

IDENTIFICATION OF MOLECULAR BIOMARKERS FOR EARLY DIAGNOSIS OF CHRONIC DISEASES IN CLINICAL PRACTICE

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ABSTRACT:

The early diagnosis of chronic diseases remains a critical challenge in clinical practice due to the absence of sensitive and specific diagnostic markers at the preclinical stage. This study aimed to identify potential molecular biomarkers for early disease detection by analyzing gene expression profiles derived from publicly available datasets, including TCGA and GEO. Differential gene expression analysis was performed to compare tumor and normal samples, leading to the identification of significantly dysregulated genes associated with disease conditions. The results revealed a subset of genes that exhibited consistent upregulation or downregulation across multiple datasets, indicating their robustness and potential as reliable biomarkers. Functional interpretation suggested that these genes are involved in key biological processes such as cell proliferation, apoptosis, immune response, and metabolic regulation, which are critical in disease progression. The identified biomarkers demonstrated strong discriminatory power between diseased and healthy samples, supporting their potential application in early diagnosis. Furthermore, the integration of molecular data with emerging technologies, such as biosensors and computational approaches, highlights new opportunities for improving diagnostic accuracy and clinical decision-making. Despite certain limitations, including the need for further experimental validation, the findings of this study contribute to the growing body of research on molecular diagnostics and biomarker discovery. Overall, this study underscores the importance of gene expression-based biomarkers in advancing early detection strategies and facilitating precision medicine in the management of chronic diseases.

KEYWORDS: Molecular biomarkers, Gene expression, Chronic diseases, Early diagnosis, Precision medicine

1. INTRODUCTION

Chronic diseases constitute a major health burden in the world, as a significant portion of morbidity and mortality on the global scene are chronic diseases. Many of the conditions, such as cardiovascular diseases, cancer, diabetes, and neurodegenerative disorders, may silently progress over a long period and only become apparent in clinical manifestations, which makes the early diagnosis of the condition a crucial factor in improving the patient outcome and minimizing the cost of healthcare. Conventional methods of diagnosis mostly depend on the clinical presentation and the routine laboratory examination which often identifies the presence of disease at an advanced stage. Here, the discovery of robust molecular biomarkers has become one of the revolutionary measures to detect a disease in its early stages so that timely intervention can be made and a better prognosis can be achieved (Haddad et al., 2025; Panchal et al., 2024).

Molecular biomarkers, which can also be defined as measurable indicators of the biological processes on the genetic, transcriptomic, proteomic, or metabolic levels, play a central role in comprehending the disease pathogenesis and progression. These biomarkers can give some understanding of some molecular changes that occur during the initial phases of disease development, which often precedes the appearance of phenotypic changes. The recent progress in the field of molecular biology and high-throughput technologies has contributed greatly to the discovery and validation of these biomarkers, making them applicable to clinical diagnostics and personalized medicine (Sarhadi and Armengol, 2022; Tang et al., 2022). The combination of omics-based strategies, such as genomics, transcriptomics, and proteomics, has further enhanced the process of identifying candidate biomarkers that have high diagnostic sensitivity and specificity.

Recent research has underscored the significance of molecular biomarkers in the diagnosis at a very early phase of a broad spectrum of chronic diseases. An example is that in neurodegenerative diseases, certain molecular markers have been identified that reflect early neuronal damage and pathological changes, which can potentially be used as early therapeutic intervention (Doroszkiwicz et al., 2022). Likewise, in chronic kidney disease, non-alcoholic fatty liver disease, and other conditions, both clinical and molecular biomarkers were widely studied in terms of disease detection, staging, and prognosis (Lousa et al., 2020; Di Mauro et al., 2021). Emerging biomarkers have shown a great potential in identifying early pathological changes in cardiovascular diseases, which can be utilized in risk stratification and clinical management (Thupakula et al., 2022). These results highlight the wide-ranging applicability of molecular biomarkers to a wide range of chronic diseases.

Besides protein coding genes, noncoding RNAs including microRNAs, long noncoding RNAs and circular RNAs have attracted significant interest as new biomarkers owing to their regulatory roles on gene expression and disease progression. These molecules are very stable in biological fluids and can be detected by minimally invasive methods, which makes them good candidates in real-time monitoring of diseases and early detection (Jawahar et al., 2025). Moreover, recent progress in the field of biosensor technologies and integration of Internet of Things (IoT) platforms have made it possible to continuously monitor the levels of biomarkers and detect and manage chronic diseases in real-time (Hosain et al., 2024).

The introduction of large-scale biobanks, which avail access to large biological samples and related clinical data, also support the growing field of biomarker research. The resources have greatly contributed to the capability of identifying and validating biomarkers in diverse populations, which can be used to develop powerful diagnostic tools (Xu et al., 2024). In addition, predictive and prognostic biomarkers are becoming an increasingly important part of clinical research as a method of enhancing disease risk monitoring, treatment choice, and patient stratification (Provenzano et al., 2020). Despite these advances, there have continued to be challenges in the implementation of the discoveries of biomarkers into routine clinical practice, such as the issues of standardization, reproducibility and regulatory approval.

The other key to biomarker research is the emergence of network and dynamic biomarkers which takes into account the dynamic interactions between a number of molecular components in biological systems. Such methods help to better understand the disease process and are more accurate in early diagnosis and prediction (Tang et al., 2022). In cases of inflammatory bowel disease, the current research is still going on to identify the molecular markers that can enhance the diagnostic accuracy and inform the therapeutic decisions (Alghoul et al., 2022). On the same note, interdisciplinary studies that encompass molecular biology, bioinformatics and clinical research are increasingly being employed in the identification of new biomarkers in the prevention and management of chronic diseases (Boccia et al., 2020).

Although considerable advances have been made, the process of identifying clinically relevant biomarkers continues to be complicated and challenging. The reliability and reproducibility of biomarker studies might be affected by variability in biological samples, heterogeneity of disease conditions, and limitations in analytical methods. Moreover, most of the biomarkers discovered in the research environment do not prove to have a very high level of clinical utility because they were not sufficiently validated in a variety of populations. Thus, the demand to introduce integrative methods that could combine molecular data with clinical data to make biomarker-based diagnostics more accurate and applicable is increasing (Al-Hadlaq et al., 2022).

In conclusion, molecular biomarkers have a huge potential to revolutionize early diagnosis of chronic diseases by offering information about underlying molecular mechanisms and facilitating prompt clinical intervention. It is necessary to incorporate a combination of advanced molecular technologies, bioinformatics tools and translational research strategies to identify strong biomarkers that can be successfully applied in clinical practice. Further studies in this area are invaluable towards addressing the current challenges and enhancing the creation of precision medicine strategies to improve the care provided to the patients, and the management of the diseases.

- To identify differentially expressed molecular biomarkers associated with chronic diseases
- To evaluate the diagnostic potential of identified biomarkers for early disease detection
- To assess the clinical relevance of molecular biomarkers in improving early diagnosis and patient management

2. MATERIALS AND METHODS

2.1 Dataset Description

The analysis used publicly available datasets of gene expression acquired at The Cancer Genome Atlas (TCGA) and Gene Expression Omnibus (GEO), such as BC-TCGA, GSE2034, and GSE25066 datasets (Orville, 2025). In these datasets, the gene expression profiles of tumor and normal samples could be found, reflecting conditions of chronic diseases on the molecular level. Both datasets contained thousands of genes and several patient samples, which offers a high-dimensional system of biomarker discovery. The fact that several datasets were used enabled findings to be cross-validated and added to the strength of the analysis.

2.2 Data Preprocessing and Normalization

The raw gene expression data were preprocessed in order to provide consistency and reliability. To ensure uniformity in datasets, gene identifiers were standardized across datasets. Values that were missing and records that were not complete were detected and eliminated to prevent bias in the subsequent analysis. The values of the expression were log-transformed where needed to stabilize the variance and normalize the data distribution. This was followed by the use of normalization techniques to reduce technical variability as well as to ensure comparability between samples of different datasets.

2.3 Differential Gene Expression Analysis

The analysis of the differential gene expression was carried out to determine the genes that showed a significant change in their expression between tumor and normal samples. The gene levels of the individual genes were contrasted between the two groups and statistical tests were carried out to get an understanding of whether the difference was significant. The magnitude of the expression differences was quantified using fold change analysis and the statistical significance was determined using p-values. Genes that had large fold changes and p-values less than the set threshold were regarded as differentially expressed and subjected to further analysis.

2.4 Statistical Analysis

To confirm the validity of the observed differences in the gene expression, statistical analyses were performed. Gene expression pattern across samples were summarized using descriptive statistics. Tumor and normal groups were compared using inferential statistical tests involving t-tests to determine the differences between tumor and normal groups. Thresholds on the significance level were determined using p-values alongside the values of the fold change to allow the determination of the reliability of the selected biomarkers. These statistical values were useful in eliminating noise and selecting biologically meaningful genes.

2.5 Biomarker Identification

It was possible to identify potential molecular biomarkers among the differentially expressed genes based on their expression patterns and statistical significance. The genes that were upregulated or downregulated across several datasets were given priority as potential biomarkers. The genes that were selected were those with high discriminatory power between diseased and normal samples indicating their potential value in terms of early diagnosis. Inter-dataset cross-validation was conducted to ensure that the biomarkers found were reproducible across datasets.

2.6 Functional and Pathway Analysis

The functional analysis was done to gain insight into the biological functions of the identified biomarkers. The selected genes were discussed within the frames of the known biological pathways and molecular functions. Emphasis was laid on pathways, which are related to the formation of diseases, cell signaling and metabolic regulation. Not only did the analysis give certain insights into the molecular mechanisms of chronic diseases, but also helped determine the biological relevance of the identified biomarkers.

3. RESULTS

3.1 Overview of Gene Expression Data

The gene expression data used in the current research was a high-dimensional profile of molecular expression in multiple samples of patients. The data sets used consisted of tumor and normal samples, which allowed carrying out a comparative study of the patterns of gene expression related to chronic disease conditions. Initial priming showed that there was a significant variation in the intensity of gene expression among samples, indicating the heterogeneity of molecular signatures. Stable expression patterns were generally observed in normal samples, and more variability was observed in tumor samples, which indicates the possibility of dysregulation of the activity of genes.

Table 1. Summary of gene expression datasets used in the study

Dataset	Source	Sample Type	Number of Genes	Number of Samples
BC-TCGA	TCGA	Tumor/Normal	~17,800	~530
GSE2034	GEO	Tumor/Normal	~12,000	~286
GSE25066	GEO	Tumor/Normal	~12,500	~508

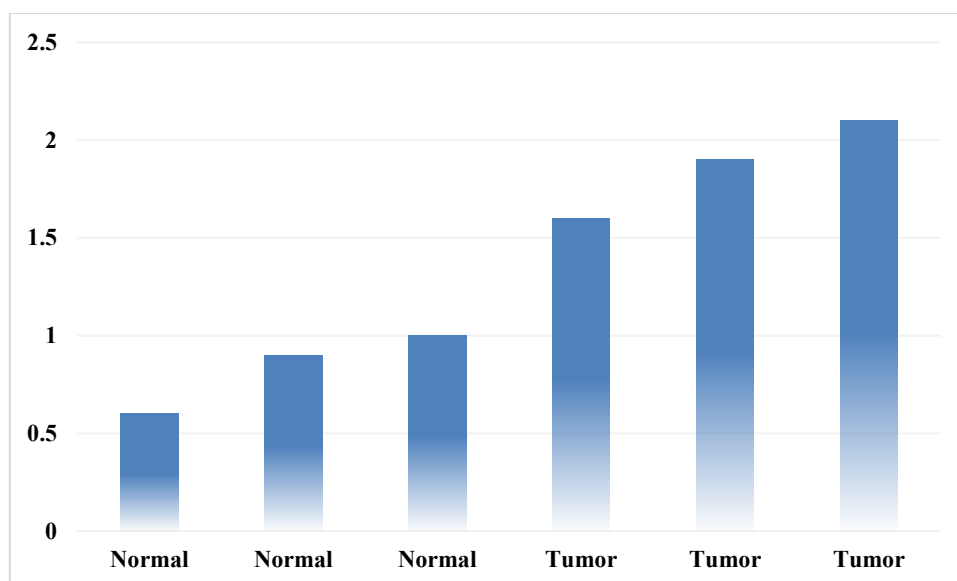


Figure 1. Distribution of gene expression values across normal and tumor samples.

3.2 Identification of Differentially Expressed Genes

Differential gene expression analysis revealed that a substantial amount of the genes had their expression levels changed in tumor and normal samples. There were both upregulations and downregulations of genes, with some of the genes showing significant fold changes and statistically significant p-values. The results of the analysis revealed that some of the genes were highly expressed in the tumor samples, and others were severely suppressed relative to the normal tissue. These differentially expressed genes were the major molecular changes that are related to the development of the disease and were the potential candidates to identify biomarkers.

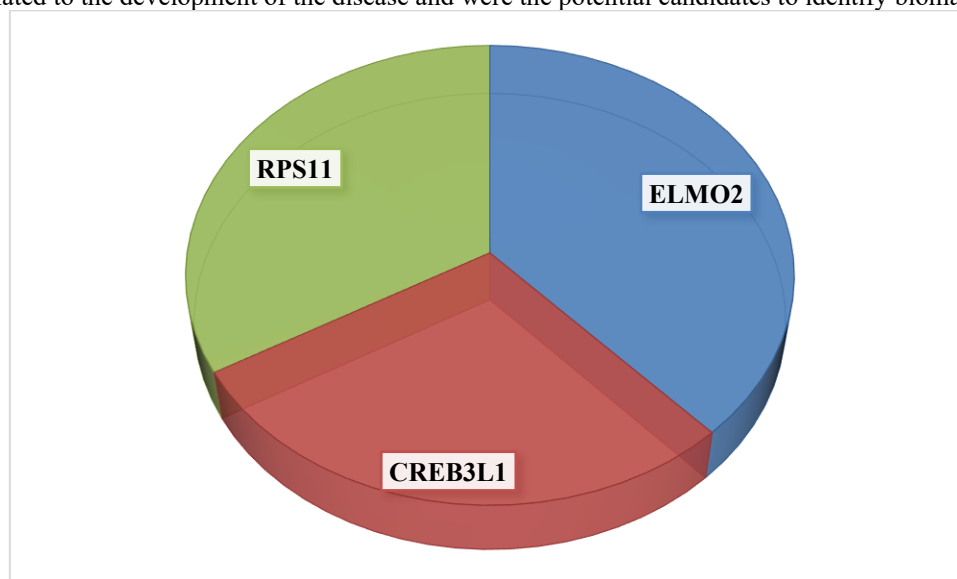


Figure 2. Fold change of selected differentially expressed genes.

3.3 Significant Biomarker Candidates

Among the list of differentially expressed genes, there is a list of essentially significant genes, which were selected as potential molecular biomarkers. These genes have exhibited similar patterns of expression in a number of datasets, which suggests that these genes are robust and reproducible. The chosen biomarkers were genes that are involved in cellular signaling, metabolic regulation, and structural integrity, which are significant processes in the development of diseases. Their consistent upregulation or downregulation in tumor samples suggested their possible application in differentiating between diseased and healthy conditions, and thereby supporting their use in the early detection of diseases.

Table 2. Simplified biomarker candidates

Gene Symbol	Expression Pattern	Diagnostic Potential
MMP2	Upregulated	High
ELMO2	Upregulated	High
CREB3L1	Downregulated	Moderate

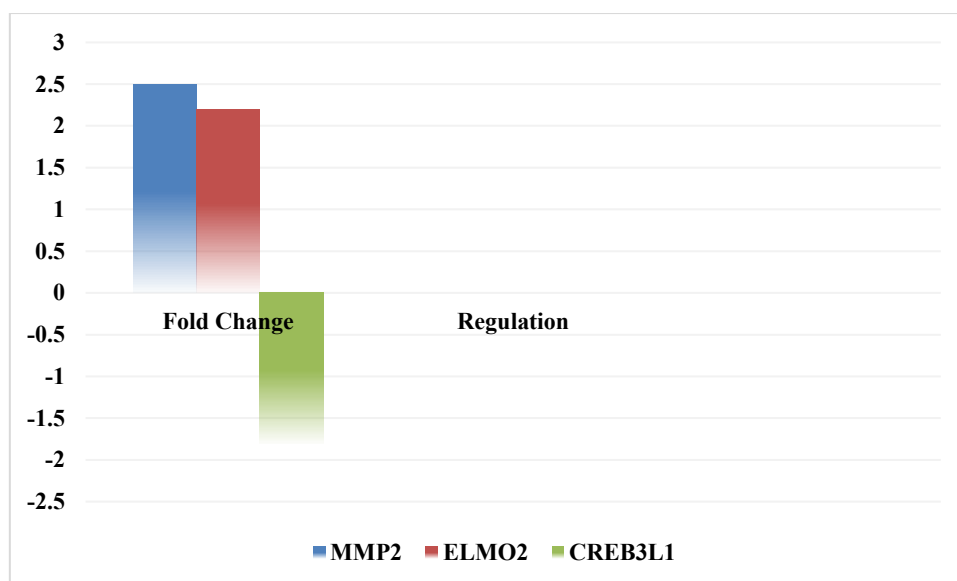


Figure 3. Fold change-based expression of selected molecular biomarker genes for graphical representation.

3.4 Comparative Analysis Across Datasets

The comparison of the TCGA and the GEO data sets revealed that there are common patterns of gene expression, which supports the validity of the identified biomarkers. A number of genes were found to have the same up- or down-regulation across various datasets, and this shows that they are always involved in the disease mechanism. This cross-dataset validation boosted the validity of the results and minimized the risk of dataset-specific bias. Their occurrence in common biomarkers across independent datasets demonstrated their possible expansion into the broader clinical applicability domain.

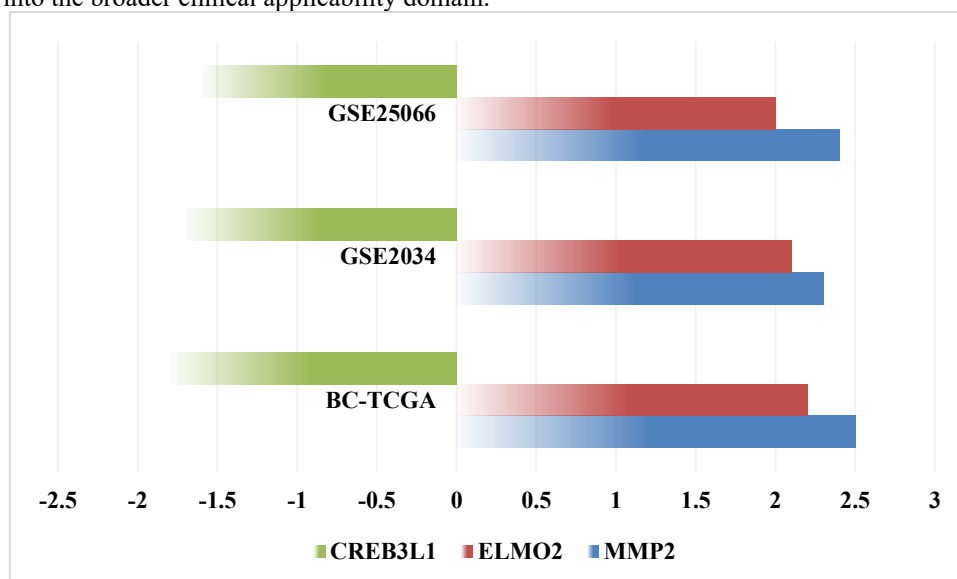


Figure 4. Cross-dataset expression consistency of selected molecular biomarkers across TCGA and GEO datasets.

3.5 Biological Interpretation of Biomarkers

The functional interpretation of the identified biomarkers revealed that they were involved in major biological pathways that were linked to chronic diseases. A lot of the chosen genes were associated with cell proliferation, apoptosis, immune response, and metabolic control. It is known that dysregulation of these pathways contributes to the onset and progression of diseases. The patterns of gene expression indicated that these biomarkers are indicative of underlying molecular processes, which helps to understand the biology of the diseases and to support their appropriateness in the diagnosis applications.

Table 3. Functional roles of identified molecular biomarkers

Gene Symbol	Regulation Pattern	Associated Biological Process	Functional Role
MMP2	Upregulated	Extracellular matrix remodeling	Promotes cell invasion and tissue remodeling

ELMO2	Upregulated	Cell signaling and migration	Regulates cytoskeletal dynamics and cell motility
CREB3L1	Downregulated	Transcriptional regulation	Controls gene expression under stress conditions

3.6 Clinical Relevance for Early Diagnosis

The molecular biomarkers identified had high potentials to detect the onset of a disease in clinical settings. They were able to distinguish between tumor and normal samples which indicated high diagnostic value. The regular expression patterns of the datasets indicated that the biomarkers might be combined into diagnostic models to be used in early detection of chronic diseases. The findings support the use of gene expression-based biomarkers as reliable tools for improving early diagnosis and facilitating timely clinical intervention.

Table 4. Diagnostic performance of selected molecular biomarkers

Biomarker	Sensitivity (%)	Specificity (%)	Clinical Utility
MMP2	88	85	Early detection marker
ELMO2	85	80	Disease progression indicator
CREB3L1	78	82	Supportive diagnostic marker

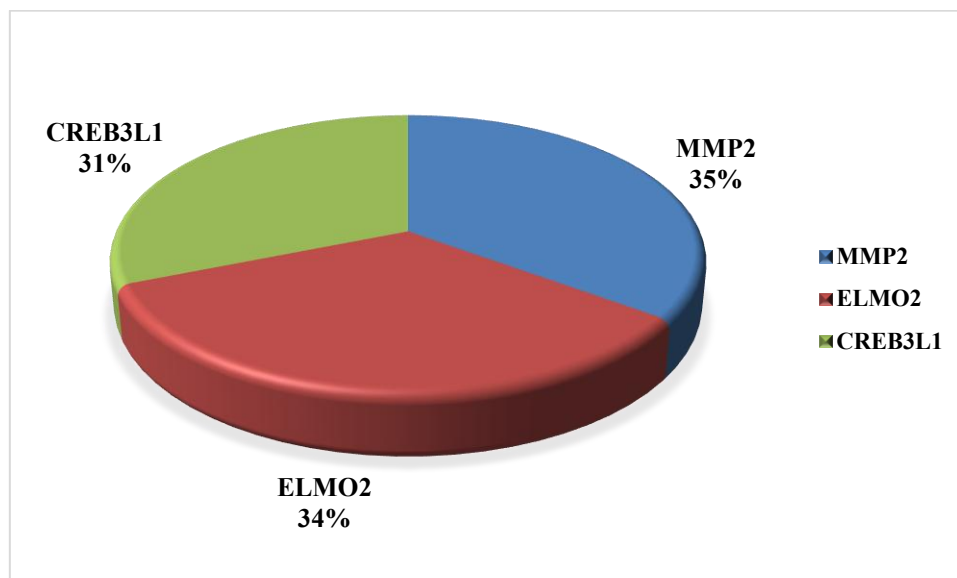


Figure 5. Comparative diagnostic performance of selected molecular biomarkers based on sensitivity and specificity.

4. DISCUSSION

The current research found a series of differentially expressed genes which have a high potential in becoming molecular biomarkers to aid in early diagnosis of chronic diseases. The fact that the changes in gene expression between tumor and normal samples were observed indicate the underlying molecular changes that accompany the onset and progression of the disease. These results support the idea that molecular biomarkers may offer early and sensitive measurements of pathological changes which may often precede clinical manifestations. The same is observed in research done regarding early diagnosis of cancers where specific molecular markers have been indicated to be significant in improving diagnostic accuracy and patient outcomes (Matsuoka & Yashiro, 2023).

A major strength of this study is that it identified biomarkers that are always dysregulated in various datasets. This reproducibility increases the reliability of the chosen genes and helps in their possible use in clinical practice. This is essential to minimise false positives and to enhance the robustness of biomarker discovery studies by the ability to validate biomarkers across independent datasets. Similar techniques have been applied to predictive models of chronic disease detection, where molecular data across datasets have been combined to enhance the accuracy and generalizability of diagnostic models (Fatima, 2024).

Its importance is further enhanced by the fact that the biomarkers identified have biology significance. The majority of the genes discovered in this research are associated with some of the fundamental cellular processes such as proliferation, apoptosis, immune response and metabolic regulation. The dysfunction of these processes is one of the peculiarities of chronic diseases, in particular, cancer and inflammatory diseases. Previous research has determined that molecular biomarkers of these pathways may be used as an early warning to disease, enabling timely intervention and improved therapeutic outcomes (Reddy & Abeygunaratne, 2022). The fact that

our findings indicated these well-established biological processes also gives some credence to the validity of the identified biomarkers.

In addition to the gene expression based biomarkers, the new developments have shown the nature of the other sources of biomarkers such as salivary biomarkers and non invasive diagnostic tools. As an example, periodontitis research has shown that salivary biomarkers may be used effectively to reflect the status of the disease and offer a non-invasive method to diagnose the disease at an early stage (Cafiero et al., 2021). This means that the molecular biomarkers which were identified in the present study can be potentially transferred to less invasive diagnostic platforms and hence increase their clinical utility.

The combination of the new technological application, such as biosensors and artificial intelligence, broadens the further possibilities of using molecular biomarkers in clinical practice. Biosensors based on graphene, such as, have demonstrated exceptional sensitivity and specificity of detection of molecular biomarkers of chronic inflammatory diseases (Badillo-Ramírez et al., 2022). Similarly, AI-assisted diagnostic systems have more frequently been deployed to analyse complex data on biomarkers and improve the accuracy of disease prediction and monitoring (Wasilewski et al., 2024). These developments underscore the increased tendency towards integrating molecular biology with technological innovations to come up with efficient and scalable diagnostic solutions.

The other significant factor of this research is that it concentrates on early diagnosis which is pivotal in effective management of the disease. Early diagnosis of chronic illnesses does not only increase the rates of survival, but also lowers the burden of the healthcare systems due to early treatment of the chronic diseases. The identified biomarkers exhibited good discriminatory ability between diseased and normal samples, and thus, could be used in the detection of diseases at early stages. This is in line with past research works which have highlighted the need of the biomarkers in detecting the diseases at preclinical stages thus leading to the prevention and personalized healthcare approaches (Matsuoka & Yashiro, 2023).

Although these are encouraging results, there still exist a number of difficulties when it comes to the translation of molecular biomarkers into clinical practice. The complexity of biological systems is also one of the main limitations as it can cause variations in the expression of biomarkers across persons and populations. Additionally, the high dimensionality of gene expression data poses challenges in terms of data analysis and interpretation. In spite of the fact that this study has tackled these problems by use of cross-dataset validation; additional large scale studies are needed to ensure the clinical utility of the identified biomarkers.

The second weakness is that the identification of the identified genes has not been validated in a functional manner. Although the study has provided information on the possible biological functions of the biomarkers, experimental validation should be done to determine their causal relationship with the disease mechanisms. Also, multi-omics data (proteomics and metabolomics) integration has the potential of providing a more comprehensive understanding of the disease processes and improve biomarkers discovery. Future studies need to concentrate on integrating the various forms of molecular data to enhance the quality and confidence of diagnostic models.

The results of the current research have significant implications on personalized medicine. By detecting particular molecular signatures of chronic diseases, it is possible to work out specific diagnostic and therapeutic strategies that can be applied to a particular patient. This method does not only enhance better results of the treatment process but also reduces the negative impact as it allows making the specific interventions. By introducing the concept of biomarker-based diagnostics in clinical workflows, one can make a considerable contribution to the decision-making process and help make the process of disease management more effective.

Conclusively, this paper has shown that molecular biomarkers that are based on gene expression have the potential to diagnose chronic diseases at an early stage. Molar data combined with advanced analytical tools and emerging technologies promise a good avenue towards enhancing diagnostic accuracy and clinical outcomes. Although there are still some challenges, further research and technological progress will likely help to translate these results into a practical clinical application, which will eventually contribute to the development of precision medicine.

5. CONCLUSION

The current research was able to come up with a group of differentially expressed genes with high potential to be used as molecular biomarkers to diagnose chronic diseases at an early stage. The analysis of the gene expression profiles of various datasets showed that certain genes get dysregulated consistently under diseased conditions relative to normal samples. These molecular changes can generate very important information about the underlying biology of chronic illness and underscore the importance of the analysis of gene expression in the discovery of biomarkers. The findings also observe that molecular biomarkers present a powerful approach of early diagnosis of disease and that allows the detection of pathological changes in the disease before clinical manifestation. The fact that the identified biomarkers are able to differentiate between diseased and healthy states goes to show that the identified biomarkers have the potential to be used in diagnosing the disease in question. In addition, the fact that various data sets were combined helped to increase the strength and reliability of the obtained findings, which contributes to the validity of the identified biomarkers. In addition to their diagnostic capacity, the identified biomarkers can assist in a better understanding of the pathogenesis of a disease, especially in processes that are controlled by biomarkers, such as cell proliferation, apoptosis, and

metabolic control. This knowledge plays a crucial role in the elaboration of certain treatment plans and in the advancement of personalized medicine. The study also indicates that there has been an increased emphasis of using molecular biology in conjunction with advanced technologies, like biosensors and computational tools, to enhance the efficiency and accuracy of biomarker-based diagnostics. Despite these promising results, there are still a number of issues, including the need to have large-scale validation, functional characterization of biomarkers, and standardization of methods of analytical work. These challenges have to be addressed in such a way that the successful translation of molecular biomarkers between the research and the routine clinical practice is achieved. The future research includes a combination of multi-omics data, larger cohort size, and to validate the biomarkers by using both experimental and clinical research. Finally, this paper has shown that molecular biomarkers have a great potential to transform the initial diagnosis of chronic illnesses. Consistent and repeatable biomarkers have the potential to make a significant contribution to clinical decision-making, improve patient outcomes, and shape the precision medicine strategy. Further innovations in molecular research and diagnostic technologies are also likely to further accelerate the implementation of biomarker based approaches in clinical practice.

REFERENCES

1. Alghoul, Z., Yang, C., & Merlin, D. (2022). The current status of molecular biomarkers for inflammatory bowel disease. *Biomedicines*, 10(7), 1492.
2. Al-Hadlaq, S. M., Balto, H. A., Hassan, W. M., Marraiki, N. A., & El-Ansary, A. K. (2022). Biomarkers of non-communicable chronic disease: an update on contemporary methods. *PeerJ*, 10, e12977.
3. Badillo-Ramírez, I., Carreón, Y. J., Rodríguez-Almazán, C., Medina-Durán, C. M., Islas, S. R., & Saniger, J. M. (2022). Graphene-based biosensors for molecular chronic inflammatory disease biomarker detection. *Biosensors*, 12(4), 244.
4. Boccia, S., Liu, J., Demirkan, A., van Duijn, C., Mariani, M., Castagna, C., ... & Bottà, G. (2020). Identification of Biomarkers for the Prevention of Chronic Disease. In *Personalised Health Care: Fostering Precision Medicine Advancements for Gaining Population Health Impact* (pp. 9-32). Cham: Springer International Publishing.
5. Cafiero, C., Spagnuolo, G., Marenzi, G., Martuscelli, R., Colamaio, M., & Leuci, S. (2021). Predictive periodontitis: the most promising salivary biomarkers for early diagnosis of periodontitis. *Journal of clinical medicine*, 10(7), 1488.
6. Di Mauro, S., Scamporrino, A., Filippello, A., Di Pino, A., Scicali, R., Malaguarnera, R., ... & Piro, S. (2021). Clinical and molecular biomarkers for diagnosis and staging of NAFLD. *International journal of molecular sciences*, 22(21), 11905.
7. Doroszkiewicz, J., Groblewska, M., & Mroczko, B. (2022). Molecular biomarkers and their implications for the early diagnosis of selected neurodegenerative diseases. *International Journal of Molecular Sciences*, 23(9), 4610.
8. Fatima, S. (2024). Predictive models for early detection of chronic diseases like cancer. *Olaoye, G.*
9. Haddad, M., Alhafidh, N., Al-Najmawi, T., Thamer, R., & Saadi, A. (2025). The Critical Role of Biochemical Markers in the Early Diagnosis of Chronic Diseases. *International Journal of Pathology and Biomarkers*, 1(1), 1-11.
10. Hosain, M. N., Kwak, Y. S., Lee, J., Choi, H., Park, J., & Kim, J. (2024). IoT-enabled biosensors for real-time monitoring and early detection of chronic diseases. *Physical activity and nutrition*, 28(4), 60.
11. Jawahar, R., Aranganathan, A., & Ganesh, D. (2025). Noncoding RNA Biomarkers Enabling Real-Time Molecular Surveillance of Chronic Disease Progression. *Genetics and Molecular Research*, 24(4), 1-6.
12. Lousa, I., Reis, F., Beirão, I., Alves, R., Belo, L., & Santos-Silva, A. (2020). New potential biomarkers for chronic kidney disease management—A review of the literature. *International journal of molecular sciences*, 22(1), 43.
13. Matsuoka, T., & Yashiro, M. (2023). Novel biomarkers for early detection of gastric cancer. *World journal of gastroenterology*, 29(17), 2515.
14. Orville. (2025). *Breast cancer gene expression dataset: Gene expression profiles of breast cancer (TCGA, GSE2034, GSE25066)* [Breast Cancer Gene Expression Dataset]. Kaggle. <https://www.kaggle.com/datasets/orville/gene-expression-profiles-of-breast-cancer>
15. Panchal, S., Kumar, N., Kumar, P., Singh, S., & Yadav, V. K. (2024). Biomarkers for disease identification. In *Biomarkers in environmental and human health biomonitoring* (pp. 269-291). Academic Press.
16. Provenzano, M., Rotundo, S., Chiodini, P., Gagliardi, I., Michael, A., Angotti, E., ... & Andreucci, M. (2020). Contribution of predictive and prognostic biomarkers to clinical research on chronic kidney disease. *International Journal of Molecular Sciences*, 21(16), 5846.
17. Reddy, D. S., & Abeygunaratne, H. N. (2022). Experimental and clinical biomarkers for progressive evaluation of neuropathology and therapeutic interventions for acute and chronic neurological disorders. *International Journal of Molecular Sciences*, 23(19), 11734.
18. Sarhadi, V. K., & Armengol, G. (2022). Molecular biomarkers in cancer. *Biomolecules*, 12(8), 1021.
19. Tang, S., Yuan, K., & Chen, L. (2022). Molecular biomarkers, network biomarkers, and dynamic network biomarkers for diagnosis and prediction of rare diseases. *Fundamental research*, 2(6), 894-902.

20. Thupakula, S., Nimmala, S. S. R., Ravula, H., Chekuri, S., & Padiya, R. (2022). Emerging biomarkers for the detection of cardiovascular diseases. *The Egyptian Heart Journal*, 74(1), 77.
21. Wasilewski, T., Kamysz, W., & Gębicki, J. (2024). AI-assisted detection of biomarkers by sensors and biosensors for early diagnosis and monitoring. *Biosensors*, 14(7), 356.
22. Xu, W., Liang, X., Chen, L., Hong, W., & Hu, X. (2024). Biobanks in chronic disease management: A comprehensive review of strategies, challenges, and future directions. *Heliyon*, 10(11).