mRNA and microRNA Profiling of Frozen and FFPE Biopsy Specimens for Predicting the Therapeutic Effectiveness of Chemo-radiotherapy Treatment in Head and Neck Squamous Cell Carcinomas

Dumur CI, Schaum JC, Garrett CT, Wilkinson D, Dinardo L, Powers CN
1Department of Pathology, 2Department of Otolaryngology, Virginia Commonwealth University, Richmond, VA

ABSTRACT

BACKGROUND

Head and neck squamous cell carcinomas (HNSCC) may arise in diverse locations and have a common etiologic association with tobacco and/or alcohol exposure. The management of HNSCC often consists of resection, followed by postoperative chemoradiotherapy (CRT).1

Recently, the results from the Radiation Therapy Oncology Group (RTOG) Trial 91-11 have demonstrated improved local control rates with concurrent CRT, without reducing survival in patients who would otherwise have undergone total resection, while preserving the organ functionality.2

Unfortunately, a significant percentage of patients treated with concomitant CRT alone do not respond and must subsequently undergo post-CRT resection, which is associated with high morbidity. This subset of patients might benefit from pre-CRT surgery and their identification remains a clinical challenge that may benefit from the discovery of new biomarkers.

Previously, we identified tumor aggressiveness and cell motility related genes as good chemoradiotherapy response predictors of HNSCC recurrence.3 In the present study, we aimed at identifying small RNA species in these samples, which may regulate those molecular pathways, which will allow a deeper understanding of the biological processes of CRT response, as well as expanding the sample cohort to include archival material to the study.

MATERIALS AND METHODS

RESULTS

CONCLUSIONS

In the study presented herein, we were able to successfully isolate small RNA species from snap-frozen and paired-FFPE HNSCC specimens using an automated method.

In addition, we have identified global microRNA expression profiles in snap-frozen HNSCC correlating to CRT response, which were preserved in paired FFPE specimens. Our findings were further validated by qRT-PCR, identifying several highly variable microRNAs in HNSCC specimens.

We have also demonstrated that specific microRNAs show significant inverted correlation with the expression of significantly altered microRNAs in CR versus NR HNSCC in the same individuals.

These findings suggest that microRNAs may play a role in regulating the gene expression in response to CRT in HNSCC.

MicroRNA profiles obtained from snap-frozen and/or FFPE samples might therefore serve as biomarkers for HNSCC prognosis and help elucidate the regulatory mechanisms involved in CRT response in this cancer.

REFERENCES