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Detection of *human papillomavirus* DNA in tumors from Rwandesebreast cancer patients

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During the last decades, a great interest was given to viral etiology of breast cancer. Indeed, due to recent technical improvements and some encouraging new results, it has been a resurgence of interest in the possibility that a substantial proportion of human breast cancers may be caused by viral infections. High-risk genotypes of *human papillomavirus* (HPV) have been found in breast cancer cases. In the present study, we aimed to assess the presence of HPV DNA in breast cancer cases from Rwanda and to evaluate the association between HPV infection and clinicopathological features. Therefore, a total of 47 archived formalin-fixed paraffin-embedded biopsies were collected and complete information was recorded. HPV detection and genotyping were done by PCR amplification and DNA sequencing. Overall, HPV DNA was found in 46.81% of cases, HPV16 being the most prevalent subtype (77.27%) followed by HPV33 (13.64%) and HPV31 (9.09%). Comparison of HPV with clinicopathological features showed no significant difference between HPV infection and breast localization, histological subtype, clinical stage, tumor grade, and intrinsic molecular subtypes. These findings provide evidence of a high prevalence of high-risk HPV in Rwandese patients with breast cancer and suggest that high-risk HPV infections could be a risk factor associated with human breast cancer development.

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