

Epstein-Barr Virus Detection in Gastric Adenocarcinoma: A comparative analysis using quantitative PCR and In-Situ Hybridisation in Formalin-Fixed Paraffin-Embedded tissue samples from South Africa

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Background: Epstein-Barr virus-associated gastric carcinoma (EBVaGC) accounts for approximately 10% of all gastric carcinomas worldwide. It is characterised by distinct genomic alterations and notable unique clinicopathological traits. This study aimed to investigate Epstein-Barr virus (EBV) status in gastric adenocarcinoma and correlate EBV infection with clinicopathological characteristics significant for patient management.

Materials and Methods: An Analytical cross-sectional study design was applied to analyse 64 cases of gastric adenocarcinoma diagnosed from 01 January 2018 to 31 December 2022 at an academic laboratory in Ga-Rankuwa, South Africa. The demographic and clinicopathological characteristics were retrieved from histological reports. Comparative molecular pathology analysis for EBV was done on cases from formalin-fixed paraffin-embedded tissue samples using quantitative polymerase chain reaction (qPCR) and RNA EBER in situ hybridisation (EBER-ISH). Statistical data analysis was done using STATA v18.

Results: EBV was detected in 61% (n=39) and 11% (n=7) of cases using qPCR and EBER-ISH, respectively. All EBER ISH-positive cases (n=7) were concordant with qPCR, however a low concordance of 36.1% was observed between qPCR and EBER-ISH. In these cases, there was a female predominance with a mean age of 70 ± 8.94 years. No statistical significance was found in the association between clinicopathological features and EBV status.

Conclusion: The qPCR method was more sensitive than EBER ISH in identifying EBV infection in gastric adenocarcinoma, however, it was less specific for identifying active versus latent EBV infection in FFPE samples. These findings may indicate that EBV infections may

be associated with gastric adenocarcinoma in our setting; however, this warrants further analysis with a bigger sample to elucidate this association.