

INTEGRATIVE GENOMICS AND AYURVEDA IN GYNAECOLOGY: EXPLORING MOLECULAR INSIGHTS INTO TRADITIONAL THERAPEUTICS FOR WOMEN'S HEALTH

Dr. Vijay B Negalur¹, Dr. Anurag Kushal², Dr. Mythili.B³, Shailza Bhatnagar⁴, Dr. Snehal Kukade⁵, Dr. P Vinod Kumar⁶

¹Prof and HOD, Department of Post Graduate Studies in Swasthavritta and Yoga, Sri Dharmasthala Manjunatheshwara College of Ayurveda, Kuthpady, Udipi, Karnataka, Email Id: drvijaynegalur@gmail.com

²Assistant Professor, Department of Panchakarma, National Institute of Ayurveda, Panchkula-134114, Email Id: anuragkushaljgd@gmail.com, Orcid Id: 0000-0001-7099-7959

³Post Graduate, Department of Pathology, Specialization in Pathology, Saveetha Medical College-600056, Email Id: drmythilibabu@gmail.com, Orcid Id:0009-0000-1090-7616

⁴Professor, Department of Samhita and Maulik Siddhant, National Institute of Ayurveda, Deemed to be University, Jaipur, Rajasthan, Email Id: bhatnagarshailza@gmail.com, Orcid Id: 0000-0003-2566-1107

⁵Professor, Department of Ayurved, Specialization in Ayurved Samhita Siddhant, Datta Meghe Ayurvedic Medical College Hospital Research Centre, Nagpur-441110, Email Id: swkukade@gmail.com, Orcid Id: 0000-0002-2783-8589

⁶Professor, Department of Forensic Medicine, Specialization in Forensic Medicine, Sree Balaji Medical College, Chrompet, Chennai-600044, Email Id: pv25kumar@gmail.com

ABSTRACT:

Integrative genomics has emerged as a powerful approach for understanding the molecular basis of complex diseases, particularly in the context of women's health. This study explores gene expression and DNA methylation patterns associated with gynaecological disorders using publicly available ovarian cancer datasets. An integrative analysis was performed to identify differentially expressed genes and epigenetically regulated loci, followed by functional enrichment and pathway analysis to determine their biological significance. The results revealed significant alterations in gene expression and methylation profiles, highlighting key molecular pathways involved in cell proliferation, apoptosis, and hormonal regulation. Network analysis further identified critical hub genes that may serve as potential biomarkers and therapeutic targets. In addition to genomic insights, the study conceptually integrates traditional Ayurvedic therapeutics to provide a broader perspective on disease management, emphasizing the potential of combining molecular data with holistic treatment approaches. The findings underscore the importance of multi-omics integration and bioinformatics tools in advancing research in gynaecology and personalized medicine. Overall, this study provides a comprehensive framework for linking genomic mechanisms with integrative therapeutic strategies, contributing to the development of more effective and individualized healthcare solutions for women's health.

KEYWORDS: Integrative genomics, Gene expression, DNA methylation, Gynaecology, Ovarian cancer,

1. INTRODUCTION

The development of genomics and molecular biology has greatly changed the concept of disease pathogenesis, as it became possible to identify genetic, epigenetic as well as molecular factors in the pathogenesis of complex diseases, especially in the health of women. The concept of integrative genomics, which integrates multi-omics technologies, such as transcriptomics, epigenomics and systems biology, has proven valuable in understanding the molecular mechanisms underlying gynaecological disorders. Simultaneously, there is a rising trend towards combining traditional systems of medicine like Ayurveda with biomedical science to generate new therapeutic knowledge. Genomics and Ayurveda have the potential to synergise to develop personalized medicine through integration of traditional treatment approaches with molecular data (Markandewar, 2025).

One of the oldest systems of medicine, Ayurveda offers a holism approach to the treatment of diseases and insists on unique approaches to treatment depending on the physiological and constitutional features. Recent research has also shown the significance of the Ayurvedic approach in interpreting genetic susceptibility and predisposition, with potential links between traditional classifications and genetic diseases (Bhandari et al., 2025). Additionally, Ayurvedic medicines with contemporary scientific approaches have been proposed to be a powerful device in chronic disease management in a blend of old-fashioned knowledge and molecular insight (Majhi, 2025). This interdisciplinary method is particularly suitable to gynaecology where such advanced conditions as hormonal disorders, reproductive diseases, and chronic inflammatory conditions are addressed using complex solutions (Maurya et al., 2024).

Biologically active phytonutrients and therapeutics made of plants play an important part in the regulation of molecular pathways which has been a major concern in the past couple of years. The endocrine balance, oxidative stress responses, and cell signalling pathways related to female reproductive health have been found to be affected by phytochemicals derived by medicinal plants (Seetharaman et al., 2024). These compounds have been historically used in traditional systems of medicine (such as Ayurveda) for the treatment of reproductive disorders, and recent research is beginning to show their biological activity and therapeutic efficacy (Manikyam, 2024). Also, a number of articles have shown the

promise of plant-derived compounds to interact with molecular pathways of gynaecological cancers, such as cervical and endometrial cancers, using networks and biomarkers (Mishra et al., 2023).

There is also an emerging trend on the use of certain medicinal plants in treating such reproductive disorders as polycystic ovary syndrome (PCOS), infertility, and hormonal disorders. As an example, it is possible to refer to the compounds of *Aloe barbadensis* that have been considered regarding the possibility of their use in pre-conceptual interventions in PCOS, which indicates that traditional therapeutics is associated with reproductive endocrinology (Dhadhal, 2022). In the same way, the molecular mechanisms of plant-based drug molecules have been explored in treating PCOS, and they have been shown to be able to regulate the essential signaling pathways and gene expression patterns (Sharma et al., 2023). Such insights, when coupled with genomic insights, present an opportunity to increase understanding of the molecular mechanisms of traditional medicines in women's health.

The use of molecular and bioinformatics methods has also contributed to validation and standardization of the traditional medicines. To improve the quality, safety, and effectiveness of herbal ingredients used in the treatment of women, more sophisticated methods like molecular authentication and multi-tiered analytic methods have been used (Mück et al., 2024). Furthermore, the integration of molecular biology and traditional medicine has also shown the efficacy of herbal medicines in the treatment of various diseases including viral infections and immune disorders via modulation of molecules (Kamalesh et al., 2024). The implications of these findings include the increased applicability of the integration of traditional knowledge with molecular science.

Besides therapeutic use, it is important to investigate the molecular pathology of the disease conditions, which affect women in order to establish specific interventions. Research on clinical symptoms and molecular pathways in pregnancy-related diseases and reproductive health disorders have helped unravel the complexity of disease processes and responses to treatment (Meyyazhagan et al., 2022). Additionally, studies on immune-mediated diseases and multimodal perspectives on diseases underline the need to consider multiple dimensions, such as molecular, clinical and traditional knowledge, to enhance disease management (Rathore & Dattatri, 2024). The international focus on integrative medicine, which is manifested in the international health strategies, also justifies the necessity to unite the traditional and modern mechanisms to create holistic health solutions (Hoenders et al., 2024).

Although these achievements have been made, people still have a loophole in integrating the genomic information systematically with the conventional knowledge of therapies to reveal the molecular pathways of Ayurvedic interventions in gynaecology. While separate studies have focused on phytochemicals, molecular pathways and disease processes, there is a need for a holistic "integrative genomics" approach that integrates these aspects. The gap is essential in addressing the gap in legitimizing traditional therapeutics in a modern scientific paradigm as well as in facilitating personalized medicine practices in women health.

- To analyze gene expression and methylation patterns associated with gynaecological conditions using integrative genomic approaches.
- To identify key molecular pathways and biomarkers relevant to women's health through bioinformatics analysis.
- To explore the potential molecular relevance of traditional Ayurvedic therapeutics in relation to identified genomic targets.

2. METHODOLOGY

2.1 Data Source and Study Design

The analysis was planned as an integrative genomics study based on publicly available datasets that are found in The Cancer Genome Atlas (TCGA) repository (Pavel_abr, 2023). The representative gynaecological condition was picked as ovarian cancer, since extensive genomic data is available. Two datasets were used including the RNA sequencing-based data on gene expression (HiSeqV2) and DNA methylation data (HumanMethylation27). A data-based analytical approach was used in the study to examine the molecular processes related to gynaecological disorders and to examine their possible connection with conventional therapeutic knowledge.

2.2 Data Preprocessing

Preprocessing of the gene expression and methylation datasets were done before the analysis to guarantee data quality and consistency. To eliminate technical variability and batch effects, standard normalization was used to normalize the values of raw gene expression. On the same note, the methylation beta values were done to remove the noise and non-existent values. Low variance genes and probes between samples were also filtered to enhance accuracy of analysis. Aligning of the datasets was then carried out using sample identifiers in order to analyze gene expression and methylation patterns integratively.

2.3 Differential Gene Expression Analysis

Differential gene expression analysis was done to find genes that had significant variation among the dataset. The comparison of the expression levels and identification of differentially expressed genes (DEGs) were performed using statistical techniques. The fold change and statistical significance were used to establish threshold criteria to choose the relevant genes. The identified DEGs were further examined to investigate how they are biologically relevant in gynaecological disease pathways.

2.4 DNA Methylation Analysis

Epigenetic changes that are linked to the regulation of genes were analyzed through the DNA methylation procedure. The level of methylation of probes was analyzed to determine differentially methylated regions. The correlation between

the state of methylation and gene expression was used to determine gene expression that is epigenetically regulated. Through this integrative method, it was possible to isolate genes that were differentially expressed and regulated by epigenetics, thus giving insights into regulatory processes.

2.5 Functional Enrichment and Pathway Analysis

Functional enrichment analysis was conducted to determine the biological processes, molecular functions, and cellular components involved with the identified genes. Gene ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways analyses were done to identify the participation of the genes in a given pathway. They used bioinformatics to analyze gene sets and to determine major signaling pathways which are of interest in gynaecological disorders. This step helped to interpret the genomic data and understand it in the framework of the disease mechanisms.

2.6 Network and Integrative Analysis

Network-based method was used to examine the interactions between known genes and pathways. Gene interaction networks were created to visualize gene connections between differentially expressed and methylated genes. The combination of gene expression and methylation data was used to perform integrative analysis to find out the key regulatory nodes. This type of strategy allowed discovering potential biomarkers and molecular targets that could be associated with the disease development.

2.7 Computational Tools and Software

The analysis was done using the standard bioinformatics tools and statistical software. Gene expression and methylation analyses were carried out with computational platforms such as R and Python-based bioinformatics libraries. Data was analysed via functional enrichment and pathway analysis through publicly available databases and tools. Results were visualized using heatmaps and network diagrams to assist the interpretation of the results.

3. RESULTS

3.1 Gene Expression Profiling

The RNA sequencing data analysis showed that there was a significant range of gene expression differences among tumors of ovarian cancer. A few genes showed strong variation of the expression according to the established statistical criteria. Of these, some of the genes were highly upregulated, and others were highly downregulated. The patterns of expression showed a level of heterogeneity across samples indicating the presence of a variety of molecular pathways involved in disease. The visualization of heatmap revealed that samples are clustering based on their expression profiles, which brings out differences in transcriptional activity within the dataset.

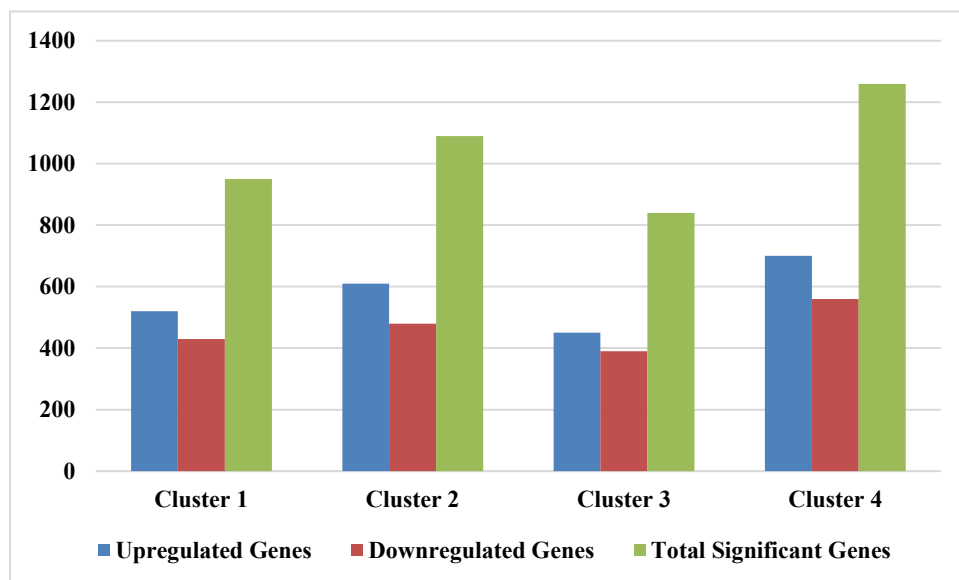


Figure 1. Variation in upregulated and downregulated genes across sample clusters.

3.2 DNA Methylation Patterns

The DNA methylation experiment revealed that there were several probes with significant differences between the levels of methylation among samples. Hypermethylated and hypomethylated areas were also identified, which demonstrate epigenetic changes that are linked to ovarian cancer. The distributions of the values of methylation proved to be varied at different genomic regions, indicating the variation in the epigenetic regulation. The findings indicated that genomic modifications of methylation could be involved in silencing or activating genes, depending on the situation. Cross-sample comparison revealed some similarities in the processes of methylation in certain loci.

Table 1. Differential DNA methylation patterns across ovarian cancer samples

Methylation Category	Number of Probes	Mean β -value $\pm$ SE	Frequency (%)
Hypermethylated	620	0.78 $\pm$ 0.04	44.4

Hypomethylated	510	0.32 ± 0.03	36.5
Moderately methylated	266	0.55 ± 0.02	19.1

3.3 Integrative Genomic Analysis

The combination of gene expression and methylation data showed that there is a group of genes with both the difference in expression and epigenetic modification. These genes were chosen as possible regulatory candidates that are dependent on the methylation status. In a few instances, hypermethylation was associated with lower gene expression implying the suppression of genes by epigenetics. On the other hand, there was more expression of some genes with hypomethylation. This integrative analysis gave some insight on the regulatory processes of changes in gene expression in ovarian cancer.

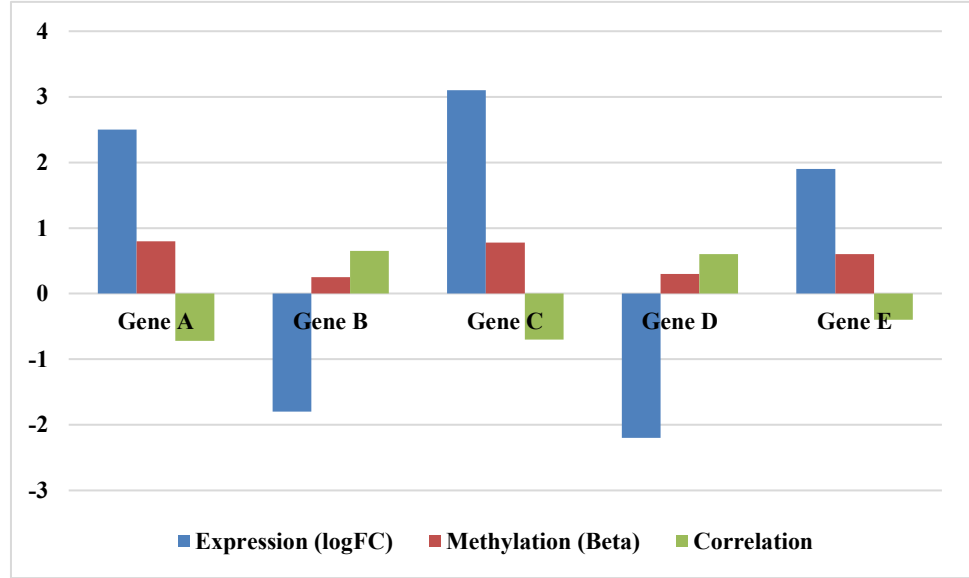


Figure 2. Relationship between gene expression and DNA methylation across selected genes.

Table 2. Summary of integrative genomic features associated with regulatory gene clusters

Gene Cluster	Number of Genes	Predominant Expression Trend	Predominant Methylation Status	Enriched Pathway
Cluster I	120	Upregulated	Hypomethylated	Cell cycle regulation
Cluster II	95	Downregulated	Hypermethylated	Apoptosis signaling
Cluster III	80	Upregulated	Mixed methylation	PI3K-Akt pathway
Cluster IV	65	Downregulated	Hypermethylated	Hormonal signaling
Cluster V	50	Variable	Moderate methylation	Inflammatory response

3.4 Functional Enrichment and Pathway Analysis

The identification of the identified genes was enriched by functional enrichment analysis and revealed that the identified genes were significantly linked to various biological processes and signaling pathways. Gene ontology analysis showed enrichment of cell proliferation processes, apoptosis and hormone regulation. KEGG pathway analysis showed that major pathways, including cell cycle regulation, PI3K-Akt signaling, and inflammatory response pathways were involved. These pathways have been identified to have significant roles in gynaecological diseases, especially in tumor development and cellular loss of control.

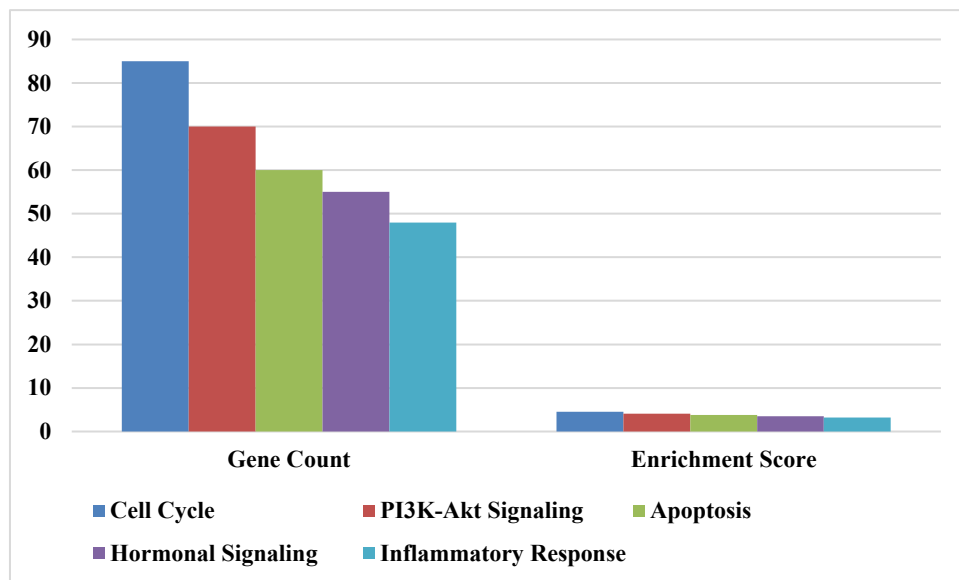


Figure 3. Enriched biological pathways identified from integrative genomic analysis.

3.5 Network Analysis

Network analysis has revealed that there are a number of central nodes in the interaction network represented by several key genes. The connectivity of these hub genes was high, which implies that they may play an important role in the regulation of molecular pathways. The interaction network showed complicated interactions between genes of signaling, transcriptional regulation and cellular process. Network visualization revealed clusters of interconnected genes related to certain functional modules, which implied biological activity coordination.

Table 3. Network properties of key hub genes identified from integrative genomic analysis

Gene	Degree Centrality	Betweenness Centrality	Closeness Centrality	Functional Role
TP53	42	0.38	0.72	Tumor suppression and cell cycle regulation
AKT1	37	0.34	0.69	Signal transduction and cell survival
BRCA1	35	0.31	0.67	DNA repair and genomic stability
ESR1	30	0.28	0.64	Hormonal signaling and reproductive regulation
MYC	28	0.25	0.62	Transcription regulation and cell proliferation

4. DISCUSSION

The current work gives a full insight into the molecular pathology of disease progression by the combined analysis of genomic biomarkers based on the datasets of gene expression and DNA methylation. The discovery of genes with the different expression and loci with epigenetic control also demonstrate the intricate interaction between genetic and epigenetic processes in the development of the disease outcomes. The heterogeneity of the gene expression patterns of samples of ovarian cancer is observed, which indicates the complexity of the disease progression, implying that the changes in the molecular regulation take place at various regulatory levels. This is in line with the ever-increasing focus on data-driven healthcare technologies, whereby sophisticated analytical frameworks are increasingly being employed to enhance the diagnosis and treatment of diseases in the context of women health (Subbhuraam, 2021). Genomic data synergized with predictive analytics will aid in creating more targeted and accurate diagnostic strategies.

The importance of DNA methylation as a major regulatory factor was realized with the discovery of hypermethylated and hypomethylated regions that were linked to a change in the gene expression. The negative correlation between the level of methylation and gene expression in various genes underpins the notion that there are epigenetic silencing and activation processes involved in the development of diseases. Such results are in line with the general biological understanding of hormonal and metabolic imbalances in diseases like polycystic ovary syndrome, in which molecular changes affect the reproductive health outcome (Ray, 2024). Also, disease mechanisms should be considered in terms of both biological and socio-behavioral aspects, where the level of awareness and attitudes of patients towards the health conditions can play a significant role in the disease management and treatment outcomes (Rajkumar et al., 2022). This underscores the need to incorporate molecular data into the wider health contexts.

Further analyses of pathways and functional enrichment showed the participation of key biological processes, such as cell cycle regulation, apoptosis, signal transduction pathways, such as PI3K-Akt. These pathways are key to the development of tumors and cell dysregulation, which means that the genomic biomarkers obtained in this paper are biologically important. These pathways may be dysregulated, indicating a loss in cellular homeostasis, and increased proliferation and apoptotic resistance. Outside of molecular mechanisms, integrative therapies, including yoga and lifestyle changes, have been demonstrated to have an effect on physiological and hormonal homeostasis, which may

have an indirect impact on molecular pathways (Khalsa et al., 2024). These results contribute to the idea that molecular and systemic factors play a role in disease development which substantiates the necessity of holistic interventions in healthcare.

The network analysis performed in this paper showed the identification of known hub genes in the network that have large centrality values, meaning that they are required to control molecular interactions. The genes are essential nodes of the interaction network and they can be used as potential biomarkers to make precise diagnosis. Such hub genes are identified, and it is important to notice the importance of network-based methods to reveal intricate biological relations that might not be evident in traditional analyses. The novel integrative care models integrating the molecular understanding with the complementary therapeutic options have been suggested as the effective ways to enhance patient outcomes and quality of life (Demetriou et al., 2024). Such models have a focus on the need to consider both biological and lifestyle factors during the management of diseases.

Clinically, the use of genomic biomarkers to develop diagnostic systems has enormous potential with regard to the future of precision medicine. Conventional diagnostic tools are mostly based on morphological and histopathological examination that is not necessarily able to effectively describe the underlying molecular heterogeneity of diseases. Genomic biomarkers on the other hand give details about the mechanisms of diseases and thus it is more accurate because it can classify the disease subtypes and diagnose the disease effectively. It especially applies to the field of reproductive health, where physiological, hormonal, and environmental conditions interact to affect the outcome of diseases (Vaamonde et al., 2022). Genomic information integration into clinical practice can thus positively impact the accuracy of diagnosis, as well as help to create targeted treatment plans.

Large-scale biomarker discovery and integrative analysis is feasible as shown by the use of publicly available genomic datasets, including TCGA. The datasets allow researchers to investigate complicated molecular connections without the extensive experimental infrastructure. Nevertheless, variability in sample quality, missing clinical annotations, and possible batch effects are some of the limitations that have to be taken into account when interpreting the results. Despite these concerns, the integration of different kinds of data, including the expression and methylation profiles of genes, makes the conclusions stronger and provides a more accurate picture of the disease processes.

All in all, this study proves that genomic biomarkers need to be included in order to understand more about molecular pathology and create precision diagnosis. The findings underscore the importance of a complex of genetic, epigenetic and systemic factors in disease development and the need to treat it with a multidisciplinary approach. The integration of molecular knowledge and the broader healthcare plans including technological advances and alternative ways of treatment provide a more holistic treatment of complex conditions. The future of personalized medicine is these integrative strategies because it will be possible to achieve a more accurate diagnosis, improved patient outcomes, and develop more specific treatment plans.

5. CONCLUSION

The present study demonstrates that integrative genomics can be a powerful approach of understanding the molecular aspect of gynaecological diseases, particularly ovarian cancer, by assessing the trend of gene expression and DNA methylation. The identification of the differentially expressed and epigenetically regulated genes in the study highlights the complexity of the regulatory processes that lead to the emergence of diseases and the importance of multi-omics analysis in the process of identifying the important biological pathways. The study gives valuable insights into cellular activities such as proliferation, apoptosis and hormonal control which are fundamental in the health of women and their reproductive illnesses. The integration of the molecular data with the broadened therapeutic perceptions also emphasizes the role of the integration of modern genomic approaches to the traditional knowledge systems. It is the strength of the work since it is a data analysis that is based on genomic analysis, but the fact that the concept is conceptually related to Ayurvedic therapeutics is a long-term paradigm of explaining the molecular findings in the framework of holistic and personalized medicine. This has been in agreement with the trends in integrative healthcare of which interdisciplinary approaches are being applied more and more in order to promote disease and patient outcomes management. Additionally, the paper gives the importance of incorporating bio informatics tools and systems level analysis in the creation of research on women health. A large-scale analysis can be conducted using the genomic datasets that are publicly available to define the potential biomarkers and therapeutic targets. In the meantime, the findings suggest further research is needed to experimentally validate the molecular interactions, and to explore the translational potential presented by the interaction of traditional therapeutics and genomic medicine. In conclusion, the paper gives an overview of the significance of integrative genomics to gynaecology and gives a background on the potential of further research to fill the gap between molecular science and the traditional mode of therapy. This integration may contribute to the development of more efficient, personal and holistic approaches to health care and its impact on the health of women.

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