Group E Sequences

HPV61  HPV62
HPVCP4173  HPVCP6108
HPVCP8304  LVX100
HPVLVX82  HPVMM7
HPVM8

INTRODUCTION

Group E consists of the novel HPV sequences CP4173, CP6108, CP8304, LVX100, LVX82, MM7, and MM8, and the previously characterized types HPV-61 and HPV-62. Viruses in this group primarily infect anogenital tissue and have relatively unknown oncogenic potential and prevalence.

CP4173, CP6108 and CP8304 were obtained through clinical studies conducted in the state of New Mexico among a tri-ethnic population [1]. LVX100 and LVX82 were isolated from the Amazonian Indian population [2]. MM7 and MM8 were identified through studies conducted in the state of California: initial prevalence data for MM7 and MM8 are similar to that obtained for characterized “intermediate risk” viruses [3]. All samples were obtained from cervical lavages or genital swabs (CP6108 and CP4173 were isolated from normal cervices).

The previously characterized HPV types HPV-61 and HPV-62 have been isolated from tissues with at least some degree of dysplasia. Both HPV-61 and HPV-62 have been derived from vulvar intraepithelial neoplasias [4].

All of the members of Group E have currently been sequenced only over the My09-My11 fragment of L1. Phylogenetic analysis of the L1 region categorizes the group E viruses as a distinct group (Part III). The comparatively small L1 region of the group E viruses makes it difficult, however, to assess the members of the group in terms of “close types” or potentially problematic members. The following sequence pairs, sequenced by different groups, differ by only a few nucleotides: HPVMM7 and HPVLVX82; HPVLVX160 and HPVCP141; HPVLVX100 and HPVCP4173; HPV66MY911 and HPV66L1AE4.

HPV61L1AE4

LOCUS HPV61L1AE4  415 bp  DNA  VRL  25-MAY-1994
DEFINITION Human papillomavirus type 61, partial L1 cds, My09/My11 region.
ACCESSION U01534
SOURCE Human papillomavirus type 61 DNA, PCR amplified clone AE4
REFERENCE 1 (bases 1 to 415)
AUTHORS Tachezy,R., Van Ranst,M.A., Cruz,Y. and Burk,R.D.
TITLE Consensus primer mediated PCR allows identification of novel human papillomavirus PCR-types in cervicovaginal lavages
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 415)
AUTHORS Van Ranst,M.A.
TITLE Direct Submission
JOURNAL Submitted (04-SEP-1993) Marc A. Van Ranst, Albert Einstein College of Medicine, Dept. of Microbiology & Immunology, 1300 Morris Park Avenue, Bronx, NY 10461, USA
COMMENT Isolate AE4 is a variant of HPV type 61 identified in a study conducted to screen cervical lavages from over 500 women for novel HPV types. All women involved in the study were seen by physicians from clinics or private practices in the Bronx, N.Y. area. Derived sequences are PCR products amplified over the My09/My11 primer region of L1.
BASE COUNT 109 a 88 c 84 g 134 t
ORIGIN

1 tattgttgtt tgtattagta tgttttgtaac cgtcgtgtat accaccqcca gttactaatgt
  61 aaccattgtt atctgtaat ccccccctgt atctgaatat aaagacacaa gtttaagaga
121 atattgtcgc atacagcttg agtttttatt tttctgattt gtaaatgtaca
181 tttaccctgtat cttcttaata ttatattat acagcttgatg tgtatgtgtg
241 gaacctatgt gccgacatc cacccctctc cagttttcgag cacacacata gttttttgca
301 tgttctagct attacatgc agaaggtgtc tgtgtcccccg ccgccccagg aaggatcgtca
361 tgccaagaat aaccttcttga ctgtgatatt acagacaag tttttcactg atttg

1-E-2
SEP 94
HPV61MY911

LOCUS HPV61MY911 455 bp ds-DNA VRL 16-OCT-1994
DEFINITION Human papillomavirus type 61 (HPV-61), partial L1 cds, My09/My11 region.
ACCESSION U12500
SOURCE Human papillomavirus type 61 DNA recovered from a patient with vulvar intraepithelial neoplasia (VaIN).
REFERENCE 1 (bases 1 to 455)
TITLE Identification and assessment of known and novel human papillomaviruses by PCR amplification, restriction fragment length polymorphisms, nucleotide sequence, and phylogenetic algorithms
COMMENT HPV-64 has recently been characterized and isolated from a vulvar intraepithelial neoplasia by Dr. T. Matsukura. The cloned DNA was subsequently sequenced by Dr. H. Delius over the L1 MY09/MY11 segment. HPV-64 and the several other types recently sequenced over the MY09/MY11 primer region by Dr. Delius were used as type-specific probes to screen DNA for novel genital HPV types. The screened DNA was obtained from four recent epidemiological studies. Similar to sequence with accession number U01534. Primer regions are annotated in the sequence; information in this region is not accurate due to primer degeneracy.
BASE COUNT 116 a 99 c 96 g 144 t
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HPV62MY911

LOCUS HPV62MY911 449 bp ds-DNA  VRL 16-OCT-1994
DEFINITION Human papillomavirus type 62 (HPV-62), partial L1 cds, My09/My11 region.
ACCESSION U12499
SOURCE Human papillomavirus type 62 DNA isolated from a patient with vulvar intraepithelial neoplasia (VaIN).
REFERENCE 1 (bases 1 to 449)
TITLE Identification and assessment of known and novel human papillomaviruses by PCR amplification, restriction fragment length polymorphisms, nucleotide sequence, and phylogenetic algorithms
COMMENT HPV-62 has recently been characterized and isolated from a vulvar intraepithelial neoplasia by Dr. T. Matsukura. The cloned DNA was subsequently sequenced by Dr. H. Delius over the L1 MY09/MY11 segment. HPV-62 and the several other types recently sequenced over this region by Dr. Delius were used as type-specific probes to screen DNA for novel genital HPV types. The screened DNA was obtained from four recent epidemiological studies. Primer regions are annotated in the sequence; information in this region is not accurate due to primer degeneracy.
BASE COUNT 116 a 92 c 99 g 142 t
ORIGIN

1 gcacagggtc ataatattgttgg ttaatgaac tgttgttac tgtgtggat
L1 cds ->

-> MY11 PCR primer <-
61 actaccagaa gtactaattt tactattgtt acqcctcca ctgctgacgc agaatcaacg
121 ggttgggcat ttggctgaat acggaggaat ttgatttgca attatatatt
181 caattgtgca aaatacagtt aacccccgaa attatggcct acctgcataa tatgaacaag
241 gacccctttgg atgaactggaa ctttggtgatt ttacccctccc ctctctctag ttttactag
301 atatatcact atatcagtt ctggactgtt attcatatatatc atatcagttt gggctgcc taccctttt
361 aaggtggacc cgtatgcgca aatgacattt tggactgtgg atcttaagga caagttgtct
421 actgatttgg atcagtttcc cttgggttg
L1 cds ->

-> MY09 PCR primer <-
LOCUS       HPVCP4173  455 bp ds-DNA   VRL    16-October-1994
DEFINITION  Human papillomavirus, isolate CP4173, partial L1 cds, My09/My11 region.
ACCESSION  U12477
SOURCE      Human papillomavirus DNA derived from a cytologically normal cervical sample from a non-Hispanic white woman, 18 years of age, isolate CP4173.
REFERENCE   1 (bases 1 to 455)
AUTHORS     Peyton, C.L. and Wheeler, C.M.
TITLE       Identification of five novel human papillomaviruses in the New Mexico triethnic population
COMMENT     Data kindly provided prior to publication by Dr. C. Wheeler, University of New Mexico, School of Medicine, New Mexico Tumor Registry, 900 Camino del Salad NE, Albuquerque, NM, 87131-5306.

Five novel HPV sequences were identified in a study in which 3655 cervical specimens were screened against known genital HPV DNA [1]. The specimens were obtained from clinical investigations conducted at the University of New Mexico. The study subjects included Native Indians, Hispanics, and non-Hispanic whites. CP4173 was derived from a cytologically normal cervical sample from a non-Hispanic white woman, 18 years of age. The viral DNA was PCR amplified using the L1 consensus primer MY09/MY11 pair, which can hybridize to a broad spectrum of HPV types. Resultant fragments range from 449 to 458 nucleotides in length. The amplification products were initially screened against 2 sets of type-specific probes and a generic probe. If hybridization to the generic probe and not to the type-specific probes occurred, the samples were further analyzed by restriction fragment length polymorphisms. RFLP patterns which did not match reference patterns were considered to be derived from novel HPVs. The five novel samples which were identified in this study include CP8304, CP6108, CP8061, CP141, CP4173. Peyton et al. also identified two HPV45 subtypes and one HPV56 subtype. They conclude that since the existence of subtypes appears to be relatively rare, it suggests that HPV45 and HPV56 are more divergent than many HPV types. It should be noted that CP141 (U12476) is almost identical to LVX160 (U12486) and HPVLIAE1 (U01535) and that CP4173 (U12477) is almost identical to LVX100 (U12485). Both LVX160 and LVX100 were identified by Ong et al. in a 1994 study which examined Amazonian Indian subjects (Ong et al., J. Infect. Dis., 1994, in press). Primer regions are annotated in the sequence; information in this region is not accurate due to primer degeneracy.

In a subsequent study Bernard et al. evaluated ten novel genital HPV types, including the five identified in the Peyton et al. study, and other known genital types to determine phylogenetic relationships. They observed that the genital types CP6108, CP8304, CP4173 and CP8061 form a branch with HPV types 61 and 62. This emergent minor branch is positioned between two others which contain cutaneous types. Bernard et al. speculate as to whether other low-risk genital types have escaped detection because of considerable sequence divergence from the common genital types (Bernard et al., J. Infect. Dis., 1994, in press). Bernard et al. also assessed the linear correlation coefficients for the MY9/MY11 fragments against the rest of L1 (.851) and against the E6 gene (.888). Since these values are close, the authors suggest that the evolutionary distance information obtained for the primer pair region should be comparable to that available from the other regions of the genome (Bernard et al., J. Infect. Dis., 1994, in press).

BASE COUNT  117 a  95 c  85 g  158 t
ORIGIN

1 gcacattgtc ataataatgg catctattgg tttaatgagc tttttgtgac agttgtagat
L1 cds ->

-> MY11 PCR primer <-

61 actactcgca gtactaatgt aactatattt gctctctctg atcagaaat
121 acagtctctta attttcgtga gtatctctgc cacactgagg aatattgattt gcsgtttata
181 tttcaactgt gtaaaattca cttactctct gaaattatgg cctacttgca caataatgaat
241 aaggccctat tgggtgactg gatattgtgt gtgggtgcttc ttctttctac cagtttagat
301 gataccctata ggttttttaca gtctctgtgc ccctactgtc aaaaaggggc tgccacccct
361 cctctctaaag aagatccata tgctaactta tccttttgga ctgtggattt aaaggacaaa
421 tttccactg actttgatca gttttctctt ggacq

L1 cds ->

-> MY09 PCR primer <-
LOCUS  HPVC6108  452 bp ds-DNA  VRL  16-OCT-1994
DEFINITION  Human papillomavirus, isolate CP6108, partial L1 cds, My09/My11 region.
ACCESSION  U12478
SOURCE  Human papillomavirus DNA derived from a cytologically normal cervical sample from a non-Hispanic white woman, 20 years of age, isolate CP6108.
REFERENCE  1 (bases 1 to 452)
AUTHORS  Peyton, C.L. and Wheeler, C.M.
TITLE  Identification of five novel human papillomaviruses in the New Mexico triethnic population
COMMENT  Data kindly provided prior to publication by Dr. C. Wheeler, University of New Mexico, School of Medicine, New Mexico Tumor Registry, 900 Camino del Salad NE, Albuquerque, NM, 87131-5306.

Five novel HPV sequences were identified in a study in which 3655 cervical specimens were screened against known genital HPV DNA [1]. The specimens were obtained from clinical investigations conducted at the University of New Mexico. The study subjects included Native Indians, Hispanics, and non-Hispanic whites. CP6108 was derived from a cytologically normal cervical sample from a non-Hispanic white woman, 20 years of age. The viral DNA was PCR amplified using the L1 consensus primer MY09/MY11 pair, which can hybridize to a broad spectrum of HPV types. Resultant fragments range from 449 to 458 nucleotides in length. The amplification products were initially screened against 2 sets of type-specific probes and a generic probe. If hybridization to the generic probe and not to the type-specific probes occurred, the samples were further analyzed by restriction fragment length polymorphisms. RFLP patterns which did not match reference patterns were considered to be derived from novel HPVs. The five novel samples which were were identified in this study include CP8304, CP6108, CP8061, CP141, CP4173. Peyton et al. also identified two HPV45 subtypes and one HPV56 subtype. They conclude that since the existence of subtypes appears to be relatively rare, it suggests that HPV45 and HPV56 are more divergent than many HPV types. It should be noted that CP141 (U12476) is almost identical to LVX160 (U12486) and HPVL1AE1 (U01535) and that CP4173 (U12477) is almost identical to LVX100 (U12485). Both LVX160 and LVX100 were identified by Ong et al. in a 1994 study which examined Amazonian Indian subjects (Ong et al., J. Infect. Dis., 1994, in press). Primer regions are annotated in the sequence; information in this region is not accurate due to primer degeneracy.

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BASE COUNT  122 a  101 c  87 g  142 t
ORIGIN

1 gcacagggtc atataatgg tatttgttgg tttaatgagt tgttgttgtc tgtgtagat
L1 cds ->
-> MY11 PCR primer <->
61 acaccctgtcttacctgat gctgttttcc aagtaagcag cagtgcagttg
121 tctacacctt tattaagactc ttaacactc actgacactc atgctttttc aagagacttg
181 caactaacaat acaaccaactc ataacacactc atgtgtttttc ttttacactc agtacactc
241 acattgtgat gtaagcactc tttggtttc cccccccttc cccccccttc tttggtttc
301 acctatcgcgct tcggtgtttt cccccccttc cccccccttc cccccccttc tttggtttc
361 cctaaaaaggg atccataatg tagttatagc ttttggagtgc tggatccataa gagaagcttg
421 tccactgatc ttcgcttgatg tcccctttgag cgc
L1 cds ->
-> MY09 PCR primer <->
LOCUS HPVCP8304  452 bp ds-DNA  VRL  16-OCT-1994
DEFINITION Human papillomavirus, isolate CP8304, partial L1 cds, My09/My11 region.
ACCESSION U12480
SOURCE Human papillomavirus, isolate CP8304.
REFERENCE 1 (bases 1 to 452)
AUTHORS Peyton, C.L. and Wheeler, C.M.
TITLE Identification of five novel human papillomaviruses in the New Mexico triethnic population
REFERENCE 2
AUTHORS Ong, C.-K., Bernard, H.-U. and Villa, L.L.
TITLE Identification of genomic sequences of three novel human papillomaviruses in cervical smears of Amazonian Indians
REFERENCE 3
TITLE Identification and Assessment of Known and Novel Human Papillomaviruses by PCR Amplification, Restriction Fragment Polymorphisms, Nucleotide Sequence, and Phylogenetic Algorithms
COMMENT Data kindly provided prior to publication by Dr. C. Wheeler, University of New Mexico, School of Medicine, New Mexico Tumor Registry, 900 Camino del Salad NE, Albuquerque, NM, 87131-5306.

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BASE COUNT

125 a 93 c 95 g 139 t

ORIGIN

1 gcacagggac ataataatgg tatttttgtg tttaatgaaa tgtttttac agtgggtgat

L1 cds ->

-> MY11 PCR primer <-

61 actacccaga gacaccaattt tactatcctgc acagctcagc atggcttgtgc agatacaag
121 gctcactact ttaagcattt tctgcgcctt caagagctagt atgtttgctc gtttatccttc
181 caatatgta aaatacgtta aacaccacaa attatggcct acttacatca tatgaacaag
241 gcacgttcttg atgttccctt ttttgggtgtg ttcctacact gctcctcaag ctctagatcag
301 acatatcctct cttttaggctt tctggcctattt acgtgcaaaa cccggttggc gctccctgag
361 cccaaagagg acccttatgc gcacatgctc ttgggacacg tgtacccattaa gagaagaattg
421 tctactgttt tggatcagta tctctggga cgg

L1 cds ->

-> MY09 PCR primer <-
HPVLVX100

LOCUS        HPVLVX100  452 bp ds-DNA
DEFINITION   Human papillomavirus, isolate LVX100, partial L1 cds, My09/My11 region.
ACCESSION    U12485
SOURCE       Human papillomavirus, isolate LVX100 from cervical smear.
REFERENCE    1 (bases 1 to 452)
AUTHORS      Ong, C.-K., Bernard, H.-U. and Villa, L.L.
TITLE        Identification of genomic sequences of three novel human papillomaviruses in cervical smears of Amazonian Indians
COMMENT      HPVLVX82, HPVLVX100 and HPVLVX160 were found in cervical smears taken from members of isolated Amazonian tribes. The samples were PCR-amplified using the MY09/My11 consensus primers, then examined in hybridization experiments in order to determine their homology with known HPV types. In addition to many previously characterized HPV types, these three novel variants were discovered to be more than 10% divergent from their closest known relatives, suggesting that they may qualify to be considered new types. Although the tribes were thought to have been sexually isolated from non-Amerindian populations for at least 12,000 years, sequences closely related to these novel variants have since been detected in other distinct populations. The authors of [1] state that this may be evidence for the hypothesis that papillomavirus types evolved before the speciation of Homo sapiens, and consequently before the divergence of ethnic groups. Primer regions are annotated in the sequence; information in this region is not accurate due to primer degeneracy. All similarity calculations exclude data from this region.

BASE COUNT 116 a 96 c 85 g 155 t
ORIGIN
1 gcccagggtc ataataatgg catctgttgg tttaatgagc tttttgtgac agttgtagat
   L1 cds ->
   -> MY11 PCR primer <-
   61 actactcgca gtactaatgt aactatttgt actgccacag cgtcctctgt atcagaatat
121 acagcttcta attttcgtga gtatcttcgc cacactgagg aatttgattt gcagtttata
181 tttcaactgt gtaaaattca cttaactcct gaaattatgg cctacttgca caatatgaat
241 aaggccttat tggatgactg gaattttggt gtggtgcctc ctccttctac cagtttagat
301 gatacctata ggtttttaca gtctcgtgcc attacctgtc aaaaggctgc cacccctcct
361 cctaaagaag atccatatgc taacttatcc ttttggactg tggatttaaa ggacaaattt
421 tccactgact tggatcagta tcctcttgga cg
   L1 cds ->
   -> MY09 PCR primer <-

I-E-11
SEP 94
DEFINITION Human papillomavirus, isolate LVX82, partial L1 cds, My09/My11 region.

SOURCE Human papillomavirus, isolate LVX82 from cervical smear.

REFERENCE 1 (bases 1 to 452)

AUTHORS Ong, C.-K., Bernard, H.-U. and Villa, L.L.

TITLE Identification of genomic sequences of three novel human papillomaviruses in cervical smears of Amazonian Indians


COMMENT HPVLVX82, HPVLVX100 and HPVLVX160 were found in cervical smears taken from members of isolated Amazonian tribes. The samples were PCR-amplified using the MY09/My11 consensus primers, then examined in hybridization experiments in order to determine their homology with known HPV types. In addition to many previously characterized HPV types, these three novel variants were discovered to be more than 10% divergent from their closest known relatives, suggesting that they may qualify to be considered new types. Although the tribes were thought to have been sexually isolated from non-Amerindian populations for at least 12,000 years, sequences closely related to these novel variants have since been detected in other distinct populations. The authors of [1] state that this may be evidence for the hypothesis that papillomavirus types evolved before the speciation of Homo sapiens, and consequently before the divergence of ethnic groups. Primer regions are annotated in the sequence; information in this region is not accurate due to primer degeneracy. All similarity calculations exclude data from this region.

BASE COUNT 123 a 104 c 87 g 138 t

ORIGIN

1 gcccagggtc ataataatgg cattttgttg tttatgtagt tattttgttac agttgtagat
   L1 cds ->
   -> MY01 PCR primer <-
   61 actacccgca gtaccaatat tactatttca gctgctgcta cacaggctaa tgaatactg
   121 gcctctaact ttaaggaata cctccgccac accgaggaat atgacttaca ggttatattg
   181 caactttgca aaatacatct tacccctgaa attatggcat acctacatag tatgaatgaa
   241 catttattgg atgagtggaa ttttggcgtg ttaccgcctc cctccaccag ccttgatgat
   301 acctatcgct atttgcagtc ccgtgctatt acctgccaaa agggtccttc cgcccctgcc
   361 cctaaaaagg atccttatga tggccttgta ttttgggagg ttgattttaaa ggacaaacta
   421 tccacagatt tagatcagtt tcctttggga cg
   L1 cds ->
   -> MY09 PCR primer <-
LOCUS   HPVMM7
DEFINITION Human papillomavirus, isolate MM7, partial L1 cds, My09/My11 region.
ACCESSION U12489
SOURCE Human papillomavirus DNA recovered from a genital swab sample, isolate MM7.
REFERENCE 1 (bases 1 to 452)
TITLE Epidemiology and partial nucleotide sequence of four novel genital human papillomaviruses
COMMENT MM7, also known as PAP291, was isolated from a genital swab sample. Samples were obtained from over 500 patients examined at either the Shasta/Diablo planned parenthood clinic or at a private practice in the state of California over the course of seventeen months. Each of the samples were cervical or vulvar/intraoital in origin. DNA was PCR amplified over the MY09/MY11 region and subsequently sequenced if the HPV digested products yielded unique RFLP patterns. This procedure resulted in the identification of four novel HPV types: W13B, PAP291, PAP155, and PAP238a, which have subsequently been renamed MM4, MM7, MM8, and MM9. Oligonucleotide probes over the MY9/MY11 region from these viruses have been reported by Hildesheim et al. (J Infect Dis 169: 235-40). These probes were used to determine prevalence in different populations. Prevalence for each of these viruses was similar to that seen in other characterized "intermediate risk" viruses probed for in these studies. It should be noted that MM4 is extremely similar (90.8%) to novel HPVIS39 (U12481) and MM7 is virtually identical to LVX82 (U12487). Primer regions are annotated in the sequence; information in this region is not accurate due to primer degeneracy. All similarity calculations exclude data from this region.
BASE COUNT 125 a 104 c 87 g 136 t
ORIGIN

1 gccagggac ataataatgg cattgttgtg tttatgtagt tatatttgtac agttgtagat
L1 cds ->

-> MY11 PCR primer <-

61 actacccgca gtaccaatat tactatttca gctgctgca taacgctgta tgaatatcag
121 gcctctaact ttaaggaata cctccgccac accgaggaat atgacttaca ggttatattg
181 caactttgcc caaattctca taccctgaa attatgcat acctacatac tatgcatgaa
241 cattatttgt atggtaggtac ttttgggctgt taccacactc ctgccacacag ccttgatgat
301 acctgtgcc aatctcactc taccctgaa attatgcat acctacatac tatgcatgaa
361 cctaaaaagg atccttatga tggccttgta ttttgggagg tgttatattaag ggacaaacta
421 tccacagatt tgatgcagta tctttttggga cg
L1 cds ->

-> MY09 PCR primer <-

I-E-13
SEP 94
**HPVMM8**

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<tr>
<td>DEFINITION</td>
<td>Human papillomavirus, isolate MM8, partial L1 cds, My09/My11 region.</td>
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<td>ACCESSION</td>
<td>U12490</td>
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<td>SOURCE</td>
<td>Human papillomavirus DNA recovered from a genital swab sample, isolate MM8.</td>
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<td>REFERENCE</td>
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<tr>
<td>TITLE</td>
<td>Epidemiology and partial nucleotide sequence of four novel genital human papillomaviruses</td>
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<tr>
<td>COMMENT</td>
<td>MM8, also known as PAP155, was isolated from a cervical swab sample. Samples were obtained from over 500 patients examined at either the Shasta/Diablo planned parenthood clinic or at a private practice in the state of California over the course of seventeen months. Each of the samples were cervical or vulvar/intraoital in origin. DNA was PCR amplified over the MY09/MY11 region and subsequently sequenced if the HPV digested products yielded unique RFLP patterns. This procedure resulted in the identification of four novel HPV types: W13B, PAP291, PAP155, and PAP238a, which have subsequently been renamed MM4, MM7, MM8, and MM9. Oligonucleotide probes over the MY9/MY11 region from these viruses have been reported by Hildesheim et al. (J Infect Dis 169: 235-40). These probes were used to determine prevalence in different populations. Prevalence for each of these viruses was similar to that seen in other characterized &quot;intermediate risk&quot; viruses probed for in these studies. It should be noted that MM4 is extremely similar (90.8%) to novel HPVIS39 (U12481) and MM7 is virtually identical to LVX82 (U12487). Primer regions are annotated in the sequence; information in this region is not accurate due to primer degeneracy. All similarity calculations exclude data from this region.</td>
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<tr>
<td>BASE COUNT</td>
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