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Clustering of a Polymorphic Membrane Protein E Clade in *Chlamydia trachomatis* Lineages from Men who have Sex with Men

Appendix 2

Appendix 2 Table 1. Summary of the *ompA* genotypes detected according to the study population and anatomic site*

Category	Genotype									
	G	D	J	F	E	K	B	H	I	Total
MSM										
Rectal	95 (46.1%)	49 (23.8%)	52 (25.2%)	0 (0%)	5 (2.4%)	1 (0.5%)	4 (1.9%)	0 (0%)	0 (0%)	206 (100%)
Pharyngeal	12 (44%)	6 (22%)	7 (26%)	0 (0%)	0 (0%)	0 (0%)	1 (4%)	1 (4%)	0 (0%)	27 (100%)
Urogenital	6 (50%)	3 (25%)	1 (8%)	0 (0%)	1 (8%)	0 (0%)	1 (8%)	0 (0%)	0 (0%)	12 (100%)
Total	113 (46.1%)	58 (23.7%)	60 (24.5%)	0 (0.0%)	6 (2.4%)	1 (0.4%)	6 (2.4%)	1 (0.4%)	0 (0.0%)	245 (100%)
Non-MSM										
Urogenital	3 (9%)	11 (31%)	3 (9%)	6 (17%)	7 (20%)	4 (20%)	0 (0%)	1 (3%)	0 (0%)	35 (100%)
Cervix	1 (6%)	3 (17%)	3 (17%)	1 (6%)	5 (28%)	3 (17%)	0 (0%)	0 (0%)	2 (11%)	18 (100%)
Total	4 (7.5%)	14 (26%)	6 (11%)	7 (13%)	12 (23%)	7 (13%)	0 (0%)	1 (2%)	2 (4%)	53 (100%)

*The proportions of each genotype in the collection source are shown in parentheses. The numbers for genotypes G, D, and J are indicated in bold.

Appendix 2 Table 2. STs detected in this study and major STs detected in previous studies*

MSM/Non-MSM	ST	n	<i>ompA</i> (n)	PmpE	Comments and findings in previous studies†
MSM	ST108	55	J (35), G (19), D (1)	p1	Major MSM ST (1–4)
	ST33	42	G (42)	p1	Major MSM ST (1,2,4)
	ST109	28	D (28)	p1	Major MSM ST (1–4)
	ST194	16	D (16)	p1	SLV of MSM ST109 and ST571
	ST52	14	G (14)	p1	Major MSM ST (1–4)
	ST112	13	J (13)	p1	SLV of MSM ST108
	ST139	13	G (12), J (1)	p1	SLV of MSM ST108
	ST150	12	G (12)	p1	SLV of MSM ST33 and ST108
	ST346	7	G (7)	p1	SLV of MSM ST33 and ST108
	ST210	4	B (4)	p1	
	ST603	3	J (3)	p1	SLV of MSM ST108
	ST54	2	G (2)	p1	SLV of MSM ST52
	ST83	2	B (2)	p1	
	ST121	2	D (2)	p1	SLV of MSM ST109
	ST132	2	J (2)	p1	SLV of MSM ST108
	ST318	2	D (2)	p1	SLV of MSM ST109
	ST3	1	E (1)	p2	
	ST131	1	D (1)	p1	SLV of MSM ST109
	ST145	1	E (1)	p2	
	ST149	1	D (1)	p1	SLV of MSM ST109
	ST151	1	D (1)	p1	SLV of MSM ST109
	ST162	1	J (1)	p1	
	ST170	1	D (1)	p1	SLV of MSM ST109
	ST185	1	D (1)	p1	
	ST192	1	G (1)	p1	
	ST196	1	G (1)	p1	SLV of MSM ST33
	ST199	1	J (1)	p1	SLV of MSM ST108
	ST237	1	E (1)	p2	
	ST305	1	E (1)	p1	
	ST354	1	J (1)	p1	SLV of MSM ST33 and ST108
	ST391	1	D (1)	p1	
	ST403	1	D (1)	p1	

MSM/Non-MSM	ST	n	<i>ompA</i> (n)	PmpE	Comments and findings in previous studies†
	ST435	1	G (1)	p2	
	ST442	1	H (1)	p2	
	ST553	1	E (1)	p1	
	ST559	1	J (1)	p1	
	ST601	1	E (1)	p1	
	ST602	1	G (1)	p1	
	ST604	1	D (1)	p1	
	ST605	1	J (1)	p2	
	ST606	1	G (1)	p1	SLV of ST33, ST58, and ST108
	ST608	1	J (1)	p2	
	ST626	1	K (1)	p1	
	ST628	1	D (1)	p1	
Non-MSM	ST208	6	D (5), I (1)	p2	
	ST609	5	K (5)	p2	
	ST264	4	J (4)	p2	
	ST3	3	E (3)	p2	
	ST110	2	F (2)	p2	
	ST620	2	E (2)	p2	
	ST27	1	G (1)	p2	
	ST30	1	K (1)	p2	
	ST35	1	D (1)	p2	
	ST100	1	I (1)	p2	
	ST148	1	F (1)	p2	
	ST166	1	E (1)	p2	
	ST172	1	E (1)	p2	
	ST281	1	D (1)	p2	
	ST381	1	D (1)	p2	
	ST426	1	E (1)	p2	
	ST435	1	G (1)	p2	
	ST444	1	H (1)	p2	
	ST499	1	D (1)	p2	
	ST592	1	E (1)	p2	
	ST607	1	K (1)	p2	
	ST608	1	J (1)	p2	

MSM/Non-MSM	ST	n	<i>ompA</i> (n)	PmpE	Comments and findings in previous studies†
	ST610	1	G (1)	p2	
	ST611	1	E (1)	p2	
	ST612	1	F (1)	p2	
	ST613	1	F (1)	p2	
	ST614	1	D (1)	p2	
	ST615	1	D (1)	p2	
	ST616	1	E (1)	p2	
	ST617	1	F (1)	p2	
	ST618	1	G (1)	p2	
	ST619	1	J (1)	p2	
	ST621	1	D (1)	p2	
	ST622	1	D (1)	p2	
	ST623	1	E (1)	p2	
	ST624	1	F (1)	p2	
	ST625	1	D (1)	p2	
References‡					
MSM	ST33				Major MSM ST (1,2,4)
	ST52				Major MSM ST (1–4)
	ST58				Major MSM ST (2,3,4)
	ST108				Major MSM ST (1–4)
	ST109				Major MSM ST (1–4)
	ST571				Major MSM ST (1)
*MSM, men who have sex with men; PmpE, polymorphic membrane protein E; SLV, single-locus variant; ST, sequence type.					
†Major STs in References 1–4 and SLVs are shown.					
‡References 1 and 3 declared major STs in their text, whereas the top 5 STs in References 2 and 4 were picked up as their major STs for MSM.					

Appendix 2 Figure (following pages). Sequence alignments of PmpE. The numbers at the right ends indicate the amino acid number of *Chlamydia trachomatis* D/UW-3/CX PmpE (AE001273). Variable regions (VRs) 1 to 5 as described previously (5) are shown.

D/UW-3/CX DPTKESLSNKISLTGDTHNLTNCYLDNLRYLALAIQKTPNEGAAVTITDYLSFFDTQKEGIYFAKNLTPESGGAIGYASP 113

p1-1R.....
p1-2R.....
p1-3V.....R.....
p1-4R.....
p1-5R.....
p2-1
p2-2
p2-3
p2-4R.....
p2-5
p2-6
p2-7
p2-8
p2-9
p2-10R.....

VR1

D/UW-3/CX NSPTVEIRDITGPVIFENNTCCRLFTWRNP-YAADKIREGGAIHAQNLYINHNHDVVGFMKNFSYVQGGAI Stanton FVVS 192

p1-1P...S...RA..N.....
p1-2P...S...RA..N.....
p1-3P...S...RA..N.....
p1-4P...S...RA..N.....
p1-5P...S...RA..N.....
p2-1
p2-2
p2-3
p2-4P.....LT.VN.....
p2-5
p2-6
p2-7R.....
p2-8
p2-9S...RA..N.....
p2-10P.....LT.VN.....

D/UW-3/CX ENQSCFLFMDNICIQTN TAGKGGAIYAGTSNSFESNNCDLFFINNACCAGGAI FSPICSLTGNRGNIVFYNNRCFKNVET 272

p1-1
p1-2
p1-3
p1-4I.....
p1-5
p2-1
p2-2
p2-3
p2-4
p2-5
p2-6
p2-7
p2-8
p2-9
p2-10I..

D/UW-3/CX ASSEASDGGAIKVTTTRLDVTGNRGRIFSDNITKNYGGAIYAPVVTLVDNGPTYFINNIANNKGGAIYIDGTSNSKISAD 352

p1-1E.....
p1-2E.....
p1-3E.....
p1-4E.....
p1-5E.....
p2-1
p2-2
p2-3
p2-4E.....
p2-5
p2-6
p2-7
p2-8D.....
p2-9
p2-10P.....E.....

VR2

D/UW-3/CX RHAIIFNENIVTNTNANGTSTSANPPRRNAITVASSSGEILLGAGSSQNLIFYDPIEVSNAGVSVSFNKEADQTGSVVF 432

p1-1SND.I.....T.....I.....EG.....F.....
p1-2SND.I.....T.....I.....EG.....F.....
p1-3SND.I.....T.....I.....EG.....F.....
p1-4SND.I.....T.....I.....EG.....F.....
p1-5	..T.....SND.I.....T.....I.....EG.....F.....
p2-1
p2-2
p2-3
p2-4F.....
p2-5
p2-6
p2-7
p2-8
p2-9
p2-10F.....

VR3

D/UW-3/CX SGATVNSADFHQRNLQTKPAPLTLNGLFCIEDHAQLTVNRFTQTGGVVS LGNGAVLSCYKNGTGDSASNASITLKHIG 512

p1-1T...NH.....K...A.....---NST...V.....
p1-2T...NH.....K...A.....---NST...V.....
p1-3T...NH.....K...A.....---NST...V.....
p1-4T...NH.....K...A.....---NST...V.....
p1-5T...NH.....K...A.....---NST...V.....
p2-1
p2-2
p2-3
p2-4
p2-5
p2-6
p2-7
p2-8
p2-9
p2-10

VR3

VR4

D/UW-3/CX LNLSSILKSGAEIPLLWVEPTNNSNN----YTADTAATFSLSDVKLSLIDDYGNSPYESTDLTHALSSQPMLSISEASDN 588

p1-1	...P..	ATTS.RTTT.S	G..R.....	D.....	V...I.A.....
p1-2	...P..	ATTS.RTTT.S	G..R.....	D.....	V...V.A.....
p1-3	...P..	ATTS.RTTT.S	G..R.....	D.....	V...I.A.....
p1-4	...P..	ATTS.RTTT.S	G..R.....	D.....	V...I.A.....
p1-5	...P..	ATTS.RTTT.S	G..R.....	D.....	V...I.A.....
p2-1	-----
p2-2	-----
p2-3	-----
p2-4	-----
p2-5	-----
p2-6	-----
p2-7	-----
p2-8	-----
p2-9	-----
p2-10	-----

VR5

D/UW-3/CX QLQSENI DFSGLNVPHYGWQGLWTGWAKTQDPEPASSATITDPQKANRFHRTLLLTLWLPAGYVPSPKHRSPLIANTLWG 668

p1-1	...SM.....	L.....	N.SA.....
p1-2	...SM.....	L.....	N.SA.....
p1-3	...SM.....	L.....	N.SA.....
p1-4	...SM.....	L.....	N.SA.....
p1-5	...SM.....	L.....	N.SA.....
p2-1
p2-2
p2-3
p2-4	..R.DDM.....	N.SA.....
p2-5
p2-6G.....
p2-7
p2-8
p2-9
p2-10	..R.DDM.....	N.SA.....

D/UW-3/CX NMLLATESLKNSAELTPSGHPFWGITGGGLGMMVYQDPRENHPGFHMRSSGYSAGMIAGQTHTFSLKFSQTYTKLNERYA 748

p1-1D.....
p1-2D.....
p1-3D.....
p1-4D.....
p1-5D.....
p2-1
p2-2
p2-3
p2-4D.....
p2-5D.....
p2-6D.....
p2-7
p2-8
p2-9
p2-10D.....

D/UW-3/CX KNNVSSKNYSQGEMLFSLQEGFLLTKLVGLYSYGDHNCHHFYTQGENLTSQGTFRSQTMGGAVFFDLPMKPFGLSTHILT 828

p1-1A.....
p1-2A.....
p1-3A.....
p1-4A.....
p1-5A.....
p2-1
p2-2
p2-3A.....
p2-4A.....
p2-5A.....
p2-6A.....
p2-7
p2-8
p2-9A.....
p2-10A.....

D/UW-3/CX APFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINVLVPIGVKGSFMNATHRPQAWTVELAYQPVLRYRQEPGIAAQLLASK 908

p1-1Q.....L...T.....
p1-2Q.....L...T.....
p1-3Q.....L...T.....
p1-4Q.....L...T....Q
p1-5Q.....L...T.....
p2-1T.....
p2-2
p2-3Q.....L...T.....
p2-4Q.....L...T.....
p2-5Q.....L...T.....
p2-6Q.....L...T.....
p2-7
p2-8
p2-9Q.....L...T.....
p2-10Q.....L...T.....

D/UW-3/CX GIWFGSGSPSSRHAMSYKISQQTQPLSWLTLH 940

p1-1

p1-2

p1-3

p1-4

p1-5

p2-1

p2-2

p2-3

p2-4

p2-5

p2-6

p2-7

p2-8

p2-9

p2-10

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