

Rare HCV subtypes and retreatment outcomes in a cohort of European DAA-experienced patients

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Table S1: Countries of origin of DAA-failure patients with rare GT

Patient	Rare GT	
Country	Rare GT1 (n=6)	Number of patients n (%)
Germany	1*, 1c, 1e	n=3
France	1e	n=1
Togo	1l	n=1
Nigeria	1*	n=1
	Rare GT2 (n=2)	
Germany	2k	n=1
Niger	2k	n=1
	Rare GT3 (n=15)	
Germany	3k	n=1
Italy	3h	n=1
India	3b, 3g, 3h, 3i	n=5
Bangladesh	3b, 3g	n=3
Pakistan	3b	n=2
Syria	3*	n=1
n.d.	3b	n=2
	Rare GT4 (n=28)	
Germany	4*, 4c, 4f	n=3
Belgium	4r	n=1
France	4r	n=1
Switzerland	4f	n=1
Egypt	4n, 4o	n=4
Angola	4r	n=1
DR Congo	4r	n=5
Burundi	4b	n=1
Eritrea	4r	n=5
Nigeria	4v	n=1
Saudi-Arabia	4r	n=2
n.d.	4r	n=3
	GT5a (n=2)	
France	5a	n=1
South Africa	5a	n=1
	Rare GT6 (n=7)	
Germany	6f, 6n	n=2
Vietnam	6e, 6r	n=2
Thailand	6f, 6r	n=2
n.d.	6e	n=1

*subtype unassigned

n.d., not determined

Table S2: Primer and PCR conditions for NS5B amplification

Primer Name	Sequence	PCR*
RZ_1b_NS5B_out_fw	CTC CGT GTG GRA GGA CTT G	Outer PCR
RZ_1a_NS5_out_fw	CCG TGT GGA ARG ACC TTC TG	
P3_8713_out_rev	GAV RCR TTG GAG GAG CAN GAT GT	
NS5B_7998_out_F	CCA ATH SMY ACH ACC ATC ATG GC	Inner PCR
P3_6816_rev**	GGC GGA ATT CCT GGT CAT AGC CTC CGT GAA	
P6_8611_rev**	AAT TCC TGG TCA TAG CCT CCG TGA AGA CTC	

*outer and inner PCRs were each performed with 40 cycles at 54°C. Sequencing of PCR products was conducted using P6_8611_rev. Further details can be found in [1]

**Primer sequence adapted from [2]

Table S3: Published reference sequences

Author	Title	Citation
R. Xu	A panel of 16 full-length HCV genomes was characterized in China belonging to genotypes 1–6 including subtype 2f and two novel genotype 6 variants	[3]
C. Li	Characterization of full-length hepatitis C virus sequences for subtypes 1e, 1h and 1i, and a novel variant revealed Cameroon as an area in origin for genotype 1	[4]
L. Lu	Full-length genomes of 16 hepatitis C virus genotype 1 isolates representing subtypes 1c, 1d, 1e, 1g, 1h, 1i, 1j and 1k, and two new subtypes 1m and 1n, and four unclassified variants reveal ancestral relationships among subtypes	[5]
L. Lu	Full-length genome sequences of five hepatitis C virus isolates representing subtypes 3g, 3h, 3i and 3k, and a unique genotype 3 variant	[6]
C. Li	Complete genomic sequences for hepatitis C virus subtypes 4b, 4c, 4d, 4g, 4k, 4l, 4m, 4n, 4o, 4p, 4q, 4r and 4t	[7]
C. Li	An expanded taxonomy of hepatitis C virus genotype 6: Characterization of 22 new full-length viral genomes	[8]

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