



Biomarkers in Clinical Laboratory Diagnostics: Emerging Trends and Clinical Significance

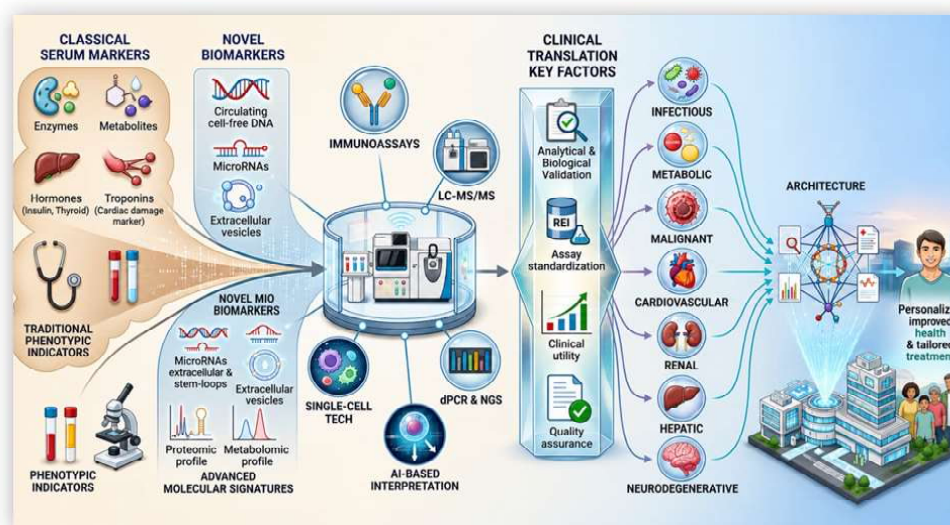
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ABSTRACT

Biomarkers are molecular, cellular, biochemical or physiological measurable parameters that reflect on normal biology, pathology changes, and/or pharmacological responses. They have now been increasingly made integrated into clinical laboratory medicine and transformed the way of laboratory procedures, moving from the traditional phenotype approach, are applied with molecular guidance for the characterisation of diseases. Classical serum markers like enzymes, metabolites, hormones, acute phase proteins, cardiac troponins, hematological indices, circulating cell-free DNA, circulating tumour DNA, microRNAs, extracellular vesicles, metabolomic signatures, proteomic profiles, immune mediators and multi-omics-derived signatures, are all indispensable things being new areas for potential diagnostic candidates. Clinical lab tests have seen significant advances with developments in immunoassays, liquid chromatographic tandem mass spectrometry, digital polymerase chain reaction, Next Generation Sequencing, single-cell technologies, and synthetic intelligence. Biomarkers are yet to be more clinically translatable beyond a mere association with disease. Advance studies suggest that analytical, biological, diagnostic, clinical utility, reference interval appropriateness, assay standardization and quality assurance are all basic factors that have to be met before a biomarker can enter into routine use. Focussing on liquid biopsy, multi-omics, high sensitivity assay, molecular diagnostics and interpretation based on artificial intelligence. In the end, the laboratory of the future will be a “lab in a lab” concept integrating an “architecture” of biomarkers which can be applied to diagnosis, molecular classification, prognosis, therapeutic decision and monitoring.

Keywords: Biomarkers, proteomics molecular diagnostics, next-generation sequencing, mass spectrometry, precision medicine.



GRAPHICAL ABSTRACT

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1. INTRODUCTION

The clinical laboratory has moved from the methodology of simply measuring relatively traditional biochemical and hematological parameters, to become a very integrated molecular diagnostic system. This transformation is in part due to new insights gained from an understanding of pathogenesis and new technologies that start to detect biological changes at lower concentrations. In this respective sense Biomarkers are considered a simple tool in order to transform molecular events to clinically interpretable information. A biomarker could be defined as an “observable property of a biological or pathological process, or a person’s reaction to an intervention, that can be measured to provide information about the process or person. biotic indicators may be molecular, cellular, histological, physiological or imaging. It is most commonly used to refer to biological entities that can be measured in biological samples like proteins, peptides, extracellular vesicles, hormones, kinases, proteins derived from body cells or tissue, metabolites, autoantibodies and antigens, circulation tumour cells and nucleic acids, which are not contained within cells, all of which can be identified in the blood. There is a relationship between biological relevance and importance to underlying pathophysiology of the biomarker. (Jorge et al., 2021) When tissue is damaged, blood levels of enzymes are raised, immunity may cause a cytokine response, an acute phase response and tissue malfunction causes changes in pressure levels of metabolites (including glucose, lipids and amino acids) in the bloodstream, and malignant conditions involve changes in levels of intracellular nucleotides in blood. Finally, biomarkers could provide data regarding disease, disease intensity/disease state, disease biological sub-type, prognosis, potential response to therapy, and recurrence. A key notion to bear in mind is that a diagnostic biomarker is not likely to communicate a diagnosis, and it is unlikely to suggest treatment, whereas a surrogate endpoint will do both. A diagnostic biomarker may aid in diagnosing or characterizing the disease or condition being studied, and a surrogate endpoint is surrogated in the evaluation of therapies. Not all the biomarker demonstrated to be statistically associated can be a clinically useful surrogate (Michelhaugh & Januzzi, 2023).

Precision medicine is strongly coupled to the rise in the value of biomarkers. Many patients are still classified using conventional diagnostics that are based on clinical phenotype, although there is significant molecular heterogeneity within each diagnostic category. Characterising patients using biomarkers may yield mechanistic differences in apparently similar patients that may allow for molecular stratification and individualised treatments. But, there is an important “translation problem” in biomarker science: discovery does not mean validation. Thousands of molecules could theoretically work as biomarkers for the diseases, but proportionately few are routinely used in the clinic. The analytical performance, the reproducibility (repeatability, reproducibility), the clinical validity and the incremental clinical utility

of a candidate biomarker are necessary criteria for the adoption of the biomarker in the diagnostic workflow. The modern Laboratory must therefore have the ability to fit in a comprehensive biomarker framework which includes from species collection right through to the interpretation of the results (Marjani et al., 2024). There are many pre-analytical, analytical, calibration and biological variables, reference populations, quality control and post analytical interpretation parameters which can impact the clinical value of the final measurement performed. Laboratory quality according to WHO defines “the full testing process”: accurate, reliable, timely results need to be obtained.

2. CONVENTIONAL AND EMERGING DIAGNOSTIC BIOMARKERS

2.1. Conventional biomarkers

The traditional lab-based tests are based on one or more of the markers referred to as conventional biomarkers. These consist of metabolites, enzymes, proteins, hormones, physiological assessment and cellular indices, electrolytes. Therefore, some examples of serologic assays used in assessing glucose blood levels and to evaluate diabetes mellitus include serum glucose and glycated hemoglobin; serologic assays used in determination of kidney function include creatinine and estimated glomerular filtration rate (eGFR); serologic assays used in determining hepatocellular injury include Alanine Aminotransferase (ALT) and Aspartate Aminotransferase (AST); serologic assays include Troponin for assessment of myocardial injury; serologic assays include C-reactive protein (CRP) in assessing systemic inflammation, serum thyroid-stimulating antibody (TSA) in assessing thyroid function, and lipid parameters in assessing cardiac risk (Singh et al., 2024). The greatest advantage is that conventional biomarkers are clinically very well-experienced. They have been standardized over decades with regard to their reference intervals, biological variation, analytical performance, decision limits and relationships with clinical parameters. Many of these can be automated in a high throughput and can be supported with a relatively high degree of accuracy and relative low cost. Traditional biomarkers however are frequently the end result activities of molecular occasions. A relatively large loss of GFR, for example, would not result in a normal serum creatinine level particularly in people with low muscle mass. Similarly, alanine aminotransferase levels also reflect liver cell injury and can not definitively determine the specific reason for liver injury. C-reactive protein (CRP) is an indicator of inflammation, and usually not of the specific source of the inflammation. Conventional biomarkers, therefore, have a high clinical value, but low disease specificity.

2.2. Protein biomarkers

Proteins are the most widely discussed classes of biomarkers; commonly identified protein biomarkers are directly linked to the cellular signaling, inflammation, tissue damage, metabolism, immunity and disease pathogenesis. For example, troponin, natriuretic peptides, procalcitonin, ferritin, cytokines, immunoglobulin G (IgG), complement components, tumour associated proteins and acute phase proteins. In addition to the pre-established biochemistry markers, these markers have been put in a new set of biomarkers based on proteomic technologies (Alkhazaali-Ali et al., 2024). High-plex protein assays (affinity-based multiplex assays, protein arrays, high-plex immunoassays and mass spectrometry) can be performed on many proteins. This will allow to develop “protein signature” rather than relying on the single analyte. An important scientific question is how to separate proteins those that are directly linked to disease from those that are just indicative of disease severity. Statistically significant association is not required both for biological specificity and clinical usefulness (Bao et al., 2024).

2.3. RNA and microRNA biomarkers

Research on messenger RNA (mRNA), circulating RNA, microRNAs (miRNAs), and long noncoding RNAs (lncRNAs) has increased significantly and is now seen as a major area of focus in the search for new biomarkers (Zhu et al., 2024). The way miRNAs function after they are made, known as post-transcriptional mechanisms, makes them particularly interesting. Additionally, miRNAs are relatively stable in extracellular fluids, possibly due to the presence of protein complexes and extracellular vesicles (EVs). Many studies have shown that certain miRNAs are not functioning properly in conditions such as cancer, cardiovascular diseases, diabetes, neurodegenerative disorders, infections, and inflammatory diseases (Zhang et al., 2024). To better understand these conditions, researchers often use multiple miRNA signatures rather than just one. However, there are some challenges in using these miRNAs, including variability during sample preparation, differences in RNA extraction methods, issues with normalization and internal controls, contamination from hemolysis, and variations depending on the platform used (Ho et al., 2022).

2.4. Metabolic biomarkers

Metabolomics is concerned with studying small molecules, called low molecular weight metabolites, that are formed in cells through biochemical reactions. The metabolome is the total effect of the genetic makeup, would you say the cell's physical state, food, gut microbe population, prescriptions, chemical exposure and health status. In the current context, with the development of metabolomics, certain metabolites such as amino acids, organic acids, lipids, bile acids, carbohydrates, nucleotides and intermediate compounds are routinely used as biomarkers (Tamber et al., 2023). These metabolites are the products of biochemical pathways, which can yield insights that are functional that may not be clear in the genetic information. There are two major technologies employed in metabolomics: mass spectrometry and Nuclear Magnetic Resonance (NMR) spectroscopy (Zetterberg & Schott, 2022). Despite all of the potential clinical applications of metabolomics, some of the complexities of the field such as diet, diurnal changes, effects of drugs, differences in sample preparation, changes in the quality of the instruments and failure of there being standard reference ranges for many metabolites hold the field back (Barnadas-Carceller et al., 2024).

2.5. Liquid-biopsy biomarkers

Liquid biopsy is one of the emerging areas of biomarker research. It can be used to diagnose disease based on blood or bodily fluid analyses, not just on tissue sample analysis. Circulating tumour DNA (ctDNA), circulating tumour cells (CTCs), and extracellular vesicles contain the tumour's genetic material and so serve as key components of liquid biopsy. The other elements are circulating RNA, cell-free DNA and tumour-educated platelets. One of the biggest benefits of liquid biopsy is that it allows for repeated testing with minimal invasiveness (Lista et al., 2024). This can be used to create a profile of a molecular marker of the disease, and then monitor whether the treatment is successful and whether the disease develops resistance over time. CtDNA plays a crucial role in oncology. It can be found in blood and genetic alterations such as mutations, copy number alterations, methylation and other markers can be detected in tumour DNA. The use of ctDNA in later stages of cancer aids in better understanding of disease and treatment decisions. (Hill & Tran, 2021) A new and exciting application is the ability to detect "minimal residual disease" (MRD) even if it is present at very low levels. In some patients, DNA detectable from the tumour can remain even after they have been believed to be cured. With

highly sensitive tests, these traces can be detected (Di Sario et al., 2023). In some forms of cancer, it also may be possible to detect positive ctDNA results before imaging reveals signs of the return of disease, providing a chance for molecular interventions earlier in the course of the disease prior to clinical relapse (Marin et al., 2024). The analysis of test results from a ctDNA test can be complex though. The factors that can impact the outcome are low fractions of tumour cells, clonal haematopoiesis, biological diversity, the sensitivity of the test, data collection error and differences in sample processes. Even so, there is great promise in this technology and cancer diagnostics and treatment seem to have a very bright future (Dong et al., 2024).

2.6. Extracellular-vesicles as biomarkers

Extracellular vesicles (EVs) are particles released by different cells and are membrane bound which include protein, lipid, DNA, mRNA, miRNA and other molecular cargo. They may represent the nature of the cell from which they released, its physiological or pathological condition. EVs are thus promising as disease biomarkers (Delaby et al., 2023). EV populations are heterogeneous, but isolation techniques are co-purifying proteins, lipoproteins and other particles. Research is therefore focused at the present time at a standardisation of EV isolation, molecular characterisation, surface-marker and single-vesicle technologies of EVs. (Strauß et al., 2024)

3. BIOMARKERS IN INFECTIOUS, METABOLIC, AND CHRONIC DISEASES

Biomarker has great potential in the field of medicine, disease diagnosis and severity evaluation. Different types of diseases will cause different type of biological changes and thus generates different type of biomarkers. So, new age laboratories are using new methods that further improve diagnoses and detection at an earlier stage of the disease, such as metabolomics, liquid biopsy, ctDNA , PCR and high-sensitivity assays. (Das et al., 2024)

Table 1; Biomarkers, their clinical importance and dection methods

Disease area	Biomarkers	Methods Used	Clinical Importance	References
Infectious Diseases	CRP, Procalcitonin, Resistance genes, Pathogen DNA/RNA, Host-response marker	Culture, Microscopy, Antigen tests, PCR, RT-PCR, qPCR, multiplex testing	Pathogen detection, Infection assessment, Sepsis evaluation, Resistance detection.	(Gupta et al., 2023)
Metabolic Disorders	HbA1c, Glucose, Lipoprotein(a), Apolipoproteins, Organic acids, Lipids, Intermediary metabolites,	Biochemical assays, HbA1c analysis, Lipid profiling, Metabolomics, Mass spectrometry, Chromatographic analysis	Glycemic monitoring, Helps to understand metabolic alterations, Insulin-resistance assessment, Estimation of cardiovascular-risk.	(Gillery, 2022)
Hepatic Disease	AST, ALT, ā-GT, Fibrosis markers, Extra cellular-matrix markers, Alkaline-phosphatase,	Immunoassays, Composite fibrosis indices, Enzyme assays, Clinical chemistry assays, Composite fibrosis assessment	Hepatocellular injury detection, Cholestasis assessment, Fibrosis evaluation & supporting non-invasive assessment	(Tamber et al., 2023)

Table (Continued)

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Disease area	Biomarkers	Methods Used	Clinical Importance	References
Cardiovascular Disorder	BNP, NT-proBNP, Vascular-risk markers, Cardiac troponin I/T,	Immunoassays, High sensitivity immunoassays, Automated laboratory systems	Myocardial injury detection, Acute coronary syndrome assessment, Heart-failure diagnosis & monitoring	(Kim et al., 2023)
Renal Disease	Creatinine, Cystatin C, Urinary albumin, Tubular injury biomarkers, Tubular stress biomarkers	Serum biochemical assays, eGFR calculation, Urine analysis, Immunoassays, Molecular assays	Kidney-function assessment, Glomerular dysfunction detection, Provide information about early kidney-injury identification	(Wang et al., 2025)
Cancer	PSA, AFP, CEA, CA-125, ctDNA, Extra cellular vesicles, Tumour-specific genetic variants.	PCR/qPCR, Digital PCR, Next-generation sequencing, Liquid biopsy, Immunoassays, Cell-based analysis, Molecular profiling	Tumour detection and monitoring, Mutation identification, Resistance detection, Minimal residual disease monitoring	(Das et al., 2024)

4. LABORATORY TECHNOLOGIES FOR BIOMARKER DETECTION

The principle of Immunoassays is depends on the immune system recognition of the antigen-antibody reaction, which is used to selectively detect particles like proteins, peptides, hormones, antibodies, and other analytes. Many automated chemiluminescent and electro-chemiluminescent systems predominately have high throughput value in clinical laboratories, and ELISA is still regarded as a key reference method in biomarker detection. Immunoassays involve affinity to antibody , specificity, epitope accessibility, antibody calibration, matrix effects, and chemistry for signal generation that are important for their analytical performance. False results can be obtained through interference from heterophile antibodies, human anti-animal antibodies, rheumatoid factor, biotin, haemolysis, lipaemia and icterus (Gupta et al., 2023). Therefore an apparent precise result does not necessarily indicate an analytical validity (Das et al., 2024).

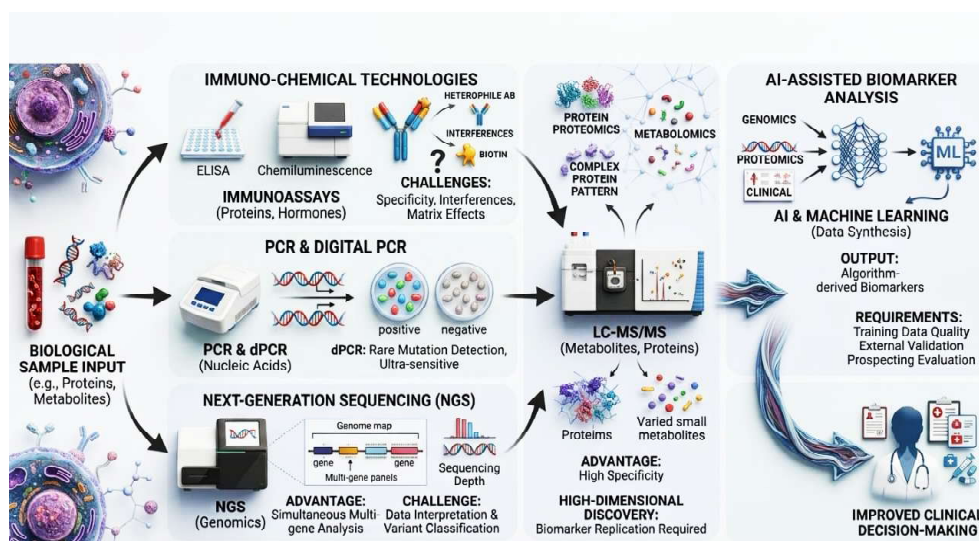


Fig 1: The laboratory technologies used for biomarker detection from immunoassays and molecular diagnostic to multi-omics and mass spectrometry AI-assisted analysis for high sensitivity detection and improved clinical decision making

4.1. PCR and digital PCR techniques

PCR is an enzymatic process that amplifies specific desirable sequences of nucleic acids repeatedly. A major development in digital PCR involves breaking the broad reaction into many small steps. Each of these smaller reactions is then amplified and classified as either positive or negative. This allows for the accurate counting of target molecules using statistical methods (Qu et al., 2021). Digital PCR is very sensitive and has many functions in molecular biology. It can detect targets present in a very low concentrations, such as rare tumors, mutations, and sequences associated with minimal residual disease.

4.2. Next-generation sequencing(NGS)

This new age laboratory technique allows the sequencing of many nucleic acid molecules at the same time and to the contrast of traditional Sanger sequencing, which usually looks at one gene at a time, this next-generation sequencing can analyze multiple genes simultaneously. It is used in clinical settings for targeted oncology panels, hereditary disease panels, transcriptomic tests, and microbial genome sequencing. A key factor in the analysis is the depth of sequencing (Pei et al., 2024). Greater sequencing depth increases the chances of detecting low-frequency genetic alterations , but also requires more undivided attention to error correction and bioinformatics filtering. Another challenge is to correctly understand these genetic changes ,a change in a sequence does not always mean it is harmful. To make sense of these changes in a clinical context, factors such as population databases, functional data, inheritance patterns, tumor biology, and validated classification systems must be considered.

4.3. Mass spectrometry

It identifies molecules depending on their mass-to-charge ratio and how they get separated. LC-MS/MS is commonly used for smaller molecules, steroidal hormones, drugs, metabolites, and some proteins. It integrates chromatography with tandem mass analysis. One of the major benefit of this technique is it's high specificity for molecules (Rankin-Turner & Heaney, 2022).However, it requires significant laboratory resources, including specialized equipment, technical expertise, sample preparation, calibration, handling of matrix effects, and interpretation of data (Gillery, 2022).

4.4. Proteomics and metabolomics

Proteomic helps to examine complex protein expression patterns, while metabolomics investigates the small-molecule composition of biological systems (Baron, 2023). These investigations can helps to identify the molecular alterations associated with disease mechanisms. However, high-dimensional biomarker discovery requires rigorous statistical control. A biomarker identified through exploratory proteomics should undergo independent replication, analytical and clinical ,and assessment of incremental value over existing tests.

4.5. Artificial intelligence-assisted biomarker analysis

AI has introduced new possibilities for biomarker identification , discovery and interpretation. Machine-learning algorithms can identify nonlinear relationships among laboratory parameters, genomic features, clinical characteristics, and longitudinal data. However, algorithmic performance is strongly dependent on training data (Stone & van der Gugten, 2023). Dataset imbalance, spectrum bias, population differences, missing data, and inappropriate validation can result in apparently impressive but clinically

unreliable models. Accordingly, external validation and prospective evaluation are essential before AI-derived biomarkers are incorporated into clinical decision-making (Wilson *et al.*, 2024).

5. CLINICAL UTILITY, LIMITATIONS, AND QUALITY ASSURANCE

The main query in biomarker medicine is not ,whether a marker differs between diseased and healthy populations, but whether its measurement provides actionable clinical information. Diagnostic performance can be estimated by using few factors like sensitivity, specificity, likelihood ratios, predictive values, and ROC analysis. The area under the ROC curve provides an overall measure of discrimination, but an excellent AUC does not automatically demonstrate clinical utility (Mayerhoefer *et al.*, 2025). Like if a new biomarker produces an AUC of 0.90 but provides essentially the similar information as an inexpensive established biomarker, its incremental clinical value may be limited.

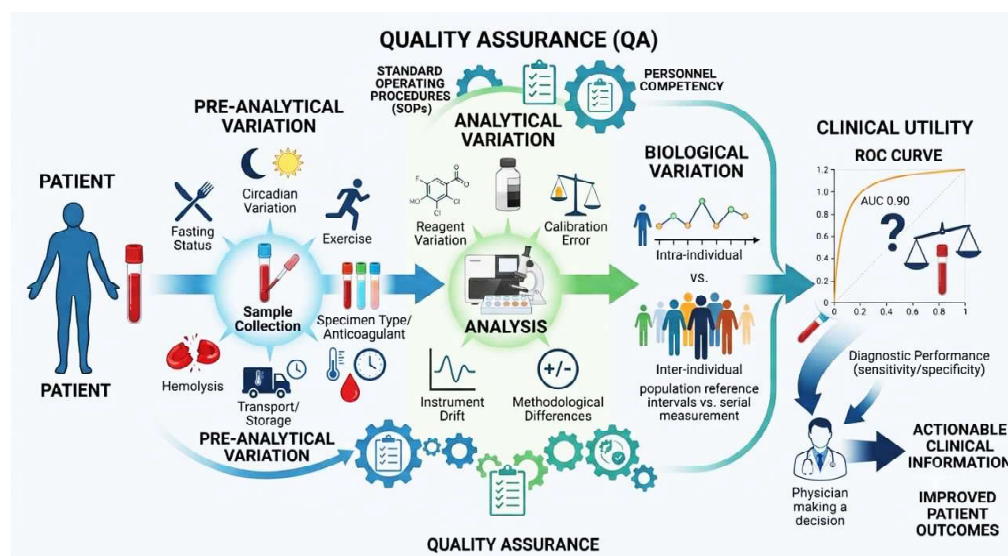


Fig 2: Clinical utility of biomarkers from pre-analytical and analytical variation to quality assurance and enabling reliable biomarker interpretation and actionable clinical decisions

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Pre-analytical variation: Biomarker concentrations can be substantially affected before analysis begins. Relevant factors include: patient preparation; fasting status; circadian variation; exercise; specimen type; anticoagulant selection; venous stasis; haemolysis; sample transport; temperature; processing delay; centrifugation conditions; storage duration; For molecular biomarkers, degradation of nucleic acids and cellular contamination is very important factor that can directly effect the result..

Analytical variation: Analytical variation arises from the measurement system itself. Sources include reagent variation, calibration error, instrument drift, analytical interference, imprecision, and methodological differences. Biomarkers cannot be interpreted reliably unless the laboratory has established acceptable analytical high performance system (Assfaw *et al.*, 2024).

Biological variation: Biological variation rises within individuals and in-between individuals. Few analytes demonstrate substantial intra-individual variation despite stable health status. Therefore, population reference intervals alone may not precisely describe meaningful change in an individual patient (Feng et al., 2021). Concepts such as biological variation, reference change values, and serial measurement become highly important in longitudinal biomarker monitoring.

Quality assurance: Biomarkers related laboratory examinations requires a precise and quality management architecture. For biomarkers, testing and standardization is particularly challenging because assays may differ in calibrators, extraction methods, amplification chemistry, reporting units, and sequencing systems. WHO's guidelines emphasizes the integration of pre-examination, examination, and post-examination processes within laboratory quality systems (Cohen & Banerjee, 2024). WHO specifically identifies the documentation, SOPs, quality-control materials, and quality assessment as key elements of laboratory quality assurance. So, quality assurance should include : valid standard operating procedures; appropriate calibration; internal and external quality control; reagent and equipment maintenance; personnel competency assessment; documentation and record management; method verification; and continuous quality improvement (Song et al., 2025).

6. FUTURE PERSPECTIVES

There will be no single dominant biomarker family to dominate the future of clinical biomarker, but rather the combination will do the job (Skov et al., 2021). The data and the source that will need to be analyzed include genomics, transcriptomics, proteomics, metabolomics, microbiomics, imaging, and clinical chemistry and electronic health-record (EHR) data (Zheng et al., 2024).

6.1. Multi-omics biomarkers:

The disease phenotype can be only partially captured by a single cellular/biological layer. Genomic information can yield a potential description of transcriptomic information, proteomics can yield a downstream description of functional cellular processes and metabolomics can yield a downstream description of biochemical information. The layers could be fused together to create more robust disease signatures (Sempionatto et al., 2022). The difficulty lies in the statistics and computations to perform for integration of the multi-omics. These properties of strong normalisation, dimension reduction, feature selection and independent validation and interpretable modelling can be important (Zeng et al., 2024).

6.2. Artificial Intelligence and machine learning:

Use of AI tools in detection, discovery, classification, prediction, analysis and laboratory quality control of biomarkers is increasingly common. Machine learning can also identify intricate patterns in a large set of variables that could be very difficult to see any of these sufficiently by conventional statistical methods (Kim et al., 2023). The key element in the large requirement is how well validated. The models should be validated externally with respect to institutions, population, instruments and disease spectrum of the models. An additional aspect of importance is explainability in a clinical context, in particular for high-stakes decisions (based on working algorithms) (Bhat et al., 2021). Lab system of the future can include laboratory biomarkers, imaging, pathology, patient history, medications, and physiology.

6.3. Personalized reference ranges:

Standard RI assumes well distributed population which can be interpreted. However, individual normal range may be more useful than the normal range developed for the general population. Individually oriented reference distributions and alert thresholds may be possible with longitudinal laboratory data (Filella et al., 2023). Those procedures may help them to more effectively see that slight difference from a “normal” biology.

6.4. Early cancer detection:

Cancer is one of the most ambitious targets in cancer research, detection. Concentrating on the liquid biopsy strategies, the data of ctDNA, methylation signatures, circulating RNA, proteins are analyzed, as well as multi modal signatures. Not only the goal to identify cancer associated molecules, but the goal is to identify them earlier in the molecular process, in the absence of having to undergo multiple tests and treatments, anxiety and various false positive results (Sharma et al., 2024). However, ongoing research is more directed towards the clinical validation and demonstration of clinical benefits.

6.5. Minimal residual disease:

MRDs are a very interesting paradigm since they are responsive to molecular markers of a possible residual tumour after treatment. On the basis of this, ctDNA has been aggressively evaluated in different solid tumor types and some studies revealed that the molecular relapse may precede as compared to conventional imaging in some patient conditions. The next step will be to evaluate if treating MRD (with better survival rates) is taking place (Paver & Morey, 2024). If a clinically-transformative prognostic biomarker association with biomarker-directed treatment results in a change in patient outcome.

6.6. Examine and talk about the spatial and single cell diagnostics that are under development:

Pathology and lab medicine will switch from the tissue level “average” to a cell resolved evaluation of molecular characterisation in the future. Single cell sequencing allows for assays of rare populations of malignant cells or/immune cells and anatomical context coupled with spatial (Hou et al., 2024). They might be of relevance in clinical applications such as in tumour therapy, autoimmune diseases, as well as in neurodegenerative and infectious diseases, where the outcome of therapy and the clinical phenotype relies on the heterogeneity of cells (Mielke & Fowler, 2024).

6.7. Obtain advanced diagnostics:

In remote areas, highly complicated biomarker assays can be carried out thanks to miniaturization and microfluidics, isothermal amplification and biosensors, and portable sequencing. Numerous of these technologies can have an impact on worldwide diagnostics for resource-limited settings. But there needs to be a robust quality system, link to reference materials, competency assessment and external quality assurance in place which go hand-in-hand with a decentralisation process (López-López et al., 2024). The goal is to make testing equally and simply accessible instead of testing in an unknown and uncontrolled environment.

7. CONCLUSION

Use of biomarkers to assess individuals' health and the severity of health problems began with the traditional biochemical tests. In present day, cutting edge technologies such as molecular biology and multi-omics are used to gain insight into the mechanisms underlying the body's operation when it's sick. In term of applications. Previously identified health issues, such as the diagnosis of glucose, creatinine, troponin, liver enzymes, markers of the inflammation, and level of lipids, which have been used for years and years in medicine, are still used for diagnosis. At the same time, the new technologies make it possible to make the timely diagnosis and with high accuracy (Wan et al., 2025). Liquid biopsy and its constituents including the circulating tumor DNA (ctDNA), single cell analysis, spatial profiling, and multi-omics, could provide answers in some aspects of the tumor, the response to treatment and the minimal residual disease (MRD). For reliable laboratory results, such standards as ISO 15189 and CLSI are important (Wang et al., 2025). In the future, complexity of diagnostics will continue to increase: AI and advanced molecular diagnostics and demographics will also come into play together with the analysis of various panels of biomarkers.

Author contribution B.M.: Data curation, Methodology, Visualization, Writing original draft, Editing; N.K.M.: Data search and collection, writing original draft, editing draft.

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