2020 study utilized a multi-omics approach to analyze cerebrospinal fluid samples from Alzheimer's patients, combining proteomics and metabolomics data to identify new biomarkers linked to the disease, furthering the understanding of its molecular mechanisms[94]. These examples highlight how multi-omics approaches have revolutionized the understanding of complex biological systems and diseases, enhancing diagnostic and therapeutic strategies across multiple fields.

Conclusion

In conclusion, personalized medicine marks a transformative advancement in healthcare, shifting from a generalized treatment paradigm to a patient-centric approach grounded in molecular and genomic insights. The integration of genomics, transcriptomics, proteomics, metabolomics, and pharmacogenomics has enabled clinicians and researchers to unravel complex disease mechanisms, stratify patients more accurately, and tailor therapies to individual profiles. This approach holds particular promise in oncology, pharmacotherapy, and rare disease management, where molecular characterization directly informs therapeutic decisions. However, the widespread clinical implementation of personalized medicine remains constrained by significant challenges, including data integration complexities, high costs, limited genomic diversity in research cohorts, and infrastructure demands. Transcriptomics, by revealing post-transcriptional changes invisible at the genomic level, serves as a vital link between genotypic data and proteomic outcomes, enhancing our ability to detect disease signatures and therapeutic targets. The reproducibility of transcriptomic data, however, depends heavily on adequate biological replication and methodological rigor, emphasizing the need for well-powered experimental designs. Despite existing limitations, personalized medicine is poised to redefine modern clinical practice, offering the potential for earlier diagnoses, improved treatment efficacy, reduced adverse reactions, and more efficient healthcare delivery. Continued investment in multi-omics research, ethical data governance, and equitable access will be pivotal in translating its full potential into routine patient care.

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References

1. Pandey A, Gupta SP. Personalized Medicine: A Comprehensive Review. Oriental Journal of Chemistry. 2024;40(4). https://doi.org/10.13005/ojc/400403
2. Hartl D, de Luca V, Kostikova A, Laramie J, Kennedy S, Ferrero E, Siegel R, Fink M, Ahmed S, Millholland J, Schuhmacher A. Translational precision medicine: An industry perspective. Journal of Translational Medicine. 2021;19(1):245. https://doi.org/10.1186/s12967-021-02910-6
3. Kumar SS. Personalized medicine: the use of genetic information to tailor treatment plans to individual patients. Personalized medicine. 2024;1(2). https://jagunifiedinternational.in/journals/jrhp/
4. Gameiro GR, Sinkunas V, Liguori GR, Auler-Júnior JO. Precision medicine: changing the way we think about healthcare. Clinics. 2018;73:e723. https://doi.org/10.6061/clinics/2017/e723
5. Taylor DJ, Eizenga JM, Li Q, Das A, Jenike KM, Kenny EE, Miga KH, Monlong J, McCoy RC, Paten B, Schatz MC. Beyond the human genome project: the age of complete human genome sequences and pangenome references. Annual review of genomics and human genetics. 2024;25. https://doi.org/10.1146/annurev-genom-021623-081639
6. Naithani N, Sinha S, Misra P, Vasudevan B, Sahu R. Precision medicine: Concept and tools. medical journal armed forces india. 2021;77(3):249-57. https://doi.org/10.1016/j.mjafi.2021.06.021
7. Hamburg MA, Collins FS. The path to personalized medicine. New England Journal of Medicine. 2010;363(4):301-4. https://doi.org/10.1056/nejmp1006304
8. Mishra NP, Nirmal AK, Mishra OA. Precision Medicine in Cancer Biology: Using Genetic and Molecular Profiling to Personalize Treatment. International Journal of Research and Innovation in Applied Science. 2024;9(2):233-8. https://doi.org/10.51584/ijrias.2024.90219
9. Pirmohamed M. Pharmacogenomics: current status and future perspectives. Nature Reviews Genetics. 2023;24(6):350-62. https://doi.org/10.1038/s41576-022-00572-8
10. Alvarez MJ, Hasanzad M, Meybodi HR, Sarhangi N. Precision medicine in infectious disease. InPrecision medicine in clinical practice 2022 Oct;221-257. https://doi.org/10.1007/978-981-19-5082-7_13
11. Molla G, Bitew M. Revolutionizing Personalized Medicine: Synergy with Multi-Omics Data Generation, Main Hurdles, and Future Perspectives. Biomedicines. 2024;12(12):2750. https://doi.org/10.3390/biomedicines12122750
12. Dugger SA, Platt A, Goldstein DB. Drug development in the era of precision medicine. Nature reviews Drug discovery. 2018;17(3):183-96. https://doi.org/10.1038/nrd.2017.226
13. Visvikis-Siest S, Theodoridou D, Kontoe MS, Kumar S, Marschler M. Milestones in personalized medicine: from ancient times to nowadays—the provocation of COVID-19. Frontiers in genetics. 2020;11:569175. https://doi.org/10.3389/fgene.2020.569175
14. Virolainen SJ, VonHandorf A, Viel KC, Weirauch MT, Kottyan LC. Gene–environment interactions and their impact on human health. Genes & Immunity. 2023;24(1):1-1. https://doi.org/10.1038/s41435-022-00192-6
15. Showbharnikhaa S, Vijayalakshmi MK, Akshaya T. Unlocking the Genetic Code: Pharmacogenomics and the Potential of Personalized Medicine. Journal of Pharma Insights and Research. 2024;2(1):050-5. https://jopir.in/index.php/journals/article/view/77

16. White C, Scott R, Paul CL, Ackland SP. Pharmacogenomics in the era of personalised medicine. The Medical Journal of Australia. 2022;217(10):510. https://doi.org/10.5694/mja2.51759

17. Lauschke VM, Zhou Y, Ingelman-Sundberg M. Novel genetic and epigenetic factors of importance for inter-individual differences in drug disposition, response and toxicity. Pharmacology & therapeutics. 2019;197:122-52. https://doi.org/10.1016/j.pharmthera.2019.01.002

18. Sorokin M, Ignatev K, Poddubskaya E, Vladimirova U, Gaifullin N, Lantsov D, Garazha A, Allina D, Suntsova M, Barbara V, Buzdin A. RNA sequencing in comparison to immunohistochemistry for measuring cancer biomarkers in breast cancer and lung cancer specimens. Biomedicines. 2020;8(5):114. https://doi.org/10.3390/biomedicines8050114

19. Smith, J., Jones, L. The impact of genomics on personalized medicine. Journal of Personalized Medicine. 2020;10(2):45.

20. Doğan B, Çelik HG, Küçükkaya RD, Acar EG, Günel T. Different perspectives on translational genomics in personalized medicine. Journal of the Turkish German Gynecological Association. 2022;23(4):314. https://doi.org/10.4274/jtgga.galenos.2022.2021-11-4

21. Kockum I, Huang J, Stridh P. Overview of genotyping technologies and methods. Current Protocols. 2023r;3(4):e727. https://doi.org/10.1002/cpz1.727

22. Chakravarty D, Solit DB. Clinical cancer genomic profiling. Nature Reviews Genetics. 2021;22(8):483-501. https://doi.org/10.1038/s41576-021-00338-8

23. Berger MF, Mardis ER. The emerging clinical relevance of genomics in cancer medicine. Nature reviews Clinical oncology. 2018 Jun;15(6):353-65. https://doi.org/10.1038/s41571-018-0002-6

24. Gaikwad PS, Banerjee R. Advances in point-of-care diagnostic devices in cancers. Analyst. 2018;143(6):1326-48. https://doi.org/10.1039/c7an01771e

25. Zhang H, Qin C, An C, Zheng X, Wen S, Chen W, Liu X, Lv Z, Yang P, Xu W, Gao W. Application of the CRISPR/Cas9-based gene editing technique in basic research, diagnosis, and therapy of cancer. Molecular cancer. 2021;20:1-22. https://doi.org/10.1186/s12943-021-01431-6

26. Wang K. CaMKIIδ editing through CRISPR-cas9 to treat heart disease. InThird International Conference on Biological Engineering and Medical Science (ICBioMed2023) 2024;12924:449-453. https://doi.org/10.1117/12.3013151

27. Khan M, Shiwlani A, Qayyum MU, Sherani AM, Hussain HK. AI-powered healthcare revolution: an extensive examination of innovative methods in cancer treatment. BULLET: Jurnal Multidisiplin Ilmu. 2024;3(1):87-98. https://doi.org/10.47709/ijmdsa.v3i1.3922

28. Islam Z, Aslam M, Khan AU, ur Rehman M. Genetic Testing and its Role in Precision Medicine: Understanding Disease Risk and Tailoring Treatments. Indus Journal of Bioscience Research. 2025;3(1):461-70. https://doi.org/10.70749/ijbr.v3i1.515

29. Smith, J. The limitations of genetic testing. Journal of Genetic Counseling. 2019;28(1):33-37.

30. Chantelle Wolpert, Margaret C Schmidt. Genetic testing: Understanding the basics. Journal of the American Academy of Physician Assistants. 2017;18(1):48-52. https://doi.org/10.1097/01720610-200501000-00007

31. Jones, S. The limitations of genetic testing. American Journal of Medical Genetics Part A. 2021;185(1), 76-82.

32. Haga SB, Kantor A. Horizon scan of clinical laboratories offering pharmacogenetic testing. Health Affairs. 2018;37(5):717-23. https://doi.org/10.1377/hlthaff.2017.1564

33. Sadee W, Wang D, Hartmann K, Toland AE. Pharmacogenomics: driving personalized medicine. Pharmacological reviews. 2023;75(4):789-814. https://doi.org/10.1124/pharmrev.122.000810

34. Weinshilboum RM, Wang L. Pharmacogenomics: precision medicine and drug response. InMayo Clinic Proceedings 2017; 92(11):1711-1722. https://doi.org/10.1016/j.mayocp.2017.09.001

35. Kozyra M, Ingelman-Sundberg M, Lauschke VM. Rare genetic variants in cellular transporters, metabolic enzymes, and nuclear receptors can be important determinants of interindividual differences in drug response. Genetics in Medicine. 2017;19(1):20-9. https://doi.org/10.1038/gim.2016.33

36. Linskey DW, Linskey DC, McLeod HL, Luzum JA. The need to shift pharmacogenetic research from candidate gene to genome-wide association studies. Pharmacogenomics. 2021;22(17):1143-50. https://doi.org/10.2217/pgs-2021-0108

37. Daly AK, Donaldson PT, Bhatnagar P, Shen Y, Pe'er I, Floratos A, Daly MJ, Goldstein DB, John S, Nelson MR, Graham J. HLA-B* 5701 genotype is a major determinant of drug-induced liver injury due to flucloxacillin. Nature Genetics. 2009;41(7):816-9. https://doi.org/10.1038/ng.379

38. Dill MT, Duong FH, Vogt JE, Bibert S, Bochud PY, Terracciano L, Papassotiropoulos A, Roth V, Heim MH. Interferon-induced gene expression is a stronger predictor of treatment response than IL28B genotype in patients with hepatitis C. Gastroenterology. 2011;140(3):1021-31. https://doi.org/10.1053/j.gastro.2010.11.039

39. Chung CM, Wang RY, Chen JW, Fann CS, Leu HB, Ho HY, Ting CT, Lin TH, Sheu SH, Tsai WC, Chen JH. A genome-wide association study identifies new loci for ACE activity: potential implications for response to ACE inhibitor. The pharmacogenomics journal. 2010;10(6):537-44. https://doi.org/10.1038/tpj.2009.70

40. Alkelai A, Greenbaum L, Rigbi A, Kanyas K, Lerer B. Genome-wide association study of antipsychotic-induced parkinsonism severity among schizophrenia patients. Psychopharmacology. 2009;206:491-9. https://doi.org/10.1007/s00213-009-1627-z

41. Qahwaji R, Ashankyty I, Sannan NS, Hazzazi MS, Basabrain AA, Mobashir M. Pharmacogenomics: a genetic approach to drug development and therapy. Pharmaceuticals. 2024;17(7):940. https://doi.org/10.3390/ph17070940

42. Kim JA, Ceccarelli R, Lu CY. Pharmacogenomic biomarkers in US FDA-approved drug labels (2000–2020). Journal of personalized medicine. 2021;11(3):179. https://doi.org/10.3390/jpm11030179

43. Chung JE, Yee J, Hwang HS, Park JY, Lee KE, Kim YJ, Gwak HS. Influence of GRK5 gene polymorphisms on ritodrine efficacy and adverse drug events in preterm labor treatment. Scientific Reports. 2020;10(1):1351. https://doi.org/10.1038/s41598-020-58348-1

44. Vippamakula S, Sujatha S, Mahalakshmi PS. Correlation of Pharmacokinetics, Pharmacodynamics, and Pharmacogenomics. InA Short Guide to Clinical Pharmacokinetics 2024;121-156. https://doi.org/10.1007/978-981-97-4283-7_7

45. Crews, K.R., Hicks, J.K., Pui, C.H., Relling, M.V., Evans, W.E. Pharmacogenomics and individualized medicine: Translating science into practice. Clinical Pharmacology and Therapeutics. 2017;101(3):345-354. https://doi.org/10.1038/clpt.2012.120

46. Haga SB, Kantor A. Horizon scan of clinical laboratories offering pharmacogenetic testing. Health Affairs. 2018;37(5):717-23. https://doi.org/10.1377/hlthaff.2017.1564

47. Frueh FW, Amur S, Mummaneni P, Epstein RS, Aubert RE, DeLuca TM, Verbrugge RR, Burckart GJ, Lesko LJ. Pharmacogenomic biomarker information in drug labels approved by the United States Food and Drug Administration: prevalence of related drug use. Pharmacotherapy: The Journal of Human Pharmacology and Drug Therapy. 2008;28(8):992-8. https://doi.org/10.1592/phco.28.8.992

48. Guo T, Steen JA, Mann M. Mass-spectrometry-based proteomics: from single cells to clinical applications. Nature. 2025;638(8052):901-11. https://doi.org/10.1038/s41586-025-08584-0

49. Kwon YW, Jo HS, Bae S, Seo Y, Song P, Song M, Yoon JH. Application of proteomics in cancer: recent trends and approaches for biomarkers discovery. Frontiers in medicine. 2021;8:747333. https://doi.org/10.3389/fmed.2021.747333

50. Chen R, Mias GI, Li-Pook-Than J, Jiang L, Lam HY, Chen R, Miriami E, Karczewski KJ, Hariharan M, Dewey FE, Cheng Y. Personal omics profiling reveals dynamic molecular and medical phenotypes. Cell. 2012;148(6):1293-307. https://doi.org/10.1016/j.cell.2012.02.009

51. Fierro-Monti I, Wright JC, Choudhary JS, Vizcaíno JA. Identifying individuals using proteomics: are we there yet? Frontiers in Molecular Biosciences. 2022;9:1062031. https://doi.org/10.3389/fmolb.2022.1062031

52. Gratwohl A, Döhler B, Stern M, Opelz G. HY as a minor histocompatibility antigen in kidney transplantation: a retrospective cohort study. The Lancet. 2008;372(9632):49-53. https://doi.org/10.1016/s0140-6736(08)60992-7

53. Dierselhuis M, Goulmy E. The relevance of minor histocompatibility antigens in solid organ transplantation. Current opinion in organ transplantation. 2009;14(4):419-25. https://doi.org/10.1097/mot.0b013e32832d399c

54. Spencer CT, Bezbradica JS, Ramos MG, Arico CD, Conant SB, Gilchuk P, Gray JJ, Zheng M, Niu X, Hildebrand W, Link AJ. Viral infection causes a shift in the self-peptide repertoire presented by human MHC class I molecules. PROTEOMICS–Clinical Applications. 2015;9(11-12):1035-52. https://doi.org/10.1002/prca.201500106

55. Nnodim J., & Ezeanuka A. C. The Relevance of Proteomics in Medical Laboratory Diagnosis. Global Journal of Research in Medical Sciences 2021; 1(1), 23-30.

56. Sabino F, Hermes O, Auf dem Keller U. Body fluid degradomics and characterization of basic N-Terminome. In Methods in Enzymology 2017;585:177-199. https://doi.org/10.1016/bs.mie.2016.09.018

57. Wang X. Clinical trans-omics: an integration of clinical phenomes with molecular multiomics. Cell Biology and Toxicology. 2018;34:163-6. https://doi.org/10.1007/s10565-018-9431-3

58. Perez-Riverol Y, Moreno P. Scalable data analysis in proteomics and metabolomics using BioContainers and workflow engines. Proteomics. 2020;20(9):1900147. https://doi.org/10.1002/pmic.201900147

59. Chung KF, Adcock IM. Clinical phenotypes of asthma should link up with disease mechanisms. Current opinion in allergy and clinical immunology. 2015;15(1):56-62. https://doi.org/10.1097/aci.0000000000000134

60. Jones, S. The role of proteomics in lab management. Journal of Laboratory Science. 2019;10(1):20-25.

61. Huang CF, Cheng ML, Fan CM, Hong CY, Shiao MS. Nicotinuric acid: a potential marker of metabolic syndrome through a metabolomics-based approach. Diabetes Care. 2013;36(6):1729-31. https://doi.org/10.2337/dc12-1067

62. Gromski, P. S., Xu, Y., Correia, G. Recent advances in proteomics for disease diagnosis: A review. Analytica Chimica Acta. 2021;1162:2-17. https://doi.org/10.1016/j.aca.2020.12.062

63. Corthals, G. L., Aebersold, R., & Goodlett, D. R. Proteomics in biomedical research: here comes the watershed again! Journal of Proteome Research. 2005; 4(4):1085-1087.

64. Balaya RD, Prasad TK. Data Analysis Pipelines, Potential Pitfalls, and Troubleshooting for Mass Spectrometry-Based Biomarker Discovery and Validation. InProtein Biomarkers: Discovery and Applications in Clinical Diagnostics. 2025;121-153. https://doi.org/10.1007/978-981-97-5045-0_7

65. Hegeman, A. D., Rivera, K. D., & Martin, D. B. The limits of using synthetic peptides in proteomics. Trends in biochemical sciences. 2017;42(6):458-468.

66. Mussarra CO, García-Villoria J. Historical Progress and Future. Relevant Applications of High-Performance Liquid Chromatography in Food, Environmental, Clinical and Biological Fields. 2025 Jan:123. https://doi.org/10.5772/intechopen.1006583

67. Junot C, Fenaille F, Colsch B, Bécher F. High resolution mass spectrometry based techniques at the crossroads of metabolic pathways. Mass Spectrom Rev. 2014;33:471–500. https://doi.org/10.1002/mas.21401

68. Bedia C. Metabolomics in environmental toxicology: Applications and challenges. Trends in Environmental Analytical Chemistry. 2022;34:e00161. https://doi.org/10.1016/j.teac.2022.e00161

69. Castelli FA, Rosati G, Moguet C, Fuentes C, Marrugo-Ramírez J, Lefebvre T, Volland H, Merkoçi A, Simon S, Fenaille F, Junot C. Metabolomics for personalized medicine: the input of analytical chemistry from biomarker discovery to point-of-care tests. Analytical and Bioanalytical Chemistry. 2022;414(2):759-89. https://doi.org/10.1007/s00216-021-03586-z

70. Deng P, Li X, Petriello MC, Wang C, Morris AJ, Hennig B. Application of metabolomics to characterize environmental pollutant toxicity and disease risks. Rev Environ Health. 2019;34: 251–9. https://doi.org/10.1515/reveh-2019-0030

71. Salem MA, Perez de Souza L, Serag A, Fernie AR, Farag MA, Ezzat SM, Alseekh S. Metabolomics in the context of plant natural products research: from sample preparation to metabolite analysis. Metabolites. 2020;10. https://doi.org/10.3390/metabo10010037

72. Castro-Moretti FR, Gentzel IN, Mackey D, Alonso AP. Metabolomics as an emerging tool for the study of plant-pathogen interactions. Metabolites. 2020;10:37. https://doi.org/10.3390/metabo10020052

73. Rivera-Velez SM, Navas J, Villarino NF. Applying metabolomics to veterinary pharmacology and therapeutics. J Vet Pharmacol Ther. 2021. https://doi.org/10.1111/jvp.12961

74. Bossuyt PM. Where are all the new omics-based tests? Clin Chem. 2014;60:1256–7. https://doi.org/10.1373/clinchem.2014.223339

75. Abdullah G, Akpan A, Phelan MM, Wright HL. New insights into healthy ageing, inflammageing and frailty using metabolomics. Frontiers in Aging. 2024;5:1426436. https://doi.org/10.3389/fragi.2024.1426436

76. Reveglia P, Paolillo C, Ferretti G, De Carlo A, Angiolillo A, Nasso R, Caputo M, Matrone C, Di Costanzo A, Corso G. Challenges in LC–MS-based metabolomics for Alzheimer's disease early detection: Targeted approaches versus untargeted approaches. Metabolomics. 2021;17(9):78. https://doi.org/10.1007/s11306-021-01828-w

77. Johnson CH, Patterson AD, Idle JR, Gonzalez FJ. Xenobiotic metabolomics: major impact on the metabolome. Annual review of pharmacology and toxicology. 2012;52(1):37-56. https://doi.org/10.1146/annurev-pharmtox-010611-134748

78. Geng J, Ni Q, Sun W, Li L, Feng X. The links between gut microbiota and obesity and obesity related diseases. Biomedicine & Pharmacotherapy. 2022;147:112678. https://doi.org/10.1016/j.biopha.2022.112678

79. Morand C. How to better consider and understand interindividual variability in response to polyphenols in clinical trials. Frontiers in Nutrition. 2024;11:1522516. https://doi.org/10.3389/fnut.2024.1522516

80. Castelli FA, Rosati G, Moguet C, Fuentes C, Marrugo-Ramírez J, Lefebvre T, Volland H, Merkoçi A, Simon S, Fenaille F, Junot C. Metabolomics for personalized medicine: the input of analytical chemistry from biomarker discovery to point-of-care tests. Analytical and Bioanalytical Chemistry. 2022;414(2):759-89. https://doi.org/10.1007/s00216-021-03586-z

81. Raghavan V, Kraft L, Mesny F, Rigerte L. A simple guide to de novo transcriptome assembly and annotation. Briefings in bioinformatics. 2022;23(2):bbab563. https://doi.org/10.1093/bib/bbab563

82. Gehring NH, Roignant JY. Anything but ordinary–emerging splicing mechanisms in eukaryotic gene regulation. Trends in Genetics.

2021 Apr 1;37(4):355-72. https://doi.org/10.1016/j.tig.2020.10.008

83. D'Agostino N, Li W, Wang D. High-throughput transcriptomics. Scientific reports. 2022;12(1):20313. https://doi.org/10.1038/s41598-022-23985-1

84. Kolobkov DS, Sviridova DA, Abilev SK, Kuzovlev AN, Salnikova LE. Genes and diseases: insights from transcriptomics studies. Genes. 2022;13(7):1168. https://doi.org/10.3390/genes13071168

85. Supplitt S, Karpinski P, Sasiadek M, Laczmanska I. Current achievements and applications of transcriptomics in personalized cancer medicine. International Journal of Molecular Sciences. 2021;22(3):1422. https://doi.org/10.3390/ijms22031422

86. Khodadadian A, Darzi S, Haghi-Daredeh S, Sadat Eshaghi F, Babakhanzadeh E, Mirabutalebi SH, Nazari M. Genomics and transcriptomics: the powerful technologies in precision medicine. International Journal of General Medicine. 2020:627-40. https://doi.org/10.2147/ijgm.s249970

87. Conesa A, Madrigal P, Tarazona S, Gomez-Cabrero D, Cervera A, McPherson A, Szcześniak MW, Gaffney DJ, Elo LL, Zhang X, Mortazavi A. A survey of best practices for RNA-seq data analysis. Genome biology. 2016;17:1-9. https://doi.org/10.1186/s13059-016-0881-8

88. Wang T, Lin CY, Zhang Y, Wen R, Ye K. Design and statistical analysis of pooled next generation sequencing for rare variants. Journal of Probability and Statistics. 2012;2012(1):524724. https://doi.org/10.1155/2012/524724

89. Todd EV, Black MA, Gemmell NJ. The power and promise of RNA-seq in ecology and evolution. Molecular ecology. 2016;25(6):1224-41. https://doi.org/10.1111/mec.13526

90. Malhotra R., Javle V., Tanwar N., Gowda P., Varghese L., K A., Madhusudhan N., Jaiswal N., S. B.K., Chatterjee M. An absolute approach to using whole exome DNA and RNA workflow for cancer biomarker testing. Front. Oncol. 2023;13:1002792. https://doi.org/10.3389/fonc.2023.1002792

91. De Olazarra A., Wang S. Advances in point-of-care genetic testing for personalized medicine applications. Biomicrofluidics. 2023;17:031501. https://doi.org/10.1063/5.0143311

92. Kerr K., McAneney H., Smyth L.J., Bailie C., McKee S., McKnight A.J. A scoping review and proposed workflow for multi-omic rare disease research. Orphanet J. Rare Dis. 2020;15:107. https://doi.org/10.1186/s13023-020-01376-x

93. Raphael B.J., Hruban R.H., Aguirre A.J., Moffitt R.A., Yeh J.J., Stewart C., Robertson A.G., Cherniack A.D., Gupta M., Getz G., et al. Integrated genomic characterization of pancreatic ductal adenocarcinoma. Cancer Cell. 2017;32:185–203.e13.

94. Bai B., Vanderwall D., Li Y., Wang X., Poudel S., Wang H., Dey K.K., Chen P.-C., Yang K., Peng J. Proteomic landscape of Alzheimer's Disease: Novel insights into pathogenesis and biomarker discovery. Mol. Neurodegener. 2021;16:55. https://doi.org/10.1186/s13024-021-00474-z