

Identification of genetic and epigenetic biomarkers associated with cisplatin and radiotherapy response in head and neck squamous cell carcinoma cell lines

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Background: Recent advances in next-generation sequencing and high-throughput technologies have enabled the discovery of genetic and epigenetic markers that provide insights into therapeutic mechanisms. Despite this progress, no biomarker has yet been implemented in clinical practice to guide treatment for HNSCC, where molecular biomarkers could help in predicting treatment response, for example to cisplatin or radiotherapy. This study aims to identify predictive genetic and epigenetic biomarkers for HNSCC by comparing cisplatin- and radiotherapy resistant versus sensitive HNSCC cell lines.

Methods: We analyzed 61 HNSCC cell lines with previously characterized sensitivity to cisplatin and radiotherapy using Genotyping by Sequencing coupled with methylated DNA Immunoprecipitation (GBS-MeDIP). This method simultaneously tests for genetic and methylomic modifications in a reduced genomic fraction, allowing efficient identification of candidate biomarkers.

Results: We identified 30 single-nucleotide polymorphisms (SNPs) and 6 differentially methylated regions (DMRs), some of which were significantly associated with treatment response. These included both resistance- and sensitivity-associated SNPs, as well as DMRs that potentially modulate expression in therapy-resistant cell lines.

Conclusions: Our results identified 30 SNPs and 6 DMRs that could serve as predictive biomarkers for cisplatin and radiotherapy response in HNSCC, highlighting their potential for personalized treatment strategies and improved clinical outcomes.