ABSTRACT BOOK ABSTRACTS



MELANOMA AND MELANOCYTIC NAEVI

## GENETIC VARIANTS IN FOLATE METABOLIC PATHWAY PREDICT MELANOMA-SPECIFIC SURVIVAL IN TWO PATIENT COHORT GWAS STUDIES

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Background: Some single-nucleotide polymorphisms (SNPs) have been identified to be associated with cutaneous melanoma-specific survival (CMSS) though hypothesis-free genome-wide association studies (GWAS), but no SNPs were found in genes involved in the folate metabolic pathway.

Objective: We examine the contribution of SNPs in folate metabolic pathway genes to CMSS.

Methods: We used one published GWAS of 858 patients from The University of Texas M.D. Anderson Cancer Center and the other of 409 patients from the Harvard Nurses' Health Study and Health Professionals Follow-up Study as the discovery and validated datasets, respectively. During the follow-up, there were 95 (11.1%) and 48 (11.5%) patients died of CM in both studies, respectively.

Results: We identified two independent SNPs (MTHFD1 rs1950902 G>A and ALPL rs10917006 C>T) associated with CMSS in both datasets, and their meta-analysis yielded an allelic hazards ratio of 1.75 (95% confidence interval=1.32-2.32, P=9.96×10-5) and 2.05 (1.39-3.01, P=2.84×10-4), respectively. Additional genotype-phenotype correlation analyses provided the support for biological plausibility of these two variants in tumor progression, thus affecting CMSS.

Limitations: A lack of detailed information in the validation dataset.

Conclusion: We found that two possibly functional genetic variants, MTHFD1 rs1950902 and ALPL rs10917006, were likely to independently or jointly associated with CMSS.





