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Global attribution of HPV genotypes to invasive cervical cancer: a systematic analysis

Lyon, France, 1 August 2024 – A new systematic analysis by scientists from the International Agency for Research on Cancer (IARC) sheds light on the global impact of different human papillomavirus (HPV) genotypes in causing cervical cancer. The study, published today in *The Lancet*,¹ is based on a novel methodology comparing HPV genotypes in more than 110 000 women with cervical cancer with those in more than 2.5 million cancer-free women (controls). It aimed to evaluate which HPV genotypes caused cancer as well as their carcinogenic strength and their contribution to the cervical cancer burden.

"This study marks the most comprehensive attempt to date to estimate the proportion of invasive cervical cancer caused by different HPV genotypes globally, regionally, and nationally," says Dr Gary Clifford, Deputy Head of the Early Detection, Prevention, and Infections Branch at IARC and senior author of the article. "These findings directly inform strategies for prevention of invasive cervical cancer, emphasizing targeted approaches through HPV vaccination and screening."

Results

In the analysis, 17 HPV genotypes were judged to be causal to invasive cervical cancer, but with huge differences in their carcinogenic strength. HPV types 16 and 18 caused approximately three quarters of cervical cancer cases across all global regions. HPV types 31, 33, 45, 52, and 58 contributed an additional 15–20% of cases. The remaining 10 causal genotypes caused only about 5% of cases worldwide, with some notable regional variations, including a higher proportion (~4%) for HPV 35 in Africa than in other regions.

The eight HPV genotypes that had the highest attributable fractions (HPV types 16, 18, 31, 33, 35, 45, 52, and 58) were also the most carcinogenic and are therefore also clear priority targets for inclusion in HPV-based screening tests. Other HPV genotypes, which each cause only a small fraction of cases of invasive cervical cancer, have a lower positive predictive value. Including these genotypes in cervical cancer screening tests makes the screening less efficient and less cost-effective.

¹ Wei F, Georges D, Man I, Baussano I, Clifford GM (2024). Causal attribution of human papillomavirus genotypes to invasive cervical cancer worldwide: a systematic analysis of the global literature. *Lancet*. Published online 1 August 2024; <u>https://doi.org/10.1016/S0140-6736(24)01097-3</u>





"These insights suggest that future HPV vaccines might target HPV 35 to reduce regional disparities," says Dr Clifford. "Efficient and equitable cervical cancer prevention could be attained by focusing on at least the major eight HPV types in vaccines and diagnostics, especially in the resource-limited regions where the burden is highest."

Note to the Editors

Invasive cervical cancer is widely acknowledged to be caused by a set of carcinogenic HPV genotypes. In the most recent evaluation by the *IARC Monographs* programme (in 2009), 12 HPV genotypes were classified as carcinogenic to humans (16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, and 59).

Cervical cancer represents a significant global health burden, with an estimated 662 301 incident cases and 348 874 deaths in 2022. In response to this high preventable burden, in 2020 the World Health Organization (WHO) launched the Global Strategy to Accelerate the Elimination of Cervical Cancer, emphasizing the vital role of vaccination against HPV, screening, and treatment.

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The International Agency for Research on Cancer (IARC) is part of the World Health Organization. Its mission is to coordinate and conduct research on the causes of human cancer, the mechanisms of carcinogenesis, and to develop scientific strategies for cancer control. The Agency is involved in both epidemiological and laboratory research and disseminates scientific information through publications, meetings, courses, and fellowships. If you wish your name to be removed from our press release emailing list, please write to <u>com@iarc.who.int</u>.