

Human papillomavirus in lung carcinomas among three Latin American countries.

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The presence of human papillomavirus (HPV) genome in lung carcinomas has been reported worldwide but its frequency varies from country to country. We examined HPV genome in 36 lung carcinomas, consisting of 14 squamous cell carcinomas, 13 adenocarcinomas, and 9 small cell carcinomas, collected from Colombia, Mexico and Peru. PCR analysis using GP5+/GP6+ primers, combined with Southern blot hybridization, found the presence of HPV genome in 10 (28%) of 36 cases. This percentage is similar to the value of 22% reported by Syrjanen, who conducted a meta-analysis of nearly 2500 lung carcinomas examined to date. Genotype analysis revealed that the most predominant genotype was HPV-16 (7 cases), followed by HPV-18 (2 cases) and HPV-33 (1 case). HPV-16 was more frequently found among female than male cases ($P=0.008$) but was not detected in any adenocarcinoma cases. On the other hand, HPV-18 and HPV-33 were detected only among male cases.

These HPV genotypes were detected only in adenocarcinomas, and all the HPV genotypes detected in this histological type were HPV-18 or HPV-33. The frequency of HPV-16 positive cases among all the HPV positive cases differed in the sexes ($P=0.033$) and differed in the three histological types ($P=0.017$). The presence of HPV tended to be more frequent in well-differentiated tumors when squamous cell carcinomas and adenocarcinomas were combined. However, it was not statistically significant ($P=0.093$). Neither p16 nor p53 expression in carcinoma cells was related to the proportion of HPV-positive cases. In conclusion, high-risk HPV DNA was detected in 28% of lung carcinomas. The predisposition of HPV-16 to female cases and to non-adenomatous carcinomas warrants further investigation