

**Semiautomated typing of human  
papillomaviruses by restriction fragment  
length polymorphism analysis of  
fluorescence-labeled PCR fragments**

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摘要

**Abstract**

A simplified version of a PCR-based reductional restriction fragment length polymorphism (rRFLP) approach for typing of human papillomaviruses (HPVs) is described previously [Wang et al., 1997]. It is achieved by the use of a biotin-labeled primer in PCR which, on restriction digestion and staining, is associated with only a single restriction fragment. In this report, we describe a further development of the rRFLP approach with the use of a fluorescence-labeled primer in PCR and fragment detection by laser scanning in an automatic sequencer. HPV typing is achieved by computer-assisted matching of the fluorescence-labeled rRFLP patterns with a database of rRFLP patterns of all known anogenital HPV types. On analysis of the typing of 133 HPV-positive cases using this procedure, 20 different HPV types were detected in exfoliated cervical cells in PAP smear samples derived from Taiwanese women. The results indicate the existence of a heterogeneous population of HPV types in Taiwan. Although most cases were associated with the more common HPV types, a significant fraction (about 20%) of the HPV types detected was related to the less common genotypes, which are often not included in commercial kits available for HPV typing. The results indicate the importance of covering as many HPV types as possible in clinical HPV genotyping protocols. Copyright 1999 Wiley-Liss, Inc.