Molecular Identification of Human Papilloma Virus Genotypes in Patients with Cervical Cancer

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Introduction: The principal cause of cervical cancer is human papillomavirus. In Camaguey population, molecular study about human papillomavirus does not exist. The Polimerase chain reaction is a molecular procedure often used for medical diagnostic; it allow to confirm the Human papillomavirus DNA in the total DNA purified of cervical cancer patients sample.

Objective: The first time demonstration the human papillomavirus circulating in the cancer cervical patients of Camaguey population, Cuban.

Methods: The analytic study was carrier out with 22 patients of the pathology consult of Genecology hospital of Camaguey. The identification and characterization of human papillomavirus genotype was carrier out through fragment restriction length polymorphic procedure.

Results: The 63.3 percent of patients showed exophytic lesion, 4.5 percent endophytic lesion and 3.8 percent another lesion. The 16 and 31 was the circulation genotypes in the Camaguey population and the 16 genotype was the most frequently.

Conclusions: This is the first report of molecular study of human papillomavirus in cervical cancer patients on Camaguey, Cuban. Present research and the other research of Cuban authors is an important contribution to therapeutic and prevent vaccine more effective in the solution anticipate for the cervical cancer in Cuban.

Key words: Human Papilloma Virus, Cervical Cancer, Polimerase chain reaction