Human papillomavirus: a potential risk factor for colorectal carcinoma?

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To the Editor

We read the recent paper entitled “The frequency of human papillomaviruses in colorectal cancer samples in Mashhad, northeastern Iran” by Meshkat et al. (1) with great interest. In the mentioned article, by using GP5+/GP6+ primers, the authors suggested a possible role of human papillomavirus (HPV) in colorectal carcinogenesis. We would like to thank Meshkat et al. for their valuable contribution.

It is known that most of the broad spectrum HPV detection methods, including GP5+/GP6+ consensus primers, are used to detect common or high risk HPV types, which are seen mainly in the anogenital region. Therefore, out of approximately 200 known HPV types, GP5+/GP6+ consensus primers have the ability to detect only about 30 of them (2). Since the distribution of HPV types varies in a wide range in different regions or organ systems in the human body, HPV type distributions may reveal some differences in colorectal cancer from the anogenital region. With these issues, to assess the presence of not only anogenital but also other HPV types, in our recent study we have used different HPV detection primer sets including GP5+/GP6+ consensus primers and novel broad spectrum primer sets covering a wide range of HPV types in 93 colorectal cancer specimens. The preliminary results of our research revealed the presence of HPV DNA in 3 colorectal cancer tissues. Interestingly, while two of the HPV DNA positive specimens were found to have common mucosal HPV types, in the third case we have identified an unclassified HPV type that was identical to the reported sequence of HPV isolate FAIMVS6.3 found in a patient with skin cancer by Forslund et al. (3). Considering the known number of HPV types is about 200, using different HPV DNA detection systems in a combined approach may enable the identification of rare HPV types that have an oncogenic potential for colorectal cancer. Our results demonstrated the presence of a rare HPV genotype in a colorectal cancer and point out the possible role of HPV genotypes other than common mucosal types in the etiology of colorectal cancer. Therefore, the selected method for detecting HPV DNA would directly influence the frequency and genotype distribution of HPV infections in colorectal cancer.

As a result, to find out the exact frequencies and type distributions of HPV types in colorectal cancer, studies performed with different primer sets covering a wide range of HPV types are required.

References


Reply to Letter to the Editor: “Human Papillomaviruses in colorectal cancer” by Tanoğlu et al.

To the Editor

The authors are grateful to Tanoğlu et al. for providing us with feedback on our previous article entitled “The frequency of human papillomaviruses in colorectal cancer samples in Mashhad, northeastern Iran” (1).

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462
mind that GP primers (PCR with GP5+/GP6+ primers) are generally used to determine the most prevalent types of HPVs.

The authors have to note that the previous study was not a comprehensive study and was aimed at providing an overview regarding the frequency of HPV among colorectal cancer samples in Mashhad. The study was performed on merely 100 samples. Therefore, future studies should include larger samples. In addition, several procedures should be employed to ensure that the result of each method corresponds to other methods.

Since HPV is found in the colon and rectum of the majority of patients suffering from colorectal adenocarcinoma, HPV was previously suggested to be the cause of the pathogenesis of colorectal cancer (2). However, the association of HPV and colorectal cancer does not seem to follow a similar pattern. In part, this could be caused by cultural differences and different trends of sexual relationships among people of different nations. In our population, at least, the association does not seem to be strong (one (1%) out of 100 patients with colorectal cancer was found to be positive for HPV DNA).

References


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