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One of the main challenges in cancer management relates to the discovery of reliable biomarkers, which could guide decision-making and predict treatment outcome. In particular, the rise and democratization of high-throughput molecular profiling technologies bolstered the discovery of "biomarker signatures" that could maximize the prediction performance. Such an approach was largely employed from diverse OMICs data (i.e., genomics, transcriptomics, proteomics, metabolomics) but not from epitranscriptomics, which encompasses more than 100 biochemical modifications driving the post-transcriptional fate of RNA: stability, splicing, storage, and translation. We and others have studied chemical marks in isolation and associated them with cancer evolution, adaptation, as well as the response to conventional therapy. In this study, we have designed a unique pipeline combining multiplex analysis of the epitranscriptomic landscape by high-performance liquid chromatography coupled to tandem mass spectrometry with statistical multivariate analysis and machine learning approaches in order to identify biomarker signatures that could guide precision medicine and improve disease diagnosis. We applied this approach to analyze a cohort of adult diffuse glioma patients and demonstrate the existence of an "epitranscriptomics-based signature" that permits glioma grades to be discriminated and predicted with unmet accuracy. This study demonstrates that epitranscriptomics (co)evolves along cancer progression and opens new prospects in the field of omics molecular profiling and personalized medicine.

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Acknowledgements

References

[1] S. Relier, A. Amalric, A. Attina, I.B. Koumare, V. Rigau, F. Burel Vandenbos, D. Fontaine, M. Baroncini, J.P. Hugnot, H. Duffau, L. Bauchet, C. Hirtz, E. Rivals, and A. David. Multivariate analysis of rna chemistry marks uncovers epitranscriptomics-based biomarker signature for adult diffuse glioma diagnostics. *Analytical Chemistry*, Aug 2022.