AIDS RESEARCH AND HUMAN RETROVIRUSES
Volume 17, Number 2, 2001, pp. 161–168
Mary Ann Liebert, Inc.

Sequence Note

Near Full-Length Clones and Reference Sequences for Subtype C Isolates of HIV Type 1 from Three Different Continents

CYNTHIA M. RODENBURG,[1] YINGYING LI,[1] STANLEY A. TRASK,[1] YALU CHEN,[1] JULIE DECKER,[2] DAVID L. ROBERTSON,[3] MARCIA L. KALISH,[4] GEORGE M. SHAW,[1,2,6] SUSAN ALLEN,[5] BEATRICE H. HAHN,[1,6] FENG GAO,[1] and the UNAIDS AND NIAID NETWORKS FOR HIV ISOLATION AND CHARACTERIZATION*

ABSTRACT

Among the major circulating HIV-1 subtypes, subtype C is the most prevalent. To generate full-length subtype C clones and sequences, we selected 13 primary (PBMC-derived) isolates from Zambia, India, Tanzania, South Africa, Brazil, and China, which were identified as subtype C by partial sequence analysis. Near full-length viral genomes were amplified by using a long PCR technique, sequenced in their entirety, and phylogenetically analyzed. Amino acid sequence analysis revealed 10.2, 6.3, and 17.3% diversity in predicted Gag, Pol, and Env protein sequences. Ten of 13 viruses were nonmosaic subtype C genomes, while all three isolates from China represented B/C recombinants. One of them was composed primarily of subtype C sequences with three small subtype B portions in *gag*, *pol*, and *nef* genes. Two others exhibited these same mosaic regions, but contained two additional subtype B portions at the *gag/pol* overlap and in the accessory gene region, suggesting ongoing B/C recombination in China. All subtype C genomes contained a prematurely truncated second exon of *rev*, but other previously proposed subtype C signatures, including three potential NF-κB-binding sites in the viral promoter–enhancer regions, were found in only a subset of these genomes.

HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 has been classified into three major groups: M, O, and N.[1] Group M viruses are responsible for the global AIDS pandemic and have been further subdivided into 10 subtypes or clades (A through H, J, and K).[1,2] Compared with group M, group O and N viruses are many fewer in numbers and mainly found in West Central Africa.[1–3] The genetic variation between members of the three different groups is extraordinary: 30 and 47% amino acid sequence variation in Gag and Env proteins, respectively. Variation among members of the different subtypes within group M is also high: 15 and 22%, on average, for Gag and Env proteins, respectively. Although there is of yet no correlation between genotype and phenotype,[4–7] this high degree of genetic variation remains a concern for AIDS vaccine development.[8–9] On the basis of the latest survey, subtype C appears to constitute 56% of all the circulating subtypes of HIV-1 group M viruses in the world.[10] Therefore, it is important to characterize subtype C viruses at the full-length genome level and to generate reference reagents for phylogenetic, biologic, and vaccine development studies.

[1]Department of Medicine, University of Alabama at Birmingham, Birmingham, Alabama 35294.
[2]Howard Hughes Medical Institute, University of Alabama at Birmingham, Birmingham, Alabama 35294.
[3]Department of Zoology, University of Oxford, Oxford OX1 3P3, UK.
[4]Division of AIDS, STD, and TB Laboratory Research, CDC, Atlanta, Georgia 30333.
[5]Department of Epidemiology and International Health, University of Alabama at Birmingham, Birmingham, Alabama 35294.
[6]Department of Microbiology, University of Alabama at Birmingham, Birmingham, Alabama 35294.
*Participants are listed in the Appendix.

TABLE 1. EPIDEMIOLOGICAL INFORMATION ON HIV-1 ISOLATES

Isolate	*Gender*	*Age (years)*	*City*	*Country*	*Year of isolation*	*Source*	*Subtype*	*GenBank Acc. No.*
98BR004	M	39	Porto Alegre	Brazil	1998	UNAIDS/NIAID	C	AF286228
98CN006	M	25	Gansu	China	1998	UNAIDS/NIAID	B/C[a]	AF286229
97CN001	M	24	Wulumuqi	China	1997	UNAIDS/NIAID	B/C[a]	AF286226
98CN009	M	21	Wulumuqi	China	1998	UNAIDS/NIAID	B/C[a]	AF286230
98IN012	n/a	40	T'Nagar Madras	India	1998	UNAIDS/NIAID	C	AF286231
98IN022	M	27	Churachandpur	India	1998	UNAIDS/NIAID	C	AF286232
94IN476	n/a	n/a	Pune	India	1994	ADARC	C	AF286223
98IS002	n/a	n/a	n/a	Israel	1998	UNAIDS/NIAID	C	AF286233
98TZ013	F	23	Dar es Salaam	Tanzania	1998	UNAIDS/NIAID	C	AF286234
98TZ017	F	23	Dar es Salaam	Tanzania	1998	UNAIDS/NIAID	C	AF286235
97ZA012	F	29	Durban	South Africa	1997	UNAIDS/NIAID	C	AF286227
96ZM651	M	47	Lusaka	Zambia	1996	ZUHRP	C	AF286224
96ZM751	M	26	Lusaka	Zambia	1996	ZUHRP	C	AF286225

Abbreviations: n/a, Not available; UNAIDS/NIAID, the Joint United Nations programme on HIV/AIDS and National Institute of Allergy and Infectious Diseases, NIH; ZUHRP, the Zambian–UAB HIV Research Project; ADARC, Aaron Diamond AIDS Research Center; M, male; F, female.

[a]B/C recombinant viral strains initially classified as subtype C based on partial p17 and V3 sequence analysis.

Since the first description of near full-length sequences for two subtype C viruses from Ethiopia and Brazil,[11,12] only two other studies have reported complete subtype C genomes. One characterized five nonrecombinant subtype C viruses from India and the other analyzed 23 nonrecombinant subtype C viruses from eight individuals in Botswana.[13,14] Many other countries, in Africa and elsewhere, also appear to have a high subtype C virus prevalence. To understand more fully the extent of subtype C genetic variation, we studied 13 additional subtype C viruses that were identified as such on the basis of partial *gag* and *env* nucleotide sequences. The samples were collected in seven countries (Zambia, India, Tanzania, South Africa, Brazil, Israel, and China) where subtype C viruses are either known to be predominant or to represent one of the major epidemic strains.

All viruses were isolated from patient peripheral blood mononuclear cells (PBMCs) by cocultivation with normal donor PBMCs. The majority of the HIV-1 isolates were obtained as part of an international collaborative study sponsored by the WHO–UNAIDS and NIAID Virus Networks on Characterization of Globally Prevalent HIV Strains in Relation to HIV Vaccine Development.[15] Available epidemiological information is summarized in Table 1. Genomic DNA was extracted from short-term PBMC cultures and used for polymerase chain reaction (PCR) amplification. Near full-length proviral genomes were amplified as previously reported.[12] PCR products were cloned either directly into vector pCR-XL-TOPO (InVitrogen, Carlsbad, CA) or vector pTZ18MluI at the *Mlu*I site. In three cases (98BR004, 98CN006, and 98IN022) two overlapping half-genomes were amplified. The complete genome sequences were determined by the primer walking method on both strands of DNA and aligned with a set of reference sequences, using the profile alignment option of CLUSTAL W.[12] The final sequence alignment was manually adjusted for optimal alignment. Columns containing gaps were stripped from the alignment to ensure that an equal number of bases were compared. Phylogenetic trees were constructed using the neighbor-joining algorithm and the Kimura two-parameter model. Nine of the 13 genomes encoded intact open reading frames for all nine genes; the remaining four (98BR004, 94IN476.104, 98TZ013.10, and 96ZM751.3) contained defective genes due to in-frame stop codons, deletions, or insertions. Comparison of amino acid sequences of the newly characterized strains revealed that the average amino acid distances for Gag, Pol, Env, and Nef proteins were 10.2, 6.3, 17.3, and 15.7%, respectively. This variation is within the range of intrasubtype diversity.

A complete genome nucleotide sequence tree depicting the phylogenetic positions of the 13 newly characterized HIV-1 strains is shown in Fig. 1. Of note, only viruses from Brazil and China formed subclusters within subtype C according to their geographic origin, suggesting a relatively more recent introduction of subtype C viruses into these countries. HIV-1 strains from Zambia, India, and Tanzania were highly divergent and did not cluster by country, suggesting a more long-standing epidemic in these areas. Similar findings were reported for subtype C viruses from South Africa, Botswana, and Burundi.[14,16,17] Phylogenetic analysis also showed that viruses from China were more closely related to certain viruses from India, supporting the previous suggestion that subtype C viruses now circulating in China might have been introduced from India.[18,19] Analyses of additional *env* gene sequences confirmed these observations (Fig. 2). Moreover, the *env* tree also revealed a third geographic cluster involving viruses from Ethiopia and Djibouti (supported by 97% bootstrap values), suggesting epidemiological linkage of viruses from these neighboring countries (Fig. 2).

Recombination between representatives of different group M subtypes is a frequent occurrence and many HIV-1 sequences in the database (both partial and full length) are known to be mosaic.[12,20,21] Most viruses in this study were collected in geographic areas where multiple subtypes are known to cocirculate. To examine whether any of our newly characterized viruses were recombinant, we performed detailed diversity and bootstrap plot analyses as previously described.[12] The results from those analyses revealed that 10 of the 13 genomes represented nonrecombinant subtype C viruses (data not shown). However, the remaining three, all from China, comprised complex B/C

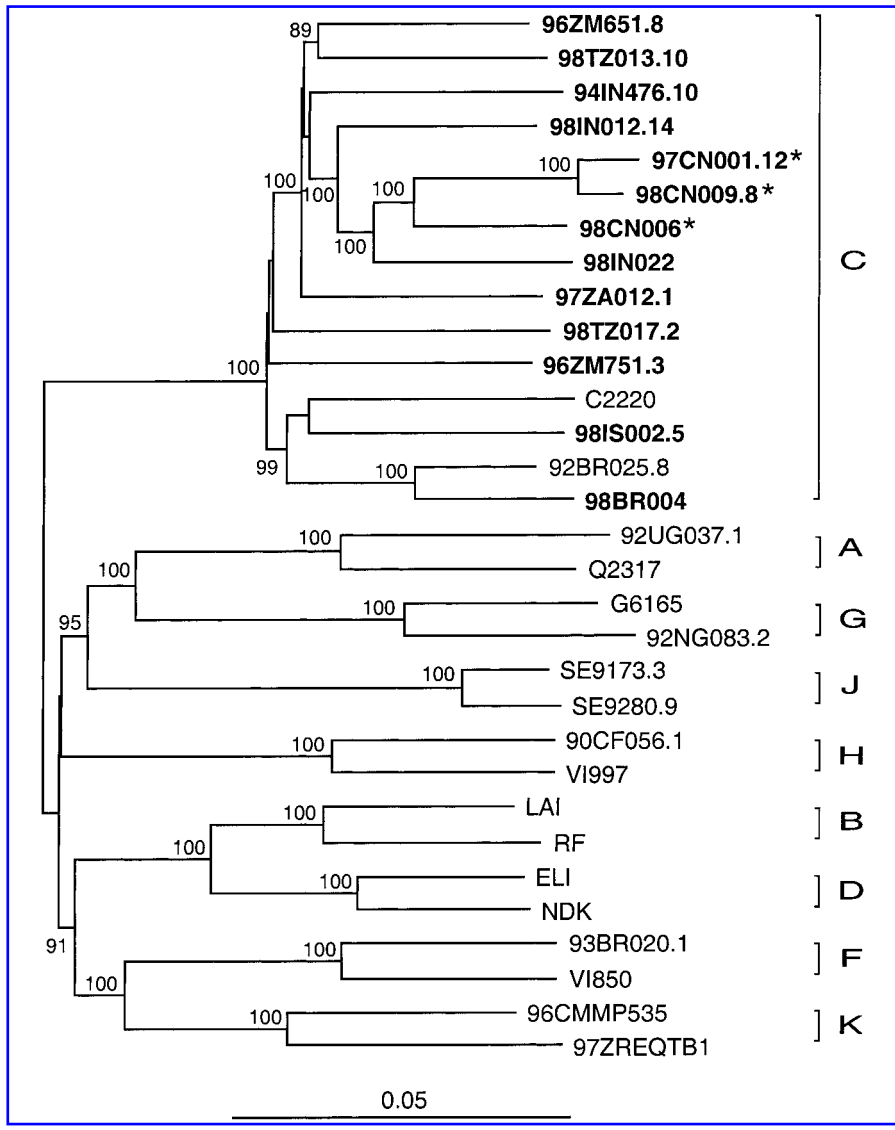

FIG. 1. Phylogenetic relationships of the newly characterized near full-length subtype C viruses with HIV-1 subtype reference sequences from the database. The phylogenetic tree was constructed from nucleotide sequences, using the neighbor-joining method and the Kimura two-parameter model. Branch lengths are drawn to scale. The bootstrap values at each node represent the percentage of 1000 bootstrap replicates that support the branching order. Only bootstrap values of 80% or higher are shown. The new sequences are in boldface. Full-length clones are identified with a number after the period; concatenated sequences lack a clone number. Asterisks denote B/C recombinant viruses.

recombinants. Since nonrecombinant subtype B and C reference sequences are available, we defined the recombination breakpoints by informative site analysis.[12,20,21] This was done with a four-sequence alignment analyzed in windows of 10 informative sites moving in increments of 1 informative site. Probable breakpoints were found by calculating a maximum χ^2 value for each window and assessing its significance by performing 1000 simulations. Using this approach, we found three subtype B regions in 98CN006 and five subtype B regions in both 97CN001.12 and 98CN009.8. All subtype B regions of 98CN006 were shared by the other two B/C recombinants. However, both 97CN001.12 and 98CN009.8 contained two additional subtype B regions at the *gag/pol* overlap and in the accessory gene region (Table 2). Their recombination boundaries were also identical, suggesting that both 97CN001.12 and 98CN009.8 shared a common ancestor and might represent a new circulating recombinant form (CRF). However, it cannot be ruled out that they represent epidemiologically linked viruses, since both were collected from the same city. The inferred structures of 97CN001, 98CN006, and 98CN009.8 are summarized in Fig. 3. Since both subtype B and C viruses have been reported to circulate in China,[18,19,22] the finding of B/C recombinants in this country is not surprising. However, it is of interest that there were two distinguishable yet clearly related B/C mosaic forms, suggesting ongoing recombination between subtypes B and C in China.

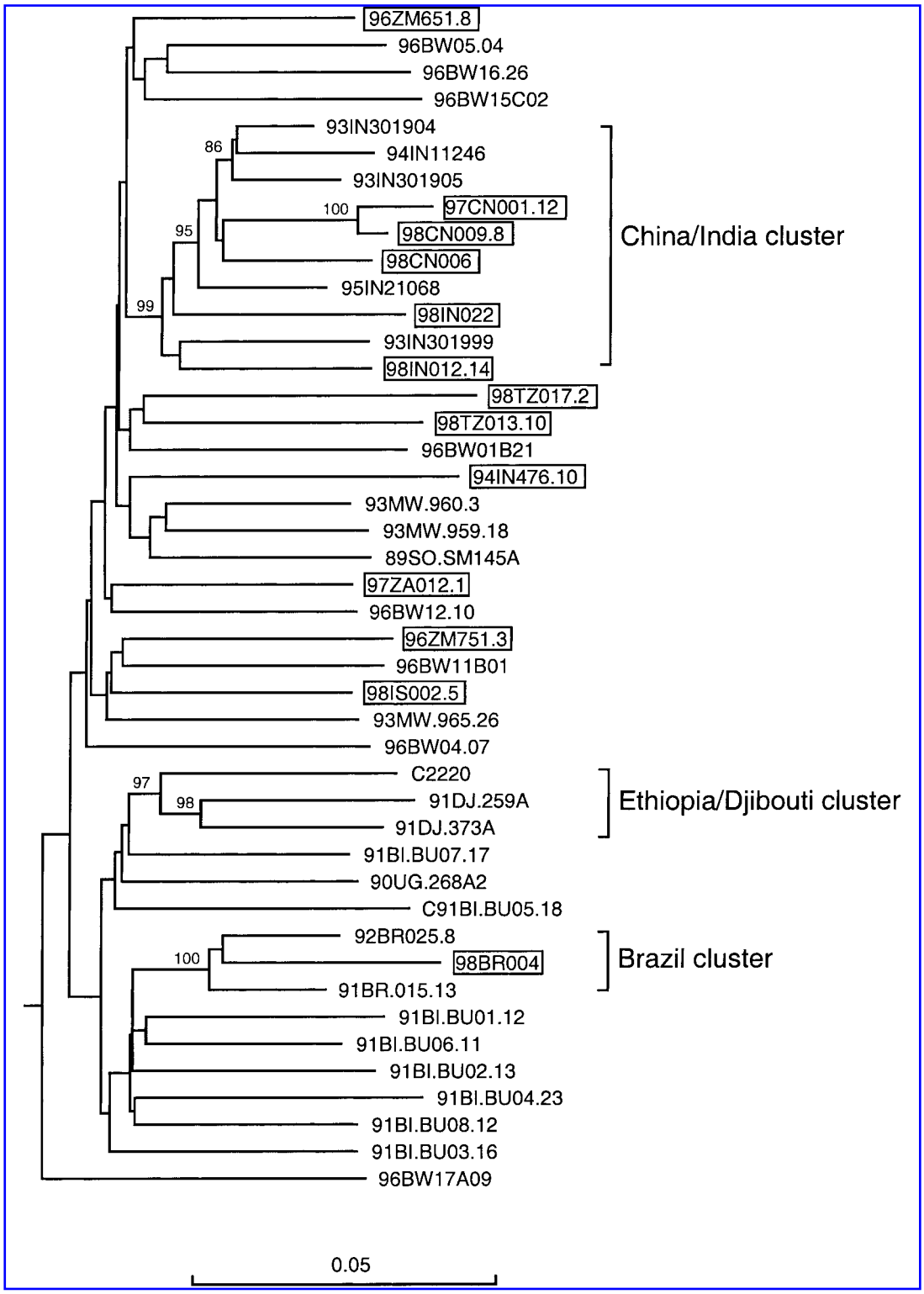

FIG. 2. Phylogenetic tree of complete subtype C envelope nucleotide sequences. The phylogenetic tree was constructed using the neighbor-joining method and the Kimura two-parameter model. Branch lengths are drawn to scale. The bootstrap values at each node represent the percentage of 1000 bootstrap replicates that support the branching order. Only bootstrap values of 80% or higher are shown. The new sequences are boxed. Subclusters supported by significant bootstrap values are indicated with brackets.

TABLE 2. INFORMATIVE SITE ANALYSIS OF B/C RECOMBINANTS FROM CHINA[a]

No. of informative sites in:														
98CN006					*97CN001.12*					*98CN009.8*				
Region	*Subtype*	*B*	*C*	*Outgroup*	*Region*	*Subtype*	*B*	*C*	*Outgroup*	*Region*	*Subtype*	*B*	*C*	*Outgroup*
1–347	C	1	18	0	1–356	C	1	18	0	1–347	C	3	18	0
383–798	B	11	4	1	383–798	B	8	4	2	383–798	B	8	4	2
821–1971	C	5	42	5	821–1188	C	3	14	1	821–1188	C	2	14	1
					1209–1595	B	11	1	1	1209–1595	B	12	1	1
					1607–1971	C	1	16	1	1607–1971	C	1	16	1
1982–2241	B	8	0	2	1982–2246	B	11	1	2	1982–2246	B	11	2	2
2271–7551	C	31	198	50	2271–4742	C	15	78	16	2271–4742	C	15	78	17
					4790–5401	B	27	8	5	4790–5401	B	26	8	7
					5449–7523	C	10	85	23	5449–7523	C	12	84	24
7570–7653	B	10	1	3	7524–7713	B	14	1	2	7524–7713	B	12	1	2
7695–8034	C	2	16	6	7761–8034	C	2	15	4	7761–8034	C	2	14	4

[a]To determine the recombination breakpoints, each putative recombinant sequence was compared with two parental sequences (B_LAI and C_92BR025.8) and an outgroup (A_92UG037.1) are reported previously.[12,20–21] Recombination breakpoints were mapped by examining the linear distribution of phylogenetically informative sites supporting the clustering of the hybrid with each of the two parental subtypes. All recombination breakpoints were evaluated in 1000 simulations.

Previous analysis of subtype C viruses revealed unique sequence signatures that were not observed among members of other subtypes.[11–14,23] The newly characterized subtype C viruses thus provided an opportunity to examine whether these signatures were also conserved among geographically more representative virus strains. One of the proposed subtype C sequence signatures is an additional NF-κB-binding site in the long terminal repeat (LTR) promoter-enhancer region. Only two NF-κB sites have been identified in the majority of subtypes, except for members of subtype A and CRF01_AE viruses, in which only one NF-κB site is generally observed. By contrast, almost all subtype C viruses thus far characterized have three NF-κB sites. This finding, along with gene expression studies demonstrating increased reporter gene expression for LTR promoter-enhancer elements containing three NF-κB-binding sites,[23,24] has led to the notion that three NF-κB sites might be one of the reasons why subtype C viruses are spreading more rapidly than other subtypes.[24] When we compared the newly characterized subtype C viral LTR sequences with other full-length subtype C sequences, we noticed that the putative third NF-κB site frequently contained deletions or mutations that changed its consensus sequence (GGGRNNYYCC), suggesting that this site may not be functional. Since about half of the subtype C LTRs contained only two consensus NF-κB sites (13 of 28; Fig. 4), the suggested causal role of the extra NF-κB site for the explosive epidemic of subtype C viruses requires further study.

A five-amino acid insertion in the Vpu transmembrane domain has also been described in all previously reported subtype C sequences.[12,14] However, in our newly derived data set, 10 of 27 subtype C sequences did not have this insertion. For example, of nine subtype C sequences from India, eight lacked this insertion. One other Chinese isolate also did not have this insertion, further strengthening the close relationship between

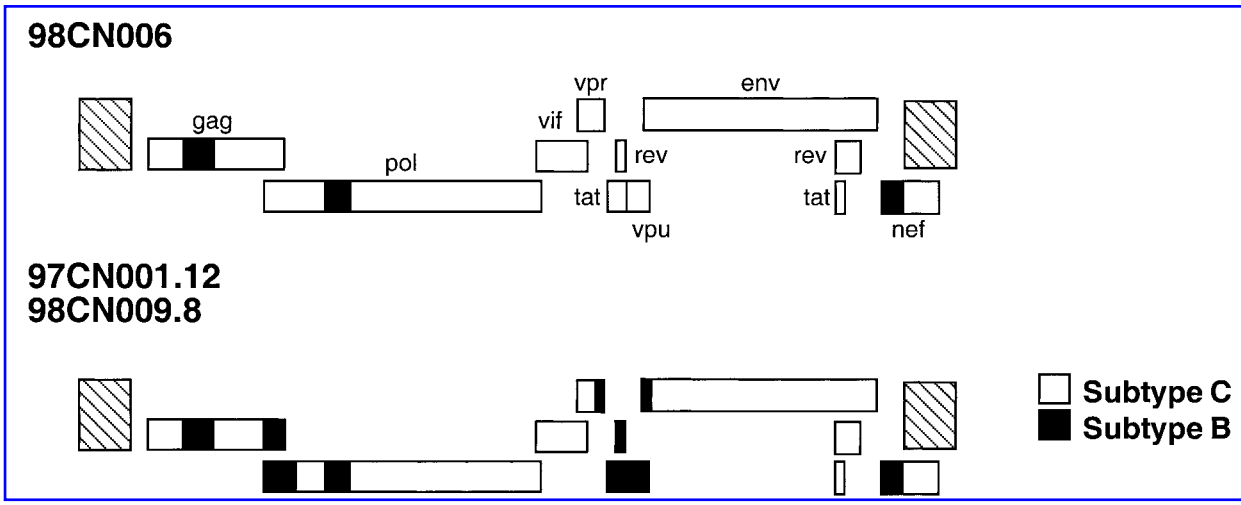

FIG. 3. Schematic representation of the inferred structures of the B/C recombinant HIV-1 genomes from China. LTR regions (hatched) were not analyzed.

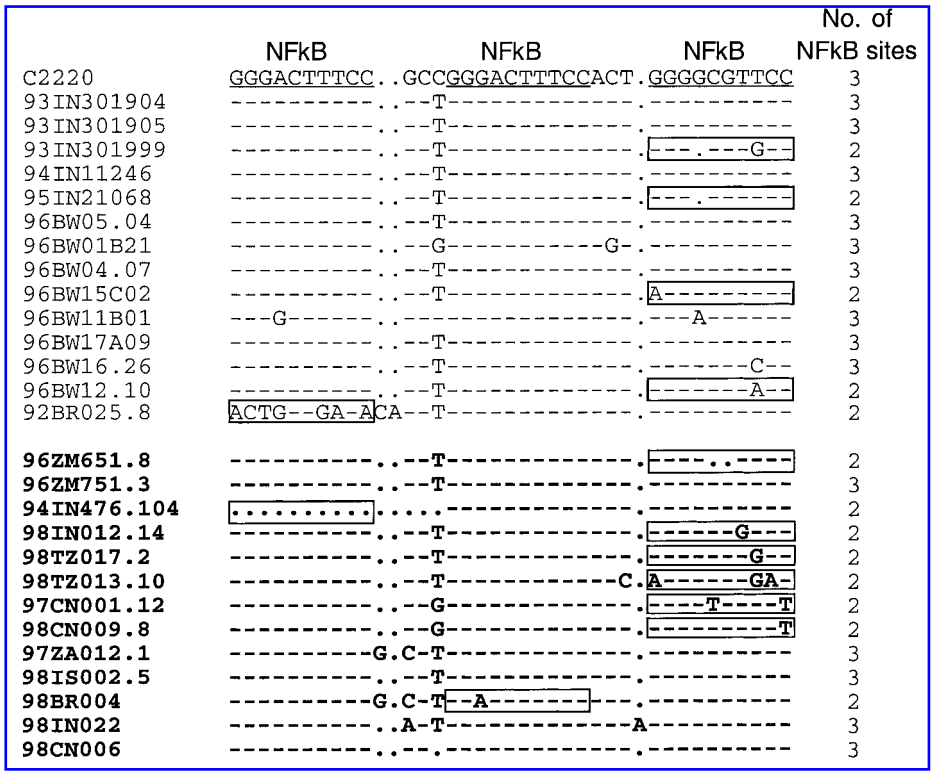

FIG. 4. Alignment of HIV-1 subtype C LTR nucleotide sequences in the promoter-enhancer region. The newly characterized sequences are in boldface and listed at the bottom. NF-κB sites that do not conform to the GGGRNNYYCC consensus are boxed. Sequences were compared with the C2220 reference strain. Dashes indicate sequence identity. Periods denote gaps introduced to improve the alignment.

the viruses from India and China. While two of the previously reported subtype C sequence signatures were not conserved, truncated *rev* genes were highly conserved in every single new subtype C isolate.[12–14] This signature thus remains a reliable subtype C sequence marker.

Subtype C viruses have become predominant epidemic strains in the world and thus a main target for vaccine development. They also have been reported to differ from viruses of other subtypes in some of their biological properties, e.g., preferential usage of CCR5.[25,26] To elucidate whether subtype C viruses indeed differ from other group M subtypes in biologically important ways, a comprehensive set of well-defined reference reagents is required. The newly characterized near full-length subtype C virus clones reported here have been deposited into the AIDS Research and Reference Reagent Program.

ACKNOWLEDGMENTS

We thank the staff of the Zambia-UAB HIV Research Project in Lusaka, Zambia for their assistance, and Y. Cao and D.D. Ho from the Aaron Diamond AIDS Research Center (New York) for providing an expanded PBMC culture for the 94IN476 isolate. This work was supported by grants NO1 AI 85338 and RO1 AI 40951 from the National Institutes of Health, and by the Howard Hughes Medical Institute.

APPENDIX

Participants in the WHO–UNAIDS and NIAID Virus Networks on Characterization of Globally Prevalent HIV Strains in Relation to HIV Vaccine Development who contributed to this study: S. Osmanov, L. Jacobs, and J. Esparza (Global Programme on AIDS, World Health Organization, Geneva, Switzerland); B. Galvao-Castro (Centro de Pesquisas Goncalo Moniz, Fundacao Oswaldo Cruz, Bahia, Brazil); Y. Shao (National AIDS Reference Laboratory, Beijing, China); N. Samuel (The Tamil Nadu Dr. M.G.R. Medical University, Chennai, India); S. Maayan (Hadassah University Hospital, Jerusalem, Israel); A. Bobkov (Russian Academy of Medical Sciences, Moscow, Russia); T. Smolskaya (St. Petersburg Pasteur Institute, St. Petersburg, Russia); W. Makgoba (Medical Research Council of South Africa, Tygerberg, South Africa); C. Williamson (University of Cape Town, Cape Town, South Africa); S. M'Boup (Université Cheikh Anta Diop, Dakar, Senegal); F. Mhalu (Muhumbili Medical Centre, Dar es Salaam, Tanzania); P. Auewarakul (Siriraj Hospital, Bangkok, Thailand); P. Kaleebu and S. Sempala (Uganda Virus Research Institute, Entebbe, Uganda); U. Dietrich and H. von Briesen (Chemotherapeutisches Forschungsinstitut, Georg-Speyer-Haus, Frankfurt, Germany); S. Nick, M. Nubling, and J. Halbauer (Paul-Ehrlich Institute, Langen, Germany); O. Hamouda and C. Kücherer (Robert Koch Institute, Berlin, Germany); R.

Riedl (Dr. Riedl and partner, Frankfurt, Germany); H. Wolf (University of Regensburg, Regensburg, Germany); M. Hoelscher (University of Munich, Munich, Germany); H. Holmes (National Institute for Biological Standards and Control, London, United Kingdom); S. Beddows (Imperial College School of Medicine, London, United Kingdom); G. Giraldo and L. Buonaguro (Instituto Nazionale Tumori, Naples, Italy); G. Scarlatti (San Raffaele Scientific Institute, Milan, Italy); M. Salminen (National Public Health Institute, Helsinki, Finland); G. van der Groen (Institute of Tropical Medicine, Antwerp, Belgium); F. Barré-Sinoussi (Institut Pasteur, Paris, France); M. Peeters (Laboratoire Retrovirus, IRD, Montpellier, France); E. Fenyö (Karolinska Institute, Stockholm, Sweden); C. López Galíndez (Instituto de Salud Carlos III, Madrid, Spain); B. Lukashov (University of Amsterdam, Amsterdam, The Netherlands); J. Bradac (National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, MD); J. Mullins (University of Washington, Seattle, WA); B. Hahn and F. Gao (University of Alabama, Birmingham, AL); A. Abimiku (Institute of Human Virology, University of Maryland, Baltimore, MD); P. Berman (VAXGEN, Brisbane, CA); D. Birx (Walter Reed Army Institute of Research, Rockville, MD); C. Chappey (National Center for Biotechnology Information, Bethesda, MD); G. Ferrari (Duke University Medical Center, Durham, NC); M. Kalish (Centers for Disease Control and Prevention, Atlanta, GA); F. McCutchan (Henry M. Jackson Foundation Research Laboratory, Rockville, MD); S. Zolla-Pazner (New York University Medical Center, New York, NY).

REFERENCES

1. Kuiken CL, Foley B, Hahn BH, Marx PA, McCutchan F, Mellors JW, Mullins JI, Wolinsky S, and Korber B: *Human Retroviruses and AIDS 1999: A Compilation and Analysis of Nuclei Acid and Amino Acid Sequences*. Theoretical Biology and Biophysics Group, Los Alamos National Laboratory, Los Alamos, New Mexico, 1999.
2. Robertson DL, Anderson JP, Bradac JA, Carr JK, Foley B, Funkhouser RK, Gao F, Hahn BH, Kalish ML, Kuiken C, Learn GH, Leitner T, McCutchan F, Osmanov S, Peeters M, Pieniazek D, Salminen M, Sharp PM, Wolinsky S, and Korber B: HIV-1 nomenclature proposal. Science 2000;288:55–56.
3. Peeters M, Gueye A, Mboup S, Bibollet-Ruche F, Ekaza E, Mulanga C, Ouedrago R, Gandji R, Mpele P, Dibanga G, Koumare B, Saidou M, Esu-Williams E, Lombart JP, Badombena W, Luo N, Vanden Haesevelde M, and Delaporte E: Geographical distribution of HIV-1 group O viruses in Africa. AIDS 1997;11:493–498.
4. Cao H, Kanki P, Sankale JL, Dieng-Sarr A, Mazzara GP, Kalams SA, Korber B, Mboup S, and Walker BD: Cytotoxic T-lymphocyte cross-reactivity among different human immunodeficiency virus type 1 clades: implications for vaccine development. J Virol 1997;71:8615–8623.
5. Ferrari G, Humphrey W, McElrath MJ, Excler JL, Duliege AM, Clements ML, Corey LC, Bolognesi DP, and Weinhold KJ: Clade B-based HIV-1 vaccines elicit cross-clade cytotoxic T lymphocyte reactivities in uninfected volunteers. Proc Natl Acad Sci USA 1997;94:1396–1401.
6. Moore JP, Cao Y, Leu J, Qin L, Korber B, and Ho DD: Inter- and intraclade neutralization of human immunodeficiency virus type 1: Genetic clades do not correspond to neutralization serotypes but partially correspond to gp120 antigenic serotypes. J Virol 1996; 70:427–444.
7. Weber J, Fenyö EM, Beddows S, Kaleebu P, and Bjorndal A: Neutralization serotypes of human immunodeficiency virus type 1 field isolates are not predicted by genetic subtype. The WHO Network for HIV Isolation and Characterization. J Virol 1996;70:7827–7832.
8. van der Groen G, Nyambi PN, Beirnaert E, Davis D, Fransen K, Heyndrickx L, Ondoa P, Van der Auwera G, and Janssens W: Genetic variation of HIV type 1: Relevance of interclade variation to vaccine development. AIDS Res Hum Retroviruses 1998;14(Suppl. 3):S211–S221.
9. Zolla-Pazner S, Gomy MK, and Nyambi PN: The implications of antigenic diversity for vaccine development. Immunol Lett 1999; 66:159–164.
10. Esparza J and Bhamarapravati N: Accelerating the development and future availability of HIV-1 vaccines: Why, when, where, and how? Lancet 2000;355:2061–2066.
11. Salminen MO, Johansson B, Sonnerborg A, Ayehunie S, Gotte D, Leinikki P, Burke DS, and McCutchan FE. Full-length sequence of an ethiopian human immunodeficiency virus type 1 (HIV-1) isolate of genetic subtype C. AIDS Res Hum Retroviruses 1996;12: 1329–1339.
12. Gao F, Robertson DL, Carruthers CD, Morrison SG, Jian B, Chen Y, Barré-Sinoussi F, Girard M, Srinivasan A, Abimiku AG, Shaw GM, Sharp PM, and Hahn BH: A comprehensive panel of near-full-length clones and reference sequences for non-subtype B isolates of human immunodeficiency virus type 1. J Virol 1998;72: 5680–5698.
13. Lole KS, Bollinger RC, Paranjape RS, Gadkari D, Kulkami SS, Novak NG, Ingersoll R, Sheppard HW, and Ray SC: Full-length human immunodeficiency virus type 1 genomes from subtype C-infected seroconverters in India, with evidence of intersubtype recombination. J Virol 1999;73:152–160.
14. Novitsky VA, Montano MA, McLane MF, Renjifo B, Vannberg F, Foley BT, Ndung'u TP, Rahman M, Makhema MJ, Marlink R, and Essex M: Molecular cloning and phylogenetic analysis of human immunodeficiency virus type 1 subtype C: A set of 23 full-length clones from Botswana. J Virol 1999;73:4427-4432.
15. UNAIDS Network for HIV Isolation and Characterization: Meeting report, April 28–30, 1999, Frankfurt, Germany.
16. Van Harmelen JH, Van der Ryst E, Loubser AS, York D, Madurai S, Lyons S, Wood R, and Williamson C: A predominantly HIV type 1 subtype C-restricted epidemic in South African urban populations. AIDS Res Hum Retroviruses 1999;15:395–398.
17. Penny MA, Thomas SJ, Douglas NW, Ranjbar S, Holmes H, and Daniels RS: *env* gene sequences of primary HIV type 1 isolates of subtypes B, C, D, E, and F obtained from the World Health Organization Network for HIV Isolation and Characterization. AIDS Res Hum Retroviruses 1996;12:741–747.
18. Yu XF, Chen J, Shao Y, Beyrer C, and Lai S: Two subtypes of HIV-1 among injection-drug users in southern China. Lancet 1998; 351:1250.
19. Neild PJ and Gazzard BG: HIV-1 infection in China. Lancet 1997; 350:963.
20. Robertson DL, Sharp PM, McCutchan FE, and Hahn BH: Recombination in HIV-1. Nature 1995;374:124–126.
21. Robertson DL, Gao F, Hahn BH, and Sharp PM: Intersubtype recombinant HIV-1 sequences. In: *Human Retroviruses and AIDS 1997: A Complication and Analysis of Nucleic Acid and Amino Acid Sequence* (Korber B, Foley B, Kuiken C, Leitner T, McCutchan F, Mellors JW, and Hahn BH, eds.). Theoretical Biology and Biophysics Group, Los Alamos National Laboratory, Los Alamos, New Mexico, 1997, pp. III-25–III-30.

22. Beyrer C, Razak MH, Lisam K, Chen J, Lui W, and Yu XF: Overland heroin trafficking routes and HIV-1 spread in south and southeast Asia. AIDS 2000;14:75–83.
23. Naghavi MH, Schwartz S, Sonnerborg A, and Vahlne A: Long terminal repeat promoter/enhancer activity of different subtypes of HIV type 1. AIDS Res Hum Retroviruses 1999;15:1293–303.
24. Montano MA, Novitsky VA, Blackard JT, Cho NL, Katzenstein DA, and Essex M: Divergent transcriptional regulation among expanding human immunodeficiency virus type 1 subtypes. J Virol 1997;71:8657–8665.
25. Peeters M, Vincent R, Perret JL, Lasky M, Patrel D, Liegeois F, Courgnaud V, Seng R, Matton T, Molinier S, and Delaporte E: Evidence for differences in MT2 cell tropism according to genetic subtypes of HIV-1: Syncytium-inducing variants seem rare among subtype C HIV-1 viruses. J Acquir Immune Defic Syndr Hum Retroviral 1999;20:115–121.
26. Cecilia D, Kulkarni SS, Tripathy SP, Gangakhedkar RR, Paranjape RS, and Gadkari DA: Absence of coreceptor switch with disease progression in human immunodeficiency virus infections in India. Virology 2000;271:253–258.

Address reprint requests to:
Feng Gao
Department of Medicine
University of Alabama at Birmingham
701 S. 19th Street, LHRB 639
Birmingham, Alabama 35294

This article has been cited by:

1. Evrim Atas, Alon Singer, Amit Meller. 2012. DNA sequencing and bar-coding using solid-state nanopores. *ELECTROPHORESIS* **33**:23, 3437-3447. [CrossRef]
2. Aditya Pattani, Paul F. McKay, Martin J. Garland, Rhonda M. Curran, Katarzyna Migalska, Corona M. Cassidy, R. Karl Malcolm, Robin J. Shattock, Helen O. McCarthy, Ryan F. Donnelly. 2012. Microneedle mediated intradermal delivery of adjuvanted recombinant HIV-1 CN54gp140 effectively primes mucosal boost inoculations. *Journal of Controlled Release* **162**:3, 529-537. [CrossRef]
3. Qijian Su, Hao Liang, Ping Cen, Zhiyou Bi, Ping Zhou. 2012. HIV Type 1 Subtypes Based on the pol Gene and Drug Resistance Mutations Among Antiretroviral-Naive Patients from Guangxi, Southern China. *AIDS Research and Human Retroviruses* **28**:7, 725-728. [Abstract] [Full Text HTML] [Full Text PDF] [Full Text PDF with Links]
4. Alon Singer, Srinivas Rapireddy, Danith H. Ly, Amit Meller. 2012. Electronic Barcoding of a Viral Gene at the Single-Molecule Level. *Nano Letters* 120224151028004. [CrossRef]
5. J.F.S. Mann, D. Stieh, K. Klein, D.S. Miranda de Stegmann, M.P. Cranage, R.J. Shattock, P.F. McKay. 2011. Transferrin conjugation confers mucosal molecular targeting to a model HIV-1 trimeric gp140 vaccine antigen. *Journal of Controlled Release* . [CrossRef]
6. Qiang Liu, Yue Li, GuiBo Yang, JieJie Dai, Ruth M. Ruprecht, Yiming Shao. 2011. Molecularly cloned SHIV-CN97001: a replication-competent, R5 simian/human immunodeficiency virus containing env of a primary Chinese HIV-1 clade C isolate. *Journal of Medical Primatology* no-no. [CrossRef]
7. Louise Donnelly, Rhonda M. Curran, John S. Tregoning, Paul F. McKay, Tom Cole, Ryan J. Morrow, Vicky L. Kett, Gavin P. Andrews, A. David Woolfson, R. Karl Malcolm, Robin J. Shattock. 2011. Intravaginal immunization using the recombinant HIV-1 clade-C trimeric envelope glycoprotein CN54gp140 formulated within lyophilized solid dosage forms. *Vaccine* **29**:27, 4512-4520. [CrossRef]
8. Martin P. Cranage, Carol A. Fraser, Alethea Cope, Paul F. McKay, Michael S. Seaman, Tom Cole, A. Nasir Mahmoud, Joanna Hall, Elaine Giles, Gerald Voss, Mark Page, Neil Almond, Robin J. Shattock. 2011. Antibody responses after intravaginal immunisation with trimeric HIV-1CN54 clade C gp140 in Carbopol gel are augmented by systemic priming or boosting with an adjuvanted formulation. *Vaccine* **29**:7, 1421-1430. [CrossRef]
9. Leopold Kong, Neil C. Sheppard, Guillaume B.E. Stewart-Jones, Cynthia L. Robson, Hongying Chen, Xiaodong Xu, George Krashias, Camille Bonomelli, Christopher N. Scanlan, Peter D. Kwong. 2010. Expression-System-Dependent Modulation of HIV-1 Envelope Glycoprotein Antigenicity and Immunogenicity. *Journal of Molecular Biology* **403**:1, 131-147. [CrossRef]
10. Daniela Teixeira, Patricia Munerato, Shirley Cavalcante Vasconcelos Komninakis, Erika Etsuko Fusuma, Luiz Mario Janini, Maria Cecilia Araripe Sucupira, Ricardo Sobhie Diaz. 2010. The Detection of in Vivo and in Vitro HIV Type 1 B/F Profiles in Brazil Using a Real-Time PCR Assay for Five HIV Type 1 Genomic Regions. *AIDS Research and Human Retroviruses* **26**:9, 981-990. [Abstract] [Full Text HTML] [Full Text PDF] [Full Text PDF with Links]
11. Ravindra K Gupta, Arinder Kohli, Adele L McCormick, Greg J Towers, Deenan Pillay, Chris M Parry. 2010. Full-length HIV-1 Gag determines protease inhibitor susceptibility within in-vitro assays. *AIDS* **24**:11, 1651-1655. [CrossRef]
12. Yutaka Takebe, Huanan Liao, Saiki Hase, Rie Uenishi, Yue Li, Xiao-Jie Li, Xiaoxu Han, Hong Shang, Adeeba Kamarulzaman, Naoki Yamamoto, Oliver G. Pybus, Kok Keng Tee. 2010. Reconstructing the epidemic history of HIV-1 circulating recombinant forms CRF07_BC and CRF08_BC in East Asia: The relevance of genetic diversity and phylodynamics for vaccine strategies. *Vaccine* **28**, B39-B44. [CrossRef]
13. George Krashias, Anna-Katharina Simon, Frank Wegmann, Wai-Ling Kok, Ling-Pei Ho, David Stevens, John Skehel, Jonathan L. Heeney, Amin E. Moghaddam, Quentin J. Sattentau. 2010. Potent adaptive immune responses induced against HIV-1 gp140 and influenza virus HA by a polyanionic carbomer. *Vaccine* **28**:13, 2482-2489. [CrossRef]

14. M P Cranage, C A Fraser, Z Stevens, J Huting, M Chang, S A Jeffs, M S Seaman, A Cope, T Cole, R J Shattock. 2010. Repeated vaginal administration of trimeric HIV-1 clade C gp140 induces serum and mucosal antibody responses. *Mucosal Immunology* **3**:1, 57-68. [CrossRef]

15. Caroline Pereira Bittencourt Passaes, Monick Lindenmeyer Guimarães, Gonzalo Bello, Mariza Gonçalves Morgado. 2009. Near Full-Length Genome Characterization of HIV Type 1 Unique BC Recombinant Forms from Southern Brazil. *AIDS Research and Human Retroviruses* **25**:12, 1339-1344. [Abstract] [Full Text HTML] [Full Text PDF] [Full Text PDF with Links]

16. Elizabeth Cavalieri, Camila Florido, Élcio Leal, Daisy Maria Machado, Michelle Camargo, Ricardo S. Diaz, Luiz Mario Janini. 2009. Intrahost and Interhost Variability of the HIV Type 1 nef Gene in Brazilian Children. *AIDS Research and Human Retroviruses* **25**:11, 1129-1140. [Abstract] [Full Text HTML] [Full Text PDF] [Full Text PDF with Links]

17. Shaolin Hong, Jingjiang Cao, Ya-ting Tu. 2009. Evolution of HIV-1 in a patient population failing multiple-drug therapy. *Microbiology and Immunology* **53**:9, 535-539. [CrossRef]

18. Nimisha Gandhi, Zainulabedin Saiyed, Samikkannu Thangavel, Jose Rodriguez, K.V.K. Rao, Madhavan P.N. Nair. 2009. Differential Effects of HIV Type 1 Clade B and Clade C Tat Protein on Expression of Proinflammatory and Antiinflammatory Cytokines by Primary Monocytes. *AIDS Research and Human Retroviruses* **25**:7, 691-699. [Abstract] [Full Text PDF] [Full Text PDF with Links]

19. Bernhard J. Fromme, Marla Coetsee, Pauline Van Der Watt, Mei-Chi Chan, Karin M. Sperling, Arieh A. Katz, Colleen A. Flanagan. 2008. High-Affinity Binding of Southern African HIV Type 1 Subtype C Envelope Protein, gp120, to the CCR5 Coreceptor. *AIDS Research and Human Retroviruses* **24**:12, 1527-1536. [Abstract] [Full Text PDF] [Full Text PDF with Links]

20. C. V. Santhosh, Mayur C. Tamhane, Rita Mukhopadhyaya, Robin Mukhopadhyaya. 2008. Full-Length Genome Characterization of an HIV Type 2 Isolate from India. *AIDS Research and Human Retroviruses* **24**:10, 1315-1317. [Abstract] [Full Text PDF] [Full Text PDF with Links]

21. H. Chen, X. Xu, H.-H. Lin, S.-H. Chen, A. Forsman, M. Aasa-Chapman, I. M. Jones. 2008. Mapping the immune response to the outer domain of a human immunodeficiency virus-1 clade C gp120. *Journal of General Virology* **89**:10, 2597-2604. [CrossRef]

22. Zhiwei Chen, Yaoxing Huang, Xiuqing Zhao, Lei Ba, Wenyong Zhang, David D Ho. 2008. Design, Construction, and Characterization of a Multigenic Modified Vaccinia Ankara Candidate Vaccine Against Human Immunodeficiency Virus Type 1 Subtype C/B′. *JAIDS Journal of Acquired Immune Deficiency Syndromes* **47**:4, 412-421. [CrossRef]

23. Atima Agarwal, Sumathi Sankaran, Madhu Vajpayee, V. Sreenivas, Pradeep Seth, Satya Dandekar. 2007. Correlation of immune activation with HIV-1 RNA levels assayed by real-time RT-PCR in HIV-1 subtype C infected patients in Northern India. *Journal of Clinical Virology* **40**:4, 301-306. [CrossRef]

24. Dayse Locateli, Patrícia H. Stoco, Artur T.L. de Queiroz, Luiz C.J. Alcântara, Luiz G.E. Ferreira, Carlos R. Zanetti, Rosângela Rodrigues, Edmundo C. Grisard, Aguinaldo R. Pinto. 2007. Molecular epidemiology of HIV-1 in Santa Catarina State confirms increases of subtype C in Southern Brazil. *Journal of Medical Virology* **79**:10, 1455-1463. [CrossRef]

25. Mario P.S. Chin, Jianbo Chen, Olga A. Nikolaitchik, Wei-Shau Hu. 2007. Molecular determinants of HIV-1 intersubtype recombination potential. *Virology* **363**:2, 437-446. [CrossRef]

26. Carmen Elena Gómez, Jose Luis Nájera, Victoria Jiménez, Kurt Bieler, Jens Wild, Linda Kostic, Shirin Heidari, Margaret Chen, Marie-Joelle Frachette, Giuseppe Pantaleo, Hans Wolf, Peter Liljeström, Ralf Wagner, Mariano Esteban. 2007. Generation and immunogenicity of novel HIV/AIDS vaccine candidates targeting HIV-1 Env/Gag-Pol-Nef antigens of clade C. *Vaccine* **25**:11, 1969-1992. [CrossRef]

27. Catherine M. Bell, Bridgette J. Connell, Alexio Capovilla, Willem D.F. Venter, Wendy S. Stevens, Maria A. Papathanasopoulos. 2007. Molecular Characterization of the HIV Type 1 Subtype C Accessory Genes vif, vpr, and vpu. *AIDS Research and Human Retroviruses* **23**:2, 322-330. [Abstract] [Full Text PDF] [Full Text PDF with Links]

28. Gustavo H. Kijak, Sodsai Tovanabutra, Eric Sanders-Buell, Veerachai Watanaveeradej, Mark S. de Souza, Kenrad E. Nelson, Vidhaya Ketsararat, Vilawan Gulgolgarn, Manu Wera-arpachai, Somchai Sriplienchan, Chirasak Khamboonrueng, Deborah L. Birx, Merlin L. Robb, Francine E. McCutchan. 2007. Distinguishing molecular forms of HIV-1 in Asia with a high-throughput, fluorescent genotyping assay, MHAbce v.2. *Virology* **358**:1, 178-191. [CrossRef]

29. Diana Safarian, Xavier Carnec, Fotini Tsamis, Francis Kajumo, Tatjana Dragic. 2006. An anti-CCR5 monoclonal antibody and small molecule CCR5 antagonists synergize by inhibiting different stages of human immunodeficiency virus type 1 entry. *Virology* **352**:2, 477-484. [CrossRef]

30. Hsi-Hsun Lin, Yi-Li Shih, Yung-Ching Liu, Susan Shin-Jung Lee, Chun-Kai Huang, Ya-Lei Chen, Chuen Chin, Chung-Hsu Lai, Hung-Chin Tsai, Yi-Chi Guo, Linqi Zhang. 2006. An Epidemic of HIV Type I CRF07_BC Infection Among Injection Drug Users in Taiwan. *JAIDS Journal of Acquired Immune Deficiency Syndromes* **42**:2, 248-255. [CrossRef]

31. Roy W. Johnson, Bing Li, Susan Sunay, Renee H. Moore, Joseph Mulenga, Eric Hunter, Susan Allen, Jerry L. Blackwell, Cynthia A. Derdeyn. 2006. Real-time PCR Quantitation of Subtype C HIV DNA in a Zambian Discordant Couple Cohort. *AIDS Research and Human Retroviruses* **22**:5, 438-444. [Abstract] [Full Text PDF] [Full Text PDF with Links]

32. Vladimir A. Novitsky, Peter B. Gilbert, Kimberly Shea, Mary F. McLane, Natasha Rybak, Ilyana Klein, Ibou Thior, Thumbi Ndung'u, Tun-Hou Lee, Myron E. Essex. 2006. Interactive association of proviral load and IFN-γ-secreting T cell responses in HIV-1C infection. *Virology* **349**:1, 142-155. [CrossRef]

33. Kalpana Dhiraj Agnihotri, Srikanth P. Tripathy, Abhay P. Jere, Sameer M. Kale, Ramesh S. Paranjape. 2006. Molecular Analysis of gp41 Sequences of HIV Type 1 Subtype C from India. *JAIDS Journal of Acquired Immune Deficiency Syndromes* **41**:3, 345-351. [CrossRef]

34. Toby D Gottfried, Ronald W Mink, Praphan Phanuphak. 2006. Calypte ® AWARE™ HIV-1/2 OMT antibody test using oral fluid: special challenges of rapid HIV testing in the developing world. *Expert Review of Molecular Diagnostics* **6**:2, 139-144. [CrossRef]

35. Andr?? F Santos, Thatiana M Sousa, Esmeralda AJM Soares, Sabri Sanabani, Ana MB Martinez, Eduardo Sprinz, Jussara Silveira, Ester C Sabino, Am??lcar Tanuri, Marcelo A Soares. 2006. Characterization of a new circulating recombinant form comprising HIV-1 subtypes C and B in southern Brazil. *AIDS* **20**:16, 2011???2019. [CrossRef]

36. Peter B. Gilbert, Vladimir Novitsky, Max Essex. 2005. Covariability of Selected Amino Acid Positions for HIV Type 1 Subtypes C and B. *AIDS Research and Human Retroviruses* **21**:12, 1016-1030. [Abstract] [Full Text PDF] [Full Text PDF with Links]

37. Li Liu, Bo Su, Ke Zhuang, Po Tien, Zhiwei Chen, Linqi Zhang. 2005. Genetic Characterization of Full-Length HIV Type 1 Genomes From 3 Infected Paid Blood Donors in Henan, China. *JAIDS Journal of Acquired Immune Deficiency Syndromes* **40**:4, 501-503. [CrossRef]

38. Esmeralda AJM Soares, Ana MB Martínez, Thatiana M Souza, André FA Santos, Vanusa Da Hora, Jussara Silveira, Francisco I Bastos, Amilcar Tanuri, Marcelo A Soares. 2005. HIV-1 subtype C dissemination in southern Brazil. *AIDS* **19**:Suppl 4, S81-S86. [CrossRef]

39. Miguel A Arroyo, Michael Hoelscher, Warren Sateren, Eleuter Samky, Leonard Maboko, Oliver Hoffmann, Gustavo Kijak, Merlin Robb, Deborah L Birx, Francine E McCutchan. 2005. HIV-1 diversity and prevalence differ between urban and rural areas in the Mbeya region of Tanzania. *AIDS* **19**:14, 1517-1524. [CrossRef]

40. Nagadenahalli Byrareddy Siddappa, Prashanta Kumar Dash, Anita Mahadevan, Anita Desai, Narayana Jayasuryan, Vasanthapuram Ravi, Parthasarathy Satishchandra, Susarla K Shankar, Udaykumar Ranga. 2005. Identification of unique B/C recombinant strains of HIV-1 in the southern state of Karnataka, India. *AIDS* **19**:13, 1426-1429. [CrossRef]

41. Hongying Chen, Xiaodong Xu, Alexandra Bishop, Ian M Jones. 2005. Reintroduction of the 2G12 epitope in an HIV-1 clade C gp120. *AIDS* **19**:8, 833-835. [CrossRef]

42. Thomas J. Scriba, Jan zur Megede, Richard H. Glashoff, Florette K. Treurnicht, Susan W. Barnett, Estrelita Janse van Rensburg. 2005. Functionally-inactive and immunogenic Tat, Rev and Nef DNA vaccines derived from sub-Saharan subtype C human immunodeficiency virus type 1 consensus sequences. *Vaccine* **23**:9, 1158-1169. [CrossRef]

43. Miguel A. Arroyo, Michael Hoelscher, Eric Sanders-Buell, Karl-Heinz Herbinger, Eleuter Samky, Leonard Maboko, Oliver Hoffmann, Merlin R. Robb, Deborah L. Birx, Francine E. McCutchan. 2004. HIV Type 1 Subtypes among Blood Donors in the Mbeya Region of Southwest Tanzania. *AIDS Research and Human Retroviruses* **20**:8, 895-901. [Abstract] [Full Text PDF] [Full Text PDF with Links]

44. C APETREI, P MARX, S SMITH. 2004. The evolution of HIV and its consequences. *Infectious Disease Clinics of North America* **18**:2, 369-394. [CrossRef]

45. Xu G. Yu, Marylyn M. Addo, Beth A. Perkins, Feili Wej, Almas Rathod, Shaun C. Geer, Mark Parta, Daniel Cohen, David R. Stone, Christopher J. Russell, Giancarlo Tanzi, Shan Mei, Alysse G. Wurcel, Nicole Frahm, Mathias Lichterfeld, Laura Heath, James I. Mullins, Francesco Marincola, Philip J. R. Goulder, Christian Brander, Todd Allen, Yunzhen Cao, Bruce D. Walker, Marcus Altfeld. 2004. Differences in the Expressed HLA Class I Alleles Effect the Differential Clustering of HIV Type 1-Specific T Cell Responses in Infected Chinese and Caucasians. *AIDS Research and Human Retroviruses* **20**:5, 557-564. [Abstract] [Full Text PDF] [Full Text PDF with Links]

46. Matthew E. Harris, Shlomo Maayan, Bohye Kim, Michael Zeira, Guido Ferrari, Deborah L. Birx, Francine E. McCutchan. 2003. A Cluster of HIV Type 1 Subtype C Sequences from Ethiopia, Observed in Full Genome Analysis, Is Not Sustained in Subgenomic Regions. *AIDS Research and Human Retroviruses* **19**:12, 1125-1133. [Abstract] [Full Text PDF] [Full Text PDF with Links]

47. Xiao-Fang Yu, Xueren Wang, Penyong Mao, Shiyi Wang, Zong Li, Jinbing Zhang, Rebecca Garten, Wei Kong, Shenghan Lai. 2003. Characterization of HIV Type 1 Heterosexual Transmission in Yunnan, China. *AIDS Research and Human Retroviruses* **19**:11, 1051-1055. [Abstract] [Full Text PDF] [Full Text PDF with Links]

48. M. A. Papathanasopoulos, T. Patience, T. M. Meyers, F. E. McCutchan, L. Morris. 2003. Full-Length Genome Characterization of HIV Type 1 Subtype C Isolates from Two Slow-Progressing Perinatally Infected Siblings in South Africa. *AIDS Research and Human Retroviruses* **19**:11, 1033-1037. [Abstract] [Full Text PDF] [Full Text PDF with Links]

49. Bo Su, Li Liu, Fusheng Wang, Xien Gui, Min Zhao, Po Tien, Linqi Zhang, Zhiwei Chen. 2003. HIV-1 subtype B' dictates the AIDS epidemic among paid blood donors in the Henan and Hubei provinces of China. *AIDS* **17**:17, 2515-2520. [CrossRef]

50. Michel P. de Baar, Almaz Abebe, Aletta Kliphuis, Girma Tesfaye, Jaap Goudsmit, Georgios Pollakis. 2003. HIV Type 1 C and C′ Subclusters Based on Long Terminal Repeat Sequences in the Ethiopian HIV Type 1 Subtype C Epidemic. *AIDS Research and Human Retroviruses* **19**:10, 917-922. [Abstract] [Full Text PDF] [Full Text PDF with Links]

51. Feng Gao, Yingying Li, Julie M. Decker, Fred W. Peyerl, Frederic Bibollet-Ruche, Cynthia M. Rodenburg, Yalu Chen, Denise R. Shaw, Susan Allen, Rosemary Musonda, George M. Shaw, Allan J. Zajac, Norman Letvin, Beatrice H. Hahn. 2003. Codon Usage Optimization of HIV Type 1 Subtype C gag, pol, env, and nef Genes: In Vitro Expression and Immune Responses in DNA-Vaccinated Mice. *AIDS Research and Human Retroviruses* **19**:9, 817-823. [Abstract] [Full Text PDF] [Full Text PDF with Links]

52. Ping Zhong, Laiyi Kang, Qichao Pan, Frank Konings, Sherri Burda, Liying Ma, Yile Xue, Xiaohong Zheng, Zicheng Jin, Phillipe Nyambi. 2003. Identification and Distribution of HIV Type 1 Genetic Diversity and Protease Inhibitor Resistance???Associated Mutations in Shanghai, P. R. China. *JAIDS Journal of Acquired Immune Deficiency Syndromes* **34**:1, 91-101. [CrossRef]

53. Mara Biasin, Adriano Boasso, Luca Piacentini, Daria Trabattoni, Giuliana Magri, Ranjana Deshmuks, Alaka Deshpande, Mario Clerici. 2003. IL-4 and CXCR4 upregulation in HIV-infected and uninfected individuals from Maharashtra-Mumbai. *AIDS* **17**:10, 1563-1565. [CrossRef]

54. Marcelo A Soares, Tulio de Oliveira, Rodrigo M Brindeiro, Ricardo S Diaz, Ester C Sabino, Luís Brigido, Ivone L Pires, Mariza G Morgado, Maria C Dantas, Draurio Barreira, Paulo R Teixeira, Sharon Cassol, Amilcar Tanuri. 2003. A specific subtype C of human immunodeficiency virus type 1 circulates in Brazil. *AIDS* **17**:1, 11-21. [CrossRef]

55. Jan zur Megede, Susan Engelbrecht, Tulio de Oliveira, Sharon Cassol, Thomas J. Scriba, Estrelita Janse van Rensburg, Susan W. Barnett. 2002. Novel Evolutionary Analyses of Full-Length HIV Type 1 Subtype C Molecular Clones from Cape Town, South Africa. *AIDS Research and Human Retroviruses* **18**:17, 1327-1332. [Abstract] [Full Text PDF] [Full Text PDF with Links]

56. Monick Lindenmeyer Guimarães, Aline dos Santos Moreira, Regina Loureiro, Bernardo Galvão-Castro, Mariza Gonçalves Morgado. 2002. High Frequency of Recombinant Genomes in HIV Type 1 Samples from Brazilian Southeastern and Southern Regions. *AIDS Research and Human Retroviruses* **18**:17, 1261-1269. [Abstract] [Full Text PDF] [Full Text PDF with Links]

57. F.E. McCutchan, J.K. Carr, D. Murphy, S. Piyasirisilp, F. Gao, B. Hahn, X.-F. Yu, C. Beyrer, D.L. Birx. 2002. Precise Mapping of Recombination Breakpoints Suggests a Common Parent of Two BC Recombinant HIV Type 1 Strains Circulating in China. *AIDS Research and Human Retroviruses* **18**:15, 1135-1140. [Abstract] [Full Text PDF] [Full Text PDF with Links]

58. Maria A. Papathanasopoulos, Tonie Cilliers, Lynn Morris, John L. Mokili, William Dowling, Deborah L. Birx, Francine E. McCutchan. 2002. Full-Length Genome Analysis of HIV-1 Subtype C Utilizing CXCR4 and Intersubtype Recombinants Isolated in South Africa. *AIDS Research and Human Retroviruses* **18**:12, 879-886. [Abstract] [Full Text PDF] [Full Text PDF with Links]

59. Thomas J. Scriba, Tania de Villiers, Florette K. Treurnicht, Jan zur Megede, Susan W. Barnett, Susan Engelbrecht, Estrelita Janse van Rensburg. 2002. Characterization of the South African HIV Type 1 Subtype C Complete 5′ Long Terminal Repeat, nef, and Regulatory Genes. *AIDS Research and Human Retroviruses* **18**:2, 149-159. [Abstract] [Full Text PDF] [Full Text PDF with Links]

60. Tumelo Mashishi, Shayne Loubser, Win Hide, Gillian Hunt, Lynn Morris, Gita Ramjee, Salim Abdool-Karim, Carolyn Williamson, Clive M. Gray. 2001. Conserved Domains of Subtype C Nef from South African HIV Type 1-Infected Individuals Include Cytotoxic T Lymphocyte Epitope-Rich Regions. *AIDS Research and Human Retroviruses* **17**:17, 1681-1687. [Abstract] [Full Text PDF] [Full Text PDF with Links]

61. Susan Engelbrecht, Tania de Villiers, Candice C. Sampson, Jan zur Megede, Susan W. Barnett, Estrelita Janse van Rensburg. 2001. Genetic Analysis of the Complete gag and env Genes of HIV Type 1 Subtype C Primary Isolates from South Africa. *AIDS Research and Human Retroviruses* **17**:16, 1533-1547. [Abstract] [Full Text PDF] [Full Text PDF with Links]

62. Feng Gao, Nicole Vidal, Yingying Li, Stanley A. Trask, Yalu Chen, Leondios G. Kostrikis, David D. Ho, Jinwook Kim, Myoung-Don Oh, Kangwon Choe, Mika Salminen, David L. Robertson, George M. Shaw, Beatrice H. Hahn, Martine Peeters. 2001. Evidence of Two Distinct Subsubtypes within the HIV-1 Subtype A Radiation. *AIDS Research and Human Retroviruses* **17**:8, 675-688. [Abstract] [Full Text PDF] [Full Text PDF with Links]

63. Michael H. Malim, Michael Emerman. 2001. HIV-1 Sequence Variation. *Cell* **104**:4, 469-472. [CrossRef]

64. Iain D. Tatt, Katrina L. Barlow, Angus Nicoll, Jonathan P. Clewley. 2001. The public health significance of HIV-1 subtypes. *AIDS* **15**, S59-S71. [CrossRef]