

Dataset	genomic region	PS	SS	interval transmission	#time points recipient	# sequences recipient	# sequences donor
BC							
Andreo <i>et al.</i> [1]	env	exp	exp	180-210	2	13	16
Blanchard <i>et al.</i> [3]	env	exp	exp	1149-1514	1	2	6
Cornelissen <i>et al.</i> [6]	gag	con	con	"	"	2	5
	env	con	con	21	2	20	8
	gag	exp	exp	"	"	20	9
Diaz-Zhang <i>et al.</i> [8]							
source→recipA	env	con	con	580-609	4	39	61
source→recipB	"	"	"	646-675	5	56	"
Kao <i>et al.</i> [15]	env	log	log	316	1	11	31
Metzker <i>et al.</i> [19]	env	exp	exp	150-420	1	50	50
Wolfs <i>et al.</i> [22]	env	con	con	30	1	8	9
	gag	exp	exp	"	1	10	8
			mean	384	2,1	19,3	20,3
			median	248	1,5	12	9
HET							
Boeras <i>et al.</i> [4]							
RW36	env	exp	exp	14-114	1	41	59
RW56	env	exp	exp	5-20	1	39	58
ZM201	env	log	log	10-41	1	46	93
ZM216	env	log	log	10-41	1	59	75
ZM221	env	exp	log	10-41	1	72	71
ZM238	env	exp	exp	10-50	1	38	72
ZM242	env	exp	exp	10-41	1	31	44
ZM292	env	exp	exp	16-34	1	39	71
Derdeyn <i>et al.</i> [7]							
13	env	con	con	14-112	1	16	23
53	env	exp	exp	24-121	1	19	34
55	env	exp	exp	14-112	1	16	36
71	env	exp	exp	14-112	1	11	10
83	env	log	log	20-127	1	11	12
106	env	con	con	53-157	1	13	12
109	env	exp	exp	14-112	1	13	13
135	env	exp	exp	26-136	1	20	32
Haaland <i>et al.</i> [12]							
RW19	env	exp	exp	14-124	1	40	40
RW35	env	log	log	14-124	1	40	37
RW41	env	exp	exp	14-122	1	40	40
RW53	env	exp	exp	10-45	1	42	36
RW57	env	exp	exp	14-122	1	42	40
RW66	env	exp	exp	10-47	1	41	42
ZM190	env	log	log	10-41	1	48	35
ZM198	env	exp	exp	10-88	1	41	42
ZM205	env	log	log	10-58	1	32	45
ZM229	env	exp	exp	14-122	1	27	22
ZM243	env	exp	exp	14-32	1	45	36
ZM248	env	log	log	10-89	1	57	56
Hayman <i>et al.</i> [13]							
don1→2	env	con	con	366-10y*	1	3	10
don1→3	env	con	con	366-10y*	1	3	10

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**Table 1 – continued
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Dataset	genomic region	PS	SS	interval trans- mission	#time points recipient	# se- quences recipient	# se- quences donor
	don1→19	”	”	con 366-10y*	1	3	”
	don1→22	”	”	” 731-10y*	1	6	”
	don17→23	env	log	log 731-1460	1	3	6
Liu <i>et al.</i> [18]	J	env	exp	exp 34-57	1	10	13
Scaduto <i>et al.</i> [21]	CC 01→02	env	exp	exp 451-907	1	20	20
	01→03	”	”	” 599-782	1	20	”
	01→04	”	”	” 770-494	1	20	”
	01→05	”	”	” 690-839	1	20	”
	01→06	”	”	” 700-1337	1	20	”
	01→07	”	”	” 464-644	1	20	”
	CC 01→02	pol	exp	exp ”	”	20	20
	01→03	”	”	” ”	”	20	”
	01→04	”	”	” ”	”	20	”
	01→05	”	”	” ”	”	20	”
	01→06	”	”	” ”	”	20	”
	01→07	”	”	” ”	”	20	”
	WA 04→01	env	exp	exp 97-297	1	20	20
	04→02	”	”	” 129-1216	1	20	”
	04→03	”	”	” 484-1249	1	20	”
	04→05	”	”	” 206-1680	1	19	”
	04→06	”	”	” 208-867	1	17	”
	WA 04→01	pol	exp	exp ”	”	20	20
	04→02	”	”	” ”	”	20	”
	04→03	”	”	” ”	”	20	”
	04→05	”	”	” ”	”	19	”
	04→06	”	”	” ”	”	17	”
Wolfs <i>et al.</i> [22]	env	exp	exp	14-163	1	8	8
			mean	206	1	26.1	0.5
			median	14	1	20	20
MSM							
Bailey <i>et al.</i> [2]	gag	exp	exp	1675-8248	4	38	6
Butler <i>et al.</i> [5]	sourceABC→A	env	exp	exp 83	1	10	53
	sourceABC→B	”	”	” 44	1	8	”
	sourceABC→C	”	”	” 21	1	5	”
	D	env	exp	exp 128	1	13	13
	E	env	exp	exp 73	1	17	22
	F	env	exp	exp 84	1	19	44
Edo-Matas <i>et al.</i> [9]	env	log	log	110-124	4	40	23
Edwards <i>et al.</i> [10]	env	log	log	47-62	4	67	33
	gag	log	log	”	4	64	39
Frost <i>et al.</i> [11]	004-007	env	exp	exp 5-163	1	12	12
	206-201	env	exp	exp 5-163	1	11	12
	206-204	env	exp	exp 5-163	1	12	13
	512-558	env	exp	exp 5-163	1	14	11

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**Table 1 – continued
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Dataset	genomic region	PS	SS	interval trans- mission	#time points recipient	# se- quences recipient	# se- quences donor	
	512-559	env	exp	exp	5-163	1	11	11
	551-550	env	exp	exp	5-163	1	12	13
	564-557	env	exp	exp	5-163	1	15	14
Herbeck <i>et al.</i> [14]								
	1	gag	exp	exp	13-36	15	304	20
	1	env	log	log	"	12	418	21
	1	pol	exp	exp	"	12	152	10
	2	gag	exp	exp	8-31	1	18	10
	2	env	exp	exp	"	"	18	10
	2	pol	exp	exp	"	"	18	10
	3	gag	exp	exp	30-53	1	93	10
	3	env	exp	exp	"	"	93	10
	3	pol	exp	exp	"	"	93	10
	4	gag	exp	exp	18-41	1	30	38
	4	env	exp	exp	"	"	30	38
	4	pol	exp	exp	"	"	30	38
Lawson <i>et al.</i> [16]		env	exp	exp	10-28	2	19	10
Li <i>et al.</i> [17]								
	AD18-AD17	env	exp	exp	10-28	1	25	17
	AD75-AD77	env	con	con	10-28	1	27	19
	AD83-04013240	env	exp	exp	10-28	1	66	22
	LAC-HOBR	env	exp	log	10-28	1	21	13
Liu <i>et al.</i> [18]								
	D	env	exp	exp	61-84	1	11	19
	E	env	exp	exp	56-79	1	15	16
	F	env	exp	exp	34-57	1	14	15
	G	env	exp	exp	18-41	1	13	14
	I	env	log	log	28-51	1	9	15
Rachinger <i>et al.</i> [20]								
	pat3→1	env	log	log	124-262	5	46	65
	pat3→2	"	"	"	245-272	6	61	"
	pat3→1	gag	log	log	"	5	46	63
	pat3→2	"	"	"	"	7	46	"
	pat3→1	pol	exp	exp	"	2	26	24
	pat3→2	"	"	"	"	3	15	"
				mean	93	2.6	47.2	24.7
				median	20	1	19	17

Overview of the examined transmission chains. For each article in which we found useful data, we detail from what genomic region the sequences originate (env = Envelope, gag = Gag polyprotein, pol = Polymerase). We also give the number of sequences by recipient and donor and what demographic model came out best by the path sampling (PS) and stepping stone sampling (SS) marginal likelihood estimators (exp = exponential, con = constant, log = logistic) as well as the number of available time points for the recipient. The transmission interval is specified by the number of days before the first sampling of the recipient that transmission could have occurred. The mean and median values refer to the most recent boundaries of the transmission intervals. When multiple transmission chains were available, we kept the original naming and specify all details for each chain separately. Similarly, when a chain comprises multiple transmission events, the data are specified per event. * Only a lower boundary could be established for these transmissions, and a cutoff of 10 years was set for the upper boundary.

References

- [1] Sandra Mara S Andreo, Luís Alberto C Barra, Luciana Jesus Costa, Maria Cecília A Sucupira, Inara Espinelli L Souza, and Ricardo Sobhie Diaz. Hiv type 1 transmission by human bite. *AIDS Res Hum Retroviruses*, 20(4):349–50, Apr 2004.
- [2] Justin R Bailey, Karen O’Connell, Hung-Chih Yang, Yefei Han, Jie Xu, Benjamin Jilek, Thomas M Williams, Stuart C Ray, Robert F Siliciano, and Joel N Blankson. Transmission of human immunodeficiency virus type 1 from a patient who developed aids to an elite suppressor. *J Virol*, 82(15):7395–410, Aug 2008.
- [3] A Blanchard, S Ferris, S Chamaret, D Guétard, and L Montagnier. Molecular evidence for nosocomial transmission of human immunodeficiency virus from a surgeon to one of his patients. *J Virol*, 72(5):4537–40, May 1998.
- [4] Debrah I Boeras, Peter T Hraber, Mackenzie Hurlston, Tammy Evans-Strickfaden, Tanmoy Bhattacharya, Elena E Giorgi, Joseph Mulenga, Etienne Karita, Bette T Korber, Susan Allen, Clyde E Hart, Cynthia A Derdeyn, and Eric Hunter. Role of donor genital tract hiv-1 diversity in the transmission bottleneck. *Proc Natl Acad Sci U S A*, 108(46):E1156–63, Nov 2011.
- [5] David M Butler, Wayne Delpont, Sergei L Kosakovsky Pond, Malcolm K Lakdawala, Pok Man Cheng, Susan J Little, Douglas D Richman, and Davey M Smith. The origins of sexually transmitted hiv among men who have sex with men. *Sci Transl Med*, 2(18):18re1, Feb 2010.
- [6] M Cornelissen, G Mulder-Kampinga, J Veenstra, F Zorgdrager, C Kuiken, S Hartman, J Dekker, L van der Hoek, C Sol, and R Coutinho. Syncytium-inducing (si) phenotype suppression at seroconversion after intramuscular inoculation of a non-syncytium-inducing/si phenotypically mixed human immunodeficiency virus population. *J Virol*, 69(3):1810–8, Mar 1995.
- [7] Cynthia A Derdeyn, Julie M Decker, Frederic Bibollet-Ruche, John L Mokili, Mark Muldoon, Scott A Denham, Marantha L Heil, Francis Kasolo, Rosemary Musonda, Beatrice H Hahn, George M Shaw, Bette T Korber, Susan Allen, and Eric Hunter. Envelope-constrained neutralization-sensitive hiv-1 after heterosexual transmission. *Science*, 303(5666):2019–22, Mar 2004.
- [8] R S Diaz, L Zhang, M P Busch, J W Mosley, and A Mayer. Divergence of hiv-1 quasispecies in an epidemiologic cluster. *AIDS*, 11(4):415–22, Mar 1997.
- [9] Diana Edo-Matas, Andrea Rachinger, Laurentia C Setiawan, Brigitte D Boeser-Nunnink, Angélique B van ’t Wout, Philippe Lemey, and Hanneke Schuitemaker. The evolution of human immunodeficiency virus type-1 (hiv-1) envelope molecular properties and coreceptor use at all stages of infection in an hiv-1 donor-recipient pair. *Virology*, 422(1):70–80, Jan 2012.
- [10] Charles T T Edwards, Edward C Holmes, Daniel J Wilson, Raphael P Viscidi, Elaine J Abrams, Rodney E Phillips, and Alexei J Drummond. Population genetic estimation of the loss of genetic diversity during horizontal transmission of hiv-1. *BMC Evol Biol*, 6:28, 2006.
- [11] Simon D W Frost, Yang Liu, Sergei L Kosakovsky Pond, Colombe Chappey, Terri Wrin, Christos J Petropoulos, Susan J Little, and Douglas D Richman. Characterization of human immunodeficiency virus type 1 (hiv-1) envelope variation and neutralizing antibody responses during transmission of hiv-1 subtype b. *J Virol*, 79(10):6523–7, May 2005.
- [12] Richard E Haaland, Paulina A Hawkins, Jesus Salazar-Gonzalez, Amber Johnson, Amanda Tichacek, Etienne Karita, Olivier Manigart, Joseph Mulenga, Brandon F Keele, George M Shaw, Beatrice H Hahn, Susan A Allen, Cynthia A Derdeyn, and Eric Hunter. Inflammatory genital infections mitigate a severe genetic bottleneck in heterosexual transmission of subtype a and c hiv-1. *PLoS Pathog*, 5(1):e1000274, Jan 2009.

- [13] A Hayman, T Moss, G Simmons, C Arnold, E C Holmes, L Naylor-Adamson, J Hawkswell, K Allen, J Radford, J Nguyen-Van-Tam, and P Balfe. Phylogenetic analysis of multiple heterosexual transmission events involving subtype b of hiv type 1. *AIDS Res Hum Retroviruses*, 17(8):689–95, May 2001.
- [14] Joshua T Herbeck, Morgane Rolland, Yi Liu, Sherry McLaughlin, John McNevin, Hong Zhao, Kim Wong, Julia N Stoddard, Dana Raugi, Stephanie Sorensen, Indira Genowati, Brian Birditt, Angela McKay, Kurt Diem, Brandon S Maust, Wenjie Deng, Ann C Collier, Joanne D Stekler, M Juliana McElrath, and James I Mullins. Demographic processes affect hiv-1 evolution in primary infection before the onset of selective processes. *J Virol*, 85(15):7523–34, Aug 2011.
- [15] Cheng-Feng Kao, Kan-Tai Hsia, Sui-Yuan Chang, Feng-Yee Chang, Kenrad Nelson, Chin-Hui Yang, Yen-Fang Huang, Tzu-Yu Fu, and Jyh-Yuan Yang. An uncommon case of hiv-1 transmission due to a knife fight. *AIDS Res Hum Retroviruses*, 27(2):115–22, Feb 2011.
- [16] Victoria A Lawson, Robert Oelrichs, Christophe Guillon, Allison A Imrie, David A Cooper, Nicholas J Deacon, and Dale A McPhee. Adaptive changes after human immunodeficiency virus type 1 transmission. *AIDS Res Hum Retroviruses*, 18(8):545–56, May 2002.
- [17] Hui Li, Katharine J Bar, Shuyi Wang, Julie M Decker, Yalu Chen, Chuanxi Sun, Jesus F Salazar-Gonzalez, Maria G Salazar, Gerald H Learn, Charity J Morgan, Joseph E Schumacher, Peter Hraber, Elena E Giorgi, Tanmoy Bhattacharya, Bette T Korber, Alan S Perelson, Joseph J Eron, Myron S Cohen, Charles B Hicks, Barton F Haynes, Martin Markowitz, Brandon F Keele, Beatrice H Hahn, and George M Shaw. High multiplicity infection by hiv-1 in men who have sex with men. *PLoS Pathog*, 6(5):e1000890, May 2010.
- [18] Yi Liu, Marcel E Curlin, Kurt Diem, Hong Zhao, Ananta K Ghosh, Haiying Zhu, Amanda S Woodward, Janine Maenza, Claire E Stevens, Joanne Stekler, Ann C Collier, Indira Genowati, Wenjie Deng, Rafael Zioni, Lawrence Corey, Tuofu Zhu, and James I Mullins. Env length and n-linked glycosylation following transmission of human immunodeficiency virus type 1 subtype b viruses. *Virology*, 374(2):229–33, May 2008.
- [19] Michael L Metzker, David P Mindell, Xiao-Mei Liu, Roger G Ptak, Richard A Gibbs, and David M Hillis. Molecular evidence of hiv-1 transmission in a criminal case. *Proc Natl Acad Sci U S A*, 99(22):14292–7, Oct 2002.
- [20] Andrea Rachinger, Paul H P Groeneveld, Sander van Assen, Philippe Lemey, and Hanneke Schuitemaker. Time-measured phylogenies of gag, pol and env sequence data reveal the direction and time interval of hiv-1 transmission. *AIDS*, 25(8):1035–9, May 2011.
- [21] Diane I Scaduto, Jeremy M Brown, Wade C Haaland, Derrick J Zwickl, David M Hillis, and Michael L Metzker. Source identification in two criminal cases using phylogenetic analysis of hiv-1 dna sequences. *Proc Natl Acad Sci U S A*, 107(50):21242–7, Dec 2010.
- [22] T F Wolfs, G Zwart, M Bakker, and J Goudsmit. Hiv-1 genomic rna diversification following sexual and parenteral virus transmission. *Virology*, 189(1):103–10, Jul 1992.