Complete genome sequences of three novel human papillomavirus types, 175, 178, and 180.

Johansson, Hanna K; Forslund, Ola

Published in: Genome Announcements

DOI: 10.1128/genomeA.00443-14

2014
Complete Genome Sequences of Three Novel Human Papillomavirus Types, 175, 178, and 180

Hanna Johansson, Ola Forslund
Department of Laboratory Medicine, Medical Microbiology, Lund University, Malmö, Sweden

We report the characterization of three novel human papillomavirus (HPV) types of the genus *Gammapapillomavirus*. HPV175 and HPV180 were isolated from a condyloma. HPV178 was isolated from healthy skin adjacent to an actinic keratosis.

Received 22 April 2014 Accepted 5 May 2014 Published 22 May 2014


Copyright © 2014 Johansson and Forslund. This is an open-access article distributed under the terms of the Creative Commons Attribution 3.0 Unported license.

Address correspondence to Ola Forslund, ola.forslund@med.lu.se.

We report the complete genome sequences of three novel human papillomavirus (HPV) types of the genus *Gammapapillomavirus*. HPV175 (SE87) and HPV180 (FA69) were originally detected as complete genomes in a condyloma swab sample from a 30-year-old male (1). HPV178 was isolated from a swab of healthy skin, next to an actinic keratosis of an 86-year-old male, and discovered after an attempt to amplify a closely related virus (SE46 [GenBank accession number JX198657]).

Briefly, multiple-displacement amplification (MDA)-amplified HPV DNA (1) was reamplified using the PrimeSTAR GXL DNA polymerase kit (TaKaRa Bio, Shiga, Japan). Primers were designed using the Primer Express Software v. 3.0 (Applied Biosystems). HPV175 (7,226 bp) was amplified in three parts, amplicon 1 (3,677 bp) (forward primer [fwd] 5'-ACAAATTCTCCTGGAGGA CTAATGC-3' and reverse primer [rev] 5'-GGCCTGATTCATCTTGG S DTGKS -3'), amplicon 2 (2,397 bp) (fwd 5'-CGCATG CCATGTTGTGTCTC-3' and rev 5'-GGGCTGATTCATCTTG G GTGGT-3'), and amplicon 3 (2,601 bp) (fwd 5'-GGATAATGC-3' and reverse primer [rev] 5'-GCCTCCAGTTCTTC -ATTTGGAA -3').

Amplicons were cloned using a TOPO TA cloning kit and the pCR 2.1-TOPO vector (Invitrogen, Carlsbad, CA) and sequenced using primer walking (Eurofins). Amplified HPV180 (7,314 bp) was obtained as a single amplicon (fwd 5'-GGTGGTG TGTGACCGAGTGTACTTTT-3' and rev 5'-TTCCATG AACCGG CCATTATAATCTACAAGT-3') (Eurofins). HPV180 (7,356 bp) was obtained as a single amplicon (fwd 5'-TATTTGGCAGCAAGGT GCACCAG-3' and rev 5'-AAGGAAAGGTGCAGAAAGAGAAG CT-3') (DNA Technology, Denmark).

The putative E6 proteins contained two zinc finger domains [CxxC(x)_{m}CxxxC] (2) separated by 36 amino acids. One zinc finger domain was also present in the E7 proteins. The LxCxE motif (binding site for the tumor suppressor retinoblastoma protein) (3) was observed in E7 of HPV178, whereas serine was substituted for cysteine in the corresponding domain (LxSxE) of HPV175 and HPV180. Among 55 E7 proteins of representative HPV types of the genus *Gammapapillomavirus*, 19 demonstrated the LxCxE motif and 27 the LxSxE motif.

The putative E1 protein of HPV178 had the conserved ATP-binding site (GPPDTGKS) (4, 5). For HPV175 we identified GSPDTGKS and for HPV180 GKPTNGKS. An initiation codon of the putative start of the E4 ORF was present in HPV175 and HPV180, whereas the corresponding codon was absent in the E4 ORF of HPV180. This is in agreement with the HPV types of species 10 of the genus *Gammapapillomavirus* (6).

**Nucleotide sequence accession numbers.** The complete genomic sequences are available in GenBank under these accession numbers: HPV175 (KC108721), HPV178 (KJ130020), and HPV180 (KC108722).

**ACKNOWLEDGMENTS**

This project was supported by BioCARE, a Strategic Research Program at Lund University, Sweden, and by the Swedish Cancer Society.

**REFERENCES**


