ASO AUTHOR REFLECTIONS

Annals of SURGICALONCOLOGY OFFICIAL JOURNAL OF THE SOCIETY OF SURGICAL ONCOLOGY



# ASO Author Reflections: Gene Expression-Profiling and Implications for Adjuvant Therapy in Melanoma

Norma E. Farrow, MD, MHS, and Georgia M. Beasley, MD, MHS

Department of Surgery, Duke University, Durham

# PAST

Historically, the prognosis for melanoma patients at intermediate or high risk for recurrence after resection was poor due to lack of effective adjuvant therapies (ATs). Beginning in 2015, multiple effective systemic ATs have been approved, which improve recurrence-free (RFS) for patients with resected stage 3 or 4 disease.

#### PRESENT

Consideration of AT currently is recommended for stage 3A disease or higher, particularly disease with sentinel lymph node (SLN) metastases larger than 1 mm. Although modern ATs are better tolerated than historic therapies, they have a broad range of significant side effects, and the risk of pursuing AT should outweigh the risk of recurrence and disease-specific mortality. Current clinical and histopathologic risk stratification techniques used to predict individual risk lack precision, particularly for those patients with high-risk stage 2 or low-risk stage 3 disease.

Gene expression-profiling, already used successfully for other malignancies, is a promising tool for prognosis better on an individual level for patients with melanoma.<sup>1</sup> Although gene expression in the primary tumor currently is being investigated, the SLN plays an important role in tumor control, and SLN gene expression has been shown to differ between patients with and without nodal metastases.<sup>2</sup> This study characterized expression of 730 immune-related genes in the SLNs of 60 patients in a retrospective melanoma cohort and created a multivariate prediction model for RFS that incorporated expression of 12 differentially expressed genes.<sup>3</sup> Although these results have not been validated to date and are limited by the small, retrospective nature of the study, they provide preliminary evidence that immunologic gene expression in SLNs correlate with clinical outcomes.

### FUTURE

If validated, gene expression in SLNs may be used in conjunction with currently available clinical and histopathologic factors for risk stratification to help guide adjuvant therapy decisions in melanoma and further characterize mechanisms of disease progression.

**DISCLOSURE** Dr. Beasley was a one-time consultant for Regeneron (2019). He is supported by the Society of Surgical Oncology Young Investigator award (2019) and by NIH K08 CA237726-01A1. Dr. Farrow was supported by a National Institutes of Health T-32 Grant (T32-CA093245) for translational research in surgical oncology.

## REFERENCES

- Zager JS, Gastman BR, Leachman S, et al. Performance of a prognostic 31-gene expression profile in an independent cohort of 523 cutaneous melanoma patients. BMC Cancer. 2018;18:130.
- Tarhini AA, Floros T, Lin HM, et al. A unique gene expression signature is significantly differentially expressed in tumor-positive or tumor-negative sentinel lymph nodes in patients with melanoma. Melanoma Res. 2017;27:429–38.
- Farrow NE, Holl EK, Jung J, et al. Characterization of sentinel lymph node immune signatures and implications for risk stratification for adjuvant therapy in melanoma. *Ann Surg Oncol.* 2020. h ttps://doi.org/10.1245/s10434-020-09277-w.

**Publisher's Note** Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

<sup>©</sup> Society of Surgical Oncology 2021

First Received: 4 January 2021 Accepted: 5 January 2021; Published Online: 22 January 2021

G. M. Beasley, MD, MHS e-mail: georgia.beasley@duke.edu