

Global Variation in the HIV-1 V3 Region

Priya K. Dighe, Bette T. Korber and Brian T. Foley

MS K710, Los Alamos National Laboratory, Los Alamos, NM 87545

Introduction

Due to the immunogenicity and functional importance of the V3 loop, there has been a great deal of interest in the V3 region of the envelope protein, resulting in a large international effort to obtain V3 region sequences. This section, which includes sequences taken from more than 2000 individuals and complete references, provides an overview of the variation of sequences that span this region.

Sequences

To best summarize the spectrum of international HIV-1 variants, only one representative viral sequence was included per infected individual. A complete set of references accompanies the sequence alignments, and nomenclature was preserved from the original papers so individuals and isolates can be clearly identified. HIV1 was deleted from the sequence names in this section, as all sequences included here are HIV1. Included with the references, when available, are brief descriptions of critical features of the sequences. This includes the health status of the individual from whom the virus was derived, whether or not the virus was cultured, and the year the blood sample was taken.

All sequences are prefaced by a subtype association (see phylogenetic clustering below) and a two letter country code to identify the country that the individual resided in at the time that the blood sample was taken. If the person was a recent immigrant and this information was available, we included the country of origin in the references. The two letter code was developed for Internet (Copyright 1992, Lawrence H. Landwater and the Internet Society), and incorporated here based on a suggestion made by Dr. Francine McCutchan. The key to the country codes follows this introduction. Note that this key was updated for 1997, with several country codes for Eastern European nations added since 1995.

Sometimes only one viral sequence was available from a person: a clone from an isolate, or a direct sequence of PCR amplified peripheral blood DNA. For other individuals, up to 80 viral sequences from PCR amplified DNA or RNA from blood samples were available. Consequently, over 11,000 sequences are represented by the 2087 included in this section. When two sequences were available from a person, one of the two was randomly selected. When three or more sequences were generated from a person, all available sequences were aligned (without regard to different time points of sampling) and either one representative sequence was chosen, or a consensus of the most common base found in each position in the alignment was generated. If there was a tie (e.g., 10 A's, 10 T's), the top base or amino acid in the alignment was used. If a set of sequences from two or more individuals was epidemiologically linked, and genetically very similar, only one sequence from the set was included, preferably the most recently infected. In the sequence description and references section, the short hand "PCR-direct, peripheral blood DNA" is used to signify that viral DNA was amplified from PBMCs, without culturing, and a single "direct" sequence was obtained from the amplification reaction products. The short hand "Consensus, PCR-clones, peripheral blood DNA" signifies that viral DNA was amplified from PBMCs and a set of clones was generated and sequenced from the PCR amplification products. The cloned sequences were aligned and a consensus was generated. In a handful of cases, a particular gp160 clone from an isolate was shown to be expressed and functional using a vaccinia virus T7 expression system. In these cases, the clone rather than the consensus of all sequences from a particular individual is included.

Phylogenetic clustering

Sequences have been organized according to the phylogenetic subtype association (A-J) of their envelope V3 regions only. The original sequence subtype (A-H) designations were defined based on the phylogenetic relationships determined by using both gag and env genes (when possible), are

approximately genetically equidistant in envelope, and have multiple members. The phylogenetic subtype designations and associations have generally been adopted by the HIV research community, and are now often presented with the publication of new sequences. We have either determined the subtype designations here, if not specified in the original manuscript, or else confirmed the subtype designations of the original manuscripts, and then used the subtypes to organize this section. Generally, confirmations were done by aligning a set HIV-1 V3 region sequences with longer env gene sequences (Part IIIC) that have clear subtype associations, and then using parsimony or neighbor joining trees to determine associations. Some of the shorter gene fragments from this region were given a subtype designation based on Hamming distances, using the similarity function of the MASE program (Faulkner DV, and Jurka J. *TIBS* 13:321-322 (1988)); these sequences have “.sh” appended to their name to indicate that they were too short for phylogenetic analysis. Parsimony trees were generated using PAUP (David Swofford, Illinois Natural History Survey), and neighbor-joining trees were generated with Kimura distances and a transition to transversion ratio of 1.3 using PHYLIP (Joseph Felsenstein, University of Washington). All available nucleotide sequence information was used for phylogenetic analysis; longer protein sequences were trimmed to be approximately the same length as the majority of the PCR fragments in this region, for the purposes of presentation. Some sequences were difficult to classify, and are included in the “U”, or unclassified, section. In addition, recombination between HIV-1 strains occurs when an individual is infected with more than one strain. A meeting was held in Santa Fe, New Mexico in October, 1995 to discuss the implications of recombination and methods for detecting recombinant sequences. Because inter-subtype as well as intra-subtype recombination is known to occur, the subtype designations reported in this section should be interpreted only as pertaining to the V3 region of the envelope gene. For example HIV-1 MAL from Zaire, is known to be recombinant between subtypes A and D, with the V3 loop of env resembling subtype D. D_ZR-MAL is still listed with other subtype D sequences in this study, but may be moved to the U (uncertain) group in the future. In the V3 region MAL is strongly associated with the D subtype.

The set of sequences used to help resolve subtype associations included at least two sequences from each subtype (A-H), plus a simian immunodeficiency virus outgroup sequence. The sequences were selected based on being “typical” of the subtype they represent based on phylogenetic analysis. The set has changed as more sequences have accumulated. Thus not all subtype designations were based on the same reference set.

Limitations of phylogenetic analyses

Most of the PCR derived sequences contain a sub-optimal length for phylogenetic analyses, given the level of variability in this region – typically on the order of 250 to 300 nucleotides. Due to this limitation, some of the classifications in this section are uncertain and are our best estimate given the available information. Control studies were performed to compare the phylogenetic clustering of the V3 region using available longer sequences, however, and these studies indicate that our subtype designations based on the V3 region are generally reliable. For 146 sequences, we had an approximately 700 base region of env available representing all of the subtypes A-H. (The limitation in length was due to including the H subtype sequences, which did not cover all of gp120.) After removing positions in the alignment which included gaps, 519 bases were left. When a 298 base V3 region fragment was excised from this set, and neighbor joining trees were constructed using both the 519 base and 298 base long sequences, the phylogenetic subtype designations were consistent in each case. Further, when a subset of longer gp120 sequences was analyzed (92 of the 146), including 935 bases after removing positions in the alignment which included gaps, the subtype designations were again clear in neighbor-joining trees. This indicates that the limited V3 region PCR fragments, which include more than the V3-loop, are generally able to serve as a reliable basis for subtype determination, given the limitation that the V3 loop sequence may be embedded in a recombinant genome.

Without detailed analysis, genetic recombination between subtypes may obscure phylogenetic relationships between sequences. A characteristic of recombination is an indeterminate place in phylogenetic analyses, and some of the “Uncertain” category sequences may prove to be recombinant genomes upon further inspection. Also, while a subtype designation based on a gene or gene fragment may be correct, recombination events outside the region examined may have occurred. Therefore,

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care should be taken to not overinterpret the subtype designations. If one is to discuss the subtype designations of viral isolates based on the data presented here, they should refer to the designation as “B-like over the V3 loop region,” rather than as “subtype B”.

Limitations of V3 amino acid consensus sequences

The V3 amino acid consensus sequences generated for each subtype have interesting features; however, one should be wary about assuming that any of the consensus sequences may broadly represent their subtype. Certainly many V3 loop variants in each of the subtypes are extremely divergent from the consensus sequences. These divergent forms may have very different biological and immunological characteristics from viruses which are similar to the consensus. Additionally, because of the relatively small sample size of most of the subtypes, consensus sequences can be dominated by a small group of highly similar sequences, which may in turn be a sampling artifact. Hence, these consensus sequences are “evolving” as new sequences from each subtype become available.

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ALL_CONSENSUS  IIRSENITDNAKTIIVQLNESVEIN  CTRPNNTRK.SIHI..GPGQ..AFYATGD..I.I.GDIRO.AHC NISRTWNN.TLQOAVAKL..RE.HF.....NK...T.IIF..PS.SGGDL.EIITHSF.NCGG.EFFYCVNT
A_CONSENSUS_97  VM-----N-----V-P-K-----VR-----TQ-----K.Y-----AM-----
B_CONSENSUS_97  WV-----F-----L-N-V-----H-----T-----R-----E-----R-----IV-----O-G-----V-----NO-----P-----VM-----
C_CONSENSUS_97  -----L-N-V-----H-----T-----R-----E-----R-----G-----A-----K-----A-----R-----
D_CONSENSUS_97  -----L-N-----I-----T-----Q.RT-----L-T-----GD.LL-----T-----K-----P-----
E_CONSENSUS_97  -----L-N-----H-----K-----H-----T-----V-----R-----D-----K-----Y-----E-----NG-----K-----E-----V-----K-----TE-----K-----N-----N-----O-----P-----M-----H-----R-----
F_CONSENSUS_97  -----Q-----S-----T-----H-----T-----Q-----L-----TF-----K-----I-----V-----G-----Q-----R-----RA-----K-----S-----I-----P-----A-----K-----NS-----A-----M-----
G_CONSENSUS_97  -----L-----V-----K-----I-----T-----N-----K-----S-----P-----P-----S-----V-----K-----E-----M-----N-----TAQ-----K-----K-----I-----N-----T-----NS-----A-----R-----
H_CONSENSUS_97  -----L-----K-----T-----N-----K-----S-----P-----P-----S-----V-----K-----E-----M-----N-----TAQ-----K-----K-----I-----N-----T-----NS-----A-----R-----
I_CONSENSUS_97  -----L-----K-----T-----N-----K-----S-----P-----P-----S-----V-----K-----E-----M-----N-----TAQ-----K-----K-----I-----N-----T-----NS-----A-----R-----
J_CONSENSUS_97  -----L-----K-----T-----N-----K-----S-----P-----P-----S-----V-----K-----E-----M-----N-----TAQ-----K-----K-----I-----N-----T-----NS-----A-----R-----
O_CONSENSUS_97  -----R-----M-----G-----K-----S-----G-----N-----T-----STINMT-----E-----G-----Q-----VQ-----E-----K-----MA-----WYSMGLA-----AGNGNNS-----A-----Y-----TVNA-----D-----EK-----A-----K-----Q-----TAE-----Y-----LELV-----N-----SNVT-----TMF-----NRSSGGDAEVTHLHFNCHG
U_CONSENSUS_97  -----N-----N-----R-----R-----T-----R-----Q-----N-----Q-----N-----K-----P-----

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Subtype consensus sequences. This V3 region alignment shows a consensus sequence generated for each of the eleven subtypes. The subtype consensus sequences indicate the most common amino acid found in each position among the sequences associated with each subtype. The sequences are aligned to a consensus based on the most common amino acid in the subtype consensus sequences, which approximates a “global” consensus. It was generated in this way (rather than by using all 1651 sequences) to avoid over-representation of the B subtype, which has by far the largest number of available sequences. As is the convention in this compendium, a dash (-) indicates concurrence with the top sequence in the alignment; a period (.) indicates a deletion. The carets show where the N-linked glycosylation sites are found in the consensus. The V3 loop is set off from the surrounding sequence by a space on either side to facilitate viewing. Interesting features of the consensus alignment are: 1) Only in the B subtype is GPGR

the most common tip of the V3 loop; globally, GPGQ is more prevalent. 2) A highly conserved N-linked glycosylation site is constitutively absent in the C subtype, proximal to the first cysteine (C) in loop. 3) The D subtype consensus has 34 amino acids from cysteine (C) to cysteine (C) rather than the more common 35; at the point where the deletion occurs, it is not uncommon to find insertions of 2 to 4 amino acids, as can be observed in the sequence alignments. 4) The D subtype has two arginine (R) residues in the V3 loop that are uncharacteristic relative to the other consensus sequences; positively charged amino acids in these positions may result in a syncytia inducing, non-monocytropic phenotype (Fouchier RAM, et al., *J. Virol.* **66**:3183–3187 (1992)). 5) A higher degree of variation is seen in the region just downstream of the V3 loop than within it. This difference is also observed internally among the sequences of the different subtypes. 6) The A, C, G and H consensus sequences have very similar V3 loop sequences.

V3 Loop Amino Acids

The following pages present amino acid alignments of the V3 loop, arranged by phylogenetic subtype. For each subtype, the number of sequences used to construct the alignment is indicated. The top line in each alignment represents the consensus sequence for that subtype, where consensus simply means the most common amino acid found in each position among the sequences of the given subtype. The subscripts record the frequency with which that amino acid is observed at that location among members of the subtype. An amino acid which is conserved 100% is shown with no subscript. Directly beneath the most common amino acid in each position are the other amino acids observed in that position, listed from most common to least common. An asterisk (*) subscript means less than 0.5% of the sequences had the indicated amino acid at that location. A dash (-) indicates a gap inserted to maintain the alignment. Percentages were rounded to the nearest whole number.

For this year's alignment, the HMMER (version 1.8) hidden Markov model software (Sean Eddy, Dept. of Genetics, Washington U. School of Medicine, St. Louis, MO 63110; eddy@genetics.wustl.edu) was used to objectively align all 2035 sequences. The frequency counts are derived from this alignment. Because each subtypes required different numbers and positions of gaps in order to create the full multiple sequence alignment, some sequences with unusual insertions were trimmed from the HMMER alignment, and a few positions were adjusted by hand, using MASE, prior to printing the full alignment which appears following the country codes description. The sequences which were culled from the alignment after counting frequencies, are appended.

Both the untouched HMMER alignment, and the edited version, will be available via ftp from the LANL HIV database (<http://hiv-web.lanl.gov>). Questions about these alignments should be directed to (btf@t10.lanl.gov) (505-665-1970).

E subtype (135 sequences)

N₉₇₋₉₉ C₉₉ T₉₈ R₉₈ P₉₈ S₈₁ N₈₁ N₈₇ T₇₉ R₉₆ T₉₀ S₈₆ I₇₀ T₅₇ I₈₄ G₉₆ P₉₆ G₉₆ Q₇₈ V₉₀ F₈₈ Y₉₅ R₇₆ T₉₉ T₉₃ D₉₃ I₉₈ I₆₂ G₈₄ R₉₆ K₉₇ A₉₉ Y₉₀ C₉₉ E₉₃
 S₁ Y₁ I₁ S₁ F₁₃ K₇ K₉ I₉ K₁ I₉ K₁ I₉ R₁₀ V₁₀ R₂₂ M₁₀ Q₂ R₁₆ A₅ L₅ H₅ K₁₈ R₁ E₁₀ M₁ T₂₂ N₁₆ P₁ G₁ Q₇ P₁ F₆ S₁ K₂
 H₁ K₁ N₂ T₄ I₁ K₆ I₁ K₅ T₆ P₇ R₂ L₁ L₁ G₁ H₅ T₂ Y₂ T₃ I₁ K₁ S₄ V₁ N₄ N₂
 T₁ R₁ H₁ V₃ S₁ P₁ G₁ M₆ N₄ L₁ I₁ I₁ W₁ S₁ R₁ A₄ -₁ L₃ K₁ I₁ A₁ S₁ Q₁
 Y₁ Y₁ R₁ M₁ A₁ L₁ V₁ A₁ R₁ N₃ V₃ T₁ S₁ M₁ V₁
 A₁ G₁ S₁ R₁ Q₁ L₄ H₄ V₁ R₁ S₁ G₁ G₃ K₂ M₁ V₁
 S₁ T₁ F₁ A₂ K₁ M₁ G₁ G₁ S₁ -₁
 D₁ Y₁ -₁ E₁ -₁ S₁ -₁

F subtype (80 sequences)

N₉₀ C₉₆ T₉₆ R₉₈ P₉₈ N₉₃ N₉₈ N₉₅ T₉₆ R₉₈ K₉₀ S₈₆ I₉₈ H₇₀ L₅₈ G₉₈ P₉₆ G₉₆ Q₆₉ A₈₅ F₉₅ Y₉₁ A₇₃ T₉₄ G₉₀ D₆₆ I₉₆ I₉₁ G₉₀ D₉₀ I₉₆ R₉₉ K₉₆ A₉₉ H₈₄ C₉₆
 T₄ -₁ S₁ K₁ H₁ S₄ K₁ Y₃ I₃ I₁ R₆ G₈ M₁ R₁₀ I₃₄ A₁ L₁ R₂₉ V₁₀ I₃ H₄ T₂₆ A₅ D₅ E₁₆ -₃ T₄ N₉ K₁ Q₈ V₁ Y₁₄ I₆
 S₃ I₁ F₁ D₁ -₁ T₁ -₁ T₁ -₁ Q₅ F₃ -₁ S₁ I₁ Q₅ F₃ -₁ S₁ H₅ T₃ L₁ F₄ R₁ M₁ S₃ A₃ V₁ V₅ K₁ R₄ S₁ V₄
 D₁ -₁ Y₁ -₁ Y₁ -₁ I₄ X₃ -₁ Y₄ X₃ -₁ P₁ Q₁ S₁ V₁ N₃ V₁ Q₃ -₃ E₁ D₁ D₃ K₃
 -₁ -₁ S₃ I₁ -₁ G₁ R₁ S₁ T₁

G subtype (28 sequences)

N₄₃ C₈₆ T₈₆ R₉₆ P₉₆ N₉₃ N₉₃ N₉₃ T₉₆ R₉₆ K₉₆ S₉₆ I₉₆ R₉₆ K₉₆ S₉₆ I₉₆ F₇₅ Y₉₆ A₉₃ T₉₆ G₇₉ D₃₆ I₉₆ I₉₆ G₉₆ D₆₈ I₉₆ R₉₆ Q₉₃ A₉₆ H₇₅ C₉₆
 T₁₈ T₄ S₇ T₄ S₇ T₃₂ F₅₀ G₉₃ P₈₉ G₉₆ Q₈₂ A₇₉ F₇₅ Y₉₆ A₉₃ T₇ S₁₁ E₂₁ V₄ T₄ N₃₂ K₄ L₄ Y₂₅ K₄
 M₁₄ I₁₁ V₁₁ R₄ H₇ T₁₁ L₁₈ H₄ T₇ D₇ A₁₈ T₄ N₁₁ Q₇ G₄ S₄ K₄
 I₁₁ V₁₁ R₄ H₁₈ L₂₁ I₇ K₇ S₇ N₇ D₄

Summary of variations in the tetrameric tip of the V3 loop. This table is a tally of the different tetramers observed in the 1651 individuals analyzed. This tip is thought to form a turn, and is the focal point of the potent neutralizing antibody epitopes that have been mapped to the V3 loop, as well as of T cell epitopes. Each column shows the number of occurrences of a given tetramer in either the entire 976 sequences (combined), or in subsets consisting of subtypes A–O, and the unclassified sequences (U). Underneath the column heading is the number of sequences in each category. The most common form found in each subtype is highlighted in bold lettering. In the B subtype, GPGR is the predominant form, however globally GPGQ is more common.

	Combined	A	B	C	D	E	F	G	H	I	J	O	U
Totals	2035	320	1078	233	119	135	81	28	3	1	5	13	19
GPGQ	838	284	93	232	38	104	54	21	1	1	5		6
GPGR	800	12	724	1	16	19	20		1				7
GPGK	88	5	82										1
GWGR	36		36										
GPGS	28	1	27										
GPGG	25	2	22					1					
GLGR	25	4	17		1	1	1						1
GLGQ	22				21								1
APGR	18	1	17										
GSGQ	17	3			12		1						1
GQGQ	13		1		12								
GPGH	11	1	1			6	2	1					
GQGR	9		6		1	2							
GPMA	9											9	
GFGR	6		6										
GTGQ	6				6								
GRGQ	6	1			4				1				
GVGR	4		2		1		1						
GSGR	4	1	3										
GLGH	4	2				1		1					
APGQ	4	1						1	2				
GPRR	3		3										
GPGA	3		3										
EPGR	3		3										
APGS	3		3										
GTGR	3							2					1
RPGR	3		3										
GPKR	3		3										
GMGR	2		2										
GGGR	2		2										
GAGR	2		2										
AGGR	2		2										
GRGR	2		1										
GLGS	1		1										
GTGG	1		1										
GPMR	1											1	
GLRQ	1				1								
AQGR	1				1								
GPMS	1											1	
GPLR	1											1	
GARR	1		1										

V3 Loop Variation

	Combined	A	B	C	D	E	F	G	H	I	J	O	U
Totals	2035	320	1078	233	119	135	81	28	3	1	5	13	19
GGGQ	1					1							
GPWG	1		1										
GIGQ	1				1								
GQGI	1					1							
GPLS	1											1	
GPGN	1		1										
GPGE	1		1										
GPEK	1		1										
GLGK	1		1										
AWGR	1		1										
APGG	1		1										
AGGK	1		1										
APGE	1				1								
GPGI	1	1											
GPGI	1	1											
GPGP	1	1											
GRWQ	1				1								
IGGR	1				1								
QPGR	1		1										
TPGR	1		1										
*PGR	1						1						

Divergent patterns of V3 loop evolution in M-group subtypes.

Introduction

Individual isolates or clones of HIV-1 from within any one subtype exhibit differences in cytopathic effect and cell tropism. Although subtype B is the most thoroughly studied, syncytium-inducing (SI) and non-syncytium inducing (NSI) isolates have been described for other subtypes as well. Despite this intraclade diversity of phenotypes, to date there has been no definitive indication of intersubtype differences in pathogenicity or transmissibility. This may be due in part to a lack of controlled studies which could identify such differences. Subtype B virus infecting North Americans and Europeans cannot be directly compared to subtype A virus infecting central Africans, because of differences in factors such as diet, access to health care, and exposure to secondary pathogens. It is difficult to do longitudinal cohort studies in the developing world, where several subtypes are prevalent in the same population. The wide range of phenotypic variability within a single subtype, as well as ranges of human responses to infection, requires a large sample size for study. Finally, long-term studies including sero-incident cases are critical for detecting differences in pathogenicity, and this type of study requires many years to complete. This analysis and discussion is focussed on identifying differences in evolutionary trends of the envelope protein V3 region between the HIV-1 M group subtypes. It is hoped that this may help to identify subtypes of HIV-1 which are more likely to show differences in phenotype.

The evolution of HIV-1 is influenced not only by mutations in the viral genome and selective pressure by individual human hosts, but also by the overall temporal and geographical patterns of the epidemic. The rapid spread of subtype B into large serologically naive populations in the urban centers of North America and Europe resulted in a star phylogeny of subtype B, suggestive of large amounts of horizontal transfer of the virus in a relatively short period of time. Conversely, the evolution of subtype A has been influenced by less geographical spread, remaining largely in the sub-Saharan region of the African continent, within more rural populations, where dual infection with other subtypes of HIV-1 (and even HIV-2) has occurred. Thus the subtype A phylogenetic tree is more "bushy" and intersubtype recombinants containing subtype A are more common than those containing subtype B.

Differences in modes of transmission might lead to different evolutionary trends for HIV-1. Transmission via contaminated needles may put different selection pressures on the virus than sexual transmission for example. Thus, the analysis of HIV-1 sequence variability should be accompanied by a consideration of the natural history of the various lineages of HIV-1, as well as an understanding of the biased sampling of HIV-1 isolates submitted to sequence analysis.

A quick perusal of the tabulation of V3 loop amino acid sequences divided by subtype (pages 77–80) illustrates the variability of evolutionary patterns between subtypes. For example, while subtype C shows near perfect conservation of the GPGQ amino acid sequence at the tip of the V3 loop, subtype D has retained the proline in less than 50% of sequences sampled. An elevated rate of nonsynonymous substitutions in the third variable (V3) loop of subtype D viruses has previously been noted [Korber et al.(1994)]. Serological studies also indicated that the V3 loop of the D subtype was more diverse than other subtypes [Barin et al.(1996)]. The V3 loop is a functionally and immunogenically important domain of the viral envelope. Positively charged amino acids in certain positions in the V3 loop correlate with a syncytium-inducing phenotype in culture [de Jong et al.(1992), De Wolf et al.(1994)], and usage of the CXCR4 second receptor [Cocchi et al.(1996), Bieniasz et al.(1997)].

We examined differences in patterns of envelope V3 region variability using the V3 data set from the 1996 HIV sequence compendium [Blouin et al.(1996)], with many more sequences available than when we first attempted this study in 1994 [Korber et al.(1994)]. The data was explored using the following method: V3 region amino acid sequences were split into two regions: the V3 loop, typically including 35 amino acids between the cysteine residues which form a disulfide bond to produce the loop; and the 35 amino acids flanking the loop, including 20 amino acids from the region immediately adjacent to the NH₂-terminal side of the loop (NFTDNARVIIVQLNESVEIN for example) and 15 amino

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acids from the region immediately adjacent to the COOH-side of the loop (NLSSTKWNNTLKQIT for example). Each of these two regions (loop or flanks) was aligned and scored for pairwise similarity using the PIMA software package [Smith & Waterman(1992)], with the protein similarity scoring scheme based on amino acid substitution matrices from protein blocks [Henikoff & Henikoff(1992), Henikoff & Henikoff(1993)]. The sequences in this set are compiled such that only a single sequence from each individual patient, or from each group of epidemiologically linked patients, is represented, thus eliminating the bias of multiple sequences from the same patient.

The results from these analyses are shown in Figures 1 and 2. The median of the similarities found in the V3 loop of subtype D is much lower than in the other subtypes, an indication of much greater diversity, while the interquartile range (a measure of the variation around the median) is larger. The diversity in the flanking regions, in contrast, is very similar to that in the other subtypes. This result suggests that the loop of subtype D is unique relative to the other subtypes, and is either under greater positive selective pressure for change, or alternatively, free from evolutionary constraints that restrict the variation of other subtypes. This effect is highly statistically significant, and is associated with the charge on the V3 loop (see below for discussion, and Figure 3). For example, using the non-parametric Wilcoxon or the Kolmogorov-Smirnov tests to compare the distributions of subtype A and D protein similarity scores for the V3 loop, gave p-values of $\ll 0.00001$. (To do the statistical test, the average value of each sequence compared to all others of that subtype was used to represent that sequence, so each sequence was only counted once for the statistical comparison, although all pairwise comparisons were made to construct the figures.) The A versus D comparison is of particular interest as the samples tend to come from the same studies conducted in the same geographic regions. Another way to view this data is through comparing the cumulative distributions of the amino acid similarity scores for the different subtypes (Figure 4). In the V3 flanking region, the distributions of similarity scores for subtypes A, B, C, and D tend to be very similar. Subtype E sequences are highly conserved, paralleling the short phylogenetic branch lengths of these closely related sequences [Yu et al.(1995)], presumably reflecting the relative youth of the main (Southeast Asian) subtype E epidemic when many of the sequences were obtained. In the V3 loop, one can see profoundly different behaviors in different subtypes. The subtype D V3 loops are radically divergent. The subtype C V3 loops tend to be more conserved.

The distribution of the similarities in subtype E V3 loops, originating generally either from Thailand or the Central African Republic, is different from the other subtypes, in that the distribution in the subtype E V3 loop similarity scores seems to be bimodal (Figures 1 and 3), reflecting the presence of two subpopulations of sequences. A highly conserved set of protein domains are apparent for the Thai subtype E sequences, but it is interesting to note that some of the phylogenetically similar Thai sequences are in the more divergent group of V3 loop protein sequences ([Yu et al.(1995)], and the data underlying Figures 1 and 3), suggesting a potential for rapid divergence in this domain in subtype E.

To further analyze the greater divergence in subtype D, the sequences were subdivided into two groups, one that retains proline in the tip of the loop (GPGR or GPGQ), the other consisting of all sequences that do not have proline (GLGQ, GSGQ, etc.). As can be seen in Figure 2 (top panel), the distribution of similarity scores in the proline-containing group is very similar to that of other subtypes, while scores in the other group are much lower. Additionally, there appears to be an association between this increased variability and increased positive charge in the V3 loop sequences. Because increased positive charge is associated with the SI phenotype (at least in subtype B), this phenomenon may be related either to greater freedom to diverge or greater evolutionary pressure to change in the SI (CXCR4 using) forms.

It is possible that the observed differences in V3 variation between the subtypes result from systematic sampling artifacts from the different subtypes. This seems unlikely in light of the large number of individuals now sampled, and the efforts of the UNAIDS and DAIDS to collect international samples from recent seroconvertors. The data suggest that, in addition to the phylogenetic distinctions, there are distinctions between the subtypes resulting from different evolutionary pressures. Thus biological differences do exist, either in the history of the epidemic of the different subtypes, or in different selective pressures. It is worthy of note that subtypes B and D appear to have shared a common ancestor, after some period of divergence from the other subtypes. Although phenotypic distinctions have not

been clearly detected in the data accrued so far, potential differences are indicated by differences in genetic makeup and rate of evolution, at least within the functionally important V3 loop of the different subtypes. Despite these interesting distinctions, it will be important in the future not to focus the search for biological differences in viruses too narrowly on HIV-1 subtypes. It has already been found that important phenotypic distinctions are found between different lineages within one subtype (such as SI and NSI isolates) and too much emphasis on the subtype distinctions could conceivably result in myopia with respect to these other potential differences.

V3 Loop Evolution

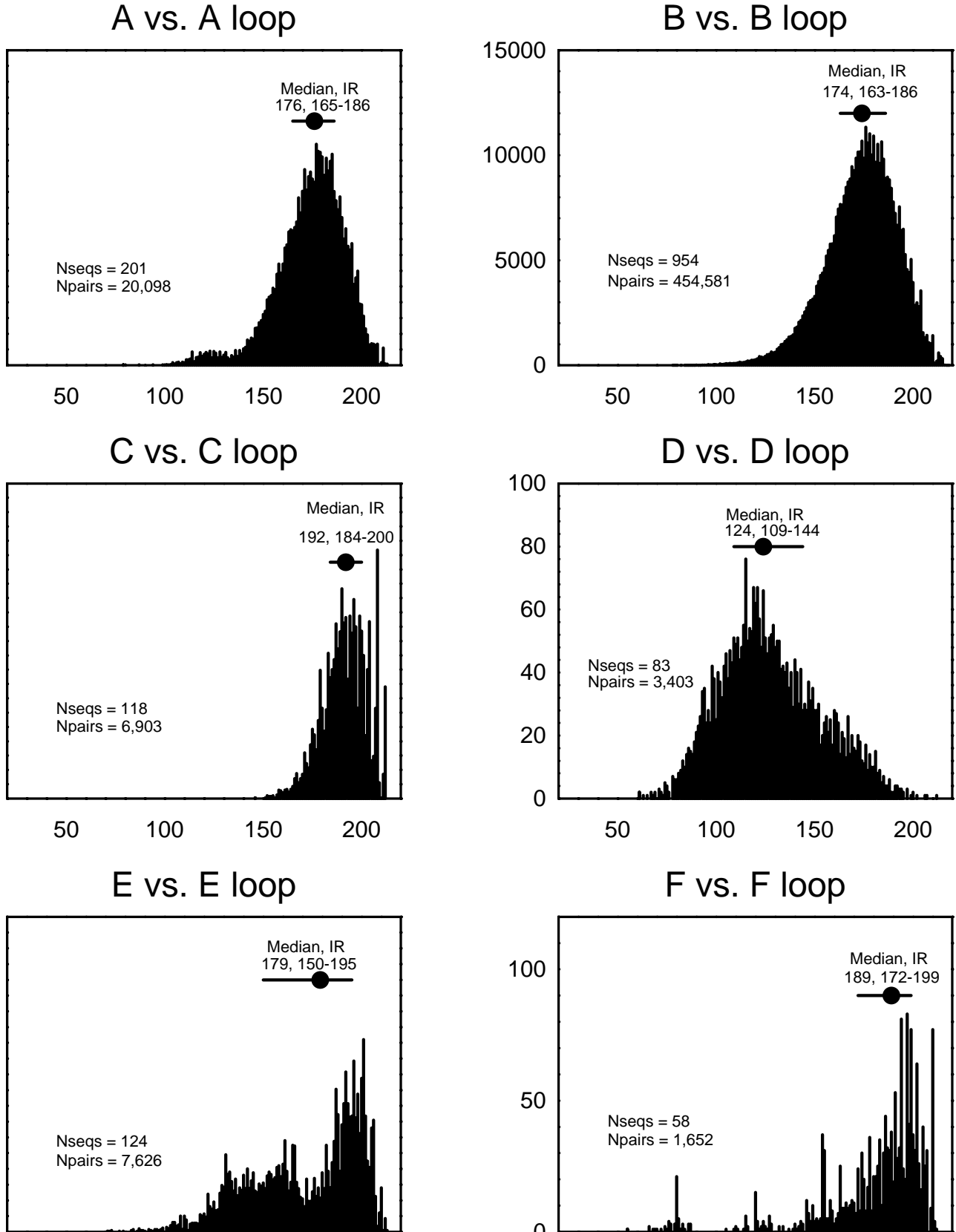


Figure 1

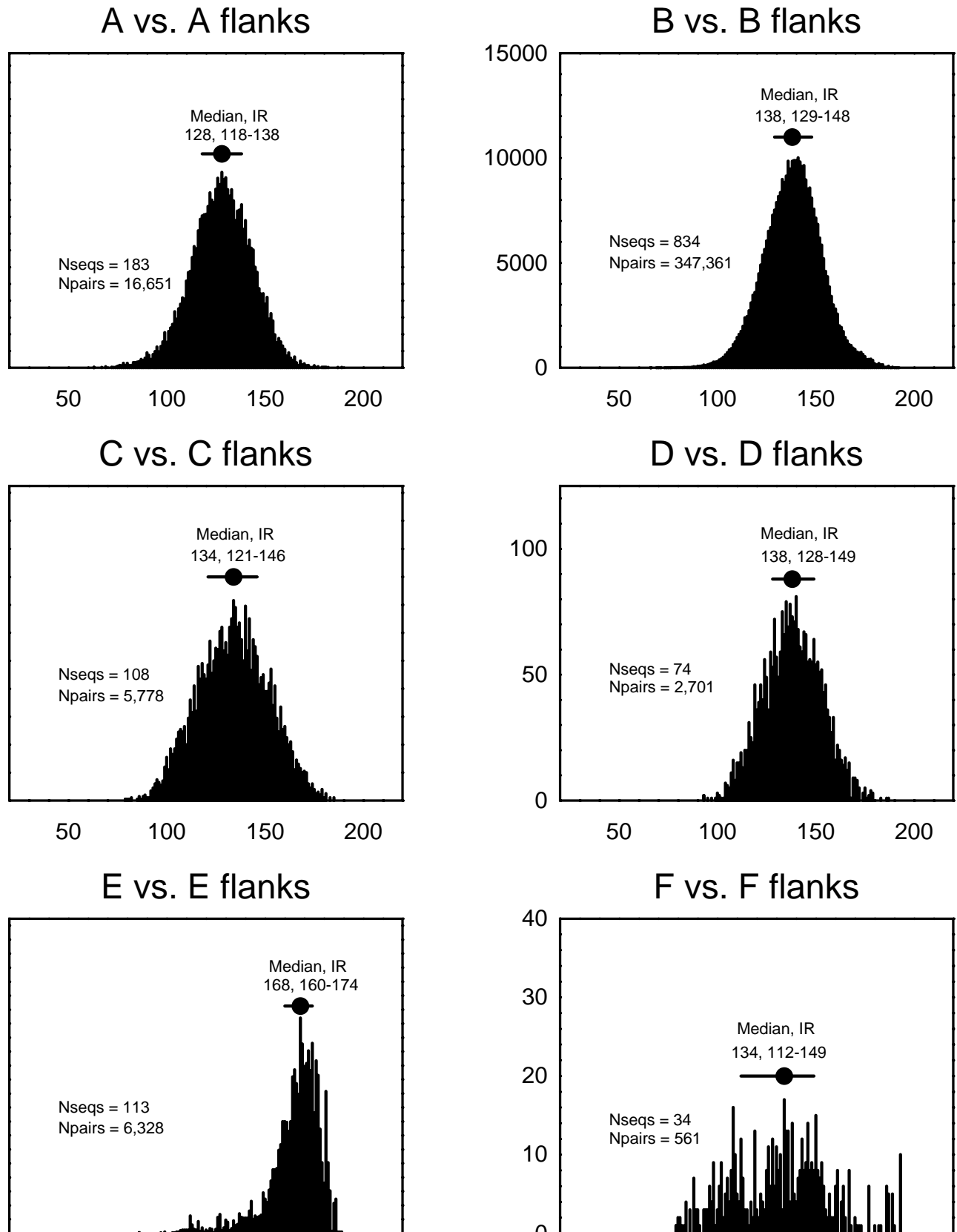


Figure 2

V3 Loop Evolution

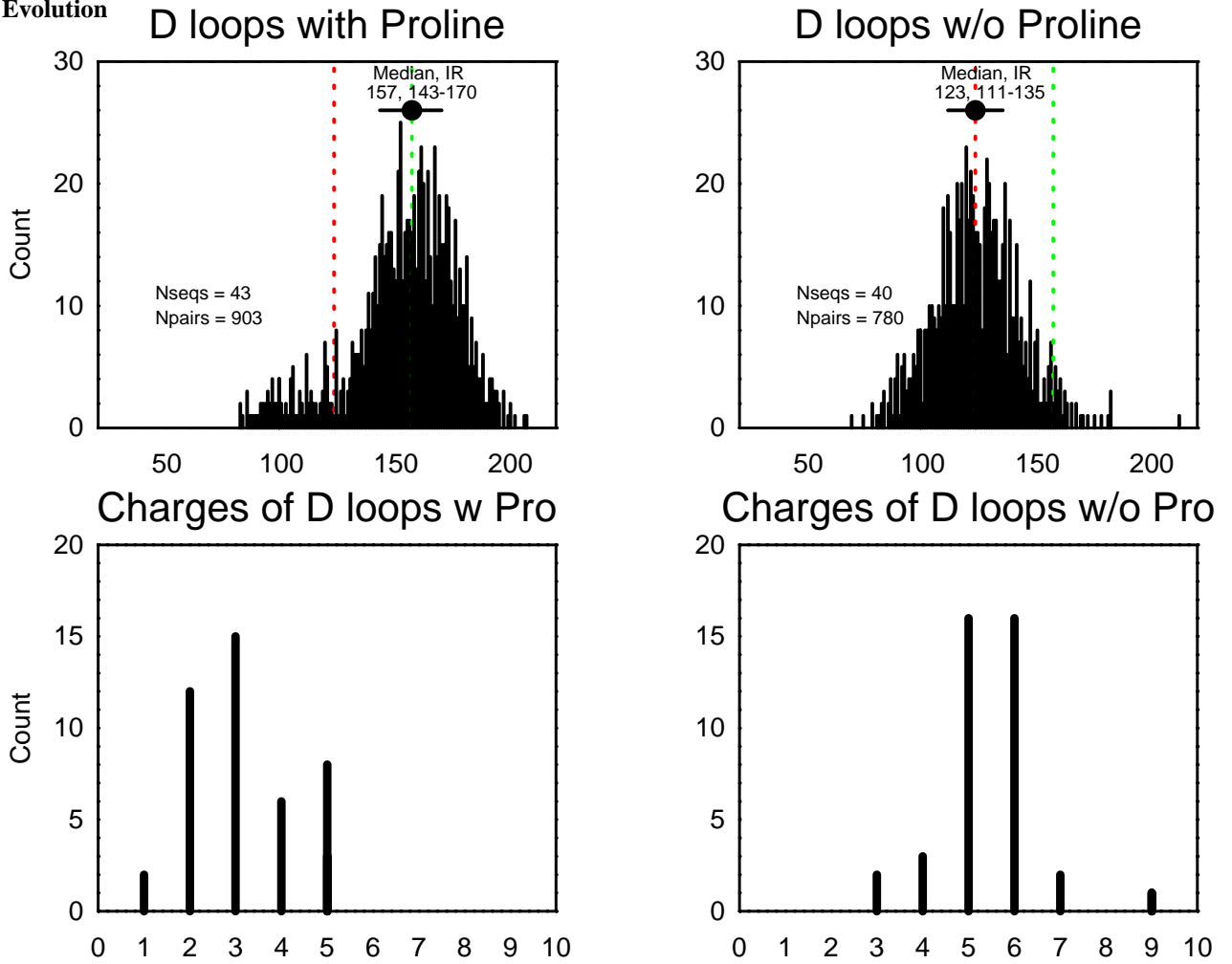


Figure 3

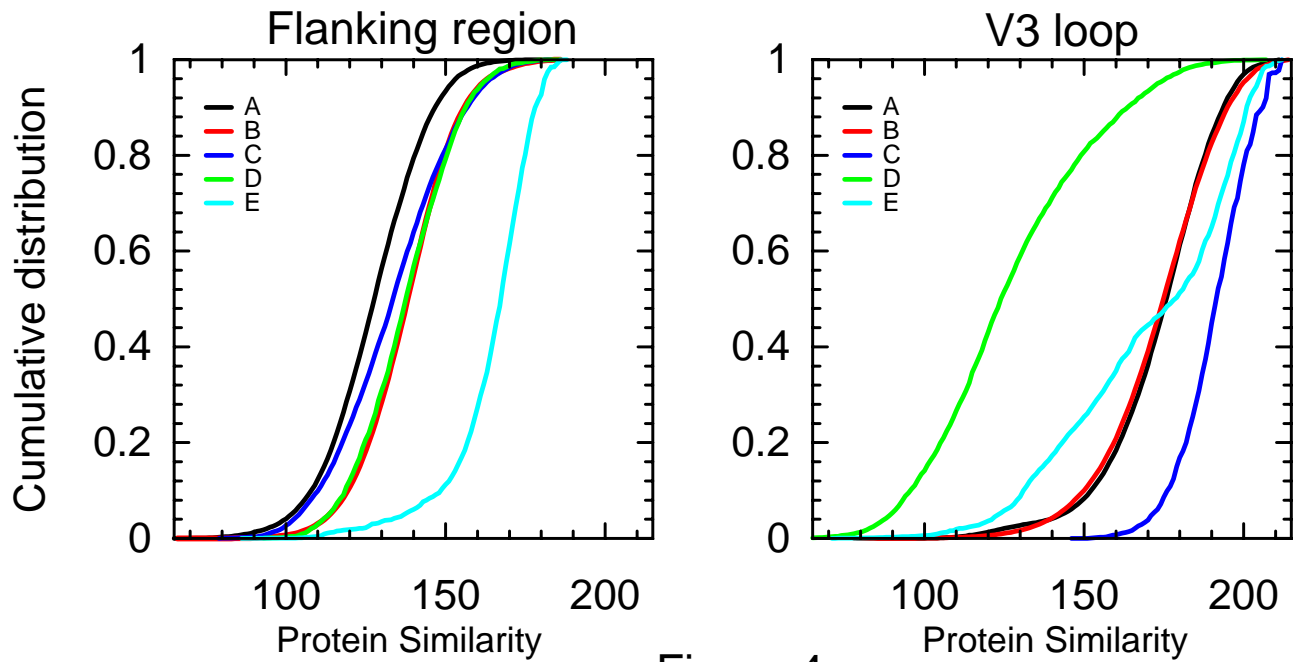


Figure 4

COUNTRY CODES

It is becoming increasingly useful to name viral isolates and samples with a country code. The following code was captured from Internet files:

`ftp://ftp.ripe.net/iso3166-countrycodes`

`gopher://sanaga.itu.ch:70/00/.1/ITU-Databases/.1/CtryCodes/.full-list.txt`

for ISO two-letter codes and for ITU three-letter codes, respectively.

This is a list based on the International Organization for Standardization (ISO) 3166:1993 standard, updated from a list prepared by Mark Horton. Note that the original standard has this same information sorted into about 6 different orders, both in English and French, therefore this is an abbreviated version not to be taken as the entire standard. While it has been checked against the standard, it may possibly contain errors; the standard and registration newsletters should be verified for any critical application.

This copy has been updated and is believed to be current through September 1997.

Table of Country Codes from ISO 3166

Country	A 2	A 3	Number
AFGHANISTAN	AF	AFG	004
ALBANIA	AL	ALB	008
ALGERIA	DZ	DZA	012
AMERICAN SAMOA	AS	ASM	016
ANDORRA	AD	AND	020
ANGOLA, REPUBLIC OF	AO	AGO	024
ANGUILLA	AI	AIA	660
ANTARCTICA	AQ	ATA	010
ANTIGUA AND BARBUDA	AG	ATG	028
ARGENTINA	AR	ARG	032
ARUBA	AW	ABW	533
AUSTRALIA	AU	AUS	036
AUSTRIA	AT	AUT	040
AZERBAIJAN	AZ	AZE	031
BAHAMAS	BS	BHS	044
BAHRAIN	BH	BHR	048
BANGLADESH	BD	BGD	050
BARBADOS	BB	BRB	052
BELGIUM	BE	BEL	056
BELIZE	BZ	BLZ	084
BENIN	BJ	BEN	204
BERMUDA	BM	BMU	060
BHUTAN	BT	BTN	064
BOLIVIA	BO	BOL	068
BOTSWANA	BW	BWA	072
BOUVET ISLAND	BV	BVT	074
BOSNIA AND HERZEGOWINA	BA	BIH	070
BRAZIL	BR	BRA	076
BRITISH INDIAN OCEAN TERRITORY	IO	IOT	086
BRUNEI DARUSSALAM	BN	BRN	096
BULGARIA	BG	BGR	100
BURKINA FASO	BF	BFA	854
BURUNDI	BI	BDI	108
BYELORUSSIAN SSR	BY	BYS	112

Country Codes

CAMBODIA	KH	KHM	116
CAMEROON	CM	CMR	120
CANADA	CA	CAN	124
CAPE VERDE	CV	CPV	132
CAYMAN ISLANDS	KY	CYM	136
CENTRAL AFRICAN REPUBLIC	CF	CAF	140
CHAD	TD	TCD	148
CHILE	CL	CHL	152
CHINA	CN	CHN	156
CHRISTMAS ISLAND	CX	CXR	162
COCOS (KEELING) ISLANDS	CC	CCK	166
COLOMBIA	CO	COL	170
COMOROS	KM	COM	174
CONGO	CG	COG	178
COOK ISLANDS	CK	COK	184
COSTA RICA	CR	CRI	188
COTE D'IVOIRE	CI	CIV	384
CROATIA	HR	HRV	191
CUBA	CU	CUB	192
CYPRUS	CY	CYP	196
CZECH REPUBLIC	CZ	CZE	203
DENMARK	DK	DNK	208
DJIBOUTI	DJ	DJI	262
DOMINICA	DM	DMA	212
DOMINICAN REPUBLIC	DO	DOM	214
EAST TIMOR	TP	TMP	626
ECUADOR	EC	ECU	218
EGYPT	EG	EGY	818
EL SALVADOR	SV	SLV	222
EQUATORIAL GUINEA	GQ	GNQ	226
ERITREA	ER	ERI	232
ESTONIA	EE	EST	233
ETHIOPIA	ET	ETH	231
FALKLAND ISLANDS (MALVINAS)	FK	FLK	238
FAROE ISLANDS	FO	FRO	234
FIJI	FJ	FJI	242
FINLAND	FI	FIN	246
FRANCE	FR	FRA	250
FRANCE, METROPOLITAN	FX		249
FRENCH GUIANA	GF	GUF	254
FRENCH POLYNESIA	PF	PYF	258
FRENCH SOUTHERN TERRITORIES	TF	ATF	260
GABON	GA	GAB	266
GAMBIA	GM	GMB	270
GEORGIA	GE	GEO	268
GERMANY	DE	DEU	276
GHANA	GH	GHA	288
GIBRALTAR	GI	GIB	292
GREECE	GR	GRC	300
GREENLAND	GL	GRL	304
GRENADA	GD	GRD	308
GUADELOUPE	GP	GLP	312
GUAM	GU	GUM	316
GUATEMALA	GT	GTM	320

Country Codes

GUINEA	GN	GIN	324
GUINEA-BISSAU	GW	GNB	624
GUYANA	GY	GUY	328
HAITI	HT	HTI	332
HEARD AND MCDONALD ISLANDS	HM	HMD	334
HONDURAS	HN	HND	340
HONG KONG	HK	HKG	344
HUNGARY	HU	HUN	348
ICELAND	IS	ISL	352
INDIA	IN	IND	356
INDONESIA	ID	IDN	360
IRAN (ISLAMIC REPUBLIC OF)	IR	IRN	364
IRAQ	IQ	IRQ	368
IRELAND	IE	IRL	372
ISRAEL	IL	ISR	376
ITALY	IT	ITA	380
JAMAICA	JM	JAM	388
JAPAN	JP	JPN	392
JORDAN	JO	JOR	400
KAZAKHSTAN	KZ	KAZ	398
KENYA	KE	KEN	404
KIRIBATI	KI	KIR	296
KOREA, DEMOCRATIC PEOPLE'S REPUBLIC OF	KP	PRK	408
KOREA, REPUBLIC OF	KR	KOR	410
KUWAIT	KW	KWT	414
KYRGYZSTAN	KG	KGZ	417
LAO PEOPLE'S DEMOCRATIC REPUBLIC	LA	LAO	418
LATVIA	LV	LVA	428
LEBANON	LB	LBN	422
LESOTHO	LS	LSO	426
LIBERIA	LR	LBR	430
LIBYAN ARAB JAMAHIRIYA	LY	LBY	434
LIECHTENSTEIN	LI	LIE	438
LITHUANIA	LT	LTU	440
LUXEMBOURG	LU	LUX	442
MACAU	MO	MAC	446
MACEDONIA, FORMER YUGOSLAV REPUBLIC OF	MK	MKD	807
MADAGASCAR, REPUBLIC OF	MG	MDG	450
MALAWI	MW	MWI	454
MALAYSIA	MY	MYS	458
MALDIVES	MV	MDV	462
MALI	ML	MLI	466
MALTA	MT	MLT	470
MARSHALL ISLANDS	MH	MHL	584
MARTINIQUE	MQ	MTQ	474
MAURITANIA	MR	MRT	478
MAURITIUS	MU	MUS	480
MAYOTTE	YT	MYT	175
MEXICO	MX	MEX	484
MICRONESIA	FM	FSM	583
MOLDOVA	MD	MDA	498
MONACO	MC	MCO	492
MONGOLIA	MN	MNG	496
MONTSERRAT	MS	MSR	500

Country Codes

MOROCCO	MA	MAR	504
MOZAMBIQUE	MZ	MOZ	508
MYANMAR	MM	MMR	104
NAMIBIA	NA	NAM	516
NAURU	NR	NRU	520
NEPAL	NP	NPL	524
NETHERLANDS	NL	NLD	528
NETHERLANDS ANTILLES	AN	ANT	530
NEUTRAL ZONE	NT	NTZ	536
NEW CALEDONIA	NC	NCL	540
NEW ZEALAND	NZ	NZL	554
NICARAGUA	NI	NIC	558
NIGER	NE	NER	562
NIGERIA	NG	NGA	566
NIUE	NU	NIU	570
NORFOLK ISLAND	NF	NFK	574
NORTHERN MARIANA ISLANDS	MP	MNP	580
NORWAY	NO	NOR	578
OMAN	OM	OMN	512
PAKISTAN	PK	PAK	586
PALAU	PW	PLW	585
PANAMA	PA	PAN	590
PAPUA NEW GUINEA	PG	PNG	598
PARAGUAY	PY	PRY	600
PERU	PE	PER	604
PHILIPPINES	PH	PHL	608
PITCAIRN	PN	PCN	612
POLAND	PL	POL	616
PORTUGAL	PT	PRT	620
PUERTO RICO	PR	PRI	630
QATAR	QA	QAT	634
REUNION	RE	REU	638
ROMANIA	RO	ROM	642
RUSSIAN FEDERATION	U	RUS	643
RWANDA	RW	RWA	646
ST. HELENA	SH	SHN	654
SAINT KITTS AND NEVIS	KN	KNA	659
SAINT LUCIA	LC	LCA	662
ST. PIERRE AND MIQUELON	PM	SPM	666
SAINT VINCENT AND THE GRENADINES	VC	VCT	670
SAMOA	WS	WSM	882
SAN MARINO	SM	SMR	674
SAO TOME AND PRINCIPE	ST	STP	678
SAUDI ARABIA	SA	SAU	682
SENEGAL	SN	SEN	686
SEYCHELLES	SC	SYC	690
SIERRA LEONE	SL	SLE	694
SINGAPORE	SG	SGP	702
SLOVAKIA	SK	SVK	703
SLOVENIA	SI	SVN	705
SOLOMON ISLANDS	SB	SLB	090
SOMALIA	SO	SOM	706
SOUTH AFRICA	ZA	ZAF	710
SOUTH GEORGIA AND THE SOUTH SANDWICH ISLANDS	GS		239

Country Codes

SPAIN	ES	ESP	724
SRI LANKA	LK	LKA	144
SUDAN	SD	SDN	736
SURINAME	SR	SUR	740
SVALBARD AND JAN MAYEN ISLANDS	SJ	SJM	744
SWAZILAND	SZ	SWZ	748
SWEDEN	SE	SWE	752
SWITZERLAND	CH	CHE	756
SYRIAN ARAB REPUBLIC	SY	SYR	760
TAIWAN, PROVINCE OF CHINA	TW	TWN	158
TAJKISTAN	TJ	TJK	762
TANZANIA, UNITED REPUBLIC OF	TZ	TZA	834
THAILAND	TH	THA	764
TOGO	TG	TGO	768
TOKELAU	TK	TKL	772
TONGA	TO	TON	776
TRINIDAD AND TOBAGO	TT	TTO	780
TUNISIA	TN	TUN	788
TURKEY	TR	TUR	792
TURKMENISTAN	TM	TKM	795
TURKS AND CAICOS ISLANDS	TC	TCA	796
TUVALU	TV	TUV	798
UGANDA	UG	UGA	800
UKRAINE	UA	UKR	804
UNITED ARAB EMIRATES	AE	ARE	784
UNITED KINGDOM	GB	GBR	826
UNITED STATES	US	USA	840
UNITED STATES MINOR OUTLYING ISLANDS	UM	UMI	581
URUGUAY	UY	URY	858
UZBEKISTAN	UZ	UZB	860
VANUATU	VU	VUT	548
VATICAN CITY STATE (HOLY SEE)	VA	VAT	336
VENEZUELA	VE	VEN	862
VIET NAM	VN	VNM	704
VIRGIN ISLANDS (BRITISH)	VG	VGB	092
VIRGIN ISLANDS (U.S.)	VI	VIR	850
WALLIS AND FUTUNA ISLANDS	WF	WLF	876
WESTERN SAHARA	EH	ESH	732
YEMEN	YE	YEM	887
YUGOSLAVIA	YU	YUG	891
ZAIRE	ZR	ZAR	180
ZAMBIA	ZM	ZMB	894
ZIMBABWE	ZW	ZWE	716

V3 Region Alignments

Table with columns for sequence identifiers (e.g., A_CONSENSUS_97, A_GAL_VI685), alignment characters (A, G, C, T, -, *), and a V3 LOOP region. The alignment shows conserved regions and variable loops across different HIV-1 strains.

V3 Region Alignments

B_CONSENSUS_97
ALL_CONSENSUS
B_AR1_06
B_AR1_13
B_AR1_21
B_AR1_22
B_AR1_24
B_AR1_29
B_AR1_33
B_AR1_34
B_AR1_35
B_AR1_36
B_AR1_56
B_AU1_MRC
B_AU1_MRC2
B_AU1_MRC3
B_AU2_C16C6
B_AU3_10631
B_AU3_10891
B_AU3_9611
B_AU3_EG2
B_AU3_JW951
B_AU3_LIF11
B_AU3_TRL1
B_BE_SIMI84
B_BR_00260n
B_BR_8Z
B_BR1_10553
B_BR1_10565
B_BR1_10575
B_BR1_1058
B_BR1_1059
B_BR1_10593
B_BR1_7930
B_BR1_7932
B_BR1_7934
B_BR1_7936
B_BR1_7940
B_BR1_7942
B_BR1_7946
B_BR1_862
B_BR1_8623
B_BR1_8625
B_BR1_8629
B_BR1_8633
B_BR1_8635
B_BR2_W2BR003
B_BR2_W2BR004
B_BR2_W2BR014
B_BR2_W2BR017
B_BR2_W2BR018
B_BR2_W2BR019
B_BR2_W2BR020
B_BR2_W2BR021
B_BR2_W2BR023
B_BR2_W2BR024

V3 Region Alignments

B_CONSENSUS_97
 ALL_CONSENSUS
 B_DE2_3499
 B_ES.03
 B_ES.06
 B_ES.07
 B_ES.09
 B_ES.10
 B_ES.13
 B_ES.14
 B_ES.15
 B_ES.17
 B_ES.18
 B_ES.20
 B_ES.26
 B_ES.106
 B_ES.108
 B_ES.D17
 B_ES.D17
 B_ES.IV
 B_ES.IX
 B_ES.P12
 B_ES.P13
 B_ES.P14
 B_ES.P17
 B_ES.P18
 B_ES.P19
 B_ES.P20
 B_ES.P21
 B_ES.F6
 B_ES.P9
 B_ES.R1
 B_ES.S1
 B_ES.S61
 B_ES.THF13A
 B_ES.THF17
 B_ES.V
 B_ES.VI
 B_ES.VIII
 B_ES.X
 B_FR.CA
 B_FR.CB
 B_FR.CC
 B_FR.CD
 B_FR.J91
 B_FR.LAI
 B_FR2.FRMP6
 B_FR2.FRMP7
 B_FR2.FRMP27
 B_FR2.FRMP29
 B_FR2.FRMP32
 B_FR2.FRMP36
 B_FR2.FRMP45
 B_FR2.FRMP47
 B_FR2.FRMP51
 B_FR2.FRMP52
 B_FR2.FRMP53
 B_FR2.FRMP54
 B_FR2.FRMP55
 B_FR2.FRMP61
 B_FR2.FRMP77
 B_FR3.FRMP78

V3 LOOP

```

VVIRSENFNTAKTIIVOLNRESVIN CTRPNNTRFKSI HIGGEGAPYYTIG.EIIG.DILROAHC NLSRAKWNT.LKQIVKLLEREFOGN.NKT.T.IVFNOSISGGDPEIVMHSF.NCGG.EFFYCNNT
II--I-N--N--VRN--G--S-G--R-Q--A-A-D--I-TE--Q-VA--H--I-AP--L-TT--*
-M-X--N--VRN--G--S-G--R-T--A-E-A-T--I-----Q-----G--V-----I-----*
I--D--S--T--K-I--S-----P-----P-----D-----Y-----*
I--D--T--AIK--T-----P-----P-----A-----D-----*
I--D--T--AIK--T-----P-----P-----A-----D-----*
A--N--V--H--K--P--R--T--S--V--N-----P-----*
D--N--V--H--K--P--R--T--S--V--N-----P-----*
D--N--V--H--K--P--R--T--S--V--N-----P-----*
V--A--I--T--K--AIO--R--N--H--K--V--A--D-----N-----*
V--A--S--T--K--PI--S--G--T--A--N-----D-----*
I--I--NHV--H--I--G-----G-----A-----D-----*
I--I--NHV--H--I--G-----G-----A-----D-----*
I--V--N--TT--T--RV--S--WR--Q--T--K--Y-----*
I--N--T--TI--Y--RV--S--L-----L-----*
D--I--S--TI--S--G--L--G--A-----A-----*
II--S--QTI--T--M--H--R--L--S--A--D-----A-----*
V--V--V--K--V--ERR--A--D--IT-----*
I--P--K--I--RG--N--A--D--N--E-----S-----*
I--D--N--L--N--P--Q--K--s--I--G--K--A--R-----*
D--N--V--T--I--S--IT--M--TVH--AI--R-----S-----*
I--D--SN--R--TI--Q--S-----*
I--D--V--KE--I--P--I--S-----*
D--N--K--IK--I--S-----*
D--N--K--AI--I--S-----*
See sequences with inserts
I--A--N--A--I-----*
D--N--H--I-----*
V--V--K--K-----*
I--N--V--K--K-----*
I--N--V--K--K-----*
KI--N--S--T-----*
I--D--AN--K--P--K-----*
D--S--S-----*
See sequences with inserts
E...PKASN--G--H--A--T-----*
IM--A--S--T-----*
I--I--V--K--P-----*
I--K--I--T--K--P-----*
#--A--L--I--P--Q-----*
AK--ISN--G--H--T-----*
SN-----T-----*
.....H--I-----*
I--N--IV-----*
#--S--I-----*
I--N--P--Q-----*
T--A--I-----*
See sequences with inserts

```

Multiple sequence alignment of V3 region proteins. Includes protein identifiers (e.g., B_CONSENSUS_97, HT2.H5996), amino acid sequences, and alignment markers (e.g., asterisks, dashes) indicating conserved regions and gaps.

V3 Region Alignments

B_CONSENSUS_97
 ALL_CONSENSUS
 HT2_H5998
 HT2_H6000
 HT2_H6002
 HT2_H6004
 HT2_H6006
 HT2_H6008
 HT2_H6010
 HT2_H6012
 HT2_H6014
 HT2_H6016
 HT2_H6018
 HT2_H6020
 HT2_H6022
 HT2_H6024
 ID1_I701
 ID1_IN93304
 ID1_IN93305
 ID1_IN93307
 ID1_IN945128
 ID1_IN94570
 ID1_IN94581
 ID1_INW01
 IN_IND9
 IN1_20016
 IN1_20023
 IN1_30005
 IN1_30008
 IT_Ed
 IT_RW1
 IT_Sala
 IT_Sala2
 IT1_115
 IT1_130
 IT1_136
 IT1_145
 IT1_190
 IT1_193
 IT1_196
 IT1_199
 IT1_20
 IT1_204
 IT2_13A
 IT2_17B
 IT2_32B
 IT3_AG7
 IT3_AL97
 IT3_BM47
 IT3_BS72
 IT3_BV76
 IT3_CM26
 IT3_DAL123
 IT3_DIV105
 IT3_MF66
 IT3_MR29
 IT3_P38
 IT3_TM59
 JP_ETR
 JP_GUNA
 JP_JH32

V3 LOOP
 VVIRSEFTDIAKTIIVOLNRSVIN
 CTRPNNTRKSI_HIGPGGAPYYTIG_EIIG_DILROAHC_NLSRAKWNNT_LKQIVKLLEREPFGN_NKT_T_IVFNQISGGDPEIVMHSF_MCGG_EFFYCNNT
 II---I-N-----R---Q---A---D-----I-TE---Q-VA-----H-----I-AP-----L-TT-----*
 See sequences with inserts
 KKP-Q-----S---D-----I-T-D---V-D---K---K---H-----H-----I-
 H---E-T---H---V---K-P-Q-----P-M---K---A---D---N---K-D-KK---HKV---G---K---H---Q---H-----H-----I-
 See sequences with inserts
 S---L-----H---Q-H-----P-----A---D---K---K---I-ETD---IH---T---Q---R---S---T---R-----R-----
 See sequences with inserts
 I---N---I---A-----P-----A---D---K---K---Y-----N-TQ-DG---T---R---R---I-S---T-----R-----
 N---N---V-----D-----A---D---N-----R-E-A---GK-AB---R---E---A-----L-N-----
 N---N---Q-----M---S---A---D---N-----T-N-T---S-----G---R---L---N-----
 P---V-----P---F---A---D---D-----I---EE---K---OK---T---G---R---L---K-----
 S-OM-----KAP-----R-----R-----I---VO---S---O-LAA---G-----G-----K-----
 HT2_H6022
 S---G-----G-----S---I---V---G-----L---T---I---N-T-----V-----R-----
 HT2_H6024
 G-L-S-----T-----S-----A---D---A---D---R-----I-TE---G---GR-AR---V-----R-----
 V-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 ID1_IN93304
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 ID1_IN93305
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 ID1_IN93307
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 ID1_IN945128
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 ID1_IN94570
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 ID1_IN94581
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 ID1_INW01
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IN_IND9
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IN1_20016
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IN1_20023
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IN1_30005
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IN1_30008
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT_Ed
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT_RW1
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT_Sala
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT_Sala2
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT1_115
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT1_130
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT1_136
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT1_145
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT1_190
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT1_193
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT1_196
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT1_199
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT1_20
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT1_204
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT2_13A
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT2_17B
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT2_32B
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT3_AG7
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT3_AL97
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT3_BM47
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT3_BS72
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT3_BV76
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT3_CM26
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT3_DAL123
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT3_DIV105
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT3_MF66
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT3_MR29
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT3_P38
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 IT3_TM59
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 JP_ETR
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 JP_GUNA
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----
 JP_JH32
 S-----I---R-G-----V---G---T---L---R-----I-KKD---D---AN---A-----L-----

B_CONSENSUS_97 VVIRSENFNDNAKTIIVOLNRSVEIN CTRPNNNTFRKSI_HIGPGRGAPYYTIG_ELIG_DILROAHC NILSRKAWNT_LKQIVKLLEREOFGN_NKT_T_IVFNQISGGDPRIYVHHSF_MCGG_EFFYCNNT *

ALL_CONSENSUS	II	I-N	PL	R	Q	A	D	O	I	TE	O	VA	H	AP	L	TT	*
B_JP_UJH1H																	
B_JP_DP23A																	
B_JP_KM03																	
B_JP1_Pat19																	
B_JP1_Pat20																	
B_JP1_Pat27																	
B_JP1_Pat48																	
B_JP1_Pat63																	
B_JP1_Pat65																	
B_JP1_Pat8																	
B_JP1_Pat9																	
B_JP1_Pat15																	
B_KP_K111																	
B_LT_LIT11A																	
B_LT_LIT17A																	
B_LT_LIT18A																	
B_LT_LIT21A																	
B_LT_LIT22A																	
B_MM1_MRN02																	
B_MM1_MRN05																	
B_MM2_1748																	
B_MM2_1755																	
B_MM2_1763																	
B_MM2_1782																	
B_MM2_M1739																	
B_MV1_9214087																	
B_MV1_9214089																	
B_MV1_9214093																	
B_MV1_9214096																	
B_MV1_9315157																	
B_MV1_9315158																	
B_MV1_9315160																	
B_MV1_9315168																	
B_MV1_9315171																	
B_MV1_9315172																	
B_MV1_9315174																	
B_NL_114C																	
B_NL_168																	
B_NL_Xicon																	
B_NL_R159																	
B_NL_wolfscon																	
B_NL1_A1																	
B_NL1_A2																	
B_NL1_A3																	
B_NL1_A4																	
B_NL1_A5																	
B_NL1_A7																	
B_NL1_A9																	
B_NL1_A10																	
B_NL1_A13																	
B_NL2_Wolfsch495																	
B_NL3_Wolfsch																	
B_NL3_NET1																	
B_NL3_NET2																	
B_NL3_NET3																	
B_NL3_NET4																	
B_NL3_NET5																	
B_NL3_NET6																	

See sequences with inserts

V3 Region Alignments

V3 LOOP

B_CONSENSUS_97
 ALL_CONSENSUS
 B_NL4_B63_84
 B_NL4_BA1_84
 B_NL4_BA206_84
 B_NL4_BA65_85
 B_NL4_BNI30_85
 B_NL4_BNI32_84
 B_NL4_BNI42_84
 B_NL4_BNI52_84
 B_NL4_BNI84_84
 B_NL4_BNI87_85
 B_NL4_BN29_85
 B_NL4_BN90_85
 B_NL4_BN93_85
 B_NL4_H1091_90
 B_NL4_H1112_90
 B_NL4_H135_90
 B_NL4_H153_82
 B_NL4_H164_90
 B_NL4_H169_85
 B_NL4_H17_82
 B_NL4_H186_85
 B_NL4_H187_90
 B_NL4_H188_90
 B_NL4_H1_85
 B_NL4_H228_90
 B_NL4_H23_82
 B_NL4_H293_85
 B_NL4_H29_82
 B_NL4_H339_82
 B_NL4_H35_80
 B_NL4_H36_82
 B_NL4_H434_85
 B_NL4_H43_90
 B_NL4_H450_85
 B_NL4_H457_85
 B_NL4_H466_82
 B_NL4_H490_85
 B_NL4_H495_85
 B_NL4_H552_90
 B_NL4_H557_82
 B_NL4_H594_85
 B_NL4_H74_81
 B_NL4_H748_90
 B_NL4_H1020_86
 B_NL4_H1025_89
 B_NL4_H1035_87
 B_NL4_H1057_87
 B_NL4_H1083_87
 B_NL4_H1164_90
 B_NL4_H117_90
 B_NL4_H138_89
 B_NL4_H141_91
 B_NL4_H142_87
 B_NL4_H221_90
 B_NL4_H257_91
 B_NL4_H3007_86
 B_NL4_H3008_88
 B_NL4_H3048_89
 B_NL4_H3057_91

VVIRSENFNTDIAKTIIVOLNESVIN CTRPNNTPRKSI_HIGPGRGAFYTTG_ELIG_DILROAHC_NLSRAKWNNT_LKQIVKLLEREOFGN_NKT_T_IVFNOSISGGDPEIVMHSF_NCGG_EFFYCNNT
 II--I-N--R--Q--A--D--N--I--TE--O--VA--H--I--AP--L--TT--*
 ---A--N--I--K--P--D--SS--YD--R--VA--O--I--O--I--R--*
 ---D--X--K--P--D--D--E--V--X--D--E--V--X--S--*
 ---D--KAP--V--G--K--E--E--E--K--E--K--E--*
 ---V--A--RM--TL--K--V--S--I--K--R--E--AT--V--R--*
 ---D--N--I--K--S--E--D--A--E--DG--S--*
 ---D--S--N--K--A--V--T--D--I--E--A--N--R--I--P--A--X--*
 ---D--R--A--V--G--TE--D--AT--I--H--*
 ---N--I--T--I--E--M--O--I--E--R--KR--*
 ---V--M--IK--D--I--R--P--L--S--D--N--T--K--*
 ---N--V--IA--E--D--N--E--X--T--K--I--P--*
 ---S--P--P--S--TIN--D--E--G--D--P--*
 ---A--N--I--K--A--R--A--D--A--D--R--T--K--R--*
 ---D--N--I--KTP--N--T--I--G--A--D--A--D--E--AT--R--I--P--A--X--*
 ---G--G--G--I--AAAT--K--D--D--E--A--K--A--*
 ---D--I--NSG--V--P--D--I--GE--T--M--R--*
 ---D--N--I--K--A--O--G--K--A--V--D--ED--AB--R--R--*
 ---D--N--I--K--K--I--G--K--A--E--A--K--Y--V--A--O--L--T--E--R--*
 ---F--D--IS--K--A--G--K--G--E--AR--E--*
 ---A--L--K--A--N--GL--I--T--D--EA--G--K--E--I--*
 ---D--N--K--K--D--DG--R--R--I--*
 ---D--N--K--K--D--E--D--S--E--AR--R--I--*
 ---D--N--K--K--D--I--G--V--T--K--Y--I--IS--*
 ---S--Q--RG--I--GE--V--T--K--Y--I--IS--*
 ---I--N--T--G--IT--AE--V--K--K--H--*
 ---D--T--K--D--IS--K--Q--K--T--I--E--*
 ---D--N--V--K--P--L--K--V--D--L--L--R--E--*
 ---D--I--I--P--P--E--D--E--R--E--S--I--S--*
 ---D--I--G--A--I--G--Q--AR--R--D--I--R--*
 ---D--N--I--H--G--K--BD--T--G--E--I--K--*
 ---D--TE--K--K--I--N--M--R--R--I--K--*
 ---D--K--K--D--N--V--T--L--Q--V--A--*
 ---D--I--T--N--A--D--N--E--I--R--E--S--V--H--*
 ---A--T--I--R--P--A--N--FLAR--R--K--QP--*
 ---A--T--I--Q--S--D--D--I--K--*
 ---D--R--F--G--D--TY--I--*
 ---D--N--G--V--D--E--T--K--R--*
 ---D--N--IG--A--O--AM--V--*
 ---A--S--ST--NT--Q--GD--R--A--T--*
 ---D--T--S--G--O--Q--T--D--I--K--*
 ---D--N--I--M--K--I--E--R--M--G--K--*
 ---A--T--S--K--K--I--Q--K--*
 ---A--I--D--I--V--R--*
 ---D--N--I--AP--D--D--I--K--S--*
 ---T--H--N--V--A--D--R--I--G--K--*
 ---N--N--I--GT--D--K--V--KD--*
 ---R--RG--V--IT--KE--E--T--V--N--K--*

B_CONSENSUS_97
 ALL_CONSENSUS
 B_NL4_13064_90
 B_NL4_13072_90
 B_NL4_13077_91
 B_NL4_13084_90
 B_NL4_13091_91
 B_NL4_133_90
 B_NL4_14004_88
 B_NL4_14008_86
 B_NL4_15020_89
 B_NL4_15032_87
 B_NL4_15037_89
 B_NL4_15038_89
 B_NL4_17025_91
 B_NL4_170_88
 B_NL4_190_89
 B_NL4_K999_86
 B_NL5_pt10con
 B_NL5_pt11con
 B_NL5_pt12con
 B_NL5_pt13con
 B_NL5_pt14con
 B_NL5_pt15con
 B_NL5_pt16con
 B_NL5_pt17con
 B_NL5_pt19con
 B_NL5_pt1con
 B_NL5_pt2con
 B_NL5_pt3con
 B_NL5_pt4con
 B_NL5_pt5con
 B_NL5_pt6con
 B_NL5_pt7con
 B_NL5_pt8con
 B_NL5_pt9con
 B_NL6_320
 B_NL7_NE1058con
 B_NL7_NE537con
 B_NL8_672
 B_NL9_H239
 B_NL9_h1054
 B_NL9_h1081
 B_NL9_h1082
 B_NL9_h1110
 B_NL9_h1135
 B_NL9_h1140
 B_NL9_h1145
 B_NL9_h159
 B_NL9_h39
 B_NL9_h411
 B_NL9_h412
 B_NL9_h424
 B_NL9_h526
 B_NL9_h569
 B_NL9_h57
 B_NL9_h571
 B_NL9_h709
 B_NL9_h716
 B_NL10_BR8914

VVIRSENFNTAKTIIVOLNRESVIN CTRPNNNTFRKSI_HIGPGRGAFYYTIG_ELIG_DILROAHC_NLSRAKWNNT_LKQIVKLLEREPFGN_NKT_T_IVFNOSISGGDPEIVMHSF_NCGG_EFFYCNNT
 II_I-N-R-Q-A-A-D-I-TE-O-VA-H-I-AP-L-TT-
 A-S-I-T-N-F-K-D-RR-I-K-A-SP-
 N-S-T-S-V-X-I-EN-I-K-K-A-
 A-N-I-P-S-G-D-EN-I-K-K-A-
 N-I-I-G-A-AI-I-
 A-N-I-V-SRG-X-K-I-K-
 D-I-PM-D-N-
 TA-I-Q-H-D-N-
 N-N-A-G-P-D-N-
 L-I-H-A-A-N-
 N-S-T-S-V-P-N-N-
 A-T-K-A-Q-N-
 A-SN-V-G-S-A-N-Y-SD-EA-V-N-E-I-ST-
 D-N-I-M-F-D-R-I-S-E-K-H-
 N-N-K-N-I-RG-A-D-K-Y-I-NST-S-V-D-K-K-H-
 See sequences with inserts
 D-N-I-M-Q
 II_I-T-H-K-II-I-AR-D-N-T-K-K-
 I-T-H-K-I-A-K-T-GK-I-K-K-T-
 N-N-K-K-R-S-R-A-T-I-G-E-E-K-K-
 N-N-I-K-IV-R-NM-A-O-VB-T-D-
 N-I-S-K-R-S-A-D-I-KE-D-AI-E-R-
 D-N-K-P-K-H-R-R-A-D-KTD-K-E-I-K-E-
 I-Q-N-IQ-B-N-A-A-Q-T-K-E-
 D-S-K-T-G-N-P-L-I-T-Q-A-K-
 A-N-I-K-K-I-KE-E-G-I-R-
 See sequences with inserts
 S-N-K-H
 D-N-V
 A-SN-H-A
 A-S-R-T
 D-S-R-M-K-A-O
 A-R-N-W-D-Y-I-D-R-T-K-K-
 D-K-TI-M-K-A-G-T-I-E-D-E-V-I-K-KD-
 I-L-A-V-L-N-A-T-N-N-V-FTE-E-ERV-I-K-A-
 I-N-I-H-I-S-R-A-K-I-GD-I-K-K-
 I-N-I-H-T-Q-P-I-K-K-E-T-K-
 D-NS-V-H-P-I-SV-R-R-K-
 N-N-K IA-D-N-A-G-H-
 N-N-h39-R-S-D-N-N-N-O-N-K-E-
 D-T-K-IV-I-Q-T-E-T-R-R-
 I-K-A-S-Q-I-O-R-E-K-H-
 K-P-K-P-S-I-G-D-N-N-K-
 SN-K-P-Q-I-T-EK-I-
 N-N-V-TD-A-E-AT-K-A-
 N-N-L-K-I-R-R-K-S-
 V-N-I-L-L-A-V-K-Y-E-NGT-AR-K-E-

V3 Region Alignments

V3 LOOP

B_CONSENSUS_97	VVIRSENFDTNAKTIIVOLNRSVEIN	CTRPNNNTFRKSI	HIGGGRGAPYYTIG	EIIG	DILROAHC	NLSRAKWNNT	LKOIVKLLLEKLEOFQGN	NKT	T	IVFNQISGGDEPIVNHSP	NCGG	EFFYCNLT	*	
ALL_CONSENSUS	II	I--I-N	--R-Q	A--D	N--	I--TE	O-VA	H--	I-AP	--L-TT			*	
B_NL10_GF921953	L-D	N--N	--V-P	D--	N--	I--GT	DA	AK	T					
B_NL10_GF93013	K	T--	K-P	D--	M--	I--E	D	AG	V					
B_NL10_MR9136	K	T	K-P	D--	M--	I--E	D	AG	V					
B_NL10_SR9038	A	L--N	--K-V	D--	D--	I--T	A	I	G					
B_NL10_SR9115	R	S--	PM	V--A	D--	I--T	A	I	G					
B_NL10_SR9235	K	I	K-PI	V--	Q	I--E	D	AD	KV					
B_NL10_SR925752	D	N--N	--N	D--	Q	I--E	D	AD	KV					
B_NL10_SR9269	D	SN--N	--T	D--	Q	I--E	D	AD	KV					
B_NL10_SR93047	V	TG-N	V--	R--F	A-R	A--	IN-T	E-AR	K-N	KT				
B_NL10_UM893272	V		T	R--P	--W	D--	I-G	Q	E-AM	K				
B_NL10_UM94038	N	VR--	T	R--P	--W	D--	I-G	Q	E-AM	K				
B_NL11_PratFoon	A	N--V	V--	PL	S	A--D	N	S	E-V	T	A-R	R	S	
B_NL11_PratNgcon	A	N--V	V--	PL	S	A--D	N	S	E-V	T	A-R	R	S	
B_NL12_0008	D	K	--R	SL	YV	A--D	Q	I--TE	D	AR	K	--E	TH	A
B_NL12_0157	D	I	K-P	S	N	I--ST	DX	R	R					
B_NL12_0211	D	N--R	--I	N		I--ST	DX	R	R					
B_NL12_0230	L	D	A	X	G	K	A	E	A					
B_NL12_0337	D	N	K	X	X	TI	N	T	A	Q				
B_NL12_0583	N	N	K		X	SL	D	E	R	V				
B_NL12_0617	N	N	K		X	SL	D	E	R	V				
B_NL1_01	S	KDP		G	A	G	DN	D	R	I				
B_NL1_03	N	N	LA	G	F	TO	T	G						
B_NL1_04	D	N	T	N	V	K	GIN	H	T	G				
B_NL1_05	N	N	T	N	S	I	K		Q	T	K			
B_NL1_06	T	K	A	V	L	G	A	D	A	T				
B_NL1_08	A	N	R	IQ	H	I	E	S	K	AL	V			
B_NL1_09	A	N	R	IQ	H	I	E	S	K	AL	V			
B_NL1_10	D	N	A		A	I	V	G	A					
B_NL1_11	D	N	A		A	I	V	G	A					
B_NL1_12	A	R		V	S	RG	K	V	A					
B_NL1_16	N	N	LN	L	L	T	NKT	D	R	V	E	K		
B_NL1_20	A	N	RN	A	A	N	F	ED	K	AI				
B_NL1_21	N	I	K		M	T	I	G	M	A				
B_NL1_22	A	N	D	H	I	S	I	N	T	R	AI			
B_NL1_23	A	N	G		R	V		A	D					
B_NL1_24	A	R		H	I	Q	P							
B_NL1_25	A	R		K		P								
B_NL1_26	A	R		A	S									
B_NL1_27	D	N	S	L	H	I	N	T	L	R	K			
B_NL1_29	D	S	L	K	H	I	N	T	L	R	K			
B_NL1_30	S	SN	I	K		I	T	S	E	RI	K			
B_NL1_31	D	I	T	K	A	R	T	E	R	I	K			
B_NL1_32	D	I	T	K	P		G	NL						
B_NL1_34	D	N	L	H	T		I	GT						
B_NL1_35	N	N			T		S	Q	K	G	T			
B_NL1_36	A	N	K	H	I	I	G	ST						
B_NL1_37	S	A	K			K	T	R	AI	G	V			
B_NL1_38	A	LS	R	I	H	I	N	T	D	S	T	A	N	
B_NL1_39	A	I	R			G	N		I					
B_NL1_40	A	N	I	A	H	I	N	T	E	K	I	G	K	T
B_NL1_41	D	N	I	KDP	V		N	A	E	Q	T	D		
B_NL1_42	V	N				I	E	AL						
B_NL1_43	S	N		V		I	E	K	G	AT				
B_NL1_44	A	L	T	H		I	E	K	G	AT				
B_NL1_45	A	N				I	E	AI	E					
B_PR1_D2PR728	N	N	KDFIK		A	E	S	H	I					
B_PR1_D2PR729						S	GH	AI						L

Table with 5 columns: ID (e.g., B_TH7.102, B_TH7.103), V3 LOOP, alignment characters (asterisks, dashes, letters), and a right-aligned column of symbols (asterisks, dashes, letters).

V3 Region Alignments

	^	^	^	*	^	^	^	^	^	*	^	^	^	*
B_CONSENSUS_97	^	^	^	^	^	^	^	^	^	^	^	^	^	^
ALL_CONSENSUS	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_TW1.236	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_TW1.257	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_TW1.261	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_TW1.358	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_TW1.366	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_TW1.382	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_TW1.384	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_TW1.386	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_TW1.391	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_TW1.646	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_TW1.84	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_TW1.91	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.AC3	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.AD39	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.ADA	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.ALA	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.BAL	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.BCSG3	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.BRVA	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.BWB	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.Diaz	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.FASH	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.HOBR	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.JFL	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.JM	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.JRCSF	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.MA	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.MN	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.NY5CG	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.P896	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.RJS	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.SBA	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.SBB	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.SBC	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.SC	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.SF128	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.SF2	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.SF33	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.TN100	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.TN1002	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.TN1003	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.TN1005	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.TN1006	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.TN1007	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.TN1009	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.WEAU	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.WM	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.WM72	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.WR27	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.TU	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US.twinABecon	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US1.HC01	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US1.HC05	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US1.HC06	^	^	^	^	^	^	^	^	^	^	^	^	^	^
B_US1.HC06	^	^	^	^	^	^	^	^	^	^	^	^	^	^

V3 Region Alignments

V3 LOOP
C_CONSENSUS_97
C_ET3_B9512
C_ET3_B9516
C_ET3_B9524
C_ET3_B953
C_ET3_B9545
C_ET3_B9552
C_ET3_B9562
C_ET3_B9585
C_ET3_B9590
C_ET3_B9595
C_ET3_B9599
C_ET3_KAZS9204
C_ET3_KAZS92109
C_ET3_KAZS9239
C_ET3_KAZS9242
C_ET3_KAZS9249
C_ET3_KAZS9258
C_ET3_KAZS9258A
C_ET3_KAZS9258B
C_ET3_KAZS9263
C_ET3_KAZS9265
C_ET3_KAZS9277
C_ET3_KAZS9294
C_ET3_KP95016
C_ET3_KP95036
C_ET3_KP95040
C_ET3_KP95043
C_ET3_KS92021
C_ET3_KS95006
C_ET3_KS95012
C_ET3_KS95020
C_ET3_KS95029
C_ET3_KS95030
C_ET3_KS95036
C_ET3_KS95038
C_ET3_KS95047
C_ET3_KS95050
C_ET3_KS95058
C_ET3_KS95077
C_ET3_KS95087
C_ET3_TKS92024
C_ET3_TKS92055
C_ET3_TKS92059
C_ET3_TKS92062
C_ET3_TKS92077
C_ET3_TKS92078A
C_ET3_TKS92078B
C_ET3_TKS92083
C_ET3_TKS92090
C_ET3_TKS92092
C_ET3_TKS92102
C_ET3_TP95001
C_ET3_TP95046
C_ET3_TP95059
C_ET3_TP95075
C_ET3_TP95091
C_ET3_TP95001
C_ET3_TS95002

Table with 4 columns: Accession ID (e.g., D_CONSENSUS_97, ALL_CONSENSUS), Protein Name (e.g., CTRPYNNITFRQRT, HIGPGSALYTTTGRIIGDGI), and sequence alignment characters (A, C, G, T, -, *, ^, *). The table shows multiple sequence alignments across various protein entries.

V3 Region Alignments

Accession	Sequence	Accession	Sequence	Accession	Sequence	Accession	Sequence
D_CONSENSUS_97	IIIRSENLTNNAKIIIVOLNRSVITN	^	^	^	^	^	^
ALL_CONSENSUS	-----I-----	^	^	^	^	^	^
D_UG1_W2UG024	-----E-----	^	^	^	^	^	^
D_UG1_W2UG035	-----V-----	^	^	^	^	^	^
D_UG1_W2UG038	-----KK-----	^	^	^	^	^	^
D_UG1_W2UG040	-----S-----	^	^	^	^	^	^
D_UG1_W2UG046	-----T-----	^	^	^	^	^	^
D_UG1_W2UG053	See sequences with inserts	^	^	^	^	^	^
D_UG1_W2UG059	-----P-----	^	^	^	^	^	^
D_UG1_W2UG065	-----S-----	^	^	^	^	^	^
D_UG1_W2UG070	-----K-E-R-----	^	^	^	^	^	^
D_UG2_1665	See sequences with inserts	^	^	^	^	^	^
D_UG2_1685	-----A-----	^	^	^	^	^	^
D_UG2_2999	-----IS-----	^	^	^	^	^	^
D_UG2_3	-----V-T-----	^	^	^	^	^	^
D_UG2_4132	-----T-----	^	^	^	^	^	^
D_UG2_4133	-----N-----	^	^	^	^	^	^
D_UG2_462	-----T-----	^	^	^	^	^	^
D_UG2_5055	-----V-T-----	^	^	^	^	^	^
D_UG2_5059	-----F-T-K-----	^	^	^	^	^	^
D_UG2_653	-----V-----	^	^	^	^	^	^
D_UG2_G1	-----D-----	^	^	^	^	^	^
D_UG2_G2	See sequences with inserts	^	^	^	^	^	^
D_UG3_109	-----N-----	^	^	^	^	^	^
D_UG3_110	-----G-----	^	^	^	^	^	^
D_UG3_114	-----P-----	^	^	^	^	^	^
D_UG3_12	-----V-----	^	^	^	^	^	^
D_UG3_120	-----A-----	^	^	^	^	^	^
D_UG3_122	-----S-----	^	^	^	^	^	^
D_UG3_7	-----VV-----	^	^	^	^	^	^
D_UG3_70	See sequences with inserts	^	^	^	^	^	^
D_UG3_74	-----F-----	^	^	^	^	^	^
D_UG3_79	-----K-----	^	^	^	^	^	^
D_UG3_83	-----I-----	^	^	^	^	^	^
D_UG4_C97111	-----I-RT-----	^	^	^	^	^	^
D_UG4_WH01523	-----K-K-T-----	^	^	^	^	^	^
D_UG5_UG266	-----I-----	^	^	^	^	^	^
D_UG5_UG269	See sequences with inserts	^	^	^	^	^	^
D_UG5_UG274	-----D-----	^	^	^	^	^	^
D_UG6_980	-----P-I-----	^	^	^	^	^	^
D_UG6_9802	-----N-----	^	^	^	^	^	^
D_UG6_9803	-----P-I-----	^	^	^	^	^	^
D_UG7_42	-----I-----	^	^	^	^	^	^
D_UG7_44	See sequences with inserts	^	^	^	^	^	^
D_UG7_963	-----S-----	^	^	^	^	^	^
D_UG8_94UG010	-----M-R-----	^	^	^	^	^	^
D_UG8_94UG013	-----G-----	^	^	^	^	^	^
D_UK1_CPHL4	-----I-D-V-N-----	^	^	^	^	^	^
D_US_AMK	-----S-----	^	^	^	^	^	^
D_ZA_ZA500	-----V-E-----	^	^	^	^	^	^
D_ZA_ZA501	-----N-----	^	^	^	^	^	^
D_ZA_ZA505	-----F-A-E-----	^	^	^	^	^	^
D_ZA_ZA506	-----N-----	^	^	^	^	^	^
D_ZA_ZA507	-----N-----	^	^	^	^	^	^
D_ZR_E51	-----N-AH-----	^	^	^	^	^	^
D_ZR_UY	See sequences with inserts	^	^	^	^	^	^
D_ZR_NAL	-----D-T-N-----	^	^	^	^	^	^
D_ZR_NDK	-----A-IV-----	^	^	^	^	^	^
D_ZR_Z2Z6	-----R-I-----	^	^	^	^	^	^
D_ZR1_6555	-----K-I-VNN-----	^	^	^	^	^	^
D_ZR1_6565.sh	-----D-L-N-----	^	^	^	^	^	^
D_ZR1_6651.sh	-----N-----	^	^	^	^	^	^
D_ZR1_6659.sh	-----D-T-----	^	^	^	^	^	^

* * * * * V3 LOOP * * * * *

F_CONSENSUS_97	QIIRSONISDMTKTIIVHINETVQIN	CITRPNNPTPRKSIHHLGPGQ	AFYSSATG	DIIG	DIGRKAHC	NYSGTQWNTALORVRAKLTGKSHFPD	NKT	..	TNIKFNSS	SGGDLEITMHSFCMCRGTEFFYCNT	*
ALL_CONSENSUS	I--E--TN--A--Q--S--E--
F_AE1_20016	V--X--X--A--I--S--S--
F_AE1_21280
F_AR2.15
F_AR2.16
F_AR2.18
F_BR_7944
F_BR_RJ103
F_BR1_BZ1126
F_BR1_BZ162
F_BR1_BZ163
F_BR2_HSP209
F_BR2_HSP229
F_BR2_HSP238
F_BR2_HSP255
F_BR2_HSP255A
F_BR4_93BR02017
F_CM_CA16
F_CM_CA20
F_CM1_CMR148
F_CM1_CMR271
F_CM1_CMR275
F_CM1_CMR304
F_CY_HO441
F_FR1_FRMP84
F_GA_V1354
F_GA1_V1354
F_NLI_BR94009
F_NLI_ZR93061
F_NLI_ZR93069
F_R01_14018
F_R01_14020
F_R01_14024
F_R01_14027
F_R01_14028
F_R01_14034
F_R01_14036
F_R01_14041
F_R01_14046
F_R02.2
F_R02.3
F_R02.4
F_R02.5
F_R02.6
F_R02.7
F_R02.8
F_R02.9
F_R02.16
F_R02.17
F_R02.18
F_R02.19
F_R02.20
F_R02.21
F_R02.22
F_R02.RMS3002
F_R02.RMS301
F_R02.RMS3012

V3 Region Alignments

V3 LOOP

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G_CONSENSUS_97 IIRSENLTDNAKVIIVOLNKSVSEIN CTRENNNT_RKSI_TFGPGQ_AFY_ATG_DIIG_DI_ROAHC NVSRDWNEM_LONVYAKLA_KRIFN_NKS_NDIPTFNSSAGGDLIITTHSPFCRGGEFFYCNT *
ALL_CONSENSUS -I-N--T---E---          RI---          -E-NT--O-AK--R-H-          T-I-AP--S---          ^ ^ ^
G_BT1_259       -M--K-F--T---ET---          -T-N---          -NK-K-YO--K-KTQ--G-Y-          S---          *
G_BT1_43        -K--I---I---M          H---L---A---          -K-D---NS-          -N-S-P-          *
G_C11.3541     .....S-T-I---R          HI---H-T---A---          -E-NT--L-          -I---          -G-
G_C11.3671     .....H-T-N-F---M          P---G---          -E-NT--L-          -I---          -G-
G_C11.3760     .....IS-T-K---M          DL-H-S---          -A-NT--H---          -L-          -V-
G_GA.LBV217   -M--F-N--N-F-ID-V          -F---          -KK-TDL--T---Q-L-H--T---Y-T-          -G-
G_GA.VI525    -Q--T---ETIG-          K-T-R-VL-          -E-RD-    .OKV--A.OLQG-          -YNK-P-          -G-
G_GA1.G98     -F-N--T---ET-          -I-RI-T---EVT-          -R-K--EK-RTQ--OKE-          -S---          -K-
G_GA1.VI526   -F-N--I---ET-          -K-K-T-R-VL-          -K-K-T-          -S---          -S-
G_GB.K        -M--I---I---ET-I          NL-I-          -GGN-ST-I-R-K-O-RIPNK-I-          -DTP-          -G-
G_GB1.22      -RV---F--T---ET-D-T-V-T-s---S-          -I---          -IN-S-TG--KE-RE--N-TDT-D-          -M-
G_GB1.NJ3     NND--K-S--T-G--I-V-s---TIG-          -R---          -TKAT-SK--K-KTQ-          -I-          -M-
G_NG1.G3      -R---S--T---D-I---          S-I-          -GQE-Q--K-O-Q--QVF-          -S-          -S-
G_NG1.JP882   -R---F---I---          -L---          -KIK-KO--MVH--R-YGI-          -I--N-          -T-S-S-
G_NG1.JV832   -I---          -A---          -KEN-EK--H-OVH--RK-YGD-          -T-S-S-          -S-
G_NL.127C    See sequences with inserts          -PI---          -IK-K--K--Q--RK-Y-          -I-          -S-
G_NL1.GH94012 -V--T---N---A-R-          -R-S---          -AE-NT-          -G-K-T--HK-EIQ--EKV-          -S-
G_NL1.LR94018 -V--N--N---A-R-          -L---          -R---          -G-K-T-          -Q-L-          -S-
G_NL1.UM92101 -V--I-N--I---ETILT          -L---          -EAE--K--HG-G-O--NK-K--YO-          -D-G-          -G-
G_RU.131lcon -V--F---I---I          -A--L---          -K---          -G---          -T---          -Y-A-
G_RU1.RUS12A -V--I-N--I---I          NL---          -R---          -G---          -T---          -G---          -K-
G_RU1.BUK3a   -V--I-N--I---I          -I---          -GRN-S--E-KG-          -Y-PR-S-          -KPA.L-          -V-I-
G_TW1.267     .....F-ETI---          RI---          -Y-KX-QK---VKK-          -I-          -I-

```


A Subtype

At this time there are viral sequences from 320 HIV-1 infected individuals associated with HIV-1 subtype A. The A subtype consensus sequence (A_CONSENSUS_97) generated from these sequences was based on the most common amino acid found in each position in an alignment of these sequences. All of these sequences have been published and/or have been made available for printing in the database by their authors.

- 1) **BJ1.ID#:** These 18 sequences are from female prostitutes, born in either Ghana or Togo, who live in Benin. 15 are from directly sequenced PCR products, derived via RT-PCR from patient serum RNA. 3 (233, 251 and 253) are from cloned PCR products, also by RT-PCR from serum RNA. Another subtype A sequence (366, U61870) is not included here, because it was nearly identical (254 of 255 bases identical) to the SF170 (M66533) sequence from Rwanda isolated in 1988, and thus it likely represents a lab artifact. [Heyndrickx et al.(1996)]. Accession numbers U61854–U61869, U61871 and U61873. Two subtype G isolates were also found in this study.
- 2) **BY.BLR10A:** This sequence is from Byelorussia. [Lukashov et al.(1995)]. Accession number L38411.
- 3) **CA.HWCL1:** This sequence is the first published sequence of subtype A HIV-1 in Canada. The patient had moved from Uganda in 1983, and was diagnosed as HIV+ in 1989. Viral RNA was recovered from archived, stored patient serum by binding viral particles to CD4-coated wells of an ELISA plate. The RT-PCR amplification product was cloned and 10 clones were sequenced. It is not clear whether this sequence is from a single clone, or a consensus of all 10. [Montpetit(1995)]. Accession number U34049.
- 4) **CF1.ID#:** These thirteen sequences are from a set of sequences obtained from 27 symptomatic patients from the Central African Republic, from whom blood was drawn in 1990–1991. The sequences are consensus sequences from cloned PCR products. DNA was isolated from co-cultured PBMCs. [Murphy et al.(1993)] Accession numbers L11457–L11458, L11461–L11463, L11469–L11471, L11474–L11475, L11477–L11479, L11484–L11496, L11498, L11518 and L11523–L11524. Some of them were sequenced again by Schmitt et al. unpublished: U43275, CF1.4023; U43109, CF1.4054; U43139, CF1.11423; U43136, CF1.1286.
- 5) **CF2.GAN and SAS:** These sequences were kindly provided prior to publication by Dr. MP Kieny of Transgene, Strasbourg, France. They are part of a set of 14 HIV-1 gp120 isolates from Bangui, Central African Republic. The gp120 proteins have been expressed in a hybrid gp160 vaccinia virus expression system. Year of isolation and health status of individuals from which the virus was isolated were not provided. Viruses were isolated in the CAR by C Mathiot and B You (Pasteur Inst., Bangui), grown by F Barre-Sinoussi and A Deslandres (Pasteur Inst., Paris), and cloned and sequenced by D Schmitt and MP Kieny. Accession numbers U43111, U43171, M81063, M81064.
- 6) **CI1.ID#:** These six sequences are from six different AIDS patients suffering from pulmonary tuberculosis at the Pneumology Hospital of Cocody, Abidjan, Ivory Coast. In this study sequences came from coculture (on donor PBMCs) supernatant viral RNA, proviral DNA from each patients' PBMCs after coculture with donor PBMCs, and proviral DNA directly from uncultured PBMCs. PCR or RT-PCR was used to amplify the env V3 region, and 4–7 cloned PCR products were sequenced. A total of 66 sequences from the six patients were published. All 66 were subtype A, and inpatient sequences were more similar than interpatient sequences [Audoly et al.(1996)]. Accession numbers U59559–U59624.
- 7) **CI2.CI-ID#:** These sequences are from 11 of 13 isolates from individuals from Abidjan, Cote d'Ivoire. CI-14 and CI-20 were symptomatic, and the others were asymptomatic. CI-14, CI-45 and CI-47 were serologically dually reactive for HIV-1 and HIV-2. The C2V3 region is part of a 900 bp sequence. Samples were collected between May 1990 and Sept. 1991. Virus was cultured with donor PBMCs, nested PCR amplified, 3–4 clones were sequenced, and the consensus of those clones is presented here. [Janssens et al.(1994a)]. Accession numbers X72024–X72027, X72030–X72039, X72043–X72056, and X72059–X72065.
- 8) **CI3.ID#:** These 21 sequences are from Abidjan, Ivory Coast. No other information is yet available. Ellenberger D.L. unpublished 1997. Subtypes A, D and G were found for Ivory Coast patients in this set. Ugandan sequences of subtype A were also part of this set. Accession numbers AF000449, AF000450, AF000452, AF000453, AF000454, AF000455, AF000456, AF000457,

- AF000459, AF000462, AF000464, AF000465, AF000466, AF000467, AF000470, AF000471, AF000472, AF000473, AF000474, AF000475, AF000493
- 9) **CM1.CA-ID#:** These sequences are 11 of 17 sequences from a very diverse set of isolates from Yaounde and Douala, Cameroon. The sequences were derived from asymptomatic (CA7, CA11, CA15, CA17, CA18, and CA21) and symptomatic (CA1, CA2, CA6, CA19 and CA22) individuals. Virus was isolated by culture with donor PBMCs, and nested PCR amplified. A single clone was sequenced representing each HIV-1 isolate. [Nkengasong et al.(1994)]. The other six sequences were subtypes B, E, F and H. Accession numbers for the subtype A sequences: X80438, X80440, X80442, X80444–X80447, X80449, X80450, X80453, X80454.
 - 10) **CM2.CMR61:** CMR61 is one of two A group sequences from a 23 year old female commercial sex worker from Cameroon who was found to be triple-infected with subtypes A and D, as well as O group HIV-1 [Takehisa et al.(1997b)]. The other subtype A sequence from the same patient is labelled as CMR709 and is from a separate blood sample. Accession numbers U58148, U58150.
 - 11) **CM3.ID#:** These 15 sequences are all from Cameroon. Takehisa et al unpublished 1997. Accession numbers U69992–U69996, U70000, U70002–U70008, U70010 and U70014 U28719 (father); U28677 (father's partner); U28665 (mother)
 - 12) **CY.HOcon:** This is a consensus sequence from four individuals who were epidemiologically linked to one another: a father, a mother, their child and a woman who was a heterosexual partner of the father. These samples, like others in this study (see also subtypes B, C, F and I) were collected in February 1994 from the AIDS clinic in Nicosia, Cyprus. PBMC DNA was PCR amplified and cloned. Individual clones were sequenced. The father (patient HO34) was 36 years old and asymptomatic. He was known to have been seropositive for at least 2 years and had a CD4 count of 410. The mother (patient HO17) was 35, had been infected for at least two years, had a CD4 count of 2 and died in May 1994. The child (patient HO49) was 2 years old, had been infected since birth, and was asymptomatic, with a CD4 count of 1,211. The partner of the father (patient HO42) was 45 years old, had been infected for at least 4 years, was symptomatic with CD4 count of 80, and died in August 1994. Because of the close epidemiological linkage, a consensus of all 5 sequences is presented here. [Kostrikis et al.(1995)]. Accession numbers U28683 (child); U28674, U28719 (father); U28677 (father's partner); U28665 (mother).
 - 13) **DJ.DJ-ID#:** These three sequences from Djibouti were from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989–1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)]. DJ258 is NSI and uses the CCR5 coreceptor [Trkola et al.(1996b)]. Accession numbers L22939, L22941, and L23064.
 - 14) **ET.TP95001:** This study describes the distribution of HIV-1 subtypes in Ethiopia. HIV-1 RNA was collected from sera (from a majority of asymptomatic individuals) and RT-PCR amplified and sequenced directly. One subtype A and numerous subtype C sequences were found [Abebe et al.(1997)]. Accession number U88756.
 - 15) **FR1.ID#:** These 6 sequences are from members of the French military who are believed to have been infected while deployed outside of France (Djibouti, Guyana, and Central African Republic). Other sequences from this study were subtypes B, C, E, F, and unclassified. [Lasky et al.(1997)]. Accession numbers for subtype A were U58800–U58806 and U58778.
 - 16) **GA.VI191:** This sequence from Gabon was from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989–1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)]. Accession number L22952. X90924, VI685
 - 17) **GA1.ID#:** These 6 sequences are from Gabon. Two (G41, G135) are from 1988-1989 samples from patients with AIDS living in Franceville Gabon. VI685 is from a 1992 sample of an AIDS patient from the Libreville General Hospital. VI1076 is from a 1993 sample of an AIDS patient from the Libreville General Hospital. LBV2310 and LBV23 are from 1988 samples from asymptomatic individuals sampled from the general population. Method of proviral DNA isolation was not described. DNA was PCR amplified and cloned. One clone per isolate was sequenced. [Delaporte et al.(1996)]. Accession numbers X90914, LBV23; X90915, G135; X90917, G41; X90918, LBV2310; X90921, VI1076; X90924, VI685. See also subtypes C, D, F, G and O sequences from this same study.

Sequence Descriptions

- 18) **GH.D687:** A single sequence from an individual from Ghana. Virus was cocultured on PBMCs and the env gene was PCR amplified. Provided by Georg-Speyer Haus, Frankfurt, Germany (Dr. Ursula Dietrich). [Dietrich et al.(1993)]. Accession numbers L07652, X68407.
- 19) **GH2.ID#:** These 9 sequences are from Ghana. Subtypes D and an A/G recombinant were also detected in this study [Takehisa et al.(1997a)]. Pol gene sequence is available for GH9 (U67040). Accession numbers for subtype A are U67051–U67054, U67057–U67059.
- 20) **GH3.ID#:** These 13 sequences are from Ghana. Subtypes D and G were also detected in this study [Ishikawa et al.(1996)]. Two additional subtype A sequences are not included here (GH14 U67689 and GH17 U67690) because they were greater than 98% identical to sequences reported by Takehisa et al [Takehisa et al.(1997a)] and may be from the same patients, although labelled differently in the two studies (GH14 here 99% identical to GH15 by Takehisa; GH17 here 98.2% identical to GH16 by Takehisa). Accession numbers for subtype A are U67685–U67700.
- 21) **IN1.ID#:** These two entries are from 1992 dried blood spot samples from Vellore near Madras, in Tamil Nadu state in southern India. DNA was extracted from the blood spots and PCR amplified. The PCR products were directly sequenced. Samples came from previously identified HIV seropositive homosexual men. Other samples from the same region were all sub (see C_IN4.#). [Cassol et al.(1996)]. Accession numbers U53286 and U53291.
- 22) **IN2.GT6:** This sequence is from India. Seven other sequences from this publication were subtype C (see C_IN5.ID#). [Tsuchie et al.(1993)]. Accession number D13425.
- 23) **KE.K89:** This sequence is named “KENYA” in the GenBank entry, but is identified as K89 in the original manuscript. It is a Kenyan sequence from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989–1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)]. Accession number L22943.
- 24) **KE.KEN-ID#:** These 19 sequences were derived from patients who were part of a 1990–1992 cohort study of maternal risk factors in mother to child transmission, including 22 pregnant women and an infant from Kenya. The C2V3 region was sequenced. [Janssens et al.(1994c)]. Accession numbers for the entire set of 23 patients surveyed in this study: U12984–U13006.
- 25) **KE1.ID#:** These 6 sequences were derived from patients who were part of a May-June 1992 study of pregnant women from the Pumwani Maternity Hospital in Nairobi, Kenya. Viral RNA was concentrated from patient serum just prior to delivery, and the envelope C2-V3 region was amplified by RT-PCR. The PCR product was cloned and 20 clones from each patient were sequenced. Two other patients from this study had viral subtypes C and D. [Zachar et al.(1996a)]. Accession numbers U32658, U33763, U33764, U33766, U33767 and U34905.
- 26) **NL1.ID#:** These 13 sequences are from recent immigrants to The Netherlands from various countries. The first two letters of the ID# represent the two letter country code for the previous residence of the patient. The next two numerals represent the year of isolation. Viral RNA was prepared from patient serum and RT-PCR was used to amplify the V3 region of the env gene. The PCR products were directly sequenced. [Lukashov et al.(1996)]. Accession numbers L76877, GH902304; L76903, GH9401488; L76883, GH915200; L76913, GH9501283; L76893, GH929927; L76896, ZR9303337; L76870, RW890388; L76875, RW893568; L76905, TZ9401664; L76881, KE913514; L76891, UG928308; L76887, AO924646; L76889, TZ925825
- 27) **RU1.ID#:** These 2 sequences are from Russia. Bobkov et al. 1996 Unpublished. Accession numbers: U33098, IVA6; U33097, GAN1.
- 28) **RU2.ID#:** These two sequences are from patients living in Kaliningrad, Russia, [Leitner et al.(1996b)]. RU21 is a 40 year old male heterosexual, believed to have become infected in the Ivory Coast in 1988. RU24 is a 44 year old heterosexual male, believed to have become infected in Zaire. Sequences were determined by direct sequencing of PCR product from uncultured PBMC proviral DNA. Although RU24 is listed in the publication as unclassified subtype, this sequence clusters in phylogenetic analyses with SAS (U43171) and BJ193 (U61859) which are classified as subtype A. Because of the A-outlier nature of the RU24 env sequence, the authors also sequenced the gag P17 region of this sample, and found that it fell with subtype A (sequence not submitted to the databases). RU21 is a more typical subtype A. Accession numbers U69656 and U69658.

- 29) **RU3.IID#**: These 12 highly related sequences are from a set of 41 sequences from 12 IV drug users in Russia. Uncultured PBMC DNA was PCR amplified and cloned and individual clones sequenced. [Bobkov et al.(1997b)]. Although the sequences are similar enough to each other to suggest direct epidemiological linkage, no such linkage, other than the fact that they are all IV drug users, is indicated. Gag p17-24 and Env V4-V5 were also sequenced. Accession numbers U93611, U93612, U93614, U93616, U93618, U93620, U93622, U93624, U93627, U93629, U93631, U93633, U93635, U93636, U93637, U93638, U93642, U93643, U93645, U93646, U93647, U93648, U93650, U93651, U93655, U93656, U93657, U93658, U93659, U93660, U93661, U93665, U93666, U93668, U93671, U93673, U93675, U93676, U93677, U93678, U93679
- 30) **RW.564C**: This sequence represents 10 identical sequences generated from PCR amplified plasma RNA from one of three infants in a Dutch mother/infant study. Patient pair 564 was from Rwanda. A sample was collected from the infant at 30 months of age. Samples were also collected from the mother at 12 and 30 months after the birth. Mother sequences are not included in this consensus. [Mulder-Kampinga et al.(1993)], [Mulder-Kampinga et al.(1995)], [Lepage et al.(1996)], and [Kampinga et al.(1997)]. The child 564 Env sequence is from the entry with Accession number Z47881. Mother 564 sequences are in entries with Accession numbers Z47882–Z47902. Mother sequences are not included in this alignment. Gag gene sequences from mother/child pairs are also available in entries with accession numbers Z47903–Z47911, Z47912–Z47928, Z47929–Z47935 and Z47936–Z47950. The second mother/child pair was from the Netherlands, see G_NL.127C. The third mother/infant pair in this study was from the Netherlands, see B_NL.114C.
- 31) **RW.SF1703**: This sequence is from Rwandan isolate sf170, a biologically active clone reported to be macrophage-tropic. [Cheng-Mayer et al.(1988)]. See also U61870, which is not reported to be from SF170, but is greater than 99% identical to it. From this same isolate; 537 bases of the 5' LTR are in M66534, 619 bases of nef are in M81729 and 508 bases of tat and rev are in M66535. For env, the Accession number is M66533.
- 32) **RW1.W2RW-ID#**: These are six of seven sequences from asymptomatic individuals from Rwanda sampled in 1992. The seventh sequence (92RW009) has now been sequenced over the complete genome and found to be A/C recombinant. Thus it has been moved to the U_RW section. Consensus, PCR-clones, cell-culture DNA and RNA. These sequences were provided by the WHO Global Programme on AIDS Vaccine Development Study. The complete set of C2V3 region WHO sequences can be found in the April supplement to the Human Retroviruses and AIDS 1993 database. Relevant papers are: [De Wolf et al.(1994)]; [Osmanov et al.(1994)]; [Gao et al.(1994a)]. Accession numbers U08630–U08640, U08645, U08647–U08665, U08763–U08766, and U08793–U08794. One of these sequences may be mislabelled in the database; U08634 is labelled as patient 016, but is identical to sequences from patient 008. Sequences from samples 92RW020 and 92RW021 were greater than 98% each other, so only 92RW021 is presented here.
- 33) **RW2-ID#**: Nine consensus sequences from Rwanda. Saah, A. Unpublished 1994. Accession numbers U23216–U23373.
- 34) **RW3.PV#**: Bex,F. et al. Unpublished. These five sequences are from Rwandese patients with AIDS. The sequencing was done by the EEC Centralized Facility for HIV genome characterization, Georg-Speyer-Haus, Frankfurt, Germany. The complete envelope gene for PVP1 is available from a clone obtained after short-term co-culture on donor PBMCs. Two other shorter sequences of PVP1 env direct from patient PBMCs are also available. Accession numbers L07082–L07091. L07088 and L07089 were withdrawn from the databases by the authors, who felt they may represent PCR artifacts.
- 35) **RW4.ID#**: These 8 consensus sequences and 2 individual sequences, are from 7 infants and 3 mothers in a study of mother-infant transmission in Rwanda [Kampinga et al.(1997)], [Lepage et al.(1996)], [Mulder-Kampinga et al.(1995)] and [Simonon et al.(1994)]. Mother 566 was apparently infected with both subtype A and subtype C HIV-1, but the env regions from the child clones were all subtype A. See also C_RW1.ID#. Accession numbers for child 566 are Z76160–Z76161, Z76167–Z76168, Z76169–Z76176, Z76233–Z76248, Z76262–Z76273 and Z76717–Z76724; mother 730, Z76353–Z76362; child 564, Z76074–Z76083; mother 226, Z76046; child 538, Z76134–Z76143, Z76373–Z76382, Z76393–Z76412; child 074, Z75958; child 082, Z75998–Z76009, Z76650; child 081, Z75959–Z75968; child 618, Z76198–Z76207; mother 439, Z76048–Z76057, Z76064–Z76068 and Z76070.

Sequence Descriptions

- 36) **SE.H4:** This sequence is from an infant, born in Sweden to a woman who was believed to have been infected sexually in Uganda. The infant was born between June 1989 and August 1992 [Contag et al.(1997)]. Accession numbers U56274–U56283 and U56328.
- 37) **TZ.TAN-ID#:** These four sequences are from a set of 14 Tanzanian samples from symptomatic individuals, using serum samples taken in 1988 to generate PCR clones from viral RNA for sequencing. [Zwart et al.(1993)]. Accession numbers L01313, L01315–L01316, L01335, L01337–L01339.
- 38) **TZ2.ID#:** These two sequences were from patients at a clinic in Dar es Salaam, Tanzania. The individuals from which the virus was cultured showed clinical signs of AIDS, and the year of viral isolation was 1988. Viral cDNA was PCR amplified from donor PBMC, and one cloned PCR product per donor was sequenced. [Siwka et al.(1994)]. Accession numbers U12408, U12409.
- 39) **TZ3.ID#:** These 4 sequences are from the Mara region of rural northwest Tanzania. [Robbins et al.(1996)]. Subtype D was also found in this study. Accession numbers U61875–U61878.
- 40) **UG.1033:** This sequence is a consensus sequence of blood and CSF samples taken from a Ugandan patient 1033, CDC class IV-A. [Keys et al.(1993)]. Accession numbers Z23177, Z23182–Z23184, and Z23220–Z23223.
- 41) **UG.92UG037:** This sequence is from a complete genome PCR amplified from proviral DNA. The patient was a 31 year old asymptomatic female from Entebe, Uganda. [Gao et al.(1996b)]. Accession number U51190. See also U09124, U09127.
- 42) **UG.964:** A single sequence used in a study of the impact of sequence variation on the distribution and seroreactivity of linear antigenic epitopes. The sequence was derived from PCR amplified DNA from peripheral blood leukocytes. The patient was an asymptomatic individual from Uganda. [Pestano et al.(1995)]. Accession number U11599. See also B_US17.ID#, C_UG1.45, and D_UG7.ID#.
- 43) **UG.U455:** This sequence is from the 1985 Ugandan isolate U455; the complete genomic sequence is available. [Oram et al.(1990)]. The env ORF in this sequence is interrupted by an in-frame stop codon beyond the COOH end of the V5 region. Accession number M62320.
- 44) **UG.UG06:** This sequence is from blood collected from the Mulago Teaching Hospital in Kampala, Uganda. Viral RNA was harvested after 10-14 days of coculture with donor PBMCs and reverse-transcribed with AMV-RT. The env V3 region was pCR amplified and cloned. This sequence is from an individual clone. [Atkin et al.(1993)], [Pestano et al.(1993)]. Accession number M98503.
- 45) **UG1.W2UG-ID#:** Three sequences from asymptomatic individuals from Uganda in 1992. Consensus, PCR-clones, cell-culture DNA and RNA. These sequences were provided by the WHO Global Programme on AIDS Vaccine Development Study. The complete set of C2V3 region WHO sequences can be found in the April supplement to the Human Retroviruses and AIDS 1993 database. Relevant papers are: [De Wolf et al.(1994)]; [Osmanov et al.(1994)]; [Gao et al.(1994a)]. Accession numbers U08666–U08669, U08767–U08770, U08788–U08792, U08795 and U09125.
- 46) **UG2-ID#:** These 11 sequences are part of a set of sequences derived from 22 Ugandans who were attending an AIDS clinic, sampled in 1990. Consensus, PCR-clones, peripheral blood DNA. [Albert et al.(1992)]. Accession numbers M98902–M98905, M98908–M98910, M98914–M98917, M98919, M98924–M98928, M98938–M98941, M98946–M98966, and M98976–M98978.
- 47) **UG4.UG-ID#:** Two Ugandan sequences from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989–1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)]. Accession numbers L22957 and L22951.
- 48) **UG5.ID#:** These 8 sequences are from Gulu, northern Uganda. They are from direct sequence of PCR product amplified from uncultured PBMCs. Blood samples were drawn from 217 pregnant women attending a clinic in Gulu, northern Uganda. Ages ranged from 17 to 37 years. The 29 seropositive women (13.4% of the 217 tested) were all asymptomatic. [Buonaguro et al.(1995)]. Accession numbers U44878–U44880, U44882, U44883 and U44885–U44887. Two subtype D sequences were also found in this study (see D_UG8).

- 49) **UG6.ID#:** These 21 sequences are from Abidjan, Ivory Coast. No other information is yet available. Ellenberger D.L. unpublished 1997. Subtypes A, D and G were found for Ivory Coast patients in this set. Ugandan sequences of subtype A were also part of this set. Accession numbers AF000496, AF000497, AF000498, AF000499, AF000500, AF000501, AF000502, AF000503, AF000504, AF000505, AF000506, AF000507, AF000508, AF000509, AF000510, AF000511, AF000512, AF000513, AF000514, AF000515, AF000516
- 50) **ZR1.ID#:** These ten sequences are part of a set of 14 A and D sequences from women from Zaire; 8 were healthy, 4 showed minor signs of illness, and 2 had AIDS. PCR-direct, peripheral blood DNA. [Potts et al.(1993a)]. Accession numbers L19624–L19626, L19628–L19630, L19632–L19634, and L19636.
- 51) **ZR2.ID#:** These sequences are from Zaire. They are unpublished, by M. Reitz et al. Accession numbers U43097–U43100.

B Subtype

At this time we have included viral sequences from 1078 HIV-1 infected individuals associated with HIV-1 subtype B. The B subtype consensus sequence (B_CONSENSUS_97) generated from these sequences was based on the most common amino acid found in each position in an alignment of these sequences. Please note that none of the studies which have published sequences of only the V3 loop sequences are included here, as the DNA sequences were deemed too short for phylogenetic analyses. (For example, LaRosa G, et al., *Science* **249**:932–935 (1990) and Fouchier RAM, et al., *J. Virol.* **66**:3183–3187 (1992).)

- 1) **AR.21281**: This sequence is from direct sequencing of PCR product from uncultured PBMCs, from a 1993 sample from Buenos Aires, Argentina. The patient had AIDS and reported promiscuous heterosexual risk behavior. Two other samples taken from unrelated patients in 1993 were subtypes F and one was found to be a subtype B/F recombinant. [Marquina et al.(1996)]. Accession number U68525.
- 2) **AR1.ID#**: These 11 sequences are from Rosario, Argentina. A total of 24 patients from different risk groups visiting a clinic in Rosario were included in this study. Of the 14 sequences determined, 11 were found to belong to subtype B and 3 were found to belong to subtype F. DNA was extracted from whole blood and PCR amplified. PCR products were directly sequenced. Subtypes of all 24 patients were tested by HMA. [Campodonico et al.(1996)]. Accession numbers U37030, U37031 and U37034–U37042.
- 3) **AU1.ID#**: Put forth as evidence that coinfection by multiple HIV-1 strains can occur in vivo, these three consensus (MRC1, MRC2, and MRC3) come from an Australian homosexual male who had been infected by more than one sexual partner, and harbored three distinct strains of HIV-1 B. The authors also found recombinant sequences, not included here. The sequences were PCR amplified from plasma RNA and PBMC DNA. [Zhu et al.(1995)]. Accession numbers U16372–U16388.
- 4) **AU2.C18CG**: This sequence is one of a group relating to an Australian blood donor infected with HIV-1 and six Australian recipients, all of whom remain symptom free with normal CD4 counts 10 to 14 years after infection. [Deacon et al.(1995)]. Samples from only the donor, D36 (U37271), and two patients, C18 (U37267, U37270) and C98 (U37268, U37269), appear to have been sequenced. These sequences have deletions in the nef gene and in the region of overlap of nef and the U3 region of LTR. The authors point to the importance of NEF or the U3 region of LTR in determining the pathogenicity of HIV-1 and suggest this strain of HIV-1 as a possible basis for a live attenuated vaccine. The complete genome of the virus from recipient C18 is in the entry with accession number U37270.
- 5) **AU3.ID#**: In this analysis of transmitting and non-transmitting mothers and the infants to whom the virus was transmitted, the authors claim that differences in variability of the env V3 loop crown octapeptide (HIGPGRAF in this clone) were significantly correlated with vertical transmission. Sequences were determined by PCR directly from uncultured PBMCs and cloned PCR products. Only seven of the sequences are presented here: from infants, and nontransmitting mothers from which at least 250 bp was sequenced. 1089, 1063, 961 and JW are the infants. Accession numbers for transmitting mothers and their infants are: U66627–U66633, U66638–U66645 and U66650–U66653. Accession numbers for nontransmitting or indeterminate mothers are: U66625, U66626, U66634–U66637, U66646–U66649 and U66654–U66660. Database entries for many of these sequences contain "nnn" in error, the paper shows these positions as deletions, not unknown sequence. Nef sequences from the LW-JW mother-infant pair of long-term survivors were published in [Wang et al.(1997b)], [Wang et al.(1997a)], [Saksena et al.(1997)] with accession numbers U73339–U73369.
- 6) **BE.SIMI84** One of two cloned env sequences from a patient with AIDS from Belgium. A vaccinia construct that expresses this gene was created to vaccinate the patient's non-infected brother with the goal of immune therapy by adoptive transfer of lymphocytes. [Bex et al.(1994)]. Accession number L07421.
- 7) **BR.002con** This consensus sequence is from entries with accession numbers L35489–L35493. These sequences were provided by the WHO Global Programme on AIDS Vaccine Development Study. Ranjbar, S. et al. Unpublished (1994).
- 8) **BR.BZ** This sequence is from an individual in a Brazilian HIV cohort study. PBMC DNA was PCR amplified in two sequential rounds, and six cloned PCR products were sequenced on both strands. A single clone containing an uninterrupted envelope open reading frame was reported. [da Costa et al.(1995)]. Accession number U28336.

- 9) **BR1.ID#:** These 21 sequences represent the B env subtype sequences found among 22 Brazilian out-patients with varying degrees of disease progression. They are consensus sequences from cloned PCR products. PCR was performed on PBMC DNA. [Potts et al.(1993b)]. Accession numbers for 21 of the 56 clones from which consensus sequences were calculated: L19225–L19237, L19240–L19246 and L20963.
- 10) **BR2.W2BR-ID#:** These 13 sequences are from individuals from Brazil. They are consensus sequences from cloned PCR products. Some of the clones were from cell-culture DNA, and some from cell-culture supernatant RNA. These sequences were provided by the WHO Global Programme on AIDS Vaccine Development Study. The complete set of C2V3 region WHO sequences can be found in the April supplement to the Human Retroviruses and AIDS 1993 database. [De Wolf et al.(1994)], [Osmanov et al.(1994)], [Gao et al.(1994a)]. Accession numbers U08670–U08714, U08771–U08778, U08780–U08782, U08792, U08796, U08797–U08800, .
- 11) **BR3.RJ- or SP-ID#:** These 32 sequences came from the Brazilian cities Rio de Janeiro and Sao Paulo. The sequences that are very short, containing V3 loop fragments insufficient for phylogenetic analysis, are not included here (5 of the 26). The full set included 20 viral sequences of the B subtype, an F subtype and a B-F recombinant (see subtypes F and U). The year of isolation for the sequences ranged from 1990–1992 for Rio de Janeiro, and 1992 for Sao Paulo. The only two with CD4+ cells < 200 were RJ636 and RJ27. The CDC clinical class ranged from II-IV. DNA extracted from PBMCs of HIV infected individuals was amplified, and the PCR product was directly sequenced. [Morgado et al.(1994)] [Sabino et al.(1994c)] and [Sabino et al.(1996)]. More recent unpublished sequences from the same isolates are also included here. Accession numbers U00400–U00401, U00403, U00405, U00407–U00414, U00416–U00418, U00421, U00424–U00425, U00427, U08975, U31586, U31587 and U31589–U31591.
- 12) **BR4.BZ-ID#:** These 2 sequences are from seropositive Brazilian patients. Virus was cultured on donor PBMCs and proviral DNA was harvested from positive cultures. PCR was used to generate sequencing templates. [Louwagie et al.(1994)]. Accession numbers L22087 and L22088. The gag gene sequences from these same isolates are also available in L11752 and L11754. See also F_BR2.BZ-ID#.
- 13) **BR5.ID#:** These 10 sequences are from entries with accession numbers L19328–L19337. Bandea, C. I. Unpublished (1993).
- 14) **BR6.ID#:** These six sequences are from patients living in cities in Brazil (P3, Sao Paulo; P4, P6 and P7, Bahia; P8, Parana; P9, Rio de Janeiro) and sampled between 1987 and 1989. Sequences were determined from directly sequenced PCR products (except P6 which was a cloned PCR product), after coculture of patient PBMCs with donor PBMCs. [Couto-Fernandez et al.(1994)]. Accession numbers X78512–X78517.
- 15) **CA1.ID#:** These 19 sequences are from 19 different Vancouver, Canada homosexuals represented in 36 database entries by N. Michael et al. Accession numbers U52888–U52906, U53103–U53119. Patients A and B (U52888–U52904) were described in [Michael et al.(1997)] as a normal-progressor rapid-progressor pair, with patient A being the rapid progressor. Only patient A sequence (U52889) is presented here, as patient B sequences were closely related. The C patients were local controls, also homosexuals from Vancouver, who are not well described in the publication. Patient A sequences from U52901 and U52902 are greater than 99% identical to JR-CSF over their entire length, and U52904 has some regions of identity to JR-CSF. Another linked pair in this set included patients C108 and C118, of which only C108 is presented here. Patient A died of AIDS-related *P. carinii* pneumonia on October 6, 1995, almost exactly 10 months after experiencing symptoms of primary HIV infection. Patient A was homozygous for for an HLA-DR1 allele previously found to be associated with rapid progression. Patient A never seroconverted for HIV, despite high viral load and the ability to seroconvert for hepatitis B after vaccination in 1990.
- 16) **CH1.ID#:** These 19 sequences came from 24 individuals living in Geneva, Switzerland who were recently infected at the time of blood drawing. Samples were collected between January 1988 and September 1993. Sequences were determined directly from PCR products of uncultured PBMC DNA or serum cDNA. All subjects were asymptomatic, 19 subjects had p24 antigen levels ranging from 5 to 6,357 pg/ml and 5 subjects had no detectable p24 antigen. Two subjects were epidemiologically linked (K11 and K16) so only one of those two is presented here. Two other individuals showed identical DNA sequences over the entire V3 region (K53 and K77) so only one of them is presented here. Three other individuals (K13, K42 and P4) had sequences nearly identical to the LAI (IIIB) laboratory strain of HIV. Although the authors

Sequence Descriptions

- are convinced that these are not contaminants, and that a IIIB-like strain of HIV is circulating in Geneva, they are not included in this alignment. [Antonioli et al.(1995)]. Accession numbers U10957–U10980.
- 17) **CI.CI-22:** A single B subtype sequence from a set of 13 isolates from individuals from Abidjan, Cote d'Ivoire. CI-22 was symptomatic. The C2V3 region is part of a 900 bp fragment that was sequenced for each individual. Samples were collected between May 1990 and Sept. 1991. Virus was cultured with donor PBMCs, nested PCR amplified, 3 clones were sequenced, and the consensus of those clones is presented here. [Janssens et al.(1994a)]. Accession numbers X72040–X72042.
 - 18) **CM.CA5:** A single B subtype sequence from a set of 17 sequences from a very diverse set of isolates from Yaounde and Douala, Cameroon. The sequences were derived from asymptomatic and symptomatic HIV infected individuals, specifically, patient CA-5 was asymptomatic. Virus was isolated by culture with donor PBMCs, and nested PCR amplified. A single clone was sequenced representing each HIV-1 isolate. [Nkengasong et al.(1994)]. Accession number X80452.
 - 19) **CN1.ID#:** These 54 sequences are from the Yunnan Province, China. No information is yet available. Unpublished 1995, Y. Shao and H. Wolf. Several of these sequences (U20009, U20012, U20013, U20018, U20023, U20024) are greater than 96% identical to the SF2 strain of HIV-1 (see B_US.SF2). Accession numbers U20001–U20054.
 - 20) **CN.1798:** This sequence is from a dried blood spot collected in 1992 from the spouse of an IV drug user in China. DNA was extracted from the blood spots and PCR amplified. The PCR products were directly sequenced. [Cassol et al.(1996)]. Accession number U53316.
 - 21) **CU.94CU053:** This sequence is from a bisexual male, most probably infected via heterosexual contact in 1992, in Cuba. Virus was isolated in 1994, 2 years after seroconversion, by cocultivation of patient PBMCs with donor PBMCs. This isolate exhibits a rapid/high, syncytium-inducing phenotype. [Gomez et al.(1996)]. Accession number U48855.
 - 22) **CY1.HO#:** These sequences are from samples, like others in this study (see also subtypes A, C, F and I), which were collected in February 1994 from the AIDS clinic in Nicosia, Cyprus. PBMC DNA was PCR amplified and cloned. Individual clones were sequenced. Patient 04 was a 24 year old man, asymptomatic with a CD4 count of 516, who had lived abroad, and had been seropositive for at least 4 years. Patient 11 was a 29 year old homosexual man, symptomatic with a CD4 count of 277, and seropositive for at least 7 years. Patient 21 was a 38 year old bisexual man, asymptomatic with a CD4 count of 743, who was infected in Greece and seropositive for at least 4 years. Patient 25 was a 34 year old heterosexual man, asymptomatic with a CD4 count of 650, who had lived in the U.S. and was seropositive for at least 6 years. Patient 27 was a 20 year old homosexual man, asymptomatic with a CD4 count of 709, infected in Cyprus and seropositive for at least 2 years. Patient 28 was a 39 year old homosexual woman, asymptomatic with a CD4 count of 430, infected in Cyprus and seropositive for at least 1 year. Patient 29 was a 49 year old heterosexual man, asymptomatic with a CD4 count of 420, infected in Cyprus and seropositive for at least 2 years. Patient 39 was a 37 year old heterosexual man, asymptomatic with a CD4 count of 470, had lived in Greece and was seropositive for at least 5 years. Patient 40 was a 29 year old heterosexual woman, symptomatic with a CD4 count of 92, who had lived in the U.S. and was seropositive for at least 6 years. Patient 43 was a 36 year old homosexual man, symptomatic with a CD4 count of 396, who had lived in the U.K. and Greece and had been seropositive for at least 6 years. Patient 45 was a 32 year old heterosexual man, asymptomatic with a CD4 count of 453, who was infected in Cyprus and seropositive for at least 1 year. Patient 46 was a 32 year old heterosexual man, whose partner had died of AIDS, asymptomatic with a CD4 count of 107, had lived in the U.K. and was seropositive for at least 4 years. Patient 48 was a 22 year old hemophiliac man, asymptomatic with a CD4 count of 276, who had been seropositive for at least 11 years. Patient 50 was 32 year old homosexual man, whose partner had AIDS, asymptomatic with a CD4 count of 315, who had been seropositive for at least 1 year. Accession numbers U28663, U28666 (04); U28664 (11); U28667–U28671 (21, 25, 27, 28, 29); U28675, U28676 (39, 40); U28678 (43); U28680–U28682 (45, 46, 48); U28684 (50).
 - 23) **CZ.BTSPR:** This sequence is from a 32 year old homosexual man from Prague, Czech Republic. It was included as part of a study of HIV-1 sequences from the neighboring Slovak Republic. DNA from cocultured PBMCs was PCR amplified and the PCR product cloned. Eight clones were sequenced from each patient, although only one sequence is presented in the publication and in the database. It is not stated whether each single sequence is a consensus of the eight clones or a single clone. [Zachar et al.(1996b)]. Accession number U53195.

- 24) **DE.D31:** This sequence is from isolate D31. [Kreutz et al.(1992)]. It has never been well described, it is only shown as HIV1-D31 in figure 3 of the paper. The complete genome has been sequenced. Accession number U43096.
- 25) **DE.HAN:** This sequence is from an infectious clone from the German isolate DE.HAN-2. [Sauermaun et al.(1990)]. Isolate HAN2 was isolated from a 39 year old homosexual German patient with AIDS related complex in 1986. This patient died from complications of AIDS in 1987. HAN2 was highly cytopathic in T cell line MT-2 it was able to productively infect MT-4, H9 or Jurkat cell lines. Genomic DNA from infected MT-2 cells was used to prepare a lambda phage genomic library. Two full-length clones, HAN2/2 and HAN2/3 were purified. HAN2/3 was used for DNA sequencing. Accession number U43141.
- 26) **DE.Serocons:** This sequence is a consensus sequence from 7 hemophilia patients who all received the same lot of beta-propiolactone and UV-light inactivated clotting factor in Bonn or Goetingen, Germany, from November 1989 to March 1990. The virus and the patients have been extensively studied over time, since initial seroconversion. The sequences which were combined to create the consensus were from proviral DNA from cultured PBMCs, PCR amplified and cloned. [Kasper et al.(1994)]. Accession numbers S76444 and S76446.
- 27) **DE1.ID#:** These 7 sequences are from a Neurology thesis by I. Weber of Rostock, Germany. They are from blood and CSF specimens from 6 patients. For each of the patients, phylogenetic analysis showed that blood and CSF sequences were more similar to each other than to other database sequences. For one patient, one of the two blood sequences was different enough from another blood and CSF pair to be included here. Accession numbers Z78482, Z78485-Z78493.
- 28) **DE2.ID#:** These 4 sequences are from a set containing 15 Dutch homosexuals, 19 Dutch intravenous drug users, 2 German homosexuals, 2 German intravenous drug users, 5 Scottish homosexuals and 6 Scottish intravenous drug users. The sequences were used in a study of HIV-1 vpr, vpu, and env V3 regions and how they vary between risk groups. [Kuiken et al.(1996b)]. Accession numbers Z68529, Z68530, Z68537 and Z68538.
- 29) **ES.ID#:** These 36 sequences are from 41 patients sampled in Madrid, Spain between 1985 and 1991. Proviral DNA was extracted from uncultured patient PBMCs and the C2V3 region was PCR amplified. The PCR products were directly sequenced. Two of the sequences reported in this set (D22-28 and D22-48) were 99.5% identical to the LAI (IIIB) lab strain of HIV-1 and are not included here. 3 other groups of sequences had members that were greater than 98% identical to each other (R1, R2 and R3; THF13-2, THF12-24; S1, S4) and only one of each of them is presented here. [Quinones-Mateu et al.(1996)]. Accession numbers U40533-U40552 and U45286-U45307.
- 30) **ES.S61:** This sequence is from a 1989 blood sample from a 4 year-old boy from Madrid, Spain with CDC stage P2CD2 disease. Virus was cocultured on PBMCs and MT-2 cells prior to sequencing. The SI/NSI phenotype of this isolate on MT-2 cells was traced to a single amino acid change in the V3 loop [Sanchez-Palomino et al.(1993)] and [Olivares et al.(1997)]. Accession numbers L04604, L04605, L04606 and L05659.
- 31) **FR.J91:** This sequence is from one of the JBB clones from the French patient Bru. [Wain-Hobson et al.(1991)] and [Guo et al.(1991)]. Accession numbers X57449-X57459 and X57461.
- 32) **FR.LAI:** This sequence is from the French isolate LAI (formerly BRU) which is also referred to as IIIB. [Wain-Hobson et al.(1985)]. Also see: [Alizon et al.(1986)], [Lukashov & Goudsmit(1995)] and [Wain-Hobson et al.(1991)]. Accession numbers K02013, L23090-L23103, X01762, L48380-L48399, M64178-M64223, M64406-M64415 and M64768-M64775. Other sequences which are of this type include: PV22, K02083; MFA, M33943 [Stevenson et al.(1990)]; F12, Z11530; BH8, K02011; BH10, M15654; TH4, L31963; MCK1, D86068; PM213, D86069; F12CG, Z11530; and HXB, K03455, M38432, M64775 and M14100. The variation of the IIIB isolate in culture was studied by [Lockey et al.(1996)], Accession numbers U54647, U54649, U54651, U54653, U54655, U54657, U54659, U54665, U54667, U54681, U54683, U54685 and U54689. The variation of IIIB/LAI in 9 years of infection in a chimpanzee has been studied by Fultz et al. unpublished, Accession numbers U56866-U56883 and U56888-U56899. The IIIB/LAI isolate of HIV-1 has also been extensively studied in cases such as the infected lab worker. See for example [Jr et al.(1994)], [Pincus et al.(1994)] U12030-U12055. The tropism of isolates from the lab worker for primary PBMCs and failure to grow in T-cell lines was localized to the V3-loop by Lishan Su et al. [Su et al.(1997)]. Recombinant virus pNL4-3, with envelope

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- from LAI(BRU) and gag-pol from NY5 has also been studied: [Adachi et al.(1986)] Accession number M19921, [Duensing et al.(1995)] Accession number L42371 and [Salminen et al.(1995)] Accession number U26942. Other database entries with IIIB-LAI sequences can be found in the patented sequences section of GenBank, in the cloning vector section, and in the primate section (for example U19867, A00647, A04321 and M18404).
- 33) **FR1.ID#:** These 4 sequences are from Toulouse, France. In this study, 4 mother-infant pairs were followed during pregnancy and after birth. The inter- and intra-patient sequence similarities of this set of 308 sequences has been controversial, because some infant sequences were identical to sequences from other mothers. For purposes of this V3 section, only one sequence from each of the 4 infants is presented here. [Briant et al.(1995)], [Korber et al.(1995)] and [Jr et al.(1996)]. Database entries for all 308 sequences are found with accession numbers U24717-U24999 and U25001-U25025.
 - 34) **FR2.ID#:** These 20 sequences are from members of the French military who are for the most part believed to have been infected while deployed outside of France (Chad, Djibouti, Gabon, Guyana, Mayotte and Cameroon). An additional sequence (FRMP040, U58787) was listed as subtype C in the paper, but clustered with subtype B in analysis done at the HIV Database and it has been listed as subtype unclassified until more information is available. Other sequences from this study were subtypes A, C, E, F, and unclassified. [Lasky et al.(1997)]. Accession numbers for subtype B were U58808–U58826 and U58777.
 - 35) **GA.OYI:** This sequence is from the Gabonese isolate OYI (designated elsewhere as isolate 397), isolated from a healthy HIV-1 infected individual. GA.OYI appears to have been the first viral sequence from Africa that phylogenetically clustered with North American viruses. [Huet et al.(1989)]. Accession number M26727.
 - 36) **GB.AIT:** This sequence is from an individual at the time of seroconversion. Proviral DNA was extracted from PBMCs from a patient who was viraemic and had an equivocal HIV-1 antibody status, and the env V3 region was PCR amplified. The PCR products were cloned and the DNA sequence determined for 15 clones. These data showed that the V3 region contained only limited sequence heterogeneity with a major variant (shown here) accounting for 66% of the protein quasispecies present. [Ait-Khaled & Emery(1993)]. Accession number S69598.
 - 37) **GB.CAM1:** This sequence is from the British isolate CAM1. McIntosh A, and Karpas A, Thesis (1991), Cambridge University, England. Accession numbers D10112, D00917.
 - 38) **GB.Man** This sequence was PCR amplified from the 1959 "Manchester sailor" kidney tissue. The sequence of the complete genome is available and clusters with subtype B contemporary HIV-1 sequences. [Zhu & Ho(1995)]. Accession number U23487.
 - 39) **GB.V-ID#:** A set of six sequences from a study of hemophiliacs from Scotland who were originally thought to have been infected by the same batch of factor VIII. (ScV12 is a sequence from a hemophiliac from the U.S., included as a control). All are consensus sequences of multiple direct PCR sequences obtained from limiting dilution of PBMCs. The Scottish hemophiliacs were infected in 1984 and the PBMCs were obtained for analysis in 1989. Although the samples were potentially related, they were deemed sufficiently divergent in this region for inclusion in this set. [Simmonds et al.(1990)], and [Balfe et al.(1990)]. Accession numbers M61327–M61346 and M61391–M61407. Database entries with accession numbers M84240–M84317 are more sequences from patient 82, taken over the period from 1984–1991. [Holmes et al.(1992)]. Database entries with accession numbers L13488–L13497 are also from these patients [Zhang et al.(1993)], as are U58393–U58465 [Cleland et al.(1996)], [Leigh Brown & Cleland(1996)], [Ludlam et al.(1985)].
 - 40) **GB1.CPHL1:** This is a consensus from the British isolate 93–08020, clones 1, 4, 7, 18, 19 and 43. It was referred to as 93–08020 in [Arnold et al.(1995c)] and was isolated from the patient referred to as CPHL1 in [Arnold et al.(1995a)]. CPHL1 is a surgeon and CPHL2 was a patient of his in 1986, approximately 7 years prior to sampling for this study. Because sequences from CPHL1 and CPHL2 are no more similar to each other than to sequences from the general population, transmission cannot be concluded, and both sequences are included in this alignment. Accession numbers U21100 (clone 1) and U23112–U23116 (clones 18, 19, 4, 43 and 7 respectively).
 - 41) **GB2.CPHL2:** This is a consensus from the British isolate 93–17305, clones 3, 11, 18 and 25 [Arnold et al.(1995c)]. It was isolated from the patient referred to as CPHL2 in [Arnold et al.(1995a)]. Accession numbers U23117–U23120 (clones 11, 18, 25 and 3 respectively).

- 42) **GB3.ID#**: The CPHL7 sequence is a sequence from the British isolate 94–24612, clone 13 [Arnold et al.(1995c)]. It was isolated from the patient referred to as CPHL7 in [Arnold et al.(1995a)]. Accession number U23126. U23127 is a second clone from this same isolate. Sequences from three other patients epidemiologically linked to CPHL7 (CPHL6, accession numbers U23130–U23132; CPHL8, U23128–U23129; CPHL9, U23133–U23135) are not included in this alignment. The 4995 sequence is from entries with accession numbers U23136–U23138.
- 43) **GB4.ID#**: These eight sequences are from British isolates from St. Bartholomew’s Hospital, London (M23470, M26864, M30156, M37677 and M37658) and Hammersmith Hospital, London (AC, JB and WB). Sequences were determined from cloned PCR products from PCR amplified DNA from either cocultured (M23470 and M26864) or uncultured (M30156, M37677, AC, JB and WB) patient PBMC proviral DNA. [Douglas et al.(1996)]. Complete envelope gp160 sequences were determined for at least one clone from each patient. Ugandan samples also sequenced in this report were subtypes D or D/A recombinant. Accession numbers for London samples were U36859–U36864, U36869, U36870, U36872–U36880 and U36882.
- 44) **GB5.ID#**: These 11 sequences are from Scotland. They are part of a set containing 15 Dutch homosexuals, 19 Dutch intravenous drug users, 2 German homosexuals, 2 German intravenous drug users, 5 Scottish homosexuals and six Scottish intravenous drug users, from which regions of vpr, vpu and env were sequenced. The authors found consistent differences in the sequences between the homosexuals and IV drug users. Only 34 of the 47 patients’ sequences are reported in the publication. [Kuiken et al.(1996b)]. See also B_NL12 and B_DE2 sets.
- 45) **GM.GM6**: A sequence from Gambia, as yet unpublished. Bobkov et al. 1996 unpublished. Accession number U33101. See also Gambian sequences of subtypes C and J.
- 46) **HT.RF**: This sequence is from the full-length lambda clone HAT-3, from Haitian isolate RF. RF is from a 28 year old Haitian male who had moved to the United States at age 25, in 1980. He had no history of IV drug use, homosexuality or blood transfusions. In October 1983 he had 20 lb weight loss, giardia with diarrhea, thrush, and diffuse lymphadenopathy. His CD4/CD8 ratio was 0.08. He died in December, 1983. Primary culture from a November 1983 blood sample was co-cultured on HUT-78 cells. [Jr et al.(1992)] [Starcich et al.(1986)] [Popovic et al.(1984)]. Accession numbers M17451 and M12508.
- 47) **HT1.D-ID#**: These seven sequences are from Haitians, and are part of a set of sequences generated as part of the DAIDS variation program in the laboratories of Dr. Beatrice Hahn at the University of Alabama, and Dr. Marcia Kalish at the Centers for Disease Control, Atlanta, GA. Except for D2HA590, the full gp160 was sequenced from clones derived from expanded culture stocks. D2HA590 is a direct sequence from PCR amplified DNA from expanded culture. The sequence ID numbers are abbreviated, for example D2HA590 can be read as DAIDS sequence (D), isolated in 1992 (2), Haitian (HA), patient 301590 (590). Full length env for some of these have been expressed [Gao et al.(1996a)]. Accession numbers: U08441–U08447, U04900. Both U08441 and U08442 are sequences from patient HT1.D1HA651 and are identical over the region of interest. Accession numbers for additional clones derived from these patients: U04901–U04906.
- 48) **HT2.H-ID#**: These 25 sequences are from Haitians. All sequences were PCR amplified from the infected individuals PBMCs, and this set includes direct sequences of PCR amplification products, consensus sequences of multiple clones of PCR products plus one direct sequence, and single clones of PCR products. Full length env for some of these have been expressed [Gao et al.(1996a)]. These sequences were provided by the Centers for Disease Control, Atlanta, GA USA (Dr. Chin-Yih Ou), and John Hopkins University School of Hygiene and Public Health, Baltimore, MD USA (Dr. Neal Halsey), and the Centers for Development and Health, Complexe Medico Sociale de la Cite Soleil, Port-au-Prince, Haiti (Dr. Reginald Boulos). Accession numbers L07145–L07161, L07163–L07165, L07167–L07207, L07209–L07239, L07241–L07246, U08441–U08447.
- 49) **ID.1701**: This sequence is from a dried blood spot collected in 1992 from a male homosexual patient in Indonesia. DNA was extracted from the blood spots and PCR amplified. The PCR products were directly sequenced. [Cassol et al.(1996)]. Accession number U53317.
- 50) **ID1.ID#**: These 7 sequences are from a set of 14 sequences from Indonesia [Porter et al.(1997)]. Accession numbers U68195–U68201. Subtype E was also identified in 7 other samples from Indonesia in this study. PCR products were directly sequenced from either uncultured PBMC DNA or cocultured PBMC DNA.

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- 51) **IN.IND9**: This sequence was from a heterosexually infected patient from New Delhi, India. DNA was isolated from cocultured PBMCs after one week of culture. PCR product was cloned and a single clone was sequenced. [Tripathy et al.(1996)]. Accession number U31364. See also C_IN3.ID#.
- 52) **IN1.ID#**: These four sequences were isolated in Hyderabad, Andhra Pradesh, in southern India. The C2V3 region of env was amplified by nested priming from DNA from PBLs from fresh blood samples. Date of sampling and health status of HIV-1 infected individuals is unknown. [Baskar et al.(1994)]. Accession numbers L29091–L29094.
- 53) **IT.ID#**: These two sequences are consensus sequences from 4 clones each. They were obtained from PCR-amplified proviral DNA from Langerhans cells from skin patches from a deceased AIDS victim in Italy [Sala et al.(1995)]. Small V1-V2 region sequences and V3-loop sequences from the same skin samples were published in [Sala et al.(1994)]. Entries with accession numbers U20670–U20677 were used here. Entries with accession numbers Z34376–Z34458, Z34470–Z34513 and Z34515 were V1-V2 and V3-loop sequences from the same patient.
- 54) **IT.PD**: This sequence is from the thymus of a 26 year old male with CDC stage III disease. Proviral DNA was PCR amplified from genomic DNA extracted from patient thymocytes, and the PCR product was directly sequenced. A V3 sequence from PBMC proviral DNA was also determined, as were gp41 sequences from both thymus and blood. [Calabro et al.(1995)]. Accession numbers U09254–U09255.
- 55) **IT.RM1**: This sequence is from a patient from Milan, Italy who was homozygous for the delta-32 deletion in CCR5 [Balotta et al.(1997b)]. Accession number U92491.
- 56) **IT1.ID#**: These 10 sequences are from infants infected in utero. The sequences came from PCR amplified DNA of uncultured PBMCs, PCR amplified DNA of cultured PBMCs, or from RNA from serum collected at or shortly after delivery. [Scarlati et al.(1993)]. Accession numbers L08277–L08286. Sequences from the mothers of these infants are also available in entries with accession numbers L08287–L08372.
- 57) **IT2.ID#**: These 3 sequences are from unpublished sequences in entries with accession numbers X92424–X92426.
- 58) **IT3.ID#**: These 12 sequences are consensus sequences from 12 individual patients in a study of long term non-progressors and rapid progressors, from Milan, Italy [Balotta et al.(1997a)]. Accession numbers U95381–U95497.
- 59) **JP.ETR**: A Japanese isolate from long-term cell culture with a truncated env gene, due to a point mutation of a CAG codon to a TAG stop codon. [Shimizu et al.(1992)]. Accession numbers D12582, D01205–D01207, D12584 and D12571.
- 60) **JP.GUNA**: A Japanese 1989 isolate HIVGUN, infectious to T cells, was adapted to grow in fibroblast-like BT cells. A single amino acid change at the tip of the V3 loop was shown to be responsible for the change in tropism, GPGR to GSGR. [Takeuchi et al.(1991)]. Accession number M59192.
- 61) **JP.JH32**: This is a sequence from a lambda clone of Japanese isolate JH3, which was isolated in 1986 from a 10 year old Japanese Hemophiliac. [Komiya et al.(1989)]. Accession number M21138.
- 62) **JP.JH23A**: This sequence is from a Japanese patient dually infected with HIV-1 subtypes B and E [Xin et al.(1995a)]. Accession number D67089. See also D67090, E_JP.JH23B.
- 63) **JP.KM03**: This sequence is from a 28 year old hemophilia B patient with CDC stage IV disease and T-cell count of 20, living in Japan. The authors [Hattori et al.(1991)] also sequenced the V3 region from 28 other Japanese individuals, but only the V3-loop amino acid sequence is available from the other patients. Accession number S70936.
- 64) **JP.JNIH1M**: This sequence is from a Myanmarese (Burmese) individual living in Japan, obtained by direct sequencing of PCR-amplified proviral DNA from peripheral blood mononuclear cells. [Weniger et al.(1994)]. Accession number L32084.
- 65) **JP1.ID#**: These 10 sequences are from 12 patients with varying rates of disease progression. Patients 1 and 2, both extremely rapid progressors who died of AIDS within 8 months (patient 1) and 3 years (patient 2) of infection by sexual contact in 1991. These two shared very similar sequences and were suspected to be epidemiologically linked, so only patient 2 sequence is presented here. Patients 8, 9, 15, 19, 47, 63 and 65 were infected between 1983 and 1985 by contaminated blood products. Patients 20 and 28 were infected by sexual contact. Sequences were determined by either RT-PCR from plasma viral RNA or PCR from uncultured PBMC proviral DNA. PCR products were cloned prior to sequencing. Each of these 11 sequences is a single clone, taken as representative of that patient. [Shioda et al.(1997)]. Accession numbers AB002829–AB002974, AB002988–AB003019. Patient 43 was infected with subtype E.

- 66) **KP.Kr111** This sequence is from an unpublished database entry with accession number X93580.
- 67) **LT.LIT#:** These 5 sequences are from Lithuania. [Lukashov et al.(1995)]. Accession numbers: L38417, LIT18A; L38412, LIT11A; L38419, LIT21A; L38416, LIT17A; L38420, LIT17A.
- 68) **MM1.ID#:** These two sequences are from Myanmarese (Burmese) individuals living in Myanmar, obtained by direct sequencing of PCR-amplified proviral DNA from peripheral blood mononuclear cells. [Weniger et al.(1994)]. Patient 02 is a male IV drug user, and 05 is a female prostitute, both were from Mandalay. Accession numbers L32088, L32089.
- 69) **MM2.ID#:** These 5 sequences are from dried blood spots collected in 1992 from a male STD patient (1782), a female prostitute (1739), and 3 IV drug users (1748, 1755 and 1763) in Myanmar. DNA was extracted from the blood spots and PCR amplified. The PCR products were directly sequenced. [Cassol et al.(1996)]. Accession numbers U53304–U53308.
- 70) **MY1.ID#:** These 11 sequences are from IV drug using prisoners in a prison in Kuala Lumpur, Malaysia. PCR products amplified from uncultured PBMCs were directly sequenced. [Brown et al.(1996)]. This report also included subtypes C and E in Malaysia. Accession numbers U65538–U65548.
- 71) **NL.114C** This consensus sequence represents sequences generated from PCR amplified plasma RNA from one of three infants in a Dutch mother/infant study. Samples were collected from the infant at birth, at 6 weeks and at 9 months of age. Samples were also collected from the mother before birth, at birth and after birth. Mother sequences are not included in this consensus. [Mulder-Kampinga et al.(1993)]. [Mulder-Kampinga et al.(1995)]. Infant 114 is from Accession numbers L21111–L21153. Mother 114 sequences are from Accession numbers L21028–L21110. Infant 127 sequences are from Accession numbers Z47817–Z47832. Mother 127 sequences are from Accession numbers Z47833–Z47880. Gag gene sequences from mother/child pairs are also available in the entries with accession numbers Z47903–Z47911; Z47912–Z47928; Z47929–Z47935; Z47936–Z47950. The second mother/child pair was also from the Netherlands, see G_NL.127C. The third mother/infant pair in this study was from Rwanda, see A_RW.564C.
- 72) **NL.168:** This is a consensus sequence of 3 clones after culturing in PBMC. The isolate was originally from an AIDS patient in Amsterdam. [Wrin et al.(1995)]. Accession numbers U15030–U15032. A V3-loop (105 bp) segment from the original isolate has been previously reported. [Fouchier et al.(1992)]. Accession number L06694.
- 73) **NL.wolfson:** This is a consensus sequence from 6 patients infected with the same unit of blood in Amsterdam. [et al(1992)]. Accession numbers U04530–U04537.
- 74) **NL.X1con:** This is a consensus sequence of 10 clones from a recipient in a donor-recipient study. Sequences from donor Y and recipient X2 are also part of this study, but are not included here. [Cornelissen et al.(1995)]. Accession numbers Z47505–Z47514 are from X1. Other new sequences analyzed in this paper include Z47411–Z47540. Sequences M91828–M91838 (donor H and recipient O, referred to as patients A14 and A13, respectively in [Wolfs et al.(1992)] see B_NL1.A13) were also re-analyzed in this study.
- 75) **NL1.ID#:** These nine sequences are part of a study of presumed donor-recipient pairs from an HIV-1 transmission study conducted in the Netherlands. If pairs were extremely close or identical, only the recipient is included here. Recipient samples were from the first sample to be antibody positive, and are numbers 1,3,5,7,9, and 13. These sequences are consensus sequences of multiple clones from PCR amplified serum RNA. [Wolfs et al.(1992)]. Recipient A1 was also studied as patient H1 in [Kuiken et al.(1993)] and so is not included here (see B_NL4.H1). Accession numbers M91819–M91827, M91829, M91831–M91832, M91839, M91857–M91870, M91872, M91874, M91881–M91884, M91891, M91893, 91895–M91908, M91910, M91911–M91926. Number 13, and the donor were also analyzed in [Cornelissen et al.(1995)].
- 76) **NL2.ID#:** These two sequences are part of a Dutch study of mutations occurring over a five year period (starting in 1985) in two patients. Serum RNA was PCR amplified and multiple clones were sequenced. The consensus for each patient is shown. [Wolfs et al.(1991)] and [Zwart et al.(1992)]. Accession numbers M74591–M74684.
- 77) **NL3.NET-ID#:** These six consensus sequences from the Netherlands are samples from AIDS patients, using serum samples to generate PCR clones from viral RNA for sequencing. [Zwart et al.(1993)]. Accession numbers L01282–L01297.
- 78) **NL4.ID#:** These 74 sequences represent a study of early seroconverters from different times with different risk factors for transmission during the AIDS epidemic in the Netherlands. The year the sample was taken

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- is indicated in the last part of the sequence name. The risk group of the individual from whom the virus is derived is indicated in the first letter of the sequence name (I, B and H for IVDUs, hemophiliacs, and homosexuals, respectively). Viral genomic RNA from sera was PCR amplified and amplification product was directly sequenced. [Kuiken et al.(1993)]. Accession numbers Z29219–Z29225, Z29256–Z29258, and Z29262–Z29325.
- 79) **NL5.ID#:** These 18 consensus sequences are from a study of patients with, and without, AIDS dementia complex (ADC) in the Netherlands. Not all patients were from the Netherlands. Samples were collected between 1986 and 1992. Viral genomic RNA from sera and/or cerebral spinal fluid was reverse transcribed and PCR amplified and clones were sequenced. [Kuiken et al.(1995)] Accession numbers Z37531–Z37534, Z37734–Z37963, Z37970–Z37971
- 80) **NL6.ID#:** 16 is a consensus sequences of four sequences used in a study of HIV-1 envelope-mediated syncytium formation. The consensus represents four clones from one patient, two clones of the consensus are SI and two are NSI. 320 is a single SI clone. The sequences were derived from PCR amplified DNA from provirus cultured in PHA-stimulated PBMCs [Andeweg et al.(1992)]. Accession numbers L08655–L08662. Complete genomes from patient 320 SI and NSI strains are found in entries with accession numbers U34603 and U34604 [Guillon et al.(1995)], *tat* and other genes from patient 320, some of the same isolates, are found with Accession numbers M64489–M64492 [Groenink et al.(1992)].
- 81) **NL7.ID#:** These two consensus sequences are from sets of sequences (Accession numbers U05797, U13240, U13241, U13243–U13247 for consensus 537 and U13242, U13248–U13252 for 1058) used in a study on the dynamics of HIV sequence changes in vivo and the utility of heteroduplex analysis. Both sequences were derived from PCR amplified PBMC DNA. Consensus 537 represents a set of sequences from a Dutch patient with a relatively stable CD4+ cell count at 62 months post-seroconversion. Consensus 1058 represents sequences from another Dutch patient whose CD4+ cell count at 73 months post-seroconversion was declining faster than 537's. [Delwart et al.(1994)]. See also US10.ID#.
- 82) **NL8.672** This is a sequence from a patient early in infection, before, or around the time of seroconversion. Three other patients studied in this paper (537, 1058 and 594), had previously been reported. See B_NL4.594, B_NL7.1058con and B_NL7.537con. [Shpaer et al.(1994)] and [Delwart et al.(1995)]. Accession numbers U23651–U23663, U23667, U23670. See also US11.ID#.
- 83) **NL9.ID#:** These 19 sequences are from a cohort of homosexual men living in Amsterdam who seroconverted between 1985 and 1989. The sequences are from direct sequencing of PCR products after RT-PCR from serum RNA. Samples for h1, h139, h491, h1140 and h1234 were obtained at seroconversion. Samples for h138 and h1136 were obtained 12 months and 29 months after seroconversion respectively. The sequence for h320 was obtained from proviral DNA, 2 months after seroconversion. [Zwart et al.(1994a)] and [Zwart et al.(1994b)]. Accession numbers L25884 and U05786–U05808. More sequences from this same cohort of men were published in [Kuiken et al.(1996b)] and [Kuiken et al.(1996a)] Accession numbers Z67875–Z67876, Z67885–Z67939, Z67941–Z67960, Z68015–Z68089, Z68109–Z68110. Some *vpr*, *vpu* and other region sequences are available from some of these patients as well. Some of the database entries for this set appear to be duplicates of sequences reported in other studies.
- 84) **NL10.ID#:** These 13 sequences are from recent immigrants to The Netherlands from various countries. The first two letters of the ID# represent the two letter country code for the previous residence of the patient. The next two numerals represent the year of isolation. Viral RNA was prepared from patient serum and RT-PCR was used to amplify the V3 region of the *env* gene. The PCR products were directly sequenced. [Lukashov et al.(1996)]. Accession numbers L76878, SR903853; L76897, SR9304737; L76879, SR911515; L76874, UM893272; L76912, UM9403860; L76888, SR925752; L76890, SR926969; L76894, GQ9301341; L76882, MA913670; L76886, SR923572; L76873, BR891413; L76910, UM9403051; L76885, GF921953.
- 85) **NL11.ID#:** These 2 sequences are consensus sequences of 81 clones (patient N) and 105 clones (patient F) from serum, sigmoid tissue and fecal matter from each patient. All sequences from patient N were more similar to other sequences from patient N than to any other sequence in the database. Likewise all sequences from patient F were most similar to other patient F sequences. [van der Hoek et al.(1996)]. Accession numbers Z76463–Z76648.
- 86) **NL12.ID#:** These sequences are part of a set containing 15 Dutch homosexuals, 19 Dutch intravenous drug users, 2 German homosexuals, 2 German intravenous drug users, 5 Scottish homosexuals and six Scottish intravenous drug users, from which regions of *vpr*, *vpu* and *env* were sequenced. The authors

- found consistent differences in the sequences between the homosexuals and IV drug users. Only 34 of the 47 patients' sequences are reported in the publication. [Kuiken et al.(1996b)]. See also B_GB5 and B_DE2 sets. Some of the patients in this study have been previously studied. For example, entries with accession numbers Z68061 and U05787 are both from the same patient.
- 87) **NO1.ID#:** These 36 sequences are from Norwegian patients who were part of the Oslo HIV cohort study [Engelstad(1996)]. Uncultured PBMC DNA was PCR amplified in two nested PCR reaction steps. PCR products were directly sequenced. Where two peaks of equal height were observed at a single position, IUPAC ambiguity codes were used. Health, sex, year of sample (1989-1992), and risk group (IVDU, Het, Homo, Hemo) for each patient were noted in a table in the publication. Four sub sequences were also part of this set (X92913, X92914, X92917, X92918). Accession numbers for the 36 subtype B sequences are X92902–X92912, X92915, X92915, X92919–X92941.
 - 88) **PR1.D-ID#:** These four sequences are from Puerto Rico, and were generated as part of the DAIDS variation program in the laboratory of Dr. Marcia Kalish at the the Centers for Disease Control, Atlanta, GA. The C2V3 region was directly sequenced from PCR amplification of DNA from viral culture. The sequence ID numbers are abbreviated; for example D2PR732 can be read as DAIDS sequence (D), isolated in 1992 (2), Puerto Rico (PR), patient 301732 (732). A full description of these sequences can be found in the April 1994 supplement to the HIV database, part III. Accession numbers U04926–U04929.
 - 89) **PY.ID#:** Ten sequences from 10 patients living in Asuncion, Paraguay. All 10 were male patients with symptoms of AIDS. Virus was propagated in tissue culture for an unstated length of time prior to harvesting proviral DNA for PCR and sequencing. PCR products were directly sequenced. PY.3614, PY.3615 and PY.12837 were syncytium-inducing and the other 7 were not. The tenth sequence, PY.3614p was PCR amplified directly from patient PBMCs with no culturing. The significant differences between the cultured sequence from this patient (PY.3614c) and the direct sequence, indicates that the virus that grew out in culture was a minority of the virus present in PBMC. The sequence of PY.3614c is not included in this alignment. [Cabello et al.(1995)]. Accession numbers U28949–U28959.
 - 90) **RU1.RUS#:** These 2 sequences are from [Lukashov et al.(1995)]. Accession numbers: L38405, RUS3A; L38407, RUS4A.
 - 91) **RU2.ID#:** These 15 sequences are from homosexuals living in St. Petersburg, Russia. Malykh et al unpublished (1995). Accession numbers U40283–U40285 and U40319–U40330.
 - 92) **RU3.ID#:** These 13 sequences are from Rostov, St. Petersburg, Sochy, Ecaterinberg, Komi Republic, and Nizhny Tagil, Russia. Sequences were determined by direct sequencing of PCR product from uncultured PBMC proviral DNA. Although several of these cases were suspected to have epidemiological linkage (RU9 and RU10 are believed to have been infected by the same individual, sequences from the index case are not available; RU11, RU13 and RU27 were all thought to share a common index case, although none of them was directly infected by the index case), the sequences do not clearly indicate such epidemiological linkage and all 13 sequences are presented here. [Leitner et al.(1996b)]. Accession numbers U69646–U69652, U69654, U69657, U69660, U69662, U69666 and U69667.
 - 93) **SE.pt11s113:** This sequence is from one (patient 11 sample 113, collected in 1988) of a set of 13 sample from 9 epidemiologically linked individuals. The index case (patient 1) was a Swedish male who is believed to have contracted HIV while visiting Haiti in 1980. Six Swedish females were infected (patients 2,4,5,7,8 and 11) by patient 1. Two males (patients 6 and 10) were then infected by these females, and two HIV-infected children (patients 3 and 9) were born to the women. Sequences from each patient were determined by PCR amplification from uncultured PBMCs and direct sequencing. Heterogeneous sites were indicated with IUPAC codes. Extensive phylogenetic analysis was done to determine which methods accurately reconstructed the true phylogeny. [Leitner et al.(1996a)]. Accession numbers U68496–U68521.
 - 94) **SE1.ID#:** Seven sequences that are consensus sequences of blood and CSF samples taken from each patient. The CDC disease stage class for the patients are as follows: II pts 930, 2815; III pt 931; IV-E pt 2951; IV-A pt 1032; and IV-C2 pts 1433, 1866. [Keys et al.(1993)]. Accession numbers Z23178–Z23181, Z23185–Z23187, Z23192–Z23195, Z23200–Z23219, Z23224–Z23227, Z23232–Z23235, and Z23240–Z23255.
 - 95) **SE2.ID#:** These five sequences are from patients in Goetebotg, Sweden each of whom had recently seroconverted at the time of sampling in 1985-1990. Sequences from the sexual partners of all five patients who were believed to have transmitted the virus to these recipients were also determined, but are

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- not shown here due to the great similarity to the recipient sequences (94% to 99% identity). Three of the recipients (R1, R3 and R4) were homosexual, and the other two were heterosexual. [Furuta et al.(1994)]. Accession numbers U10929–U10950.
- 96) **SE3.ID#:** These 5 sequences are from a study of the ability of beta-chemokines RANTES, MIP-1alpha and MIP-1beta to inhibit primary isolates with SI and NSI phenotypes. The conclusion was that NSI viruses were inhibited by these beta-chemokines, whereas SI viruses were not. Each viral isolate was cocultured on PHA-stimulated donor PBMCs for 3 days, PBMC DNA was harvested, PCR amplified, and the PCR product directly sequenced. For each of these 5 patients (labelled patients A-E) one SI and one NSI isolate were sequenced, only the NSI sequence is presented here. [Jansson et al.(1996)]. Accession numbers U76078–U76087.
 - 97) **SK1.ID#:** These nine sequences are from homosexual men living in the inner city of Bratislava, in the Slovak Republic. Patients 11, 12, 15 and 23 were classified as CDC stage A1 and were not taking any medication. Patients 18 and 20 were CDC stage B2 and were taking AZT. Patients 9 and 28 were CDC stage C3 and were taking AZT. No information is available for patient 22. Two other patients (10 and 51) were included in this study, but their sequences are not shown here because after their sequences proved to be similar to sequences from patients 9 and 28, respectively, epidemiological investigation indicated that they (9 and 10; 28 and 51) had been sexual partners. DNA from cocultured PBMCs was PCR amplified and the PCR product cloned. Eight clones were sequenced from each patient, although only one sequence is presented in the publication and in the databases. It is not stated whether the single sequence is a consensus of the eight clones or a single clone.[Zachar et al.(1996b)]. Accession numbers U53192–U53194, U53196–U53203.
 - 98) **TH.93TH067:** This sequence is from Thailand. It is one of several complete env gene sequences obtained for the World Health Organization. HMA subtyping as well as sequence-determined subtyping was done on each one. Sequences were PCR amplified from cocultured PBMCs. Two to three clones from each isolate were sequenced. [Penny et al.(1996)]. Accession numbers U39258 and U39259.
 - 99) **JP.JH23A:** This sequence is from a Japanese patient dually infected with HIV-1 subtypes B and E [Xin et al.(1995a)]. Accession number D67089. See also D67090, E_JP.JH23A.
 - 100) **TH.T8174:** This sequence comes from a study of the genetic heterogeneity and epidemiological distribution of HIV1 in Thailand. The host was an intravenous drug user and the sequence was obtained from PCR amplified PBMC DNA. [Ou et al.(1993)]. Accession number L19238. See also E_TH.T8178.
 - 101) **TH1.ID#:** These ten sequences are from individuals from Thailand. PCR-direct, peripheral blood PBMC DNA. [Ou et al.(1992b)] and [Ou et al.(1993)]. (Published erratum appears in *Lancet* **342**:250 (1993).) Accession numbers L07442, L07449–L07456 and L07460.
 - 102) **TH2.ID#:** The TB132 sequence is from a set of isolates from HIV seropositive individuals from Thailand. PCR, PBMC co-culture, DNA. Full env sequence is available. [McCutchan et al.(1992)]. Please note: the TB132 locus name in the database corresponds to the McCutchan et al. “BK132” isolate. Accession number L03697. The CM237 sequence is from PBMC proviral DNA. [Mascola et al.(1994)]. Accession number L14570. See also B_US14
 - 103) **TH3.W2TH-ID#:** 2 sequences from Thailand from asymptomatic individuals. Consensus, PCR-clones, cell-culture DNA and RNA. These sequences were provided by the WHO Global Programme on AIDS Vaccine Development Study. The complete set of C2V3 region WHO sequences can be found in the April 1994 supplement to the *Human Retroviruses and AIDS 1993* database. [De Wolf et al.(1994)]; [Osmanov et al.(1994)]; [Gao et al.(1994a)]. Accession numbers U08715–U08718, U08801–U08802, and U08783–U08784.
 - 104) **TH4.ID#:** These twelve sequences are B subtype sequences from Thailand. Ten were genetically most similar to HIV-1 found in the Americas and Europe; these sequences were derived from people infected prior to 1988 (diagnosed in 1986 or 1987). The other two (N762 and N763) were designated B' and were isolated from people with more recent infections, 1988 and 1992. The sequences were obtained from PCR amplified PBMC DNA. The naming of the sequences submitted to the databases does not correspond with the naming of the sequences in the paper. [Kalish et al.(1994)]. Accession numbers for the entire set of thirteen sequences studied in this publication: U15576–U15588.
 - 105) **TH5.ID#:** These three sequences are B subtype sequences from Thailand. Two individuals believed to be dually infected with subtypes B and E were analyzed. It is not clear from the paper or the database

- entries, which sequences came from individual 1 and which from 2. [Artenstein et al.(1995)]. Accession numbers U21471, U21473, U21475. See also E_TH6.ID#.
- 106) **TH6.ID#**: These 4 entries are from 1992 dried blood spot samples from Thailand. DNA was extracted from the blood spots and PCR amplified. The PCR products were directly sequenced. Samples came from 3 previously identified HIV seropositive IV drug users (58, 11, 15) and a homosexual (86). Other samples from the same region were all subtype E (see E_TH8.#). [Cassol et al.(1996)]. Accession numbers U53310, U53311, U53314 and U53315.
- 107) **TH7.ID#**: These 70 sequences are from IV drug users in Bangkok, Thailand, who were undergoing methadone treatment at 14 treatment clinics. Blood samples were collected between January and April, 1994. Uncultured PBMC DNA from each patient was PCR amplified, and the PCR product was directly sequenced (except for patient 108, in which PCR product was cloned and 2 clones were sequenced, one shown here). Of the 84 patients sampled, 69 were Thai B, one (091) was typical subtype B, and 14 were subtype E. [Kalish et al.(1995)]. Accession numbers U22543–U22547, U22549–U22552, U22554–U22556, U22558–U22560, U22562–U22566, U22568–U22574, U22576–U22603, U22605–U22608, U22610, U22613–U22616, U22618–U22623 and U22626. See also E_TH9.
- 108) **TT.QZ4589**: This sequence is from Trinidad. W. Blattner et al. Unpublished 1995. Accession number U32396.
- 109) **TW1.ID#**: These 16 sequences are from healthy HIV-1 carriers or AIDS patients from Taiwan [Chang et al.(1997)]. Three subtype B sequences in this set were greater than 97% identical to the HXB2/LAI lab strain (see B_FR.LAI) of HIV-1, and are not included here (TW83, U73049; TW271, U73059; and TW335, U73061). The manuscript reports that 123 of 143 sequences from Taiwan were subtype B, but only 27 of the 143 sequences were submitted to the sequence databases. Other subtypes found in Taiwan in this study were E (17 cases), C (1 case), F (1 case) and G (1 case). Accession numbers for B subtype are U73045–U73054, U73056, U73057, U73059, U73061 and U73063–U73069.
- 110) **US.ACP1**: This virus was cultured from a seronegative man with Kaposi's sarcoma. (See: [Ho et al.(1989)]). ACP1 was the sequenced after one passage in PBMCs. Accession number M80660. The sequence AC-H9 (M80661) was also derived from this patient. [Ashkenazi et al.(1991)].
- 111) **US.AD39**: This sequence is one recipient sequence from a set of 36 clones from a homosexual donor-recipient pair. Other donor-recipient pairs were studied by quantitative homoduplex tracking assay (QHTA) but only this pair was sequenced. [Zhu et al.(1996)]. Accession numbers U50780-U50815.
- 112) **US.ADA**: This sequence is from the monocytropic U.S. isolate ADA. [Westervelt et al.(1991)]. The complete genome of a derivative of this isolate has been reported to have been sequenced in [Theodore et al.(1996)]. The complete genome is from a macrophage tropic HIV-AD8 isolate, derived from HIV-AD87, which was in turn derived from HIV-ADA. Accession numbers M60472, AF004394.
- 113) **US.ALAI**: This sequence is from an infectious clone of the 1985 U.S. isolate AL-1, taken from a patient with AIDS. Buckler-White, A. et al., Unpublished (1988). Accession number M38430.
- 114) **US.BAL1**: This sequence is from the macrophage tropic U.S. isolate BAL, harvested from lung alveolar tissue. Reitz M, et al., Unpublished (1990). Accession numbers M68893, M68894. The entry with accession number M63929 is 98% identical to this sequence and is also derived from the BAL isolate [Hwang et al.(1991)].
- 115) **US.BCSG3**: This is a fragment of a full genomic sequence from the provirus SG3, cloned as a single proviral unit. This clone replicates more efficiently in chimpanzee than in human lymphocytes, and is extremely cytopathic and syncytium inducing (SI) in immortalized human T-cell lines. [Ghosh et al.(1993)]. Accession number L02317.
- 116) **US.BRVA**: This sequence is from U.S. isolate BRVA, which was taken from the brain tissue of a AIDS patient with neurological disorders. [Anand et al.(1989)]. Accession number M21098.
- 117) **US.BWB**: This consensus sequence is from sequences derived from PCR amplified PBMC DNA from brain tissue. [Monken et al.(1995)]. Accession numbers L17088–L17126.
- 118) **US.CDC42**: This sequence is from an infectious clone of the U.S. isolate CDC-451 [Desai et al.(1986)]. It was isolated in 1984 from a 16 year old hemophilia A patient, who died of AIDS in June, 1984. The viral isolate was propagated on H9 cells prior to cloning into Lambda phage and M13 phage for sequencing. Accession number M13137.

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- 119) **US.Diaz:** This sequence is one of a set of 223 closely related sequences. All 223 sequences came from 3 patients with a common source of HIV, a blood donor and two recipients of this donor's blood [Zhang et al.(1997)]. Accession numbers for all 223 sequences are U29433–U29437, U29956–U30145, and U43035–U43054. Gag sequences from 12 clones are also available in entries U31573–U31584.
- 120) **US.FASH:** This sequence is also known as 91US005.11 from the WHO Global program on AIDS. It is from a 17 year old female with primary symptomatic infection (PSI) from Birmingham, Alabama, USA. The risk factor for this individual was reported as heterosexual contact. The sequence indicates that this clone is subtype B. Blood was drawn in 1991. Although this clone has a 34 bp deletion followed by a premature stop codon in the envelope gene, relative to other subtype B sequences, the env protein was strongly positive in a CAT complementation assay. The patient from which this clone was isolated experienced rapid CD4 decline. In addition to the 17 amino acid truncation of the gp41 peptide, the env gene has a mutation at amino acid position 721 (bases 2157-2159) replacing tyrosine with cysteine (Y721C). This mutation has been shown in SIV to increase cell surface concentrations envelope glycoprotein [LaBranche,C.C. et al, J. Virol. 69: 5217- 5227 1995]. The complete gp160 coding region of this isolate was sequenced along with those of others collected at major epicenters of the AIDS epidemic [Gao et al.(1996a)]. Accession number U27434.
- 121) **US.HOBR:** This sequence is also known as 91US006.10 from the WHO Global program on AIDS. It is from a 28 year old male with primary symptomatic infection (PSI) from Birmingham, Alabama, USA. The risk factor for this individual was reported as homosexual contact. The complete gp160 coding region of this isolate was sequenced along with those of others collected at major epicenters of the AIDS epidemic [Gao et al.(1996a)]. Accession number U27443.
- 122) **US.JFL:** This sequence is from a non-infectious clone from the monocytropic U.S. isolate JFL. [McNearney et al.(1990)]. Accession number M31451. Other sequences from HIV-1 isolates epidemiologically linked to this isolate can be found in database entries with accession numbers L06256–L06273. [McNearney et al.(1993)].
- 123) **US.JM:** This sequence, along with B_US.WM, came from viral isolates after short term culture in PBMCs, PCR amplification, and cloning of PCR products. Both are from asymptomatic, seropositive individuals. [Ashkenazi et al.(1991)]. Accession number M80662.
- 124) **US.JRCSF:** This sequence is from an infectious clone of the 1986 U.S. isolate JRCSF, derived from from the CSF of a patient who died with Kaposi's sarcoma and severe AIDS encephalopathy. The infectious clone JRFL was isolated from the brain of the same patient. JRFL does not replicate in Jurkat, U937 or HUT78 cells. JRFL does replicate in mononuclear phagocytes, and the macrophage-tropic region of the virus was determined by domain swapping with NL4-3 to reside in a 157 amino acid region of gp120 including the V3 loop. [O'Brien et al.(1990)]. Accession numbers U63632, M38429, U45960. Also see: [Pang et al.(1990)], [Pang et al.(1991)], [Koyanagi et al.(1987)], [Klasse et al.(1996)].
- 125) **US.MN:** This sequence is from U.S. isolate MN, taken from a 6 year old male pediatric AIDS patient from the Newark, New Jersey area in 1984. His mother was an IV drug user who died of pneumonia in 1982. His father was also HIV seropositive. A complete genome of isolate MN is found in M17449. Other sequences from this patient from the 1984 blood sample and from a 1987 sample taken shortly before death (U72495) are available also. [Jr et al.(1992)] [Gurgo et al.(1988)]. Accession number M17449. See also L48364–L48379 [Lukashov & Goudsmit(1995)].
- 126) **US.NY5CG:** This sequence is from the 1984 U.S. isolate NY5. [Willey et al.(1986)]. Accession number M38431. See also GenBank accession number K03346. A recombinant between NY5 and LAI has also been extensively studied, see B_FR.LAI entry.
- 127) **US.P896:** This sequence represents a molecular clone from an primary isolate derived from a Jamaican man who immigrated to Philadelphia 15 years earlier. At the time of viral isolation, he had no antiviral therapy, but was an AIDS patient with < 10 CD4 cells per mm³. The infectious molecular clone from which this sequence was derived is both macrophage-tropic and extremely cytopathic in lymphocytes. [Collman et al.(1992)] and [Kim et al.(1995)]. Accession numbers M96155, U39362.
- 128) **US.RJS:** This is a consensus of six biologically characterized clones from patient RJS, isolate 4. The HIV-1 infected individual had been infected for five years at the time of isolation. Patient RJS was a 31 year old homosexual male from Claifornia, who reported having sexual encounters with at least 1000 partners while HIV-infected, from 1980 to 1985 [Hahn et al.(1986)]. Virus was isolated via coculture on

- donor PBMCs prior to cloning and sequencing. Complete env sequence is available. [Daniels et al.(1991)] and [Fisher et al.(1988)]. Accession numbers M37491 and M37573–M37577.
- 129) **US.SB(A-C)**: These three sequences are from 1988 U.S. isolates taken from a woman, her daughter and her sexual partner. The three viruses are epidemiologically linked, however the amino acids sequences appeared sufficiently divergent in this region to merit the inclusion of all three samples. Sequences were directly sequenced from PCR amplification products after the virus was briefly cultured. [Burger et al.(1991)]. GenBank accession numbers M77228–M77230.
- 130) **US.SC**: This sequence is from the 1984 U.S. isolate SC, from an AIDS patient. [Gurgo et al.(1988)]. Accession number M17450.
- 131) **US.SF128**: This clone was isolated from the spinal cord tissue of a patient with dementia, after coculture with PBMCs. It is macrophage tropic, infecting macrophages but not T-cells [Liu et al.(1990)]. Accession numbers M95292 and M38673. The ability to infect macrophages versus HUT 78 cells was mapped to the region between a *StuI* site in *env* and a *XhoI* site in *nef*, by replacing this region in SF2 with the same region from SF128.
- 132) **US.SF162**: This sequence is from an infectious clone from the U.S. isolate SF162, cultured from the cerebrospinal fluid of a patient with toxoplasmosis. [Cheng-Mayer et al.(1990)]. Accession numbers M38428, M65024.
- 133) **US.SF2**: This sequence is from an infectious clone from the U.S. isolate ARV-2. ARV-2/SF2 was isolated from a patient with oral candidiasis after co-culture with mitogen-stimulated PBMCs in 1984 [Levy et al.(1984)]. [Sanchez-Pescador et al.(1985)]. Accession numbers K02007 and I07977. HIVSF13 (Accession number L07422) is a more infectious virus taken from the same patient five months later, when he had developed Kaposi's sarcoma and *Pneumocystis carinii* pneumonia [Cheng-Mayer et al.(1991)]. SF2 and SF13 are 98% identical to one another. The variation of SF2 in 9 years of infection in a chimpanzee has been studied by Fultz et al. unpublished, Accession numbers U56884–U56887.
- 134) **US.SF33**: This sequence is from an infectious clone from the 1984 U.S. isolate SF33. [York-Higgins et al.(1990)]. Accession number M38427.
- 135) **US.TN-ID#**: These eight sequences are from asymptomatic individuals identified after donating blood in Memphis, Tennessee, USA. [Slobod et al.(1994)]. Accession numbers U09140–U09175.
- 136) **US.twinABcon**: This sequence is a consensus of a set of 27 *env* sequences from a pair of heterozygotic perinatally HIV-1 infected twins who were observed during their first 2 years of life. Twin A remained asymptomatic through her first 2 years while twin B developed AIDS at six months and died at 22 months of age. Patient PBMCs were cocultured with donor PBMCs, prior to DNA extraction and PCR amplification. Approximately 500 copies of HIV proviral DNA per PCR reaction were used. PCR products were cloned prior to sequencing. Viral phenotypes from both infants, and all time points were also assessed. All were found to be non-syncytium inducing, but they differed in their ability to infect primary macrophages. Overall, it seems that the production of neutralizing antibodies by the healthy twin was the most important clinical factor. [Hutto et al.(1996)]. GenBank accession numbers U47562–U47588 for the envelope sequences and U47589–U47613 for *tat* sequences from the same blood samples.
- 137) **US.WEAU**: This sequence was kindly provided prior to publication by Sajal K. Ghosh. It is from a cultured isolate from a patient described as "patient 1" in [Clark et al.(1991)] and as WEAU 0575 in [Jr et al.(1993)]. The sequence is from a fully infectious complete, cloned genome. It has a high tropism for T-cells and is syncytium-inducing. Accession number U21135.
- 138) **US.WM**: This sequence, along with B_US.JM, came from viral isolates after short term culture in PBMCs, PCR amplification, and cloning of PCR products. Both are from asymptomatic, seropositive individuals. [Ashkenazi et al.(1991)]. Accession number M80663.
- 139) **US.WMJ22**: This sequence is from the isolate WMJ22, isolated from a 4 year old female with AIDS, born in Florida to a woman of Haitian descent living in the U.S. Virus was cocultured on an immortalized T-cell line. [Hahn et al.(1986)] and [Starcich et al.(1986)]. Accession numbers M12507, K03457.
- 140) **US.WR27**: This sequence is from a complete genome. It represents first complete PCR-derived sequence of a U.S. clinical isolate of genotype B expanded only in primary PBMC. This provirus harbors a uniquely truncated V3 loop. WR27 was a patient with clinical progression to WR stage 5 when blood was drawn for viral isolation in 1988. This sequence is from a PCR clone from a primary isolate that was expanded in PBMC. The virus isolate had an SI phenotype. [Salminen et al.(1995)]. Accession number U26546.

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- 141) **US.YU:** This is a consensus sequence of eight lambda phage clones and 12 PCR amplified clones derived from the uncultured brain tissue of a patient with AIDS dementia complex. A macrophage tropic clone (YU-2) is almost identical to the consensus sequence of YU in this region, with only a single amino acid change (K to N) 10 amino acids from the carboxy-terminal end of the sequence. [Li et al.(1991)]. Complete genomic sequences are available for two of the HIV1YU clones, along with biological characterizations of four of the HIV1YU clones: [Li et al.(1992)]. The GenBank accession numbers for the YU-10 and YU-2 complete genomes are M93259 and M93258, respectively. Accession numbers for the other clones are M89972–M89984.
- 142) **US1.HC-ID#:** These are forty 1990–1991 U.S. samples, from the study of the dentist who was thought to have been the source of HIV-1 infection of six of his patients. Only the dentist's viral sequence and the Florida control sequences are shown here; the six epidemiologically and genetically linked patients are excluded from this alignment because their viral sequences were very similar to the dentist's. All sequences were PCR amplified from patient PBMCs. Most are direct sequences from the amplification products, although some are consensus sequences of multiple clones of PCR products and one direct sequence. [Ou et al.(1992a)]. Accession numbers for the 75 sequences in this set: M90847–M90853, M90881–M90886, M90894–M90900, M90907–M90912, M90914–M90956, M90958–M90964, M92100–M92133, L22590–L22606 and U06872–U06919. See also [Korber & Myers(1992)], [Crandall(1995)], [Smith & Waterman(1992)], [DeBry et al.(1993)], [Palca(1992b)], [Palca(1992a)], [Abele & DeBry(1992)], [Hillis & Huelsenbeck(1994)], [Ciesielski et al.(1991)] and [Ciesielski et al.(1994)]. In a related study [Delwart et al.(1995)] heteroduplex mobility tracking assays were used to re-analyze samples from this set, again supporting the dental to patient transmission hypothesis.
- 143) **US2.D-ID#:** These 15 sequences are from the USA, and are part of a set of sequences generated as part of the DAIDS variation program in the laboratory of Dr. Marcia Kalish at the the Centers for Disease Control, Atlanta, GA. The C2V3 region was directly sequenced from PCR amplification products of DNA from viral culture. The sequence ID numbers are abbreviated, for example D2US711 can be read as DAIDS sequence (D), isolated in 1992 (2), United States (US), patient 301711 (711). A full description of these sequences can be found in the April 1994 supplement to the HIV database, part III. Full length envelope genes from some of these clones have been expressed, [Gao et al.(1996a)]. Accession numbers U04907–U04915, U04918 and U04921–U04925, U08448–U08452.
- 144) **US3.D-ID#:** These four sequences are from the US, and are part of a set of sequences generated as part of the DAIDS variation program in the laboratory of Dr. Beatrice Hahn at the University of Alabama. gp160 sequences of clones from expanded culture stocks are available. The sequence ID numbers are abbreviated, for example D2US711 can be read as DAIDS sequence (D), isolated in 1992 (2), United States (US), patient 301711 (711). A full description of these sequences can be found in the April 1994 supplement to the HIV database, part III. Accession numbers U08448–U08449 and U08451–U08452. Accession numbers for additional clones from these patients: U04916–U04917 and U04919–U04920,
- 145) **US4.ZhuPt-ID#:** Sequences from five primary seroconverters. Consensus, PCR-clones, peripheral blood PBMC DNA. Although sequences were also available from two of the donors, only sequences from five recipients are shown here. [Zhu et al.(1993)]. Accession numbers L21224–L21328, L21372–L21373, L21376–L21377, L21380–L21381, L21384–L21389, L21393–L21394, L21397–L21398, L21400–L21401, L21404, L21405, L21408, L21410–L21411, L21414, L21417–L21418, L21426–L21427, L21430–L21432, L21434–L21437, L21440–L21442, L21445, L21447, L21449–L21450, L21453–L21454, L21457, L21459, L21462–L21463, L21519–L21520, L21522–L21523, L21525–L21526, L21528–L21533, L21535–L21536, L21538–L21539, L21541, L21543, L21545–L21546, L21548, L21550–L21551, L21553–L21554, L21556, L21558–L21559, L21561–L21569, L21571–L21578, L21580, L21582, L21584, L21586, L21588 and L21590.
- 146) **US5.pt-ID#:** A consensus of PCR-clones, peripheral blood DNA. These two sequences were part of a study of blood sequences compared to brain sequences from six individuals. [Korber et al.(1994)]. Accession numbers U05360–U05568.
- 147) **US6.-ID#:** Each sequence is a consensus sequence of several cloned PCR products from PBMC proviral DNA from an individual infant. These sequences were part of a study of mother-infant transmission. Infant blood samples were taken from 1 week (infant 7) to 34 months (infant 4) post-partum. Dates of sample collection were: Infant 1, 10/25/91; Infants 2–4, 10/31/91; Infant 5, 2/6/92; Infant 6, 8/30/93;

- Infant 7 5/13/93. Maternal sequences were also reported as part of this set, but are not used in building these consensus sequences. [Ahmad et al.(1995)]. Accession numbers U16390–U16652.
- 148) **US7.-ID#:** Each sequence is a consensus sequence of several cloned PCR products from PBMC proviral DNA from an individual patient. These sequences were part of a study of early samples (1984–1986) from the San Francisco region. One of the samples (552-3) was HIV negative but was determined to be contaminated with blood from another (565-3) so the six samples from 552-3 and 565-3 are made into one consensus here (565). Another sample (552-5) from patient 552 was not contaminated, and it is presented as B_US11.552, because a larger region was reported in that publication. [Sabino et al.(1994b)] Accession numbers L20371–L20380. More V3 and tat sequences from these individuals are discussed in [Sabino et al.(1994a)]. Accession numbers U00243–U00399 and U01513–U01529.
- 149) **US8.-ID#:** These sequences were from a study of three recipients of contaminated blood. Recipient 1 (R1) and recipient 2 (R2) each received blood from different donors. A third recipient, not presented here, received blood from both donors. All three recipients were neonates. R1 received erythrocytes from donor 1 on 19 October, 1984 at the age of 3.5 weeks. For R1 the sequence of one of the two clones (2E) is presented here. R2 received erythrocytes from donor 2 on 24 September, 1984 at the age of 2 months. For R2 a consensus of 6 clones is presented here. Blood samples for this study were drawn in March 1986. R1 had slow weight gain, and R2 had lymphadenopathy at time of sample collection. [Diaz et al.(1995)]. Accession numbers U11188 = R1–2E, U11189 not used; U11203, U11196, U11199, U11192–U11194 = R2 six clones. The tat and envelope V4–V5 regions of clones from these same individuals are also available in U11173–U11178, U11180, U11205–U11209.
- 150) **US9.-ID#:** These are four consensus sequences for samples taken over a range of time from four different subjects. Blood samples for S1 were drawn in Nov '85, Jul '87, Jan '88 and May '89. Blood samples for S2 were drawn in May '85, Apr '87 and Oct '87. Blood samples for S3 were drawn in Jun '87 and Dec '87. Blood samples for S4 were drawn in Jan '85, Jan '89 and Jun '89. S2, S3 and S4 had decreasing CD4 counts during the study period. S1 had fluctuating CD4 counts. [McNearney et al.(1992)]. GenBank accession numbers L03430–L03453 and L23575–L23588 = S1; L03454–L03477 and L23618–L23633 = S2; L03478–L03490 and L23589–L23600 = S3; L03491–L03515 and L23601–L23617 = S4.
- 151) **US10.ID#:** These three consensus sequences are from sets of sequences used in a study on the dynamics of HIV sequence changes in vivo and the utility of heteroduplex analysis. All sequences were derived from PCR amplified PBMC DNA. The MA145 consensus represents sequences (GenBank accession numbers U00821, U00822, U00831–U00839) taken from an asymptomatic male from Massachusetts over a period of 4.5 years starting April 1989. Patient MA, from the US, was infected in 1984 or 1985, and had been experiencing neurological disorders prior to 1989 [Kusumi et al.(1992)]. The SFBI and SFPE consensus represent sequences (Accession numbers U13373–U13380 and U13381–U13388 respectively) taken from two patients with AIDS from San Francisco. [Delwart et al.(1994)]. Other sequences from patient MA can be found in database entries with accession numbers U00804–U00822, U00831–U00850, U00873–U00888, M79342–M79354 and M90025–M90046. Other SFBI sequences can be found in U13240–U13252. See also NL7.ID#.
- 152) **US11.ID#:** These four consensus and seven individual sequences came from patients early in infection, before, or around the time of seroconversion. Sequences for 306, 419, 349, and 074 are consensus sequences. [Shpaer et al.(1994)] and [Delwart et al.(1995)]. Accession numbers U23664–U23666, U23668, U23669, U23671–U23708, L20381. See also B_NL8.ID#.
- 153) **US12.ID#:** These six sequences were used in an investigation into the transmission of HIV-1 from one child (CHA), who had received zidovudine, to another child (CHB), who harbored a zidovudine-resistant strain. The presence of the zidovudine-resistant strain in child A and B, and the lack of such a strain in child 2's mother was used to show that child B was infected by child A and not by child B's mother. LC sequences are from children used as local controls. All sequences were derived from PCR amplified PBMC DNA. [Fitzgibbon et al.(1993)]. Accession numbers L12751–L12756, L19695, L19697, S66942. L12756 is listed as "isolate 100" in the databases, but seems to be the "group B consensus sequence" used for phylogenetic analysis.
- 154) **US13.ID#:** These three consensus sequences are from three IV drug users in Florida. Proviral DNA sequences were obtained from blood, cerebrospinal fluid and dorsal root ganglia from each of the three individuals. Sequences for V1–V5 of env, were PCR amplified, cloned and sequenced. [Shapshak et al.(1995)]. [Xin et al.(1995b)]. The sequence for patient 149 is a consensus of all 24 clones in

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Accession numbers U16094–U16117. The sequence for 141 is a consensus of database entries labelled as being from patient 141 with the exception of: R5D, R6D, R7D, R2D and R4D, which were similar to IIIB strains of HIV-1; and R1R, R3R, R7R, R8R and R9R, which were similar to samples from patient 144. The sequence for 144 is a consensus of database entries labelled as being from patient 144 with the exception of: R3R, R6R, R9R, R12R, R13R and L1D, which were similar to IIIB strains of HIV-1; and C3D, C4D, C7D, C8D and C10D, which were similar to samples from patient 141. While infection of each individual with multiple strains of HIV (including one very similar to the IIIB lab strain) is a possible explanation of these findings, we are only including one consensus sequence from each patient for this alignment. The authors are currently (1996) resequencing new samples from these patients. Accession numbers for patients 141 and 144 are U16032–U16093, U25191–U25261.

- 155) **US14.ID#:** These four sequences are from DNA from PBMC. [Mascola et al.(1994)]. Accession numbers L14573–L14576. See also B_TH2, E_TH2.
- 156) **US15.ID#:** These six consensus sequences are from a study of infants. Blood samples were collected from six infants over time. [Strunnikova et al.(1995)]. Accession numbers U22682–U22810, U22834 and U22835.
- 157) **US16.ID#:** These two consensus sequences were used in a study of the impact of sequence variation on the distribution and seroreactivity of linear antigenic epitopes. Both sets of sequences were from PCR amplified DNA from peripheral blood leukocytes. Patient ARTC1 was an asymptomatic individual from New York and ARTC3 was an AIDS patient from New York. [Pestano et al.(1995)]. Accession numbers U11586–U11594. See also A_UG1.964, C_UG1.45, and D_UG7.ID#.
- 158) **US17.ID#:** CB7 is one sequence from a set of 12 clones from two different samples (six clones each) from the same patient, collected in 1988 and 1990, plus two more clones as yet unpublished. The patient seroconverted in 1985. The patient did not receive any antiviral therapy until 1992. The patient's CD4 count was 1035 in 1988 and 807 in 1990. The patient's PBMS were cocultured with donor PBMC for an unspecified length of time before cultured DNA was isolated and PCR amplified. Individual clones of PCR product were then sequenced. [Wang et al.(1995)]. Accession numbers U16324–U16335 and U19706–U19711. The other 8 sequences are individual clones from 8 different patients, all from the same clinic in Boston, MA. Individual CB7 was again included in this study, [Wang et al.(1996a)] [Wang et al.(1996b)]. Accession numbers U60152–U60162 and U27658–U27669.
- 159) **US18.ID#:** These 22 sequence are from a study of a HIV-1 infected dentist and many of his HIV-1 infected patients. In this case, no evidence was found for dentist to patient, patient to dentist, or patient to patient transmission. [Jaffe et al.(1994)]. Accession numbers U11454–U11490. Unfortunately the dentist sequences were not submitted to the databases.
- 160) **US19.ID#:** These two sequences are from a comparison of a mother who transmitted HIV to her infant and a mother who did not. One of the sequences (nontransmitter-283 accession number U07839) was 99.4% identical to the LAI strain of HIV-1 and is not included here. Sequences from the transmitter and nontransmitter were highly similar with the exception of sequence nontransmitter-217 (U07836). Thus a consensus of the similar sequences is included here as VA1-consensus, and the nontransmitter-217 outlier is presented separately as VA2. [Ayyavoo et al.(1996)]. Accession numbers U07833–U07841 and U07891–U07917.
- 161) **US20.ID#:** These three sequences are from a study of mother-infant transmission. Only child consensus sequences are used here, but mother and child clonal sequences are reported in [Roth et al.(1996)]. Proviral DNA was PCR amplified from uncultured patient PBMCs. Cloned PCR products were sequenced. Child 1 was 27 months old, child 2 was 5 months old and child 3 was 21 months old when blood was drawn for sequencing. Sequences, including those from the mothers, are in database entries with accession numbers U47745–U47807.
- 162) **US21.ID#:** These six sequences are from six different patients, all men from the Chicago, Illinois, USA MACS cohort. In the study, P1 & P2 were rapid progressors, P3 & P4 normal progressors, and P5 & P6 non-progressors. Their estimated years of seroconversion are as follows: P1, 1985; P2, 1985; P3, 1986; P4, 1986; P5, 1985; and P6, 1984. A total of 292 sequences of the C2-V5 region of envelope were completed. In the database entries the sample numbers are of the form Px.y-z, where x stands for the patient number, y is the number of months after the estimated date of seroconversion, and z is the clone number. Each of the six sequences presented here is a consensus of all clones from that patient. [Wolynsky et al.(1996)]. Accession numbers U35895–U36185.

- 163) **US22.ID#:** These 12 sequences are from a study of variability of tat and env genes. Lorenzo et al (1996) Unpublished. Accession numbers U57104–U57216. Tat sequences from these clones are also available (U57217–U57304).
- 164) **US23.ID#:** These 3 sequences are from a study of variability of vif and env genes. [Sova et al.(1995)]. Uncultured or short-term cultured PBMC proviral DNA was PCR amplified, and several clones from each PCR reaction were sequenced. Only one clone sequence from each patient is presented here. Accession numbers U50615–U50628. Vif sequences from these patients are also available (U41055, U41056, U41179–U41182 and U42229–U42282).
- 165) **US24.ID#:** These 5 sequences are from unpublished database entries by Schwartz et al. Accession numbers U49518–U49640, U51311–U51326 and U45860–U45876.
- 166) **US25.RM:** This sequence is from a blood recipient M who received a red blood cell pack from donor W in October 1984. Blood was sampled from recipient M for this sequence in January 1986, 15 months after the transmission event. Sequences from donor W (collected in January 1987, 27 months after transmission) and another recipient (O, collected in November 1986, 20 months after an RBC pack transfusion in March 1985) are also available [Delwart et al.(1995)]. Accession numbers U22826–U22828.
- 167) **US26.ID#:** These two sequences are from: A) a slow progressor, patient A, a 26 year old caucasian male who lost an average of 31 CD4+ cells/ml per year during the first 3 years of infection, and remains healthy; and B) a rapid progressor, patient B, a 38 year-old caucasian male who lost an average of 175 cells/ml per year during the first 3 years of infection. Both patients were infected from the same source but patient B picked up two divergent subtype B forms (one shared with patient A, and one unique to patient B). In the database entries, patient B is labelled as "14" and patient A as "13". [Liu et al.(1997)]. Sequences were determined by PCR from uncultured PBMC DNA and RT-PCR from plasma viral RNA. PCR products were cloned prior to sequencing. One representative clone from patient A was picked for the "13A" sequence presented here, and one of the divergent B sequences was picked for the "14B" sequence presented here. Accession numbers U56146–U56235, U79034–U79113.
- 168) **US27.ID#:** These 5 sequences are from infants infected perinatally and followed over time after birth as part of the Los Angeles Perinatal Transmission Study [Ganeshan et al.(1997)]. DNA sequences were determined from cloned PCR products from uncultured patient PBMCs.
- 169) **US28.ID#:** These 13 sequences are from studies of long-term survivors. Patient 3799 was transfused with HIV-1 infected blood in October, 1982 at the age of 30, and has remained asymptomatic, with very low viral load and fairly stable CD4 counts for over 13 years. The donor, as well as two other recipients of his blood, have all died from complications of AIDS. The husband of 3799, as well as two children born and breastfed after the 1982 transfusion, are all HIV-negative. [Michael et al.(1995)] and [Schwartz et al.(1997)]. The other patients showed varying rates of disease progression. During the study, only 101867 (sequence not available) died of AIDS. Sequences were PCR amplified directly from patient PBMC without coculture, cloned and sequenced. Only one clone from each patient is presented here. Accession numbers U60670–U60733. Entries with accession numbers U24443–U24487 are also from patient 3799, but not V3 region.
- 170) **US29.ME1:** This sequence is from a 40 year old patient in the Pittsburgh AIDS Clinical Trials Unit. [Chen et al.(1997)] describes a new method, called "progressive amplification" for obtaining full-length infectious molecular clones of HIV. In this study, two clones were generated and the env gp120 completely sequenced. One (ME1) was from the patient when asymptomatic, and both the viral isolate (367), and the molecular clone (ME1) grew on macrophages but not T-cells (Macrophage tropic) and did not show cytopathic effect on either MT-2 or PBMCs (NSI). The other (ME46) was from an isolate (828) taken from the same patient 20 months later, when the patient had AIDS. This isolate and the clone derived from it were able to grow on both macrophages and T-cells. It induced cytopathic effect in MT-2 cells and PBMCs (SI). Accession numbers U66221, U66222. The paper also reports on sequences from "patient P" in figure 5b, but those sequences are not available.
- 171) **US30.ID#:** These 10 sequences are from rapid and slow progressors who were studied in 1990-1994. The subjects were all asymptomatic and taking AZT (zidovudine) at the beginning of the study. Patients A, C, E, G and I were classified as slow progressors, while patients B, D, F, H and J were classified as rapid progressors. Two sequences appear to be mislabelled: U69410 labelled patient G clusters with patient E, and U69380 labelled as patient E clusters with patient G. Eight of the ten patient F, 1993 sequences are suspiciously similar (greater than 98% identical) to the HXB2R lab strain of LAI/IIIB. Each sequence is

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- a single clone from one patient, although several clones from each patient at two time points are available [McDonald et al.(1997)]. Accession numbers U69282–U69481.
- 172) **US31.ID#:** This study demonstrates the influence of three monoclonal antibodies IgG1b12, 2G12, and 2F5 to the HIV-1 envelope glycoprotein, and a tetrameric CD4-IgG molecule (Cd4-IgG2), for the ability to neutralize primary HIV-1 isolates from the genetic clades A through F and from group O. Each of the reagents broadly and potently neutralized B clade isolates [Trkola et al.(1996a)]. Accession numbers are U79721, U79720, U79719.
 - 173) **UY1.ID#** These 9 sequences are from 22-37 year old patients with CDC stage IV disease (except 726 at stage III). All are from Montevideo Uruguay. Four were homosexuals (270 352, 093 and 672), two were IV drug users (406 and 726), and the other 3 were heterosexuals (1699, 1193 and 376) [D. et al.(1996)]. Accession numbers U66414–U66422.
 - 174) **VE.ID#:** These 8 sequences are from 8 individuals in Venezuela. Patient PBMCs were cocultured with donor PBMCs. Proviral DNA was harvested PCR-amplified. PCR products were directly sequenced. Nearly complete env gp120 sequences were determined, as well as pol gene sequences. [Quinones-Mateu et al.(1995)]. Accession numbers U16764–U16778, even numbers are env, odd numbers are pol.
 - 175) **VN1.HCM9:** This sequence is from South Vietnam. [Menu et al.(1996)]. The sequence is from Ho Chi Minh city, from a woman infected by her HIV seropositive sexual partner who was thought to have been infected while traveling in Europe. Three other sequences in this study were found to be subtype E. Accession number U29209.
 - 176) **ZA.ID#:** These 7 sequences are from 7 individuals in South Africa. ZA504 was from a 33 year old white male homosexual with AIDS and the virus was syncytium-inducing (SI). ZA508 was from a 32 year old white male bisexual with ARC and the virus was NSI. ZA509 was from a 30 year old white male homosexual with AIDS and the virus was SI. ZA524 was from a 49 year old white male bisexual with AIDS and the virus was NSI. ZA510 was from a 29 year old white male heterosexual with ARC and the virus was SI. ZA512 was from a 26 year old white male homosexual with ARC and the virus was SI. ZA513 was from a 3 year old black male blood transfusion recipient with AIDS and the virus was SI. All samples were collected at the Tygerberg Hospital in the Western Cape region of South Africa between 1984 and 1992. DNA was harvested from cocultured PBMCs and the env gene was PCR amplified and cloned into pBSKS+ for sequencing. Each sequence is from a single cloned PCR product. [Engelbrecht et al.(1995)]. Accession numbers L48063–L48066, L48069, L48071 and L48073. Database entries U33770 and U33774–U33779 are shorter env gene fragments from these same clones.

C Subtype

At this time there are viral sequences from 233 HIV-1 infected individuals associated with HIV-1 subtype C. The C subtype consensus sequence (C_CONSENSUS_97) generated from these sequences was based on the most common amino acid found in each position of an alignment. All of these sequences have been published and/or have been made available for printing in the database by their authors.

- 1) **BR.W2BR025:** This sequence is part of a gp160 sequence from an asymptomatic individual from Brazil, sampled in 1992. A clone was derived from an expanded viral culture, expressed and sequenced. This sequence was provided by the WHO Global Programme on AIDS Vaccine Development Study. The complete set of C2V3 region WHO sequences from this patient can be found in the April supplement to the Human Retroviruses and AIDS 1993 database. Relevant papers are: [De Wolf et al.(1994)]; [Osmanov et al.(1994)]; [Gao et al.(1994a)]. Accession number U15121. This sequence is from a 23 year old male hemophilia patient from Porto Alegre, Brazil. He had seroconverted more than 1.2 months prior to the date this blood sample was collected in 1992. He was asymptomatic, and had not taken any anti-retroviral therapy prior to sampling. The HIV isolate exhibited an NSI phenotype, when assayed by the WHO [Gao et al.(1996a)]. 92BR025 is similar to another WHO sample; 91BR015. Accession number U52953. Entries with accession numbers U08720, U08785, U09126, U09132 and U09133 are also from W2BR025.
- 2) **BR1.HSP203** Although this sequence is listed as unpublished in the database, it seems to be an extension of work published in [Morgado et al.(1994)], [Sabino et al.(1994c)] and [Sabino et al.(1996)]. It is from San Paulo, Brazil. Accession number U31585.
- 3) **BR2.91BR015:** This sequence is from Brazil. It is one of several complete env gene sequences obtained for the World Health Organization. HMA subtyping as well as sequence-determined subtyping was done on each one. Sequences were PCR amplified from cocultured PBMCs. Two to three clones from each isolate were sequenced. 91BR015 is similar to another WHO sample; 92BR025. [Penny et al.(1996)]. Accession numbers U39234 and U39238.
- 4) **BI1.ID#:** These eight sequences are from Burundi. They are part of several complete env gene sequences obtained for the World Health Organization. HMA subtyping as well as sequence-determined subtyping was done on each one. Sequences were PCR amplified from cocultured PBMCs. Two to three clones from each isolate were sequenced. 91BU009 groups with subtype D in a neighbor-joining tree of the V3 region and is presented as an undetermined subtype in the section of the compendium. [Penny et al.(1996)]. Accession numbers U39252 and U39233, 91BU001; U39248 and U39237, 91BU002; U39239 and U39242, 91BU003; U39241 and U39243, 91BU004; U39240 and U39257, 91BU005; U39244 and U39246, 91BU006; U39245, U39247 and U39249, 91BU007; U39250 and U39251, 91BU008; U39253 and U39254, 91BU009.
- 5) **BY1.ID#:** These 3 sequences are from Byelorussia. [Lukashov et al.(1995)]. Accession numbers: L38410, BLR9A; L38409, BLR8A; L38408, BLR5A.
- 6) **CY.HO021:** This is a sequence from a 51 year old woman whose husband had died of AIDS. She was born and lived in Zambia, before moving to Cyprus. She was asymptomatic, with a CD4 count of 200, and she had been seropositive for at least 6 years. This sample, like others in this study (see also subtypes A, B, F and I) was collected in February 1994 from the AIDS clinic in Nicosia, Cyprus. DNA was extracted from patient PBMCs and PCR amplified. After a second round of PCR, products were cloned and sequenced. Two clones from patient 02 were sequenced. [Kostrikis et al.(1995)]. Accession numbers U28321 and U28661.
- 7) **DJ1.DJ-ID#:** These two sequences from Djibouti were from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989–1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)]. Accession numbers L22940 and L23065.
- 8) **ET2.ID#:** These nine sequences of Ethiopian isolates were part of a cohort considered to be heterosexually infected. PBMC DNA was PCR amplified and directly sequenced. [Salminen et al.(1996)]. For patient 2220, who had slim disease and AIDS, almost full length HIV-1 genome was PCR amplified from PBMC DNA and cloned. Proviral DNA from others in the cohort was PCR amplified and directly

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- sequenced. Other regions of the genome are available for these isolates as well. [Salminen et al.(1996)]. Accession numbers U45481–U45502 (V3 region), U15060–U15066 and U45503–U45504 (LTR NF-kB/NRE regions), M64001–M64009 (gag p7 region), M64015–M64018 (env gp41 region) and U46016 (C2220 complete genome).
- 9) **ET3.ID#:** These 93 sequences are from a study that describes the distribution of HIV-1 subtypes in Ethiopia. HIV-1 RNA was collected from sera (from a majority of asymptomatic individuals) and a 284bp fragment covering the V3 region was amplified by RT-PCR and directly sequenced. All sequences were subtype C except for one subtype A [Abebe et al.(1997)]. Accession numbers U88727–U88755, U88757–U88821.
 - 10) **FR1.ID#:** These 14 sequences are from members of the French military who are believed to have been infected while deployed outside of France (Djibouti). An additional sequence (FRMP040, U58787) was listed as subtype C in the paper, but clustered with subtype B in analysis done at the HIV Database and it has been listed as subtype unclassified until more information is available. Other sequences from this study were subtypes A, B, E, and F. [Lasky et al.(1997)]. Accession numbers for subtype C were U58785, U58786, U58788–U58799.
 - 11) **GA1.ID#:** These 2 sequences are from Gabon. G134 is from a 1988 or 1989 sample from a patient with AIDS living in Franceville, Gabon. LBV105 is from a 1988 sample from an asymptomatic individual sampled from the general population of Libreville. Method of proviral DNA isolation was not described. DNA was PCR amplified and cloned. One clone per isolate was sequenced. [Delaporte et al.(1996)]. Accession numbers X90912, G134; X90913, LBV105. See also subtypes A, D, F, G and O sequences from this same study.
 - 12) **GB1.00513:** This sequence is from the British isolate 93–00513. [Arnold et al.(1995c)]. Accession number U21099.
 - 13) **GM.GM3:** A sequence from Gambia, as yet unpublished. Bobkov et al. 1996 unpublished. Accession number U33098. See also Gambian sequences of subtypes B and J.
 - 14) **IN1.D-ID#:** These four sequences are from samples from high risk patients in India, PCR clones, DNA, PBMC culture. [Dietrich et al.(1993)]. Accession numbers L07651 and L07653–L07655; X65638–X65640 and X68406.
 - 15) **IN2.D-ID#:** These five sequences are from samples from high risk patients in India, primarily stage I. They were nested PCR amplified from DNA obtained from uncultured PBMC from patients serologically defined as HIV-1/HIV-2 mixed infections. [Grez et al.(1994)]. Accession numbers U07098 and U07100–U07103.
 - 16) **IN3.ID#:** These 8 sequences were isolated from Pune and New Delhi, India. All 8 sequences were from heterosexually infected patients from New Delhi, or Pune, India. DNA was isolated from cocultured PBMCs after one week of culture. PCR product was cloned and a single clone was sequenced. [Tripathy et al.(1996)]. Accession numbers U29179, U29694–U29698, U31362 and U31363. See also B_IN.IND9.
 - 17) **IN4.ID#:** These 24 sequences are from 1992 dried blood spot samples from Vellore near Madras, in Tamil Nadu state in southern India. DNA was extracted from the blood spots and PCR amplified. The PCR products were directly sequenced. Samples came from previously identified HIV seropositive STD patients (1, 3, 5, 6, 7, 11, 12, 13, 19, 20, 23, 29, 33), spouses of infected men (2, 4, 10, 16, 22, 26, 27), female prostitutes (36, 37) or bisexual men (8, 32). Two homosexual men from the same region had subtype A HIV-1 (see A_IN1.9 and 14). [Cassol et al.(1996)]. Accession numbers U53278–U53285, U53287–U53290, U53292–U53303.
 - 18) **IN5.ID#:** These 7 sequences are from India. Another sequence from this publication was subtype A (see A_IN2). [Tsuchie et al.(1993)]. Accession numbers D13420–D13424, D13426, D13427.
 - 19) **KE.NA113:** This sequence was derived from a patient who was part of a May-June 1992 study of pregnant women from the Pumwani Maternity Hospital in Nairobi, Kenya. Viral RNA was concentrated from patient serum just prior to delivery, and the envelope C2-V3 region was amplified by RT-PCR. The PCR product was cloned and 20 clones from the patient were sequenced. Seven other patients from this study had viral subtypes A and D. [Zachar et al.(1996a)]. Accession number U33762.
 - 20) **MW.SM750:** This sequence is from cloned PCR amplified cocultured PBMC DNA. SM750 was a black male sampled in the gold mines in Malawi in 1989. [Becker et al.(1995)]. Accession number U06719.

- 21) **MW1.ID#:** These 13 sequences are from pregnant women with risk factors from Malawi. PCR-direct, peripheral blood DNA. [Orloff et al.(1993)]. Accession numbers L07427–L07441, L15721–L15735.
- 22) **MW2.D-ID#:** These two sequences are from individuals from Malawi, generated as part of the DAIDS variation program in the laboratory of Dr. Beatrice Hahn at the University of Alabama. The C2V3 was excised from full gp160 sequences, derived from clones from expanded culture stocks. The sequence ID numbers are abbreviated, for example D3MA959 can be read as DAIDS sequence (D), isolated in 1993 (3), Malawi (MA), patient 301959 (959). Accession numbers U08453–U08454.
- 23) **MY.ID#:** These 2 sequences are from IV drug using prisoners in a prison in Kuala Lumpur, Malaysia. PCR products amplified from uncultured PBMCs were directly sequenced. Both of these prisoners had received medical treatment in India which included blood transfusion and organ transplants, and it is likely that they were infected in India. [Brown et al.(1996)]. This report also included subtypes B and E in Malaysia. Accession numbers U65549–U65550.
- 24) **NL1.ID#:** These 2 sequences are from a Dutch woman whose partner was a recent immigrant to The Netherlands from Zaire, and from a recent immigrant to The Netherlands from either Zambia or Zaire. The first two letters of the ID# represent the two letter country code for the previous residence of the patient (UN = unknown). The next two numerals represent the year of isolation. Viral RNA was prepared from patient serum and RT-PCR was used to amplify the V3 region of the env gene. The PCR products were directly sequenced. The sequence from the Dutch/Zaire patient is not unequivocally a sub sequence, it may be subtype A or unclassifiable. [Lukashov et al.(1996)]. Accession numbers L76908, NL9402418; L76898, UN9305091.
- 25) **NO1.ID#:** These 4 sequences are from Norwegian patients who were part of the Oslo HIV cohort study [Engelstad(1996)]. Uncultured PBMC DNA was PCR amplified in two nested PCR reaction steps. PCR products were directly sequenced. Where two peaks of equal height were observed at a single position, IUPAC ambiguity codes were used. Health, sex, year of sample (1989-1992), and risk group (IVDU, Het, Homo, Hemo) for each patient were noted in a table in the publication. The four subtype C sequences were all from heterosexuals who had sex with persons from Zambia (3) or South Africa (1). Thirty-six subtype B sequences were also part of this set (see B_NO1.ID#). Accession numbers X92913, X92914, X92917 and X92918.
- 26) **RU.ID#:** These 4 sequences are from Russia. [Lukashov et al.(1995)]. Accession numbers: L38418, RUS20A; L38404, RUS2A; L38406, RUS1A; L38414, RUS13A.
- 27) **RU1.YAN4:** This sequence is from Russia. Bobkov et al. 1996 Unpublished. Accession number U33109.
- 28) **RW1.ID#:** These two sequences are consensus sequences of many clones from mothers infected in Rwanda. Mulder-Kampinga et al., Unpublished (1996) and [Kampinga et al.(1997)]. Mother 566 was apparently dually infected with HIV-1 subtypes A and C. See also A_RW4.ID#. Accession numbers for mother 566 are Z76183, Z76188–Z76197, Z76284–Z76293, Z76295–Z76299, Z76301, Z76303–Z76311, Z76322–Z76342 and Z76725–Z76732; for mother 134, Z76039–Z76042 and Z76044.
- 29) **SN.SE364:** A Senegalese sequence from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989–1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)]. Accession number L22944.
- 30) **SO.1574:** This sequence is a consensus sequence of blood and CSF samples taken from the Somalian patient 1574, CDC classification II. [Keys et al.(1993)]. Accession numbers Z23188, Z23190–Z23191, and Z23228–Z23231.
- 31) **SO.SM145:** A Somalian sequence from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989–1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)]. Accession number L22946.
- 32) **TW1.252** This sequence is one of a set of sequences from Taiwan. Other sequences in the set were subtypes B, E, F or G. [Chang et al.(1997)]. Accession number U73055.
- 33) **TZ1.1588:** This sequence is from the Mara region of rural
- 34) **UG.45:** A single sequence used in a study of the impact of sequence variation on the distribution and seroreactivity of linear antigenic epitopes. The sequence was derived from PCR amplified DNA

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- from peripheral blood leukocytes. The patient was an asymptomatic individual from Uganda. [Pestano et al.(1995)]. Accession number U11597. See also A_UG1.964, B_US17.ID#, and D_UG7.ID#.
- 35) **UG.UG268:** A Ugandan sequence from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989–1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)]. Accession number L22948.
 - 36) **ZA.NOF:** This sequence is from a South African individual who was part of a study of HIV-1 strains in India. This sequence was found to be closer to the Indian sequences, than are other isolates from Africa. PCR amplified DNA from PBMC cultures were sequenced. [Dietrich et al.(1993)] and [Becker et al.(1995)]. Accession numbers L07426 and U06716. See also C_IN3.ID#, B_IN.IND9.
 - 37) **ZA1.ID#:** These 2 sequences are from 2 individuals in South Africa. ZA514 was from a 59 year old mixed-race male heterosexual with AIDS and the virus was NSI. ZA517 was from a 33 year old mixed-race male heterosexual with ARC and the virus was NSI. The samples were collected at the Tygerberg Hospital in the Western Cape region of South Africa between 1984 and 1992. DNA was harvested from cocultured PBMCs and the env gene was PCR amplified and cloned into pBSKS+ for sequencing. Each sequence is from a single cloned PCR product. [Engelbrecht et al.(1995)]. Accession numbers L48067–L48068. Database entries U33781 and U33782 are shorter env gene fragments from these same clones. See also B_ZA and D_ZA sequences from this same study.
 - 38) **ZA2.ID:** These 3 sequences are from clones from PCR amplified cocultured PBMC DNA. Dlu was a black male sampled at the Tygerberg Hospital in Cape Town, South Africa in 1990. Gom was a black male sampled at the Tygerberg Hospital in Cape Town, South Africa in 1990. BooyD was a mixed-race female mother sampled at the Tygerberg Hospital in Cape Town, South Africa in 1990. A short sequence from a seropositive child of BooyD is presented in entry U07015. [Becker et al.(1995)]. Accession numbers U07237, U06717 and U06718.
 - 39) **ZM1.ZAM-ID#:** Two sequences from Zambia, from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989–1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)]. Accession numbers L22954 and L22956.
 - 40) **ZW.2647:** This sequence is a consensus sequence taken from blood and CSF samples taken from Zimbabwe patient 2647, CDC classification II. [Keys et al.(1993)]. Accession numbers Z23196–Z23199 and Z23236–Z23239.

D Subtype

At this time there are viral sequences from 119 HIV-1 infected individuals associated with HIV-1 subtype D. The D subtype consensus sequence (D_CONSENSUS_97) generated from these sequences was based on the most common amino acid found in each position of an alignment. All of these sequences have been published and/or have been made available for printing in the database by their authors.

- 1) **BLBU009con:** This is a consensus sequence from 8 clones from a 36 year old female with CDC stage IV AIDS and pulmonary tuberculosis, from Bujumbura, Burundi. PBMCs from the patient were cocultured with donor PBMCs for 2 weeks, at which time large syncytia formed and the culture became antigen positive. The env region was then PCR amplified by nested PCR and cloned. [Ranjbar et al.(1995)] and [Ranjbar(1995)]. Accession numbers L35452–L35459.
- 2) **BR.RJ100** This sequence is from Rio De Janeiro, Brazil. Morgado et al. unpublished, 1997. Accession number AF000238.
- 3) **CF.4020:** This sequence was the only D subtype from a set of sequences obtained from 27 symptomatic patients from the Central African Republic, from whom blood was drawn in 1990–1991. It is a consensus from cloned PCR products, derived from cultrued proviral DNA. [Murphy et al.(1993)]. A full gp120 sequence from this isolate was kindly provided prior to publication by Dr. MP Kieny of Transgene, Strasbourg, France. It is a part of a set of 14 HIV-1 gp120 isolates from Bangui, Central African Republic. The gp120 proteins have been expressed in a hybrid gp160 vaccinia virus expression system [Richalet-Secordel et al.(1994)]. The year of isolation and health status of individuals from which the viruses were isolated were not provided. Viruses were isolated in the CAR by C Mathiot and B You (Pasteur Inst., Bangui), grown by F Barre-Sinoussi and A Deslandres (Pasteur Inst., Paris), and cloned and sequenced by D Schmitt and MP Kieny. Sequences of clones from sample 4093 (Accession numbers L11517, L11517) which was taken from the same patient as 4020 one year later, are closely related and are not included here. Accession numbers L11472–L11473, U43138.
- 4) **CI.CI-13:** A single D subtype sequence from a set of 13 isolates from individuals from Abidjan, Cote d'Ivoire. CI-13 was symptomatic, and serologically dually reactive for HIV-1 and HIV-2. The C2V3 region is part of a 900 bp fragment that was sequenced for each individual. Samples were collected between May 1990 and Sept. 1991. Virus was cultured with donor PBMCs, nested PCR amplified, 3–4 clones were sequenced, and the consensus of those clones is presented here. [Janssens et al.(1994a)]. Accession numbers X72028–X72029.
- 5) **CI.I.ID#:** These 2 sequences are from Abidjan, Ivory Coast. No other information is yet available. Ellenberger D.L. unpublished 1997. Subtypes A, D and G were found for Ivory Coast patients in this set. Ugandan sequences of subtype A were also part of this set. Accession numbers AF000469, AF000451.
- 6) **CM.CMR61D:** CMR61 is one of two D group sequences from a 23 year old female commercial sex worker from Cameroon who was found to be triple-infected with subtypes A and D, as well as O group HIV-1 [Takehisa et al.(1997b)]. The other sequence from the same patient is labelled as CMR709 and is from a separate blood sample. Accession numbers U58149, U58151.
- 7) **D_CM2.ID#:** These four sequences are all from Cameroon. Takehisa et al unpublished-1997. Accession numbers U70013, U70012, U70011
- 8) **GA1.ID#:** These 2 sequences are from 1988 or 1989 samples from patients with AIDS living in Franceville Gabon. Method of proviral DNA isolation was not described. DNA was PCR amplified and cloned. One clone per isolate was sequenced, [Delaporte et al.(1996)]. Accession numbers X90919, G109; X90920 G141. See also subtypes A, C, F, G and O sequences from this same study.
- 9) **GB1.CPHL4:** This sequence is a consensus from the British isolate 93–43424, clones 2, 6 and 35. It was referred to as 93–43424 in [Arnold et al.(1995c)] and as CPHL4 in [Arnold et al.(1995a)]. Accession numbers U21098 (clone 35) and U23121–U23122 (clones 2 and 6 respectively). CPHL4 is a female who is believed to have contracted the virus from CPHL5 through heterosexual contact. Sequences from CPHL5 are not included in this alignment due to this epidemiological relationship.
- 10) **GH.GH3:** This sequence is from Ghana. Subtypes A and an A/G recombinant were also detected in this study [Takehisa et al.(1997a)]. Accession number U67049.
- 11) **GH1.ID#:** These 2 sequences are from Ghana. Subtypes A and G were also detected in this study [Ishikawa et al.(1996)]. Accession numbers for subtype D are U67682 and U67684.

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- 12) **KE.NA116:** This sequence was derived from a patient who was part of a May-June 1992 study of pregnant women from the Pumwani Maternity Hospital in Nairobi, Kenya. Viral RNA was concentrated from patient serum just prior to delivery, and the envelope C2-V3 region was amplified by RT-PCR. The PCR product was cloned and 20 clones from the patient were sequenced. Seven other patients from this study had viral subtypes A and C. [Zachar et al.(1996a)]. Accession number U33765.
- 13) **KE1.KEN-ID#:** These three patients were part of a 1990–1992 cohort study of maternal risk factors in mother to child transmission, including 22 pregnant women and an infant from Kenya. The C2V3 region was sequenced. [Janssens et al.(1994c)]. Accession numbers for sequences from the entire set of 23 patients studied in this publication: U12984–U13006.
- 14) **NL.A11:** This sequence is from a Dutch study of presumed HIV-1 donor-recipient pairs. This sequence is from a recipient at the time of seroconversion; the donor was a Zairean woman living in the Netherlands (patient A12 accession numbers M91840–M91848). The sequences from both donor and recipient were extremely similar, so only the recipient (patient A11) is shown here. This sequence is a consensus sequences of multiple clones from PCR amplified serum RNA. [Wolfs et al.(1992)]. Accession numbers M91849–M91856.
- 15) **NL2.ID#:** These 7 sequences are from recent immigrants to The Netherlands from various countries. The first two letters of the ID# represent the two letter country code for the previous residence of the patient. The next two numerals represent the year of isolation. Viral RNA was prepared from patient serum and RT-PCR was used to amplify the V3 region of the env gene. The PCR products were directly sequenced. [Lukashov et al.(1996)]. Accession numbers L76900, UG9307184; L76907, ZR9402261; L76892, ZR929193; L76904, UG9401525; L76895, AO9302187; L76872, ZR891183; L76876, ZR901100.
- 16) **RU.RUS14A** This sequence is from [Lukashov et al.(1995)]. Accession number L38415.
- 17) **SN.SE365:** A Senegalese sequence from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989–1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)]. Accession number L22945.
- 18) **TZ1.TAN-ID#:** These ten sequences are from a set of 14 Tanzanian samples from symptomatic individuals, using serum samples taken in 1988 to generate PCR clones from viral RNA for sequencing. [Zwart et al.(1993)]. Accession numbers L01298–L01339.
- 19) **TZ2.ID#:** These eight sequences were from patients at a clinic in Dar es Salaam, Tanzania. The individuals from which the virus was cultured showed clinical signs of AIDS, and the year of viral isolation was 1988. Viral cDNA was PCR amplified from donor PBMC, and one cloned PCR product per donor was sequenced. [Siwka et al.(1994)]. Accession numbers U12406, U12407, U12410–U12415.
- 20) **TZ3.ID#:** These 4 sequences are from the Mara region of rural northwest Tanzania. [Robbins et al.(1996)]. Subtype A was also found in this study. Accession numbers U61875 and U61879–U61881.
- 21) **UG.U44342:** This sequence is from a Ugandan. Consensus of PCR-clones, peripheral blood DNA. Intact env sequences are available from this sample. [Bruce et al.(1993)]. Accession numbers M98408–M98416.
- 22) **UG.UG23:** This sequence is from blood collected from the Mulago Teaching Hospital in Kampala, Uganda. Viral RNA was harvested after 10-14 days of coculture with donor PBMCs and reverse-transcribed with AMV-RT. The env V3 region was PCR amplified and cloned. This sequence is from an individual clone. [Atkin et al.(1993)], [Pestano et al.(1993)]. Accession number M98504.
- 23) **UG1.W2UG-ID#:** Twelve sequences from asymptomatic individuals from Uganda in 1992. Each sequence is a consensus from cloned PCR products derived from cell-cultured proviral DNA or culture supernatant RNA. These sequences were provided by the WHO Global Programme on AIDS Vaccine Development Study. The complete set of C2V3 region WHO sequences can be found in the April supplement to the Human Retroviruses and AIDS 1993 database. [De Wolf et al.(1994)]; [Osmanov et al.(1994)]; [Gao et al.(1994c)]. Accession numbers U08721–U08741, U08786–U08787, U08803–U08809, U08821–U08824, U27399, U43386. Two sequences not reported to be related to these Ugandan isolates are suspected to represent lab contamination of PCR reactions with these isolates: U58827 (FRMP153) is 99% identical to 92UG046; and L38415 (RUS14A) is 99% identical to 92UG024.
- 24) **UG2.ID#:** These twelve sequences are from 1986–1987 Ugandan samples. Each sequence is a consensus from cloned PCR products derived from uncultured proviral DNA harvested directly from patient PBMCs. [Oram et al.(1991)]. No database entries exist for these sequences.

- 25) **UG3.ID#:** These 11 sequences are part of a set of sequences derived from 22 Ugandans who were attending an AIDS clinic. Blood samples were obtained in 1990. Each sequence is a consensus from cloned PCR products derived from uncultured proviral DNA harvested directly from patient PBMCs. [Albert et al.(1992)]. Accession numbers L00614–L00618, L00733–L00737, M98894–M98899, M98901, M98906–M98907, M98911–M98913, M98918, M98920–M98923, M98929–M98937, M98942–M98945 and M98967–M98975.
- 26) **UG4.ID#:** One to 4 clones of each these Ugandan isolates were sequenced, but only one clone is shown here. [Douglas et al.(1996)]. Other Ugandan isolates sequenced in this study were subtype D/A recombinant. London subtype B clones were also reported. Complete envelope gp160 sequences were reported for all isolates. Accession numbers U36867, U36868, U36871, U36884–U36887.
- 27) **UG5.UG-ID#:** Three Ugandan sequences from a set of HIV-1 viral isolates from Africa. Health status of the individuals from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989–1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)]. Accession numbers L22947 and L22949–L22950.
- 28) **UG6.ID#:** Three Ugandan sequences from a set of HIV-1 viral isolates from Africa. All three individuals from which the virus was cultured had AIDS, and the year of viral isolation was 1987. Viruses were cultured with HUT-78 cells for an unspecified length of time. The V3 region of env (gp160) was amplified, cloned and sequenced. [von A. et al.(1995)]. Accession numbers U15005, U15006 and U15007.
- 29) **UG7.ID#:** These sequences were used in a study of the impact of sequence variation on the distribution and seroreactivity of linear antigenic epitopes. Both sets of sequences were from PCR amplified DNA from peripheral blood leukocytes. All patients were asymptomatic individuals reporting for regular blood drawing at the Nakasero blood transfusion service, Kampala, Uganda. [Pestano et al.(1995)]. Accession numbers U11595, U11596, and U11598. See also A_UG1.964, C_UG1.45, and D_UG7.ID#.
- 30) **UG8.#:** These 2 sequences are from Gulu, northern Uganda. They are from direct sequence of PCR product amplified from uncultured PBMCs. Blood samples were drawn from 217 pregnant women attending the clinic in Gulu, northern Uganda. Ages ranged from 17 to 37 years. The 29 seropositive women (13.4%) were all asymptomatic. [Buonaguro et al.(1995)]. Database accession numbers U44881 and U44884. Eight subtype A sequences were also found in this study (see A_UG5).
- 31) **US.AMK:** This sequence comes from a student living in Alabama, who moved from Zaire to the US in 1988. Virus was isolated from the patients PBMCs; this isolate was PCR amplified, and amplification products from both gag (U08192) and env were subcloned and sequenced. His CD4 count was < 5 cells/mm³, and he was symptomatic at the time of viral isolation. [Gao et al.(1994c)] and [Gao et al.(1996a)]. AMK is also known as 93ZR001. Accession numbers U08193, U27419.
- 32) **ZA.ID#:** These 5 sequences are from 5 individuals in South Africa. ZA500 was from a 41 year old white male homosexual with ARC and the virus was non-syncytium-inducing (NSI). ZA501 was from a 24 year old white male bisexual with AIDS and the virus was SI. ZA505 was from a 36 year old white male homosexual with AIDS and the virus was SI. ZA506 was from a 33 year old white male homosexual with AIDS and the virus was SI. ZA507 was from a 37 year old white male homosexual with AIDS and the virus was SI. All samples were collected at the Tygerberg Hospital in the Western Cape region of South Africa between 1984 and 1992. DNA was harvested from cocultured PBMCs and the env gene was PCR amplified and cloned into pBSKS+ for sequencing. Each sequence is from a single cloned PCR product. [Engelbrecht et al.(1995)]. Accession numbers L47608, L48061, L48062, L48070 and L48072. Database entries U33769, U33771–U33773 and U33780 are shorter env gene fragments from these same clones. See also B_ZA and C_ZA1 sequences from this same publication.
- 33) **ZR.ELI:** This sequence is from the Zairean isolate ELI. [Alizon et al.(1986)] and [Goodenow et al.(1989)]. The complete genomic sequence and an infectious clone are available. In the 1995 Compendium (pages III-45 and III-47), ELI was listed as a possible D/A mosaic, with gp41 being A-like. Accession numbers M27949, K03454 and X04414.
- 34) **ZR.JY1:** This sequence is from Zairean isolate Z-84, clone JY1. [Youno et al.(1988)]. Accession number J03653.
- 35) **ZR.MAD:** This sequence is from an asymptomatic Zairean woman who was seropositive for HIV-1 by several French-approved HIV tests and by HIV-1 western blot. The viral sequences obtained for

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- the env V3 region and gp41 show that this isolate belongs to M-group subtype D. [Cohen et al.(1995)]. Accession number X83216. A region of gp41 is also sequenced, see X83215.
- 36) **ZR.MAL:** This sequence is from a non-infectious clone of the Zairean isolate MAL. [Alizon et al.(1986)]. The complete genomic sequence and an infectious clone from the isolate MAL are available. MAL is known to be recombinant between subtypes A, D and I. Accession numbers K03456 and X04415.
 - 37) **ZR.NDK:** This sequence is from an infectious clone of the Zairean isolate NDK. The molecular clone is highly cytopathic in vitro. [Spire et al.(1989)]. The complete genomic sequence is available. Accession number M27323.
 - 38) **ZR.Z2Z6:** This sequence is from an infectious clone of Zairean isolate Z2. Theodore T, and Buckler-White A, unpublished. The complete genomic sequence is available. Accession number M22639. See also [Srinivasan et al.(1987)]. The database entry with accession numbers K03458 and M16322, which is from the same isolate.
 - 39) **ZR1.ID#:** These four sequences are part of a set of 14 A and D sequences from women from Zaire. 8 were healthy, 4 showed minor signs of illness, and 2 had AIDS. Sequences were determined by directly sequencing PCR products derived from uncultured proviral DNA harvested directly from patient PBMCs. [Potts et al.(1993a)]. Accession numbers L19623, L19627, L19631 and L19635.

E Subtype

At this time there are viral sequences from 135 HIV-1 infected individuals associated with HIV-1 subtype E. The E subtype consensus sequence (E_CONSENSUS_97) generated from these sequences was based on the most common amino acid found in each position of an alignment. All of these sequences have been published and/or have been made available for printing in the database by their authors.

- 1) **CF.90CF402** 90CF402, previously named CAR-E 4002 or 90CR402, was obtained from a man from Bangui, Central African Republic, who had lymphadenopathy, diarrhea, severe weight loss and recurrent respiratory infections. He was infected through heterosexual contact, but the year of infection is unknown. The virus was first adapted to growth in chimpanzee cells, expanded in chimpanzee cells, and then re-expanded in human PBMCs before lambda cloning and sequencing. [Gao et al.(1996b)]. The complete genome is found with Accession number U51188.
- 2) **CF1.ID#:** These eight sequences are from a set of sequences obtained from 27 symptomatic patients from the Central African Republic, from whom blood was drawn in 1990–1991. Consensus, PCR-clones, cell culture, DNA. [Murphy et al.(1993)]. Accession numbers L11459–L11460, L11463–L11468, L11476, L11480–L11481, L11504–L11505, L11511–L11513, L11519–L11521 and U43137. Another sequence from patient 4039 is found with accession number U43112.
- 3) **CF2.ID#:** These three sequences were kindly provided prior to publication by Dr. M.P. Kieny of Transgene, Strasbourg Cedex, France. They are part of a set of 14 HIV-1 gp120 isolates from Bangui, Central African Republic. The gp120 proteins have been expressed in a hybrid gp160 vaccinia virus expression system. Year of isolation and health status of individuals from which the virus was isolated were not provided. Viruses were isolated in the CAR by C. Mathiot and B. You (Pasteur Inst., Bangui), grown by F. Barre-Sinoussi and A. Deslandres (Pasteur Inst., Paris), and cloned and sequenced by D. Schmitt and M.P. Kieny. Database accession numbers U43110, U43170 and U43173.
- 4) **CM.CA10:** A single E subtype sequence from a set of 17 sequences from a very diverse set of isolates from Yaounde and Douala, Cameroon. The sequences were derived from asymptomatic and symptomatic HIV infected individuals, specifically, CA10 was symptomatic. Virus was isolated by culture with donor PBMCs, and nested PCR amplified. A single clone was sequenced representing each HIV-1 isolate. [Nkengasong et al.(1994)]. Accession number X80439.
- 5) **CM.CMR10:** This sequence is from Cameroon. Takehisa et al unpublished-1997. Accession number U69991
- 6) **FR1.ID#:** These six sequences are from members of the French military who are believed to have been infected while deployed in Cambodia between 1992 and 1995. Other sequences from this study were subtypes A, B, C, F, and unclassified. [Lasky et al.(1997)]. Accession numbers for subtype E were U58779–U58784.
- 7) **GB1.11643:** This sequence is from the British isolate 94–11643. The sequence was determined from PCR-amplified lymphocyte DNA. The gag gene from this isolate was subtype A, as is the gag gene from all subtype E virus studied to date. The patient is thought to have contracted the virus in Thailand, but currently lives in the United Kingdom. [Arnold et al.(1995c)]. Accession number U21109.
- 8) **ID1.ID#:** These 7 sequences are from a set of 14 sequences from Indonesia [Porter et al.(1997)]. Accession numbers U68189–U68194. Subtype B was also identified in 7 other samples from Indonesia in this study. PCR products were directly sequenced from either uncultured PBMC DNA or cocultured PBMC DNA.
- 9) **JP.JH23B:** This sequence is from a Japanese patient dually infected with HIV-1 subtypes B and E [Xin et al.(1995a)]. Accession number D67090. See also D67089, B_JP.JH23A.
- 10) **JP1.ID#:** These three sequences are from one Japanese and two Thai individuals living in Japan, obtained by direct sequencing of PCR-amplified proviral DNA from peripheral blood mononuclear cells. [Weniger et al.(1994)]. NIH3J is from a male Japanese national. NIH2T and NIH4T are from Thai female prostitutes, living in Japan. Accession numbers L32085–L32087.
- 11) **JP2.Pat43:** This sequence is from a study of rapid versus slow progressors in Japan. Patient 43 was a rapid progressor infected through sexual contact in 1992 after testing negative in 1991, [Shioda et al.(1997)]. Other sequences in this study were subtype B. Accession numbers AB002975–AB002987.

Sequence Descriptions

- 12) **MM.1786:** This sequence is from a dried blood spot collected in 1992 from a Female STD patient in Myanmar. DNA was extracted from the blood spots and PCR amplified. The PCR products were directly sequenced. [Cassol et al.(1996)]. Accession number U53309.
- 13) **MY.9214103:** This sequence is from a Thailand infant who was adopted by Malaysians, and now lives in Malaysia. PCR products amplified from uncultured PBMCs were directly sequenced. [Brown et al.(1996)]. This report also included subtypes B and C in Malaysia. Accession number U65551.
- 14) **NL.TH94037:** This sequence is from a recent immigrant to The Netherlands from Thailand. The blood sample was collected in 1994. Viral RNA was prepared from patient serum and RT-PCR was used to amplify the V3 region of the env gene. The PCR product was directly sequenced. [Lukashov et al.(1996)]. Accession number L76911.
- 15) **RU1.1164con:** This is a consensus of 3 clones from a single patient RU1164 from Russia. [Bobkov et al.(1997a)]. The patient was a 21 year old asymptomatic commercial sex worker who first tested HIV positive in April, 1996. Blood was collected for this sequence in May, 1996. She reported having travelled to Singapore in 1994-1996 and having multiple sexual clients there. DNA from uncultured PBMCs was PCR amplified, cloned and sequenced. Patient RU1164 lives in Khabarovsk kray in the far eastern part of the Russian Federation. This is the first report of subtype E in Russia. Accession numbers U93607, U93608, U93609.
- 16) **TH.93TH253:** This sequence is from a 21-year-old man from Chiang Mai, Thailand and was previously named CMU010 or 302053. The patient had end-stage AIDS. The mode and year of infection are unknown. 93th253 was isolated in 1993 and expanded in human PBMCs, then expanded in H9 cells, and followed by lambda cloning and sequencing. The complete genome has been sequenced. [Gao et al.(1996b)]. Accession number U51189.
- 17) **THC18:** This sequence is derived from an HIV-1 infected mother enrolled in Bangkok in a perinatal transmission study. Her plasma was screened for gp120 binding antibody, CD4/gp120-binding inhibition, to subtype B (MN/H9), and Thai E (SL7/SupT1) using native gp120 antigens and neutralizing antibody to subtype B and Thai E isolates. In these assays, THC18 plasma showed a pattern of antibody reactivity similar to other E sera. The genetic subtype of this HIV-1 isolate was identified by HMA. [Louisirirochanakul et al.(1997)]. Accession number U96782.
- 18) **TH.CM240:** This sequence is from a 21 year old asymptomatic man from northern Thailand. The route of infection is believed to be heterosexual transmission. The blood sample was collected in 1990. The patient's PBMCs were cocultured with stimulated donor PBMCs and proviral DNA was harvested for PCR amplification and sequencing of a cloned full-length genome PCR product. [Carr et al.(1996)]. The complete genome is found in the databases with accession number U54771.
- 19) **TH.N764:** This sequence is from a survey of IV drug using prisoners in Thailand. 12 of 13 sequences from Thai prisoners were of subtype B; N764, from patient (THP13) represents the only subtype E sequence identified in this set, from a prisoner infected in 1989. The sequences were obtained from PCR amplified PBMC DNA. [Kalish et al.(1994)]. Accession number U15588.
- 20) **TH.T8178:** This sequence comes from a study of the genetic heterogeneity and epidemiological distribution of HIV1 in Thailand. The host was a female prostitute and the sequence was obtained from PCR amplified PBMC DNA. [Ou et al.(1993)]. Accession number L19239. See also B_TH.T8174.
- 21) **TH1.ID#:** These twelve sequences are from a set of 23 individuals from Thailand. PCR-direct, peripheral blood PBMC DNA. Referred to as Thai subtype A in [Ou et al.(1992b)] and [Ou et al.(1993)]. (Published erratum appears in *Lancet* **342**:250 (1993).) Accession numbers L07443–L07445, L07447–L07448, L07457–L07459 and L07461–L07464.
- 22) **TH2.ID#:** Six of these eight sequences are from 16 isolates from HIV seropositive individuals from Thailand. Sequences were from PCR products derived from co-cultured PBMC DNA. The full length envelope gene sequences are available. [McCutchan et al.(1992)]. Please note: the "TN-ID#" locus names in the database correspond to the McCutchan et al.'s "CM-ID#" isolates. Accession numbers L03698–L03701 and L03703–L03704. The other two (TH238, TN240) are also from Thailand, DNA from PBMC. [Mascola et al.(1994)]. Accession numbers L14571, L14572.
- 23) **TH3.W2TH-ID#:** Fifteen sequences from asymptomatic individuals from Thailand in 1992. Consensus, PCR-clones, cell-culture DNA and RNA. These sequences were provided by the WHO Global Programme on AIDS Vaccine Development Study. The complete set of C2V3 region WHO sequences can be found in the April supplement to the Human Retroviruses and AIDS 1993 database. [De Wolf et al.(1994)];

- [Osmanov et al.(1994)]; and [Gao et al.(1994a)]. Accession numbers U08810–U08811, U08825–U08836 and U08742–U08761. The entry with accession number U09131 is also TH_W2TH022.
- 24) **TH4.D-ID#:** These three sequences are part of a set of sequences generated for the DAIDS variation program in the laboratory of Dr. Beatrice Hahn at the University of Alabama. They are clones from expanded culture stocks, and are excised from full gp160 sequences. The sequence ID numbers are abbreviated, for example D3TH966 can be read as DAIDS sequence (D), isolated in 1993 (3), Thai (TH), patient 301966 (966). [Gao et al.(1996a)]. Accession numbers U08456–U08458.
 - 25) **TH5.ID#:** These seventeen consensus and five individual sequences are from twenty two patients with AIDS involved in a study of genotypic and phenotypic characteristics of Thai HIV-1. Blood samples were collected between July and December 1993. All sequences were derived from PCR amplified PBMC DNA, after patient PBMCs were cocultured with virus-free donor PBMCs. CMU01, CMU03, CMU04, CMU05, CMU07, and CMU10 are NSI, the rest are SI, as determined by syncytium formation in the cocultured cells. CM = Chang Mai University Hospital. KH = Kavila Army Hospital. All subjects were males and reported past contact with commercial female sex workers, but no history of drug injection, blood transfusion or homosexual contact. [Yu et al.(1995)]. Accession numbers U25550–U25626. Longer sequences from samples KH003, KH005, KH008, CMU02, CMU08 and CMU010 were determined in 1996 [McCutchan et al.(1996)]. Accession numbers U48264–U48269.
 - 26) **TH6.ID#:** These three sequences are E subtype sequences from Thailand. Two individuals believed to be dually infected with subtypes B and E were analyzed. It is not clear from the paper or the database entries which sequences came from individual 1 and which from 2. [Artenstein et al.(1995)]. Accession numbers U21472, U21474, U21476. See also B_TH5.ID#.
 - 27) **TH7.ID#:** These two sequences are from samples collected in 1993 in Thailand. Patients 1018 and 1110 were asymptomatic. [McCutchan et al.(1996)]. Accession numbers U48273–U48274.
 - 28) **TH8.ID#:** These two sequences were from dried blood spots collected in 1992 from a heterosexual (0289) and an IV drug user (0103). DNA was extracted from the blood spots and PCR amplified. The PCR products were directly sequenced. [Cassol et al.(1996)]. Accession numbers U53312 and U53313.
 - 29) **TH9.ID#:** These 14 sequences are from 84 IV drug users in Bangkok, Thailand, who were undergoing methadone treatment at 14 treatment clinics. Blood samples were collected between January and April, 1994. Uncultured PBMC DNA from each patient was PCR amplified, and the PCR product was directly sequenced. Of the 84 patients sampled, 69 were Thai B, one (091) was typical subtype B, and 14 were subtype E. [Kalish et al.(1995)]. Accession numbers U22542, U22548, U22553, U22557, U22561, U22567, U22575, U22604, U22609, U22611, U22612, U22617, U22624 and U22625. See also B_TH7.
 - 30) **TH10.ID#:** These sequences are from Thailand. They are part of several complete env gene sequences obtained for the World Health Organization. HMA subtyping as well as sequence-determined subtyping was done on each one. Sequences were PCR amplified from cocultured PBMCs. Two clones from each isolate were sequenced. [Penny et al.(1996)]. Accession numbers U39256 and U39260, 92TH002; U39255 and U39261, 92TH011.
 - 31) **TW1.ID#:** These 3 sequences are from healthy HIV-1 carriers or AIDS patients from Taiwan [Chang et al.(1997)]. Other subtypes found in Taiwan in this study were B, C, F and G. Accession numbers U73060, U73062 and U73070.
 - 32) **US.POC30506:** This sequence is from a U.S. serviceman who aquired an HIV-1 infection while deployed in Thailand. He was asymptomatic when the sample for this sequence was collected in 1993. [McCutchan et al.(1996)]. Accession number U48272.
 - 33) **UY.ID#:** These four sequences are from Uruguayan servicemen who aquired HIV-1 infections while deployed as United Nations peacekeepers in Cambodia in 1993. All four were asymptomatic when samples were collected for these sequences in 1993. [McCutchan et al.(1996)]. Accession numbers U48275–U48278.
 - 34) **VN1.ID#:** These 3 sequences are from South Vietnam. [Menu et al.(1996)]. The sequences were from IV drug users in Ho Chi Minh city and Dong Nai, and a female prostitute in Can Tho. A fourth sequence, from Ho Chi Minh city, was found to be subtype B. Accession numbers U29206-U29208.
 - 35) **VN2.ID#:** These 4 sequences are from South Viet Nam. VN1 and VN2 were from healthy 17 and 25 year old female prostitutes from Can Tho and An Giang. VN3 and VN 4 were from male IV drug users. VN3 was 43, had pruritus and splenomegaly, and was from Nha Trang. VN4 was 31, healthy and was also from Nha Trang. [Nerurkar et al.(1996)]. Accession numbers U45239, U45240, U48719 and U48720.

Sequence Descriptions

NOTE:

- 1) While the sequences in this subtype were distinct over this region of env from the other four env subtypes, in the gag gene it is not possible to make a distinction between this subtype and subtype A. What this means is that the isolates for which both gag and env are sequenced which cluster together as the “A” subtype in gag, are very distinctive in env and are broken down into two subtypes. env “A” and env “E”. This holds true for the E subtypes sequences that originated in Thailand, as well as the E subtype isolate from the Central African Republic for which gag sequence was obtained. [McCutchan et al.(1992)]; [Louwagie et al.(1993)]; and [Murphy et al.(1993)]. Complete genomes of subtype A and subtype E viruses became available in late 1996 [Gao et al.(1996b)], genbank accession numbers U51188–U51190.
- 2) The relative lack of diversity in the Thai sequences in this subtype relative to the other subtypes is likely to be a consequence of the short time span of the HIV-1 subtype E epidemic in Thailand. [McCutchan et al.(1992)], and [Ou et al.(1992b)].

F Subtype

At this time there are viral sequences from 80 HIV-1 infected individuals associated with HIV-1 subtype F. The F subtype consensus sequence (F_CONSENSUS_97) generated from these sequences was based on the most common amino acid found in each position of an alignment. All of these sequences have been published.

- 1) **AR1.ID#:** These two sequences are from direct sequencing of PCR products from uncultured PBMCs, from 1993 samples from Buenos Aires, Argentina. Patient 21280 had AIDS and reported IV drug abuse. Patient 20016 was asymptomatic and HIV risk behavior was unknown. Two other samples taken from unrelated patients in 1993 were subtypes B or B/F recombinant. [Marquina et al.(1996)]. Accession numbers U68522 and U68524.
- 2) **AR2.ID#:** These 3 sequences are from Rosario, Argentina. A total of 24 patients from different risk groups visiting a clinic in Rosario were included in this study. Of the 14 sequences determined, 11 were found to belong to subtype B and 3 were found to belong to subtype F. DNA was extracted from whole blood and PCR amplified. PCR products were directly sequenced. Subtypes of all 24 patients were also tested by HMA. [Campodonico et al.(1996)]. Accession numbers U37032, U37033 and U37043.
- 3) **BR.7944:** This sequence represents a single env F subtype sequence found among 22 Brazilian outpatients with varying degrees of disease progression. It was identified by Potts et al. as the single sequence which did not cluster with North American sequences in phylogenetic analysis. Consensus, PCR clones, peripheral blood PBMC DNA. [Potts et al.(1993b)]. Accession number L19237.
- 4) **BR.RJI03:** An F subtype sequence from Rio de Janeiro, Brazil. 26 additional B and a B-F recombinant were also observed in this set. Year of isolation for RJI03 was 1993, from a woman of CDC clinical stage II. [Morgado et al.(1994)]. DNA was amplified directly from PBMCs of an HIV infected woman with CDC stage II disease, and the PCR product was directly sequenced. Accession number U00422. See also [Sabino et al.(1994c)] Accession number U08974.
- 5) **BR1.BZ-ID#:** Three sequences from Brazil of the F subtype. Full length env (gp160) was amplified from proviral DNA of cultured PBMCs, cloned and sequenced. [Louwagie et al.(1994)]. Accession numbers L22082, L22084 and L22085. The gag gene of these same isolates is found in L22083, L22086 and L11751. Although shown in figure 2B of the paper as clustering with subtype F in the gag region, BZ126 (L22083) seems to be a subtype A outlier with a strong similarity to subtype C at the 3' end, and is 99A/C recombinant ZAM184. See also B_BR4.BZ-ID#.
- 6) **BR2.HSP#:** These 5 sequences are from Sao Paulo Brazil. They seem to be an extension of work published in [Morgado et al.(1994)] and [Sabino et al.(1994c)]. They are proviral DNA sequences from cloned PCR products, from uncultured PBMCs [Sabino et al.(1996)]. Accession numbers U31588, U31592-U31595.
- 7) **BR4.93BR02017:** This sequence is part of a set of sequences generated through the WHO Global Programme on AIDS. The virus was derived from a 52 year old asymptomatic male, from Rio de Janeiro, Brazil, whose route of infection is thought to be due to bisexual contact. The blood sample was taken in 1993. The env sequence clusters with HIV-1 subtype F sequences. The complete gp160 coding region of this isolate was sequenced along with those of others collected at major epicenters of the AIDS epidemic [Gao et al.(1996a)]. Accession number U27401.
- 8) **CM.CA-ID#:** These sequences are 3 of 17 sequences from a very diverse set of isolates from Yaounde and Douala, Cameroon. The sequences were derived from asymptomatic and symptomatic HIV infected individuals; specifically patients CA16 and CA20 were asymptomatic and patient CA4 was symptomatic. Virus was isolated by culture with donor PBMCs, and nested PCR amplified. A single clone was sequenced representing each HIV-1 isolate. The F subtype designation of these sequences is tentative. Although the F subtype sequences from Cameroon and Brazil consistently form a clade in phylogenetic analyses, the branch lengths between isolates from the two countries are typical of inter-subtype distances, and sequences from the two countries each form their own distinct clade within the F subtype (HIV database and Wouter Janssens, personal communication). [Nkengasong et al.(1994)]. Accession numbers for the subtype F sequences are X80443, X80448 and X80451.
- 9) **CM1.ID#:** These four sequences are all from Cameroon. Takehisa et al unpublished-1997. Accession numbers U70001, U69999, U69998, U69997

Sequence Descriptions

- 10) **CY.HO44-1:** This is a single sequence from two individuals who were heterosexual partners of one another. Patient 16 was a 29 year old bisexual male who was born and lived in Zaire, before moving to Cyprus. He was symptomatic with a CD4 count of 60 and had been seropositive for at least 6 years. Patient 44 was a 32 year old heterosexual female. She was asymptomatic with a CD4 count of 1,136. These samples, like others in this study (see also subtypes A, B, C, and I) were collected in February 1994 from the AIDS clinic in Nicosia, Cyprus. DNA was extracted from patient PBMCs and PCR amplified. After a second round of PCR, products were cloned and sequenced. One clone from patient 16 and one from patient 44 were sequenced. [Kostrikis et al.(1995)]. Because of the close epidemiological linkage, only the clone from patient 44 is presented here. Accession numbers U28662 (16) and U28679 (44).
- 11) **FR1.ID#:** This sequence is from a member of the French military who is believed to have been infected while deployed in the Central African Republic in 1992. Other sequences from this study were subtypes A, B, C, E and unclassified. [Lasky et al.(1997)]. Accession number U58807.
- 12) **GA1.VI354:** This sequence is from a 1989 sample from a patient with AIDS living in Libreville, Gabon. Method of proviral DNA isolation was not described. DNA was PCR amplified and cloned. One clone per isolate was sequenced. [Delaporte et al.(1996)]. Accession number X90923. See also subtypes A, C, D, G and O sequences from this same study.
- 13) **NL1.ID#:** These 3 sequences are from recent immigrants to The Netherlands from Brazil and Zaire. The first two letters of the ID# represent the two letter country code for the previous residence of the patient. The next two numerals represent the year of isolation. Viral RNA was prepared from patient serum and RT-PCR was used to amplify the V3 region of the env gene. The PCR products were directly sequenced. [Lukashov et al.(1996)]. Accession numbers L76899, ZR9306911; L76871, ZR890819; L76901, BR9400960.
- 14) **RO1.ID#:** These nine sequences are from isolates from Romanian children, in different clinical stages. All isolates showed cytopathic properties in peripheral blood mononuclear cells. DNA sequences are direct sequences of PCR products amplified from co-cultured PBMCs. The patients are also known as RM(A-J). [Dumitrescu et al.(1994)]. Accession numbers L19571–L19579.
- 15) **RO2.ID#:** These fifteen sequences are from isolates from Romanian children, infected nosocomially, and adults, infected through heterosexual transmission or transfusion. DNA sequences are direct sequences of PCR products amplified from co-cultured PBMCs. [Apetrei et al.(1997)]. Accession numbers Z83284–Z83303.
- 16) **RO3.RM-ID#:** These 24 sequences are from isolates from orphaned Romanian children, ranging in age from 2.5 to 6 years, admitted to a clinic in Tirgu Mures, Romania. All children were referred to this clinic with serious infections and are believed to have been infected horizontally in different orphanages. Virus was isolated after coculture with donor PBMCs. Proviral DNA from cocultured PBMCs was PCR amplified and the PCR products were directly sequenced. [Holm-Hansen et al.(1995)]. Accession numbers X77964–X77987.
- 17) **RU1.ID#:** These 3 sequences are from St. Petersburg and Armavir, Russia. Sequences were determined by direct sequencing of PCR product from uncultured PBMC proviral DNA. [Leitner et al.(1996b)]. RU26 is believed to have been infected by RU20, so only the RU26 sequence is shown here. RU20 was infected by a woman, whose husband was infected by HIV-1 while living in Congo. RU22, RU23 and RU29 were all heterosexually infected by the same HIV-1 infected man, thus only RU22 is presented here. RU30 is believed to have been infected in 1993 while traveling in the Congo. Accession numbers U69655, U69657, U69659, U69661, U69663 and U69664.
- 18) **TW1.3341:** This sequence is one of a set of sequences from Taiwan. Other sequences in the set were subtypes B, C, E or G. [Chang et al.(1997)]. Accession number U67765.

G Subtype

At this time there are viral sequences from 28 HIV-1 infected individuals associated with HIV-1 subtype G. The G subtype consensus sequence (G_CONSENSUS_97) generated from these sequences was based on the most common amino acid found in each position of an alignment. All of these sequences have been published and/or have been made available for printing in the database by their authors.

- 1) **BJ1.ID#:** These 2 sequences are from female prostitutes, born in either Ghana or Togo, who live in Benin. 43 is from directly sequenced PCR product, derived via RT-PCR from patient serum RNA. 259 is from cloned PCR product, also by RT-PCR from serum RNA. [Heyndrickx et al.(1996)]. Accession numbers U61872 and U61874. Subtype A sequences were also determined in this study.
- 2) **CF.4067:** This sequence was associated with the C subtype in first analysis of the C2V3 region ([Murphy et al.(1993)]), but when a full gp120 sequence became available from this isolate, and phylogenetic analysis was performed including some of the new subtype G sequences, it was more closely associated with G. The full length sequence was kindly provided prior to publication by Dr. MP Kieny of Transgene, Strasbourg Cedex, France. It is part of a set of 14 HIV-1 gp120 isolates from Bangui, Central African Republic. The gp120 proteins have been expressed in a hybrid gp160 vaccinia virus expression system. Year of isolation and health status of individuals from which the virus was isolated were not provided. Viruses were isolated in the CAR by C Mathiot and B You (Pasteur Inst., Bangui), grown by F Barre-Sinoussi and A Deslandres (Pasteur Inst., Paris), and cloned and sequenced by D Schmitt and MP Kieny. Accession numbers L11499 and L11500, U43169.
- 3) **CF1.15166:** A single sequence from a set of sequences obtained from 27 symptomatic patients from the Central African Republic, from whom blood was drawn in 1990–1991. It is a consensus from PCR clones from cultured proviral DNA. [Murphy et al.(1993)]. Accession number L11525. Other sequences from this study were subtypes A, D, E and unclassified. This sequence was originally listed as subtype C in the publication, as was the 4067 isolate.
- 4) **CI1.ID#:** These 4 sequences are from Abidjan, Ivory Coast. No other information is yet available. Ellenberger D.L. unpublished 1997. Subtypes A, D and G were found for Ivory Coast patients in this set. Ugandan sequences of subtype A were also part of this set. Accession numbers AF000458, AF000460, AF000463, AF000468.
- 5) **GA.LBV217:** A sequence from Gabon from a set of HIV-1 viral isolates from Africa. This sequence was derived from a clone of PCR amplified DNA from cultured PBMCs. It represents a fragment of a full length env sequence. [Janssens et al.(1994b)]. Accession number U09664.
- 6) **GA.VI525:** A sequence from Gabon from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989–1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1994)] and [Janssens et al.(1994b)]. Accession numbers L22953 and U09665. The same isolate was classified as subtype H in gag, [Louwagie et al.(1993)], Accession number L11792.
- 7) **GA1.ID#:** These 2 sequences are from Gabon. G98 is from a 1988 or 1989 sample from a patient with AIDS living in Franceville, Gabon who moved there from Niger. VI526 is from a 1990 sample from an AIDS patient at the Libreville General Hospital. Method of proviral DNA isolation was not described. DNA was PCR amplified and cloned. One clone per isolate was sequenced. [Delaporte et al.(1996)]. Accession numbers X90916, G98; X90922, VI526. See also subtypes A, C, D, F and O sequences from this same study.
- 8) **GB1.22:** This sequence is a consensus of three clones from an infected infant in a mother-infant transmission study. The sequences were obtained via PCR from cell lysates, with sequencing of cloned PCR products. The infant was 3 months old at the time of blood drawing, and had pneumonia. [Arnold et al.(1995b)]. Accession numbers U26304–U26306. Envelope sequences for the mother are found in database entries U26301–U26302, and gag sequences for mother and infant are in U26303 and U26307.
- 9) **GH3.ID#:** This sequence is from Ghana. Subtypes A and D were also detected in this study [Ishikawa et al.(1996)]. Another report from Ghana [Takehisa et al.(1997a)] showed that a Ghana env subtype G isolate was A/G recombinant, with pol gene related to subtype A. Although this sequence appears to be phylogenetically related to that one, we have no pol sequence for this isolate, and thus no solid evidence of it being A/G recombinant. Accession numbers for subtype G is U67683.
- 10) **KP.Kr121** This sequence is from an unpublished database entry with accession number X93469.

Sequence Descriptions

- 11) **NG1.ID#:** These four sequences are G subtype sequences from Nigeria [Abimiku et al.(1994)]. JP882 and JV832 were derived from AIDS patients, and G3 and G9 from healthy women. G9 was cultured on the T cell line CEM-SS, and the other three isolates were cocultured with uninfected donor PBMCs. DNA from viral cultures was PCR amplified, cloned and sequenced. Accession numbers U13208–U13209, U13211 and U13213. Complete genomes for JV1083 (aka JV832, 92NG083) and G3 (aka 93NG003) are available in database entries U88826 and U88825, respectively.
- 12) **NL.127C** This consensus sequence represents sequences generated from PCR amplified plasma RNA from one of three infants in a Dutch mother/infant study. A sample was collected from the infant at 1.5 months of age. Samples were also collected from the mother before birth, at birth and after birth. Mother sequences are not included in this consensus. [Mulder-Kampinga et al.(1993)]. [Mulder-Kampinga et al.(1995)]. Infant 127 sequences are from Accession numbers Z47817–Z47832. Mother 127 sequences are from Accession numbers Z47833–Z47880. Gag gene sequences from mother/child pairs are also available in entries with accession numbers Z47903–Z47911; Z47912–Z47928; Z47929–Z47935; Z47936–Z47950. The second mother/child pair was also from the Netherlands, see B_NL.114C. The third mother/infant pair in this study was from Rwanda, see A_RW.564C.
- 13) **NL1.ID#:** These 4 sequences are from recent immigrants to The Netherlands from Brazil and Zaire. The first two letters of the ID# represent the two letter country code for the previous residence of the patient. The next two numerals represent the year of isolation. Viral RNA was prepared from patient serum and RT-PCR was used to amplify the V3 region of the env gene. The PCR products were directly sequenced. [Lukashov et al.(1996)]. Accession numbers L76880, ZR911976; L76906, LR9401885; L76884, UM9210113; L76902, GH9401230.
- 14) **RU1.ID#:** RU16 is from Volgograd, Russia. The sequence was determined by direct sequencing of PCR product from uncultured PBMC proviral DNA. [Leitner et al.(1996b)]. RU16 is a 21 year old female who was infected nosocomially. The nosocomial outbreak in southern Russia began with an index case, an infant born in Elista, to a HIV-1 infected mother whose husband is believed to have been infected in the Congo. Over a period of several months in 1988-1989, over 250 patients, mostly children, were infected perenterally with contaminated needles in several hospitals [Bobkov et al.(1994a)], [Lukashov et al.(1995)], [Bobkov et al.(1997b)]. This sequence clusters with the other Russian subtype G sequences, which were also part of this nosocomial outbreak. Accession number U69653. Other sequences from this Russian outbreak can be found with accession numbers L38413, U08355–U08368, U30312, U30313, U27445, U51295. Several of these are from the WHO isolate 92RU131 (U27445), from a 3.5 year old female from Rostov-on-Don, isolated in 1992, which has been classified as G/A recombinant [Gao et al.(1996a)]. The CF.4067 sequence is more closely related to these Russian G sequences, than are some other G sequences from Russia, such as BUK3a from Uzbekistan. Other sequences, with only 105 bp of V3 loop data are available in entries with accession numbers U10701-U10859, these include a mother who is thought to have been infected by her infant during breast feeding [Bobkov et al.(1994b)].
- 15) **TW1.267:** This sequence is from directly sequenced PCR product from uncultured PBMCs from Taiwan. [Chang et al.(1997)]. Most of the Taiwanese sequences determined in this study were subtype B, but subtypes C, E and F were also found. Database accession number U73058.
- 16) **UG.JW3:** This single sequence of subtype G HIV-1 is from a female patient with stage IV disease and CD4 count of 20, from Uganda. The patient had recently migrated to the United Kingdom from Uganda, but contracted the HIV in Uganda. The sequence is referred to as JW3 in [Kaleebu et al.(1995)] but was previously referred to as K1, by the HIV database. It has been given the name 92UG975.10 by the World Health Organization. Accession numbers U22010, U27426.
- 17) **UZ1.BUK3a:** This sequence is from a 39 year old male caucasian heterosexual who lived in Uzbekistan [Bobkov et al.(1996a)]. The patient tested HIV-1 seropositive in June 1991, blood was collected for this sequence in November, 1992. He reported living in Mozambique in 1984-1985 where he was admitted to the hospital several times, but reported having no sexual relations during this time. His wife in Uzbekistan was HIV-1 seropositive in 1991 and died of AIDS in 1995. He reported having sexual relations with a woman in Uzbekistan in 1986-1987 shortly after returning from Mozambique, and this woman and her husband were both found to be HIV-1 seropositive in 1991. Patient BUK died of AIDS in November, 1993. Proviral DNA from uncultured PBMCs was PCR amplified in nested double reactions. The PCR product was cloned into pUC18 plasmid prior to sequencing. Accession numbers U33095, U33096.

H Subtype

At this time there are viral sequences from 3 HIV-1 infected individuals associated with HIV-1 subtype H. The H subtype consensus sequence (H_CONSENSUS_97) generated from these 2 sequences was based on the most common amino acid found in each position of an alignment. Both of these sequences have been published and/or have been made available for printing in the database by their authors. Eight sequences that are too short for classification are closer to H than to other subtypes. The locus names (ID's) and sources of the sequences are:

- 1) **CF.90CF056:** This sequence is from a 1990 blood sample from the Central African Republic. It was originally published as an unclassified subtype, [Murphy et al.(1993)], with accession number L11497. It was later classified as subtype H, [Janssens et al.(1994b)]. The complete genome was sequenced in 1997, Feng Gao unpublished 1997, and appears to be subtype H throughout the genome, accession number AF005496. L11497 contains an 8 base-pair, frameshifting insertion, relative to AF005496, near the 3' end of its sequence, which is a third copy of an 9 bp direct repeat.
- 2) **CM.CA13:** A sequence from Cameroon from a set of HIV-1 viral isolates from Africa used to define the prototype G and H env sequences. This sequence was derived from a clone of PCR amplified DNA from cultured PBMCs. It represents a fragment of a 900 base pair sequence. [Janssens et al.(1994b)] and [Nkengasong et al.(1994)]. The H subtype association is not always clearly apparent using some sets of background sequences for comparison, and neighbor joining trees (HIV database, Wouter Janssens, personal communication), although parsimony trees confirmed the original association documented in [Janssens et al.(1994b)]. Accession numbers X80441 and U09667.
- 3) **RU1.MLY10:** This sequence is from Russia [Bobkov et al.(1996c)]. Patient MLY was a recipient of a 1987 blood transfusion from patient SLH. Patient SLH had a history of sexual contact with an HIV-1 seropositive student from Zaire. Patient MLY gave birth to a child by caesarian section (soon after which she received the transfusion), and the child was later determined to be HIV infected, presumably via transmission during a 3-month period of breast feeding. Accession numbers: U33104 U33105, MLY; U33106 U33107 U33108, SHL.
- 4) **ZR.VI557:** A sequence from Zaire from a set of HIV-1 viral isolates from Africa used to define the prototype G and H env sequences. This sequence was derived from a clone of PCR amplified DNA from cultured PBMCs. It represents a fragment of a 900 base pair sequence. [Janssens et al.(1994b)]. Accession number U09666.

I Subtype

At this time there are viral sequences from 2 HIV-1 infected individuals associated with HIV-1 subtype I. The subtype I consensus sequence reflects the sequencing of two clones from one individual and one clone from the other. Both of these sequences have been published.

- 1) **CY.HOcon:** This is a consensus sequence from two individuals who were heterosexual partners of one another, and former IV drug users. They had lived for several years in Athens, Greece as well as in Cyprus. These samples, like others in this study (see also subtypes A, B, C, and F) were collected in February 1994 from the AIDS clinic in Nicosia, Cyprus. Patient HO31 was a 24 year old asymptomatic female known to have been HIV seropositive for at least 5 years. Patient HO32 was a 35 year old asymptomatic male, also seropositive for at least 5 years. DNA was extracted from patient PBMCs and PCR amplified. After a second round of PCR, products were cloned and sequenced. Two clones from HO32 and one from HO31 were sequenced. [Kostrikis et al.(1995)]. Accession numbers U28672, U28673 and U28685.

J Subtype

At this time there are viral sequences from 5 HIV-1 infected individuals associated with HIV-1 subtype J. The J subtype consensus sequence (J_CONSENSUS_97) generated from these sequences was based on the most common amino acid found in each position of an alignment. All of these sequences have been published or made available to the database for printing.

- 1) **GMI.GM#:** Three sequences from Gambia, as yet unpublished, which cluster with the two Swedish sequences by Leitner in the V3 loop region. Accession numbers U33099, U33100, U33102. Bobkov et al. 1996 unpublished. GM4 (U33099 U43105) has been published in [Bobkov et al.(1996b)] as a G/?/C recombinant in the env V1-V5 region, with the ? region covering the V3 loop. See also Gambian sequences of subtypes B and C.
- 2) **SE1.SE#:** Two sequences from Sweden, both from patients who were recent immigrants from Zaire. [Leitner et al.(1995)]. Sample 7022 as collected in December 1993 from an asymptomatic female with a CD4 count of 184. Her first known seropositive sample is from May 1990, but epidemiological investigation indicated that she was infected in Zaire between 1981 and 1986. Sample 7887 was collected in October 1994 from an asymptomatic male who had tested seronegative in Sweden in January 1993, and who had a seropositive sample in August 1994. His CD4 count was normal at 567. Both patients were heterosexual and a thorough epidemiological investigation revealed no contact or shared contacts between the two. The two sequences were 95% identical to each other over 255 bases of env and 98% identical to each other over 460 bases of gag. Accession numbers L41176 and L41177. Gag gene sequences from these same individuals are in L41178 and L41179.

O Subtype

At this time there are viral sequences 13 HIV-1 infected individuals associated with HIV-1 subtype O that have been published and/or have been made available for printing in the database by their authors. The O subtype consensus sequence (O_CONSENSUS_97) generated from these sequences was based on the most common amino acid found in each position of the alignment; when there was no consensus in a position an "X" was used. These sequences represent a set of sequences that are extremely divergent relative to other HIV-1's. The subtypes A-H have been grouped together under the heading "M" for main. "O" sequences are as different from one another as are sequences from different "M" subtypes.

- 1) **CM.CA9:** This sequence is from an individual living in Cameroon. [Janssens et al.(1994d)]. No database entry is yet available. The pol gene from this isolate has Accession number X78476.
- 2) **CM.ANT70:** The complete viral genome has been sequenced from this viral isolate derived from a symptomatic Cameroonian, CDC stage III. [R. et al.(1990)] and [Vanden Haesevelde et al.(1994)]. Accession number M31171. LTR and partial env sequences were also presented in L20587 and L23119.
- 3) **CM.MVP5180:** The complete viral genome has been sequenced from an isolate derived from a Cameroonian woman, sampled in 1991; the donor died of AIDS in 1992. The viral isolate MVP-5180 was grown in several human T-cell lines and the monocytic U937 line. [Gurtler et al.(1994)]. Accession number L20571.
- 4) **CM.CMR61:** This sequence is one of two O group sequences from a 23 year old female commercial sex worker from Cameroon who was found to be triple-infected with subtypes A and D, as well as O group HIV-1 [Takehisa et al.(1997b)]. Accession numbers U58152, U58153.
- 5) **ES.1158:** This sequence was from a 35 year old man from Spain. Two blood samples from this same man were collected in April and September 1995. The V3 region was PCR amplified from uncultured PBMCs, cloned into pGEM-5ZF and an individual clone sequenced. The April sequence is shown here. The sequence from the September blood sample (681, Accession number U62617) is also available. Accession number U62618.
- 6) **FR.CF#:** These seven consensus sequences are from Cameroonian patients living in France. [Loussert-Ajaka et al.(1995)]. PBMC proviral DNA was PCR amplified and 3-6 clones from each patient were sequenced. The consensus of the 3-6 clones is presented. Accession numbers U24562-U24568. Gag gene sequences for these patients are also available with Accession numbers U24706-U24712.
- 7) **FR.DUR:** This sequence is as yet unpublished, by J.H.M. Cohen et al. Accession number X84327.
- 8) **FR.VAU:** This sequence was derived from an isolate from a French woman who died of AIDS in 1992. DNA was extracted from VAU infected PBMCs, PCR amplified, cloned, and gp160 env was sequenced. The viral isolate was highly cytopathic. [Charneau et al.(1994)]. Accession number X80020.
- 9) **GA1.VI686:** This sequence is from a 1992 sample from a Gabonese woman with AIDS, taken at the Libreville General Hospital in Gabon. Method of proviral DNA isolation was not described. DNA was PCR amplified and cloned. One clone per isolate was sequenced. [Janssens et al.(1994d)], [Delaporte et al.(1996)]. Accession number X96526. The pol gene from this isolate has Accession number X78477. See also subtypes A, C, D, F and G sequences from this same study.

Uncertain Classification

At this time there are viral sequences from 19 HIV-1 infected individuals that are not clearly associated with any of the HIV-1 genetic subtypes A through J. They either appeared distinct from the subtypes A–J in phylogenetic analysis, or else the subtype association was unclear, with different associations in different analyses. For some of the shorter gene fragments, subtype associations might have been established if more sequence information was available or if a different set of sequences was included in the background set used to define subtype associations. Some of these sequences may be representatives of subtypes as divergent as A–J, but only a single limited sample is yet available. Still others may represent recombinant genomes.

- 1) **AR.20021:** This B/F recombinant sequence is from direct sequencing of PCR product from uncultured PBMCs, from a 1993 sample from Buenos Aires, Argentina. The patient was asymptomatic and HIV risk behavior was unknown. Three other samples taken from unrelated patients in 1993 were subtypes F (2) or B (1). [Marquina et al.(1996)]. Accession number U68523.
- 2) **BI1.91BU009:** This C/D sequence is from Burundi. It is one of several complete env gene sequences obtained for the World Health Organization. HMA subtyping as well as sequence-determined subtyping was done on each one. Sequences were PCR amplified from cocultured PBMCs. Two to three clones from each isolate were sequenced. 91BU009 groups with subtype D in a neighbor-joining tree of the V3 region and with subtype C in other regions. [Penny et al.(1996)]. Accession numbers U39253 and U39254.
- 3) **BR4.93BR01904** This sequence is part of the WHO Global Programme on AIDS. The virus was derived from a twenty-year old asymptomatic male patient in Rio de Janeiro, Brazil, who presumably contracted the virus through bisexual contact. Blood sample was taken in 1993 [Gao et al.(1996a)]. This sequence appears to be a recombinant of subtypes B and F. Accession numbers U27404, U27408 and U27444. All three confirm the subtype F/B recombination in env.
- 4) **BR.93BR029:** This sequence is another B/F recombinant from Brazil. It is one of several complete env gene sequences obtained for the World Health Organization. HMA subtyping as well as sequence-determined subtyping was done on each one. Sequences were PCR amplified from cocultured PBMCs. Two to three clones from each isolate were sequenced. [Penny et al.(1996)]. Another env sequence from this same patient was determined by a second group. [Gao et al.(1996a)]. Accession numbers U27413, U39235, U39236 and AF005495 (complete genome). LTR sequence from this isolate is in the entry with accession number U51291.
- 5) **BR.RJI03** This sequence is B-F recombinant in the V3 region. DNA was amplified directly from PBMCs of an HIV infected woman with CDC stage II/A disease in August, 1992, and the PCR product was directly sequenced [Morgado et al.(1994)]. More V3 region sequences from this individual (RJ549 from April 1992) and her sexual partner (RJ548 from April 1992) were also sequenced [Sabino et al.(1994c)]. Accession numbers U00420, U08953–U08955, U08957–U08960, U08962–U08964, U10019–U10029, U08972, U08973 and U08965–U08971.
- 6) **CF1.ID#:** These four sequences are from a set of sequences obtained from 27 symptomatic patients from the Central African Republic, from whom blood was drawn in 1990–1991. Consensus, PCR-clones, cell culture, DNA. [Murphy et al.(1993)]. Accession numbers L11482–L11483, L11497, L11508–L11510 and L11514–L11515. Janssens et al. classified 4056 as an H subtype sequence [Janssens et al.(1994b)]. D. Schmitt provided an unpublished sequence of CF.4081, U43174.
- 7) **FR1.ID#:** This sequence is from a member of the French military who is believed to have been infected while deployed in Djibouti in 1991. It was classified as subtype C in [Lasky et al.(1997)]. However, it has a GPGR V3 loop tip, and clusters with subtype B in phylogenetic analysis done for this section of the HIV Database Compendium. All other subtype C as of November 1997 have GPGQ at the tip of the V3 loop. Other sequences from this study were subtypes A, B, C, E, and F. [Lasky et al.(1997)]. Accession number U58787.
- 8) **GH.GH8:** This A/G recombinant sequence is from Ghana. Subtypes A and D were also detected in this study [Takehisa et al.(1997a)]. Accession number U67039.
- 9) **KE.K124:** A Kenyan sequence from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably

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- between 1989–1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)]. This isolate is not clearly associated with D subtype; however, Louwagie and colleagues found that it associated with the D subtype in env, and the A subtype in gag. Using parsimony analysis, we found that it was difficult to determine a clear association, and this observation was confirmed by Wouter Janssens (personal communication). Accession number L22942.
- 10) **KE.KEN976** This is a single unclassified sequence from a set of patients who were part of a 1990–1992 cohort study of maternal risk factors in mother to child transmission, including 22 pregnant women and an infant from Kenya. The C2V3 region was sequenced. [Janssens et al.(1994a)]. Accession number U12992.
 - 11) **NG.IBNG:** An envelope gp120 sequence from Nigeria was kindly provided by Dr. Tom Howard from the University of Southern California (USC) [Howard et al.(1994)] and the complete genome has now been sequenced [Howard & Rasheed(1996)]. Originally classified as subtype A, it has more recently been thought to be a mosaic between subtypes A and G. Accession numbers U48628 and L39106.
 - 12) **NL.RW94028:** This sequence is from a recent immigrant to The Netherlands from Rwanda. The blood sample was collected in 1994. Viral RNA was prepared from patient serum and RT-PCR was used to amplify the V3 region of the env gene. The PCR product was directly sequenced. [Lukashov et al.(1996)]. Database accession number L76909.
 - 13) **RW.92RW009:** This sequence is from a complete genome of a 1992 isolate from Rwanda. The env region clusters with subtype A, but overall the genome is A/C recombinant or mosaic, [Gao et al.(1994a)], [Gao et al.(1994b)], [De Wolf et al.(1994)]. Accession numbers U08793, U16220, U16221, U16222, U88823, U13441. A Gag gene is available with accession number U86545.
 - 14) **SE.KI4803:** This sequence is from patient number 24 described in [Asjo et al.(1986)] and [Fredriksson et al.(1991)]. Several molecular clones from this patient have been extensively characterized in [Tan et al.(1993)]. Complete env gp120 sequences for 8 clones were determined in [McKeating et al.(1996)] and one of the 8 sequences (clone 13) is presented here. Accession numbers for 7 of the 8 clones (clone 32 was not submitted to the databases) are U57788–U57794. A complete genome from isolate KI4803 has reportedly been sequenced, but not yet submitted to the databases (Fenyo,EM personal communication). The patient had AIDS at the time of viral isolation in 1985. The virus exhibited rapid/high phenotype [Asjo et al.(1986)] and when gp120 from this isolate was swapped into the HXB2 genome, the ability of the chimeras to grow in various cell lines correlated with the gp120 [McKeating et al.(1996)]. Although the amino acid sequences translated from these sequence entries are clearly subtype B, the DNA sequences do not cluster with any of the HIV-1 M-group subtypes. The codon usage of these sequences is similar to the codons used for optimal high-level expression in E.coli, and it is possible that these sequences were reverse-translated from amino acid sequences. The authors have been contacted, but have not responded.
 - 15) **UG1.ID#:** Two clones from each of these two D/A recombinant Ugandan isolates were sequenced, but only the sequences of 92UG035 clone 21 and C6080 clone 09 are shown here. [Douglas et al.(1996)]. The publication shows C6080 as subtype A, but analyses done at Los Alamos indicate that it is a D/A recombinant, like 92UG035. Other Ugandan isoaltes sequenced in this study were subtype D. London subtype B clones were also reported. Complete envelope gp160 sequences were reported for all isolates. Accession numbers U36865, U36866, U36881 and U36883.
 - 16) **ZM.ZAM184:** This Zambian sequence is an outlier, though in some phylogenetic analysis it appears most closely associated with the A subtype. In particular it is closely associated with A_CF.SAS U43171 (100/100 replicates in parsimony analysis of gp120). Health status of the individual from which the virus was cultured was a woman from Lusaka, Zambia who participated in a clinical research study. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. [Louwagie et al.(1995)], [Salminen et al.(1997)]. The Salminen paper is based on full-length gag and env genes recovered directly from peripheral blood mononuclear cells or from primary virus cultures, using serial blood samples from a Zambian woman and a sample from her spouse. DNA sequencing and phylogenetic analysis established that two different A/C recombinant forms of HIV-1 predominated at two time points in the woman. A related but distinct recombinant HIV-1 was recovered from her spouse. Intersubtype recombination apparently played a central role in the evolution of HIV-1 in this couple and may contribute substantially to the rapid emergence of HIV-1 variants whenever mixed-subtype HIV-1 infections occur. Accession number L22955. A complete genome from this isolate is now

- available with accession number U86780 and other clones from this patient and her spouse, from blood samples taken in 1989 and 1990, are found with accession numbers U86768-U86781.
- 17) **ZR.Z3:** This sequence is from the 1983 Zairean isolate Z-3 (non-infectious, possibly due to frame-shift). [Willey et al.(1986)]. Accession number K03347.
 - 18) **ZR.Z321:** This sequence is from the 1976 Zairean isolate Z321. [Srinivasan et al.(1989)]. Accession number M15896. Earlier listed as subtype A, it was subsequently shown to be recombinant between subtypes A and G [Choi et al.(1997)]. Accession numbers M15896, U76035, U50207, U50208.

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