



ABSTRACTS: VOLUME 8, SPECIAL ISSUE {8th Undergraduate Conference}

AMPLICON-BASED NGS FOR DETECTION AND GENOTYPING OF HERPESVIRUSES IN HEALTHY PALESTINIAN INDIVIDUALS IN SPECIFIC REGIONS IN PALESTINE

Bushra Mahmoud Ismail Mahmoud¹, Abed Almajeed Naseredden^{1*}. Supervisor: Abed Almajeed Naseredden Bushra Mahmoud Ismail Mahmoud¹, Abed Almajeed Naseredden^{1*}

Supervisor: Abed Almajeed Naseredden¹

¹ Al-Quds Bard College, Al-Quds University, Jerusalem, Palestine

¹ Al-Quds Bard College, Al-Quds University, Jerusalem, Palestine.

Abstract

Background: Herpesviruses, including Cytomegalovirus (CMV), Epstein-Barr virus (EBV), herpes simplex virus type 1 (HSV-1), and type 2 (HSV-2), are widespread and pose serious public health challenges due to their ability to persist in the body and spread easily. While diagnostic tools have improved over the years, commonly used methods like serological tests and PCR-based assays still have limitations. Next-generation sequencing (NGS) has opened a new era in viral diagnosis, allowing for the simultaneous detection of multiple viruses in a single test, thereby improving both speed and precision of results. In Palestine, there is a significant gap in research on herpesvirus prevalence and genotypes, and access to advanced molecular diagnostics such as NGS remains limited. Many local laboratories still rely on traditional methods, which may lead to underdiagnosis or misclassification of infections. Since herpesviruses can remain latent without causing symptoms, an NGS-based approach that screens for all herpesviruses in a single test could enhance detection while reducing costs. This study aims to investigate the prevalence and genetic diversity of herpesviruses among asymptomatic individuals, addressing a critical need for improved viral surveillance in the region.

Methods: Seventy-five cotton swab samples were collected from healthy, asymptomatic Palestinian individuals across different regions. HSV-1 and HSV-2 positive samples were used as controls. DNA was extracted from all samples. Primers for HSV-1, HSV-2, CMV, and EBV—previously published and modified for this study—were used. Viral DNA was amplified using multiplex PCR and subsequently genotyped using NGS for herpesvirus detection. Bioinformatic analysis was performed using Galaxy and SPSS statistical software.

Results: Among the 75 analyzed samples, HSV-1 was detected in 53 participants (70.7%), HSV-2 in 3 participants (4%), and HSV-1/HSV-2 co-infection in 3 participants (4%). HSV infection showed significant



associations with region ($p = 0.046$), marital status ($p = 0.050$), education level ($p = 0.048$), and field of study ($p = 0.037$), based on chi-square analysis. These findings indicate meaningful relationships between HSV positivity and several sociodemographic factors. No CMV or EBV was detected in oral samples. This study demonstrates the prevalence and distribution of HSV-1 and HSV-2 among asymptomatic individuals in Palestine using an NGS-based approach. The absence of CMV and EBV detection in oral samples may be due to tissue-specific tropism, low viral loads in asymptomatic individuals, or the generally healthy, non-immunocompromised status of participants, as these viruses are more likely to cause oral manifestations in immunocompromised individuals.

Conclusion: This study highlights the utility of NGS in improving herpesvirus detection and surveillance in Palestine. The findings may support the development of more accurate diagnostic strategies and inform public health interventions aimed at protecting vulnerable populations, including immunocompromised individuals, pregnant women, and children.

Keywords: NGS, Herpesvirus, HSV-1, HSV-2, CMV, EBV, Prevalence, Detection, Genotyping.