Human papillomavirus in esophageal squamous cell carcinoma in Colombia and Chile.


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AIM: To examine the presence of human papillomavirus (HPV) in esophageal squamous cell carcinoma (ESCC) specimens collected from Colombia and Chile located in the northern and southern ends of the continent, respectively.

METHODS: We examined 47 and 26 formalin-fixed and paraffin-embedded ESCC specimens from Colombia and Chile, respectively. HPV was detected using GP5+/GP6+ primer pair for PCR, and confirmed by Southern blot analysis. Sequencing analysis of L1 region fragment was used to identify HPV genotype. In addition, P16 (INK4A) protein immunostaining of all the specimens was conducted.

RESULTS: HPV was detected in 21 ESCC specimens (29%). Sequencing analysis of L1 region fragment identified HPV-16 genome in 6 Colombian cases (13%) and in 5 Chilean cases (19%). HPV-18 was detected in 10 cases (21%) in Colombia but not in any Chilean case. Since Chilean ESCC cases had a higher prevalence of HPV-16 (without statistical significance), but a significantly lower prevalence of HPV-18 than in Colombian cases (P = 0.011) even though the two countries have similar ESCC incidence rates, the frequency of HPV-related ESCC may not be strongly affected by risk factors affecting the incidence of ESCC. HPV-16 genome was more frequently detected in p16 positive carcinomas, although the difference was not statistically significant. HPV-18 detection rate did not show any association with p16 expression. Well-differentiated tumors tended to have either HPV-16 or HPV-18 but the association was not statistically significant. HPV genotypes other than HPV-16 or 18 were not detected in either country.

CONCLUSION: HPV-16 and HPV-18 genotypes can be found in ESCC specimens collected from two South American countries. Further studies on the relationship between HPV-16 presence and p16 expression in ESCC would aid understanding of the mechanism underlying the presence of HPV in ESCC.