

Human papillomavirus or HPV is connected with the insistence of Cervical Cancers. And while only a small percentage of those infected with HPV get cervical cancer it remains incredibly widespread. Even with the introduction of screening and vaccination programs according to the authors of “Genetic variation in cervical preinvasive and invasive disease: a genome-wide association study.” HPV-derived cervical cancer remains among the most common malignancies in women worldwide. The paper focuses on the connection between genetics and instances of cervical cancer in women. The researchers make these connections through analyzing single nucleotide polymorphisms or SNPs and their association with a cohort that does and does not have cervical cancer. Through finding these connections the authors hope to find key candidate SNPs for further analysis and study for the prevention and treatment of HPV-derived cervical cancers.

This study was a GWAS or Genome-wide association study. These sorts of studies aim to identify certain genes and their association with a certain disease. The cohort for this study was extracted from the UK Biobank and that cohort consisted of European women between the ages of 40-69 years old. In total 273377 individuals were included from this cohort along with another 128123 Finnish individuals, from the FinnGen, for the independent replication of associations. 4769 individuals with cervical cancer and carcinoma in situ were included in the analysis along with 145545 control individuals. HPV status was unavailable due to the lack of HPV-based screening data. A total of 9600464 single nucleotide polymorphisms or SNPs were assayed in this study. The authors used an additive univariate logistic regression model to analyze whether certain variations were associated with cervical cancer. The authors also used a two-sample Mendelian randomization to analyze if any co-risk factors, such as smoking, for the genetic risk of cervical cancer.

Of the 9600464 single nucleotide polymorphisms assayed 6 independent variants were associated with cervical cancer and carcinoma in situ. Three of these SNPs were replicated in the Finnish cohort. The authors interpret these results as being strong evidence for a genetic susceptibility to cervical cancers. They suspect that these SNPs may cause disruptions to immune function and apoptotic pathways. The authors did not investigate whether HPV disrupts or amplifies these pathways and suggest that further research is needed to find that connection. The authors also note that their study relies highly on European datasets and that future research should focus on non-European populations. They additionally note that rates of cervical malignancy are higher in non-European populations. The Mendelian randomization found that smoking, older age at pregnancy, and number of sexual partners were co-risks for the genetic risk of cervical cancer.

References

Bowden, S.J. et al. Genetic variation in cervical preinvasive and invasive disease: A genome-wide association study. *The Lancet Oncology*. 22, 548-557. [https://doi.org/10.1016/S1470-2045\(21\)00028-0](https://doi.org/10.1016/S1470-2045(21)00028-0) (2020).