医薬品 告書

報告	調査	報告	研究素	医薬部外品化粧品	医					
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識別番号・幸	報告回数		報告日		第一報入手日 2007年2月13日	新医	薬品等の区分 該当なし	厚生労働省処理欄
一般的名称 販売名 (企業名)	①乾燥抗 HBs 人免疫グロ ②ポリエチレングリコール ①ヘプスプリン (ペネシス ②静注用ヘプスプリンーII	·処理抗 HBs 人免疫ク 、)		報告の 表状況	Yox Sanguinis 2007; 113-120	92:	公表国 韓国	
20 例の血友病患者が、1990 年初頭以降、韓国で製造された血液凝固第 1X 因子の投与を受けてから 1~2 年後にヒト免疫不全ウイルスー1 (HIV-1) に感染していると診断された。本研究は血漿ドナーで見出されたウイルスと血友病患者で見出されたウイルスとの間の遺伝子の関連性を調べたものである。感染した血友病患者、韓国製の凝固因子製剤製造に用いられた血漿のドナー、韓国外で感染した血友病患者、および韓国ローカルの対照から得られたウイルスの nef 遺伝子と pol 遺伝子の配列を nestedPCR および直接的な DNA 配列分析で調べた。それらの配列の間の関連性を調べるために系統学的分析を用いた。その結果、血漿ドナーと血友病患者の双方とも、HIV-1 サブタップ B の韓国 subclade での感染であることが判明した。即ち、これらのデータは、20 例の血友病患者への HIV-1 の伝播が韓国製の凝固を子製剤の静脈内注射を介して起こったことを示している。 更に筆者らは、この報告の中で、当該ロットの血液凝固第 IX 因子製剤を製造した韓国 X 社の製造工程について、以下の問題点があったことを指摘している。 1) 製造法に、New York Blood Center から導入した SD 処理技術を採用していたが、当時レトロウイルスを不活化することが明らかになれていた加熱処理は行なっていなかった。 2) 1991 年半ばに、韓国 X 社の製造施設及び製造工程の査察が行われ、New York Blood Center の専門家の指摘により、以下の工程改造							との間の遺伝子	使用上の注意記載状況・ その他参考事項等 代表として静注用ヘブスプリンーIH の記載を示す。 2. 重要な基本的注意 (1)本剤の原材料となる血液については、HBs抗原、抗HCV抗体、抗HIV-1抗体、抗HIV-2抗体陰性で、かつALT (GPT) 値でスクリーニングを実施している。更に、プールした試験血漿については、HIV-1、HBV及びHCVについて核酸増幅検査(NAT)を実施し、適合した血漿を本剤の製造に使用しているが、当該NATの検出限界以下のウイルスが混入
要 ・SD 試薬添加時に二人のサインを求める。 ・SD 試薬添加の直前にろ過する。 ・SD 試薬添加前にあらかじめ定めたたん白濃度まで希釈する。								している可能性が常に存在する。本剤は、以上の 検査に適合した高力価の抗HBs抗体を含有する血 漿を原料として、Cohnの低温エタノール分画で得 た画分からポリエチレングリコール4000処理、
弊社で製造工 関第 IX 因子製 これまで、当 また、当該4製 り、工程では 下で管理して	備により、HIV-IがSD処理」 捏にSD処理を導入している 関がであるコンコエイトHT-I 該SD処理4製剤が疑われた 関剤のSD処理工程では、SD試 pH、たん白濃度、SD試薬の おり、当然のことながら全て な工程管理の不備による感勢	製剤には、血液凝固第 パ、トロンビン-ヨシ 感染症報告は受けてい 薬添加前に薬液の清潤 農度、温度および処理 この作業は担当者と確	5 伝播したとの報告 IX 因子製剤である。 トミ及びフィブリノ ない。 登化を目的としてろう 時間を管理している 認者のダブルチェッ	クリスマシ ゲン-HT の 過または返 ら。またこ	ソン-M のほか血液凝 が4 製剤がある。 な な な な い な い な い な と い る い る い る い る い る い る い る に る い る 、 に る い る 、 れ ら の こ て る の れ ら の れ ら の れ ら の れ ら の れ ら の れ ら の れ ら の れ ら の れ ら の れ ら の れ ら の れ ら の れ ら れ ら	報告は:響を与	後の対応 本剤の安全性に えないと考える みの措置はとらな	DEAEセファデックス処理等により抗HBs人免疫グロブリンを機縮・精製した製剤であり、ウイルス不活化・除去を目的として、製造工程において60℃、10時間の液状加熱処理及び濾過膜処理(ナノフィルトレーション)を施しているが、投与に際しては、次の点に十分注意すること。



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ORIGINAL PAPER

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Molecular epidemiologic study of a human immunodeficiency virus 1 outbreak in haemophiliacs B infected through clotting factor 9 after 1990

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Vox Sanguinis

Background and Objectives Twenty haemophiliacs were diagnosed as infected with human immunodeficiency virus 1 (HIV-1), 1 to 2 years after exposure to clotting factor 9 manufactured in Korea, beginning in early 1990. This study assessed the genetic relationships between viruses found in plasma donors and haemophiliacs.

Materials and Methods Sequencing of the nef and pol genes of viruses from infected haemophiliacs, plasma donors whose plasma was used in domestic clotting factor manufacture, haemophiliacs infected outside Korea, and local controls were determined by nested polymerase chain reactions and direct DNA sequencing. Phylogenetic analysis was used to investigate the relationships among the sequences.

Results Both plasma donors and the haemophiliacs were infected with a subclade of subtype B that is a founder effect lineage in Korea.

Conclusion Our data indicate that HIV-1 transmission to 20 haemophiliacs occurred through intravenous injection of Korean-made clotting factor.

Summary A clotting factor made in Korea from blood from cash-paid donors infected at least 20 haemophiliacs with HIV-1 subtype B.

Key words: domestic clotting factor 9, haemophiliacs, HIV-1, nef gene, phylogenetic analysis, plasma, pol gene.

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Introduction

One consequence of the rapid rate of human immunodeficiency virus 1 (HIV-1) mutation is that phylogenetic analysis

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Y.C. and H.S. participated in designing and performing the research; Y.C., B.T. and J.K. controlled and analysed the data; Y.C., H.S and B.T. wrote the paper; and all authors were involved in preparation and subsequent version of the paper.

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of HIV-1 DNA sequences is a powerful tool for identifying closely related viral strains and allowing the inference of transmission between individuals. Many previous studies have used phylogenetic methods to examine suspected or known viral transmission events [1-5]. There are also geographic variations in HIV-1 sequences that may be of scientific use. By comparison to the worldwide sequences, it was found that Korean subtype B (KSB) HIV-1 sequences are quite distinct [6-11], indicating a strong founder effect, with the founding event(s) occurring in the late 1980s.

Prior to 1990, Korean patients suffering from haemophilia B (HP B) were treated with imported clotting factor 9 and other blood products. Domestic clotting factor 9 (DCF), produced by a non-heat inactivation processing, was supplied to almost all Korean HP B beginning in early 1990. Before exposure to DCF through intravenous injection, 18 of the 23 HPs were screened and found to be seronegative for anti-HIV-1

antibodies. Except HP-21 who were diagnosed in 1987, between 1990 and 1994, 22 Korean HPs (19 HP B and 3 HP A) were diagnosed with HIV-1 infection after exposure to DCF. At the time of these diagnoses, there were 122 HP B registered at the Korea Haemophilia Clinic (seropositive rate 15-6%).

In this study, we performed further investigations of the 20 HIV-1-infected HP B and 3 HIV-1-infected HP A patients mentioned above, including a single HP B diagnosed in 1987 prior to receiving DCF, and two HP B who received clotting factors manufactured outside Korea. Considering the very low prevalence of HIV-1 in Korea (251 cases out of a population size of 47 million as of December 1992), the increased prevalence of HIV-1 cases occurring after 1990 within the 122 HP B was very unusual, especially compared to the very low prevalence of seropositives (less than 15 per million) among local blood donors [12]. This large cluster of HIV-1 cases within the haemophilia population prompted the Center for AIDS Research, Korean National Institute of Health, to form an investigation committee to examine this issue.

Before the first anti-HIV-1 antibody testing of HPs registering at the Korea Haemophilia Clinic, 16 of those patients had received transfusions (> 785 units in total, in Table 1). Despite multiple transfusions, they were free of HIV-1 infection until they began to inject DCF, after which time they were rarely transfused (a total 16 units in two HPs). Thus, it seems unlikely that these patients were infected with HIV-1 through transfusion. Interestingly, the only other similar outbreak was seen from 1989 to 1990 in Germany, where 9 of 48 HPs (18-8%) treated with a single contaminated batch of clotting factor 9 were infected with HIV-1 [13].

Here, we investigated whether there is a genetic association between the Korean HIV-1-infected HPs and HIV-1-infected plasma donors who are known to have seroconverted a short time after donating plasma that was used to make DCF.

Patients and methods

Twenty-three HIV-1-infected haemophiliacs

HPs 1-20 were diagnosed with HIV-1 infection between 1990 and 1994. HP 21 was infected with HIV-1 by imported factor 9 prior to 1987, and was diagnosed in 1987. Two other HPs (nos 22 and 23) were diagnosed in 1991 and 1994, but they had lived outside Korea for a prolonged period (Table 1). Two other HIV-1-infected Korean HPs were not included from this study, as one was infected with HIV-1 abroad prior to 1987, and the other was infected through mother-to-child transmission. Informed written consent was obtained from all living study participants.

Cash-paid plasma donors

In the late 1980s, cash-paid plasma collection occurred at domestic plasma centres run by Company X, which manufactures various blood products, including clotting factors. At these centres, four HIV-1-seropositive homosexual donors 0, P, Q and R were detected during primary infection (Table 2). The last four plasma units (drawn on 30 November and 8, 20 and 23 December 1989) from donor 0 were withdrawn, but the prior 79 units had already been used for manufacturing various blood products. Because of the window period between infection and seroconversion, at least four units (drawn on 4, 10, 13 and 16 October 1989) were not safe. Between 3 January 1990 and 26 March 1990, 21 units of plasma were taken from donor P. Three units of plasma (taken on 20 and 23 January and 2 March 1990) from donor P were used to produce DCF according to the manufacturer's report. Two units of plasma were taken from donor Q on 29 January and 6 February 1992. Plasma from donor R was taken nine times between 6 April 1992 and 8 June 1992. Except for last two units, seven units were used for manufacturing blood products. In addition, donors O and R were also infected with hepatitis C virus (HCV) on at least 13 March 1991 and 16 March 1993, respectively.

Sequencing of the nef and pol genes

Peripheral blood mononuclear cells (PBMC) from 23 HPs and three donors (O, P and Q) were obtained between 1991 and 2003. To amplify proviral nef sequences from the PBMC, nested polymerase chain reactions (PCR) were used as previously described [7]. In cases that were negative for the nested PCR, a second set of nested primers was applied. The primers used were as follows: first PCR, CE21 (forward) and CE22 (reverse); second PCR, primer Nef5'5 and LTR3' [14]. The PCR products were purified and used for direct sequencing. We determined the nef gene sequence at least two different times in each HP sample except HP 15. We ruled out PCR contamination by physical separation of each PCR procedure, inclusion of negative controls, BLAST search, and phylogenetic analysis. To amplify partial pol sequences from PBMC, a nested PCR was employed as described in our previous studies [11,15].

nef and pol sequence data

The GenBank accession numbers for the nef sequences from the donors and HPs are AY121450, AY221654, AY121451, AY260770, AY584756-AY584759, AY899339 and AY899340 from donor O; AF063929, AY363309 and AY363310 from donor P; AF063918 from donor Q; AF063923 and AY363311 from HP 1; AF063928 and Z98020 from HP 2; AY221675-AY221715 and AY260771-AY260791 from the other HPs. The local nef sequences from non-HPs, which were used for comparison purposes, could be found under the following accession

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Table 1 Summary on 23 HIV-1 infected Korean haemophiliaes

	Age at HIV	Deficient	Negative for	Dx of HIV		Time on the	CD4+ T cell
Hacmophiliacs	diagnosis	factor	anti-HIV antibody	infection	Total number of blood transfusion* (unit)	first use of DCF	(the earliest)
20 haemophiliacs	infected with Kore	an subclade B of	HIV-1 subtype B				7
1	19	9	April 1990	26 November 1990	Not available (death in 1994)	Early 1990	555 in 1991
2	14	9 '	No data	21 February 1991	33 from Fébruary 1986 to March 1989	May 1990	629 in 1991
3	11	9	21 February 1991	1 April 1991	3 before 1983 and 93 from 1988 to 1990	May 1990	576 in 1991
4	6	8 '	No data	24 August 1991	1 in August 1987	Not available	826 in 1994
5	11	9 .	28 February 1991	13 January 1992	155 (127 from 1981 to 1988 and 28 in 1989)	February 1991	554 in 1992
6	4	9	9 May 1989/25 February 1991	20 January 1992	90 from September 1988 to 6 December 1990 (death in 1998)	14 March 1991	771 in 1992
7	7	9	27 February 1991	22 January 1992	265 from 1 August 1987 to 23 January 1991	1 May 1990	804 in 1992
8	19	9	10 June 1989/9 April 1991	15 February 1992	16 from June 1989 to September 1990	April 1991	241 in 1992
9	23	9	27 February 1991	25 February 1992	5 in Mar 1989 and 3 in 6 April 1991	7 March 1991	589 in 1993
. 10	23	9	No data	26 March 1992	56 from March 1990 to September 1990 and 4 in March 1992	September 1990	336 in 1993
11	5	9	28 February 1990/14 March 1991	29 February 1992	4 from March 1989 to October 1989	16 April 1991	966 in 1992
12	29	9	6 March 1991	25 February 1992	4 in 1987 and 4 in 1989	March 1991	767 in 1992
13 ,	11	9	25 February 1991	29 February 1992	3 in March 1987	7 March 1987/11 ¹ January 1991	446 in 1992
14	35	9	20 October 1989/22 February 1991	19 February 1992	24 in October 24 to October 28, 1989	February 1991	420 jn 1992
15	16	9	21 February 1991	16 September 1992	1 in 1989	March 1991	507 in 1996
16	22	9	14 March 1991	5 December 1992	30 from September 1988 to October 1988	14 March 1991	315 in 1992
17	4	9	27 February 1991	26 February 1993	30 to January 1991	16 February 1991	612 in 1993
18	35	9	1 July 1991	2 March 1993	Many before February 1988, 2 in March 1988, and 12 in November 1991	2 April 1988/10 September 1989	173 in 1993
19	13	9	5 March 1991/2 March 1992	26 July 1993	0	5 March 1991	425 in 1996
20	39	8	27 February 1991	4 August 1994	0 (use of six vials of DCF instead of factor 8)	25 February 1991	234 in 1994
3 haemophiliaes i	nfected with non-	Korean subclade	B of HIV-1 subtype B	•			
21	9	9	No data	3 August 1987	Used clotting factors imported from USA	· 1990	627 in 1987
22	35	9	No data	27 March 1991	4 in January 1987, lived in USA in 1988	1990	527 in 1991
23	10	8 .	No data	13 October 1994	Lived in Iran for 10 years since birth	October 1994	561 in 1996

^{*}Blood transfusion includes fresh frozen plasma, cryoprecipitates, and so on, Haemophiliacs 13 and 18 were also exposed to DCF which was manufactured in 1987. Dx, diagnosis; DCF, domestic clotting factor 9.

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Table 2 Summary on the four HIV-1 infected cash-paid plasma donors and domestic clotting factor (DCF)

Plasma	Age at HIV	Period of plasma	Unit of plasma	Last negative for	Diagnosis of
donor	diagnosis	donation at Company X	donation	anti-HIV antibody	HIV infection
0	27	5 January 1988 to 23 December 1989	83	16 October 1989	30 November 1989
P	30	3 January 1990 to 26 March 1990	19	15 March 1990	30 March 1990
DCF has bee	n manufactured fron	late 1989 in Company X			
Q	32	29 January 1992 to 6 February 1992	. 2	29 January 1992	6 February 1992
R	22	6 April 1992 to 8 June 1992	9	30 May 1992	3 June 1992

numbers: AF462701-AF462767, AY121449-AY121471, AY363309-AY363369 and AY584754-AY584808.

The GenBank accession numbers for the 532 pol sequences from the donors, HPs and local sequences from non-HPs are as follows: AY585687 and AF407364 from donor O, AY347694 from donor P, AY347690 from HP I, AY166460-AY166503, AY219009-AY219031, AY347683-AY347709, AY392099-AY392125 and AY731184-AY731229 for other HPs and local controls.

Phylogenetic analysis

The sequences described in the current study were aligned to the HIV-1 subtype reference set from the HIV Sequence Database (http://hiv-web.lanl.gov/content/hiv-db/Subtype_REF/align.html) and phylogenetic trees were built using the maximum parsimony method in paup produced identical trees with regard to which sequences fell within KSB within HIV-1 subtype B.

Results

Characteristics of haemophiliacs

Seventeen of 20 HPs (excluding nos 2, 4 and 10) screened negative for HIV-1 antibody just before they were administered (Table 1). The test was mainly performed by the Korea Haemophilia Clinic using an internationally marketed ELISA kit manufactured by Company X. In addition, four of the HPs (nos 6, 8, 11 and 14) tested negative for HIV-1 antibody at other university hospitals 1-2 years before using DCF. This group was mainly treated with imported factors prior to the inception of domestic DCF production (officially 12 December 1989, although 154 vials were produced in 1986).

Molecular epidemiologic data from the nef gene

Phylogenetic analysis revealed that 20 of the HPs (nos 1-20) and the three plasma donors (0, P and Q) were infected with KSB HIV-1, whereas the three HPs (nos 21-23) infected abroad were infected with non-KSB HIV-1. HPs 1-4 were the

first cases among 20 HPs infected with the KSB (Fig. 1). As expected from the time period between seroconversion and sampling for DNA sequencing for this study, intrapatient DNA sequence identity among the HPs who had progressed to AIDS (HPs 3, 5, 16 and 21) was less than 95%. In contrast, in patients whose CD4+ T cell count maintained a steady state, such as HPs 7 (98·7%), 8 (95·1%), 13 (97·8%), 14 (96·6%), 19 (96·4%) and 22 (96·2%), sequence identities were > 95% after 7–9 years of infection.

Molecular epidemiologic data from the pol gene

We determined pol sequences from donor O (957 bp: AY585687), donor P (543 bp: AY347694, derived from September 1991), and 292 local control sequences from 107 local patients not known to have sold plasma for DCF production. In a phylogenetic tree including 23 domestic pol sequences (> 957 bp), sequences from eight HPs strongly clustered around those of donor O without the embedding of other local sequences (Fig. 2), and sequences from 10 HPs also strongly clustered. Although we could not include pol sequences from donor P in this phylogenetic tree or for comparison of sequence identities due to small fragment size of 543 bp, sequences from 10 HPs were clustered without an embedding of other local sequences in the lower cluster.

In regard to the frequency of the specific amino acid reverse transcriptase (RT) codons in KSB sequences, 1135V, 1202V, and R211K were detected in four, six and six of 45 local control patients (including two cash-paid plasma donors), respectively (Table 3). In contrast, the 20 HPs showed significantly higher frequencies of these three codons, in a manner consistent with their occurrence in the two cash-paid plasma donors. Specifically, two RT sequences from donor O showed 1202V but not 1135V and R211K, whereas those of donor P showed 1135V (sequences after codon 190 were not determined). The frequencies of I135V, I202V and R211K (9, 9 and 12, respectively, based on the earliest sequences from each patient) were significantly higher in the 20 HPs than in the 45 local control patients (P < 0.01 by Student's t-test for all. three codons) (Table 3). This finding also supports the epidemiological linkage for the transmission of HIV-1 from two plasma donors to at least 17 HPs.

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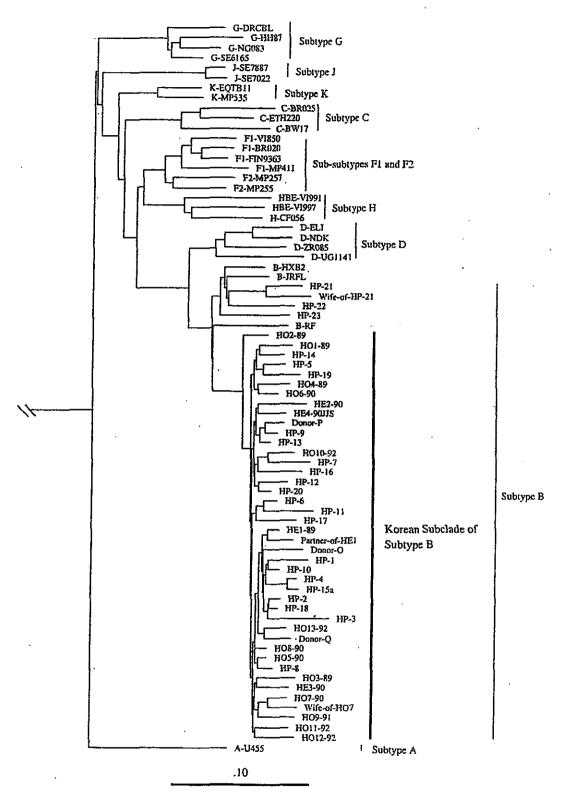


Fig. 1 Phylogenetic tree of nef sequences of 23 haemophiliacs (HP), plasma donors (O, P and O) and 19 database nef sequences that showed the highest aust score with donors O and P and the HiV Database subtype reference set (HO means sequences obtained from homosexuals and HE, heterosexuals). The sequences described in the current study were aligned to the HiV-1 subtype reference set from the HiV Sequence Database (http://www.hiv.lanl.gov/content/hiv-db/SUBTYPE_REF/align.html) and sequences scoring highly in aust, and a phylogenetic tree was built using the PMDP DIADIST (F84 model, Ts: Tv 1-7) and NBBHBOUR programs.

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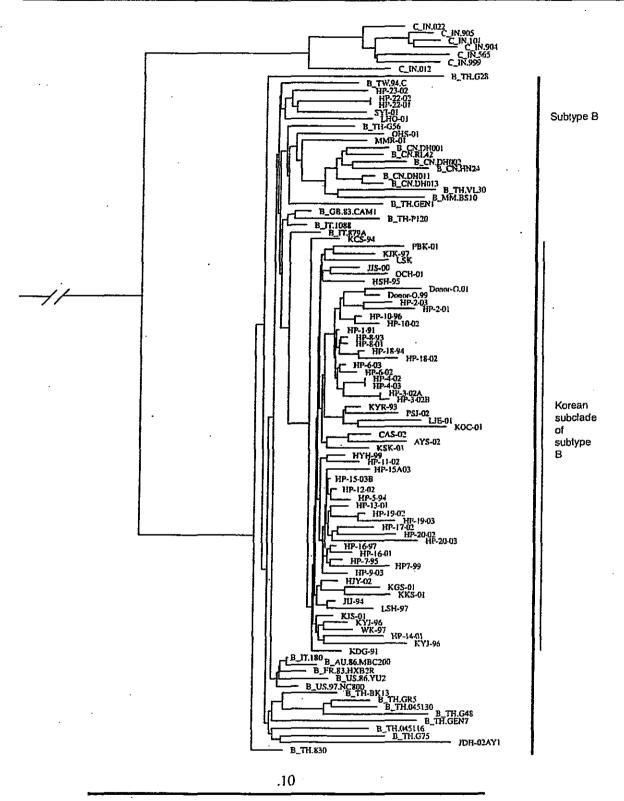


Fig. 2 Phylogenetic tree of pol sequences of 23 haemophiliaes (HP), plasma donor O and 23 local sequences. Twenty-three local pol sequences = 957 bp were selected by the highest BUST score with the two plasma donors. We did not include the pol sequences from donor P because of the shorter length (543 bp) sequenced from this sample. There are two strong clusterings with 18 HPs; sequences from eight HPs strongly clustered around those of donor O and sequences from 10 HPs also strongly clustered.

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Table 3 Frequency of specific amino acids in reverse transcriptase (RT) of haemophiliaes is statistically significantly higher than those in 45 local HIV-1 with Korean subtype B

	Reverse tr)		
Haemophiliacs	Codon 135 lle	Codon 202 lic	Codon 211 Arg	GenBank no
Donor P	Val	No data	No data	AY347694
5	Val ₂	-∕Val,	Lys2	AF273194
12	Val ₂	'n	Lys ₂	AY219017
13	Val,	·/Val,	-/Lys ₁	AY166480
15	Val ₃	' 3	Lys ₃	AY347701
17	Val ₃	'n	Lys ₃	AY219021
19	Val ₃	;	Lys,	AY219023
20	Val ₃	3	Lys,	AY219024
74	Val ₂ /.	'n	Lys ₃	AF273196
16	Val/.	-2	Lys ₂	AY392120
7	'7	7 .	Lys,	AF448137
11	72	` 2	Lys	AY219020
9	Leu ₄	`•	Lys,	AY347699
Denor 0	·2	Val ₂	ż	AF273180
1	'n	Val ₁	'n	AY347699
2	4	Val ₄	4	AF448135
3	·3	. ₁ /Val ₂	2/Lys ₁	AF273186
4	' 2	Val ₂	*2	AY219015
6	•2	Val ₂	' 2	AY219016
8	' 3	Val ₃	' 3	AF481437
10	•	Val ₃	` 3	AY219012
18	ā	Val ₁₇	1 17	AY166489

Number in subscript means times sequenced in each patient. A dot '.' indicates identity to the consensus for this codon.

Discussion

In this study, we found that 20 of 23 Korean HPs were infected with KSB HIV-1. Our investigation of molecular epidemiology rules out foreign imported factor 9 as the cause of infection in the 20 HPs and indicates that DCF is the most probable causative factor for this HIV-1 outbreak. This is further supported by medical record evidence that shows that all 20 HTV-1-infected HP with KSB were exposed to the same DCF. This was manufactured from plasma including donations of plasma from donors O and P collected a relatively short time prior to their documented seroconversion dates.

Eighteen of the 23 HIV-1-infected HPs had tested HIV-1 seronegative at the beginning of DCF therapy, but became seropositive within 2 years of using DCF. Second, more than 50% of the HPs were sexually inactive at the time of diagnosis. Third, in a case-control study taken as one arm, there were statistical associations between six lots of DCF and HIV-1 infection in HPs described in a report from an investigative committee (April 2004). Fourth, the prevalence of HIV-1

infection in the general population was very low at the time of the outbreak. A similar overseas study [6] also showed that only a portion of HPs exposed to contaminated clotting factor 9 developed HIV-1 infection.

Despite the 7-10 years time lag between the outbreak in 1991-1992 and our sampling in 1998-2002, our data show that the sequences from 20 HPs were most closely related with those from two plasma donors. Taken together, both the epidemiological data and this molecular data support the conclusion that HTV-1 transmission to most of the infected Korean HPs occurred from a common source, which is the intravenous injection of DCF, rather than transfusions or imported clotting factors.

DNA sequences and sequence analysis can indicate that virus transmission is likely to have occurred between one person and another. However, other relevant epidemiological information related to such cases must always be used in concert with the molecular epidemiology data. In this case, it is the combination of records providing the dates of cash-paid plasma donations, plus records providing the seroconversion dates of the donors and HPs, together with the molecular data establish the near certainty that the HPs were infected via the clotting factor. Even taken together, these data cannot prove that any one or more of these donors was the cause of the HP infections. It is possible that each HP received some virus from both donors, and also possible that donor Q or other, as yet unidentified donors also contributed to this problem. The only strong linkage is between the DCF product and this group of HPs. The individual cases, such as some HPs having sequences slightly closer to sequences from donor O and others having sequences slightly closer to donor P, are not highly significant. We do not have enough information about pooling of plasma donations and production sizes of batches of DCF to know if it is likely or possible that each of the HPs would have been exposed to virus from only one donor or to a combination of viruses from more than one donor.

Regarding the DCF manufacturing technique, Company X employed a solvent/detergent (tri-n-butylphosphate/Tween 80) technique adapted from the New York Blood Center (NYBC), with no heat treatment. After reporting a series of HIV-1 cases in US HPs, several improvements were implemented according to an investigator from NYBC. During an in-house audit of the Company X's manufacturing facility and processing as part of the activity of the investigation committee, a specialist from the NYBC noted that 'several improvements in processing were instituted in mid-1991, including use of a double signature addition, filtration just prior to solvent/detergent addition, and dilution to preset protein concentration' (Horowitz B: solvent/detergent usage by the Company X-summary of technology transfer and 2day site visit. Report signed on 1 June 1993). This mid-1991 time point was after the detection of the first cases of infection in this cohort (in HPs 1, 2, 3 and 4). Still no heat

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treatment that has been shown to inactivate retroviruses [16,17] was used.

Korean subtype B sequences were first detected in homosexual Korean HIV-1 patients diagnosed in 1989 [7-11]. Our previous studies [7-11] showed that the KSB sequences represent a subclade of global subtype B, indicating a founder effect. All KSB sequences were found among domestic-residing homosexuals who did not have sexual contact with foreigners. In contrast, Korean patients infected with non-KSB HIV-1 had sexual contact with US army soldiers in Korea in the late 1980s or had visited the USA, whereas overseas sailors who had visited foreign countries and their spouses showed various subtypes according to their epidemiological history [7-11]. A total of 128 HIV-1-infected patients (1 in 1985, 4 in 1986, 9 in 1987, 22 in 1988, 37 in 1989 and 54 in 1990) were diagnosed in Korea before 1991. Based on epidemiological data, 37 of those were presumed to be infected with KSB and 91 with non-KSB including 59 overseas sailors, five of their wives, and 10 prostitutes who had worked next to US military camps in Korea.

In conclusion, the *nef* and *pol* sequences from donors 0 and P showed higher DNA sequence identities with those from the tested HPs than with local sequences from Korean seropositive individuals including homosexuals diagnosed with KSB HIV-1 infection before 1991. These data coincide with the clinical and medical records, and together indicate that HIV-1 transmission to 20 HPs occurred through IV injection of DCF rather than transfusions or imported clotting factors.

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医薬品 医薬部外品 化粧品

研究報告 調査報告書

識別番号・幸	服告回数	報告日	第一報入手日 2006年12月14日	新医薬品等の区分	厚生労働省処理欄
一般的名称 販売名 (企業名)	①②③人血清アルブミン ④乾燥濃縮人血液凝固第個因子 ⑤乾燥濃縮人血液凝固第IX因子 ①献血アルブミン·Wf(ベネシス) ②献血アルブミン·S%)·Wf(ベネシス) ③アルブミン·Wf(ベネシス) ④コンコエイトーHT(ベネシス) ⑤クリスマシン-M(ベネシス)	研究報告の公表状況		公表国 ドイツ 3:	b
研究 報告 の 概 うラに動95脳るわのに 95脳るわのに AD) が で AD)	質の凝集はアルツハイマー病の発病機序としていてはほとんど明らかとなっていない。アルツェニックマウスから得たアミロイド-β(Aβ)をると、時間と濃度に依存した大脳内のβ-アミせると誘導される病変の進行が阻害された。さけ間の熱処理はアミロイド誘導を消失させなかのシーディング(seeding)活性は、Aβ免疫除去性に誘導したアミロイドーシスの表現型は、循うな、生物活性の異なる多型性 Aβ系統の存在方な、生物活性の異なる多型性 Aβ系統の存在で活することができ、プリオンの取り込みと分けオン病と同じ意味で伝播性であるというによって、特発性アルツハイマー病の起源を角によって、特発性アルツハイマー病の起源を角	ハイマー病患者、またはβ-ア 含んでいる脳抽出物の希釈し コイドーシスとそれに伴う病3 5に、70%蟻酸での1時間処理 った。 、タンパク変性、または Aβ? 主と誘導因子のソースの双方に を示唆している。プリオン病 に全身性の細胞機作が関与し 証拠はない。しかし、異常 A	ミロイド前駆体タンパク質 たものを APP トランスジ を誘導した。APP23 宿主で によりアミロイド誘導活性 を宿主に免疫することによ に依存して変わり、そのこ はさまざまな伝播効率で種 しているが、現在のところ、	${\{(APP)}$ を発現しているト エニックマウスの大脳内 アウスを Beta-1 抗体で受 を完全に消失させたが、 って、低下または消失す とは、プリオン系統を思 々の経路を介して野生型 β -アミロイドーシス(特	使用上の注意記載状況・ その他参考事項等 代表として献血アルプミン-Wf の記載を示す。 2. 重要な基本的注意 (1) 本剤の原材料となる献血者の血液については、HBs 抗原、抗 HCV 抗体、抗 HIV-1 抗体、抗 HIV-2 抗体、抗 HTLV-1 抗体陰性で、かつ ALT (GPT)値でスクリーニングを実施している. 更に、プールした試験血漿については、HIV-1、HBV 及び HCV について核酸増幅検査(NAT)を実施し、適合した血漿を本剤の製造に使用しているが、当該 NAT の検出限界以下のウイルスが混入している可能性が常に存在する。本剤は、以上の検査に適合した
との報告であ アルツハイマー 種による感染	一病患者由来のアミロイド-βの感染性を示唆 実験のみであり、アルツハイマー病が実際に愿 イマー病患者のアミロイド-βが異常プリオン	では、トランスジェニー な情報は、トランスジェニー 染・伝播したとの事例は報告	ックマウスへの脳内接 も されていない。そのた	今後の対応 ルツハイマー病に関連 る情報については、今後 注視することとする。	血漿を原料として、Cohn の低温エタノール分画で得た画分から人アルプミンを精製し、アルプミン 濃度 5w/v%に調整した製剤であり、ウイルス不活化を目的として、製造工程において 60℃、10 時間の液状加熱処理を施しているが、投与に際しては、次の点に十分注意すること。



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