

GERMLINE PALB2 GENETIC VARIATIONS OF FAMILIAL ESOPHAGEAL SQUAMOUS CELL CARCINOMA (ESCC) IN HENAN, A HIGH RISK ESCC REGION

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BACKGROUND AND AIMS: ESCC is often a deadly cancer diagnosed at late stage with a 5-year survival rate less than 10% in advanced cancers. It is important to elucidate the molecular genetic basis for this deadly cancer to achieve the ultimate goal of early cancer detection and improved clinical management. Our aim is to understand the genetic basis of inherited ESCC by deciphering PALB2 mutation status in high risk northern China. By investigation of PALB2 germline mutations and variants, as compared to healthy individuals, the genetic basis and genomic risk factor associations with inherited EC will be clarified. **METHODS:** Blood was collected from high-risk Henan familial history-positive (FH+) individuals. Blood DNAs were extracted for Sanger sequencing analysis. **RESULTS:** By Sanger sequencing with primers covering more than 90% of the PALB2 coding sequence, PALB2 variants were detected in exon 4 for 4% (2/50) FH+ ESCC patients from Henan, but no germline protein truncation variations were observed. Since mutations were only observed in exon 4, further mutation screening were confined to exon 4 of PALB2 with an additional 300 FH+ Henan ESCC, 283 FH- Henan ESCC, and 364 Henan non-ESCC control individuals. However, no mutations were detected in the validation samples. **CONCLUSIONS:** Infrequent PALB2 germline mutations were detected in Henan FH+ ESCC patients, suggesting PALB2 may be involved in a small proportion of familial ESCC in Henan. Further study is necessary to clarify if the identified mutations are pathogenic.