
Jade Cabello*, Marcela Ras*, Katelyn Tran*, Athit Voytas*, Mary Coolbaugh-Murphy, Ph.D., MB(ASCP) CM, Denise M. Juroske Short, Ph.D., MB(ASCP) CN

Undergraduate Program in Molecular Genetic Technology, School of Health Professions, UT MD Anderson Cancer Center

*Authors contributed equally & are listed in alphabetical order
Abstract

Objective: To conduct a meta-analysis of the available and relevant literature on E1/E2 genes and their affect on the epigenetics of Human Papillomavirus caused uterine cervical cancer.

Background/Significance: Human Papillomavirus is strongly linked to cervical cancer, and cervical cancer is the fourth most common type of cancer in women. 99.7% of patients with cervical cancer have a “high risk HPV genotype” which factors greatly into the causation if their diagnosis. The HPV vaccine that came out in 2006 has greatly decreased cervical cancer in the population as well as increased the preventative chances of highly susceptible individuals.

Methods: To conduct a meta-narrative review, MD Anderson databases and Google Scholar were used to access PubMed as well as Web of Science. Articles older than 5 years (2019-2024) were not considered, but articles with research from across the globe not just the United States were considered. Phrases such as “E1/E2 genes”, “Human Papillomavirus”, and “Cervical Cancer” were used.

Discussion: The genes E1 and E2 were discussed by their role in DNA application, as well as the multitude and variety of nucleotide variations and their locations. The oncogenic links between these genetic variations and their epigenetic modulations were shown to be strong but further research still needs to be conducted.

Conclusion: The articles reviewed show that genes play a factor in HPV induced uterine cancer, and that DNA methylation and histone modifications are a key factor in all stages of cervical uterine cancer.

Keywords: Human Papillomavirus, Meta-Narrative Review, Cervical Cancer, E1/E2 genes.