Letter to the Editor

Artificial Intelligence-Driven Multiomics Network Analysis Reveals Resistance Mechanisms in Oral Cancer

Dear Editor,—The recent article by Tachaveeraphong et al. in the International Dental Journal provides valuable insights into oral carcinogenesis, emphasizing the importance of genetic and epigenetic factors. Their findings on histone H3 modifications in oral epithelial dysplasia and oral squamous cell carcinoma (OSCC) are particularly noteworthy.[1]

In our work, we have explored the integration of artificial intelligence, specifically machine learning and deep learning algorithms, to advance the understanding of these processes. Utilizing multiomics network analysis, we have been able to identify molecular alterations and predict treatment responses in oral cancer.[2] This method facilitates the identification of functional interactions among molecules and pathways, yielding novel insights into disease mechanisms, biomarker discovery, and therapeutic target identification. Recent studies have demonstrated its potential in investigating cancer resistance mechanisms and uncovering genetic alterations, gene expression patterns, and protein interactions.[3,4]

Our study analyzed data from various omics platforms, including mRNA, long noncoding RNAs (lncRNA), miRNA, and proteins, to construct a comprehensive network analysis. We identified key driver genes and proteins involved in oral cancer resistance, such as BCL2, EZH2, and TP53, and explored their interactions.[3] This approach has provided novel insights into disease mechanisms and potential therapeutic targets.

The role of lncRNAs, particularly HOTAIR, was highlighted in our findings. We discovered that HOTAIR interacts with miR-613, affecting autophagy and apoptosis processes, thereby contributing to cisplatin resistance in OSCC.[4] Our network analysis revealed significant nodes and interactions, suggesting new avenues for targeted therapies.

We agree with Tachaveeraphong et al.[1] that histone modifications play a crucial role in the progression of oral cancer. Our findings further support this by demonstrating that specific lncRNAs and miRNAs are involved in chemoresistance, potentially offering new targets for improving treatment outcomes.[5]

In conclusion, the integration of artificial intelligence and multiomics analysis enhances our understanding of oral cancer and its resistance mechanisms. The multiomics network analysis highlights the roles of lncRNAs and miRNAs in promoting cisplatin resistance in OSCC cells, suggesting potential therapeutic targets for improving treatment outcomes.

These insights align with the findings of Tachaveeraphong et al.,[1] reinforcing the significance of epigenetic modifications in oral carcinogenesis.

Conflict of interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this article.

Ethical approval

Not required.

Author contributions

Both authors have made substantial contributions to the conception and design of the study, acquisition of data, analysis, and interpretation of data, drafting of the article and revising it critically for important intellectual content, and final approval of the version to be submitted.

Funding

This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

Data availability

Records were obtained from the included investigations.

REFERENCES

1. Tachaveeraphong W, Phattarataratip E. The significance of modified histone H3 in epithelial dysplasia and oral cancer. Int Dent J 2024;74:769–76.
2. Yamaguchi K, Yamamoto T, Chikuda J, Shirota T, Yamamoto Y. Impact of non-coding RNAs on chemotherapeutic resistance in oral cancer. Biomolecules 2022;12(2):284.
3. Duran-Frigola M, Cigler M, Winter GE. Advancing targeted protein degradation via multiomics profiling and artificial intelligence. J Am Chem Soc 2023;145:2711–32.
4. Dar MA, Arafah A, Bhat KA, et al. Multiomics technologies: role in disease biomarker discoveries and therapeutics. Brief Funct Genomics 2023;22:76–96.
5. Wang RS, Maron BA, Loscalzo J. Multiomics network medicine approaches to precision medicine and therapeutics in cardiovascular diseases. Arterioscler Thromb Vasc Biol 2023;43:493–503.

Pradeep K. Yadalam
Carlos M. Ardila *
Department of Periodontics, Saveetha Dental College, Saveetha Institute of Medical and Technology Sciences, SIMATS, Saveetha, University, Chennai, Tamil Nadu, India
Biomedical Stomatology Research Group, Universidad de Antioquia U de A, Medellín, Colombia

*Corresponding author. Carlos M. Ardila, Calle 70 No. 52-21, Medellín, Colombia.
E-mail address: martin.ardila@udea.edu.co (C.M. Ardila).

https://doi.org/10.1016/j.identj.2024.07.010