Identification of Pathogenic Variants in Patients with Melanoma who Meet NCCN Criteria for Hereditary Breast and Ovarian Cancer and Lynch Syndrome Testing

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INTRODUCTION
Currently, CDKN2A and CDK4 have primarily been implicated in familial melanoma. However, pathogenic variants (PVs) in these genes represent only a small percentage of familial melanoma cases, indicating that other genes may be involved.

METHODS
We evaluated the results of a multi-gene hereditary cancer panel among individuals tested between 9/2013 and 7/2019 who met NCCN testing criteria according to melanoma history.

– Personal history (PHx) and/or family history (FHx, first-degree relatives only) of melanoma (N=27,946)
– No PHx or FHx of melanoma (N=581,224)

RESULTS
Figure 1. Cancer History for Patients with Personal History of Melanoma
Among individuals with a PHx and/or FHx of melanoma, PVs were most common in ATM, BRCA1, BRCA2, CHEK2, and PALB2.

The prevalence of PVs in ATM, CHEK2, and PALB2 was similar to that observed for individuals with a history of a non-melanoma cancer.

PV Positive Rate by Melanoma History: PHx and FHx = 8.9% (108/1,208); PHx Only = 7.7% (534/6,907); FHx Only = 6.8% (1,506/22,247)

CONCLUSIONS
Early identification of PV-carrying patients with melanoma would present provider and patient with an opportunity to prevent the occurrence of a second primary cancer through increased surveillance or risk-reducing surgeries.