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## Uncommon Detection of Mixed HCV Genotype Infections in Recently Infected Men Who Have Sex with Men

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1 **Uncommon Detection of Mixed HCV Genotype Infections in Recently Infected Men Who**  
2 **Have Sex with Men**

3 **Short title: Mixed HCV Genotype Infections in Men Having Sex with Men**

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37

38 **ABSTRACT (249 words)**

39 **Introduction:** Mixed HCV genotype (GT) infections are clinically important as different  
40 genotypes have different sensitivities to direct-acting antivirals (DAAs). A high prevalence of  
41 mixed GT infections was observed in people who inject drugs due to their multiple HCV  
42 exposures. The prevalence of mixed HCV GT infections in men having sex with men (MSM)  
43 at high-risk behaviors was investigated by ultra-deep sequencing (UDS).

44 **Methods:** NS5B fragment was sequenced from viruses of patients with recent HCV infection:  
45 50 HIV-positive and 18 HIV-negative including 13 from the ANRS Pre-Exposure Prophylaxis  
46 (PrEP) IPERGAY study. UDS data were analysed by Geneious (version 10.3.2). Phylogenetic  
47 trees were constructed by FastTree (version 2.1).

48 **Results:** HCV sequencing showed GT1a (47.1%), GT4d (41.2%), GT3a (8.8%) and GT2k  
49 (2.9%). We detected three (4.4%) mixed GT infections: one between predominant GT4d and  
50 minority GT1a, one between predominant GT4d and minority GT1b, and one between  
51 predominant GT1a and minority GT4d virus. The rates of minority GT viral populations  
52 detected in virus of the three above patients were 0.32%, 10.7%, and 1.3%, respectively. The  
53 two first patients were HIV co-infected and the other was HIV-negative under PrEP. The anti-  
54 HCV treatment was successful in the three patients.

55 **Conclusion:** This work evidenced uncommon mixed HCV GT infections in MSM at high risk  
56 of multiple HCV exposures. Their impact on treatment response has not been established but  
57 further studies on more patients are necessary. To prevent treatment failure in this population,  
58 regular monitoring of treatment response is needed, particularly when pan-genotypic treatment  
59 is not used.

60 **Keywords:** mixed HCV genotype infections, deep sequencing, men who have sex with  
61 men, recent HCV infection

## 62 INTRODUCTION

63 Although current treatments of HCV infection especially pan-genotypic direct-acting antivirals  
64 (DAAs) allow a high rate of sustained virological response (SVR) [1], some failures are still  
65 observed, e.g. in case of HCV genotype (GT) 3 infection [2]. Mixed HCV genotype (GT)  
66 infections (infection with two or more HCV GTs) [3] are still a clinical concern as HCV of  
67 different GTs have different sensitivities to current GT-specific DAAs. The observed  
68 prevalence of mixed HCV GT infections ranges from 14% to 39% in people who inject drugs  
69 depending on the sensitivity of methods used [3–6]. The prevalence is high in this population  
70 mostly due to their high-risk behaviors such as ongoing injection and needle sharing. As well,  
71 the prevalence of mixed HCV GT infections in men having sex with men (MSM) at high risk  
72 of multiple HCV exposures may probably be high. However, few data about the mixed HCV  
73 GT infections are available in this population. To the best of our knowledge, a few documented  
74 case reports of superinfection defined as detection of different HCV strains after the persistent  
75 infection of primary HCV strains [3] were reported in HIV/HCV co-infected MSM via sexual  
76 transmission [7–9]. More profound knowledge about the prevalence of mixed HCV GT  
77 infections in this community could help to establish an optimized strategy for surveillance,  
78 diagnostics, and treatment regimen. Ultra-deep sequencing (UDS) allows detecting minority  
79 viral population down to 1%, which is suitable for an extensive analysis of complex viral  
80 populations. In this study, we aimed to investigate by UDS the prevalence of mixed HCV GT  
81 infections in a population MSM with high-risk behaviors who were recently diagnosed with  
82 HCV infection.

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## 86 MATERIALS AND METHODS

### 87 *Study design and patients*

88 Pre-treatment plasma samples within the period defined as recent HCV infection were collected  
89 from 55 patients (50 HIV-positive and 5 HIV-negative), followed at the Pitié-Salpêtrière, Saint-  
90 Antoine and Tenon hospitals, Paris, France and 13 HIV-negative patients from the ANRS  
91 IPERGAY study (Intervention for prevention of HIV acquisition by antiretroviral therapy for  
92 PrEP among gay men at high risk of HIV-1 infection) [10,11]. The 55 patients followed at the  
93 three hospitals were previously enrolled in the recently published study using Sanger  
94 sequencing technique and addressing HCV transmission and associated sexually transmitted  
95 infection issues in this population [12]. Overall, six patients were enrolled between July 2012  
96 and December 2013 and 62 between March 2014 and May 2016.

97 The study was carried out in accordance with the Declaration of Helsinki. This work was a  
98 retrospective non-interventional study with no addition to standard care procedures.  
99 Reclassification of biological remnants into research material after completion of the ordered  
100 virological tests was approved by the local interventional review board of Pitié-Salpêtrière  
101 hospital. According to the French Public Health Code (CSP Article L.1121-1.1) such protocols  
102 are exempted from individual informed consent.

103 Recent HCV infection was defined as a positive serology test and/or a positive HCV viral load  
104 (VL) associated with a negative HCV serology within the previous 12 months, or a positive  
105 HCV VL beyond 24 weeks of a successful treatment or spontaneous clearance with  
106 modification of genotype. Furthermore, patients with a positive HCV VL with increase of  
107 alanine aminotransferase (ALAT)  $\geq 10$  upper limit of normal without any other etiology of  
108 hepatitis, or a positive HCV VL beyond 24 weeks of a successful treatment or spontaneous

109 clearance without modification of genotype were also enrolled and considered as possible  
110 recent HCV infections.

### 111 *Extraction, amplification, and deep-sequencing*

112 HCV RNA were extracted from 1 mL plasma using NucliSENS® easyMAG® (bioMérieux  
113 Clinical Diagnostics) and the NS5B fragment of 388 bp (8256 to 8644) was reverse-transcribed  
114 and amplified by PCR in a one-step process (Superscript III One-step RT-PCR with platinum  
115 Taq kit; Invitrogen, USA) according to the manufacturers' protocol by 2 pan-genotypic primers  
116 Forward: 5'-ATATGAYACCCGCTGYTTTACTC-3' and Reverse: 5'-  
117 GCNGARTAYCTVGTTCATAGCCTC-3'. Multiplexed samples were pooled and subjected to  
118 standard Illumina Miseq paired-end sequencing at 2x250 bp.

### 119 *UDS data analysis*

120 UDS data were analyzed by Geneious software (version 10.3.2, <http://www.geneious.com>)  
121 [13]. Paired reads were firstly merged, primer-removed and quality-trimmed. Sequences of  
122 good quality were error-corrected by BBNorm from the BBtools package included in Geneious.  
123 Corrected reads of each sample were clustered by *de novo* assembly approach at 90% of  
124 similarity where almost all reads were assembled. All contigs and unassembled reads were  
125 aligned to a reference sequence corresponding to the predominant subtype with maximum  
126 mismatches allowed per reads depending on the intra-genotype variability (according to the  
127 literature, 17% of maximum mismatches for GT1, 18% for GT2 samples, 20% for GT3 and  
128 16% for GT4) [14]. Sequences unable to map to the reference were put aside and their subtypes  
129 were verified by Geno2Pheno (available at <https://www.geno2pheno.org/>) [15]. When their  
130 subtypes were different with the predominant subtype, these sequences were considered either  
131 mixed infections or contaminations. Suspected contaminations were detected by building  
132 phylogenetic trees using FastTree [16] (General Time Reversible model, available at

133 <http://www.microbesonline.org/fasttree/#Install>) with viral sequences of the other samples in  
134 the same experiment. If the genetic distance among them was superior to 3%, we considered  
135 these sequences as mixed infections. If else, we suspected contaminations.

## 136 **RESULTS**

### 137 *Sequencing results and patients' characteristics*

138 A median of 2389 sequences (interquartile range (IQR): 1851-2960) per sample was obtained  
139 after quality trimming step. The median age of patients was 38.5 years (IQR: 30.5-46.0); the  
140 median of HCV viral load was 5.9 log IU/ml (IQR: 5.3-6.6); and the median value of ALAT  
141 was 320.0 IU/L (IQR: 146.5-535.5). Most of them were MSM (85.3%) and the others were  
142 reported with unknown sexual orientation. HCV genotyping by Sanger sequencing showed  
143 GT1a, GT4d, GT3a, and GT2k infection in 47.1%, 41.2%, 8.8%, and 2.9% of patients,  
144 respectively. Fifteen patients (22.1%) experienced HCV reinfections and three (4.4%) were  
145 possible recent HCV infections. HIV-coinfection was found in 50 patients (75.3%) with a  
146 median of 673 CD4 cells/mm<sup>3</sup> (IQR: 531-873, available data on 25 patients). Five among them  
147 had a detectable HIV-RNA level (> 50 copies/mL) for reasons of antiretroviral therapy (ART)  
148 absence (n=1), loss of follow-up (n=1), resistance to the received  
149 tenofovir/emcitrabine/raltegravir (n=1), viral blips (n=1), and no resistance to the received  
150 ART but suppression of the replication after treatment intensification (n=1). Sexually  
151 transmitted infections were detected in 15 patients (22.1%) ≤ 1 month before recent HCV  
152 infection diagnosis (seven *Chlamydia trachomatis*, eight *Treponema pallidum*, two *Neisseria*  
153 *gonorrhoeae*). HCV infection mainly occurred in a context of high-risk sexual behaviours  
154 (unprotected anal sex) and frequently associated with recreative drug use. Patient characteristics  
155 are presented in table 1.

### 156 *Mixed HCV genotype infections*



157 After eliminating suspected contaminations as described in the method section, three (4.4%)  
158 mixed GT infections were detected. All the three patients were infected by HCV for the first  
159 time. Two patients were co-infected by HIV and the other was HIV negative and enrolled in  
160 the ANRS IPERGAY trial.

161 In detail, a mixed HCV GT infection between predominant GT4d (at frequency of 99.68%) and  
162 minority GT1a (at frequency of 0.32%) was detected in the viral population of one HIV-positive  
163 patient. The patient was treated by 6 months of peginterferon alfa-2a/ribavirine in 2013 and  
164 obtained undetectable HCV VL after one month. His HCV viral load remains undetectable  
165 during the 5 years of follow-up.

166 In the viral population of the second patient co-infected with HIV, another mixed infection  
167 between predominant GT4d (at frequency of 89.3%) and minority GT1b (at frequency of  
168 10.7%) was identified. This patient was treated later by 12 weeks of sofosbuvir and ledipasvir.  
169 The HCV viral load was undetectable 9 months after the end of treatment.

170 The third mixed infection between predominant GT1a (at frequency of 98.7%) and minority  
171 GT4d (at frequency of 1.3%) was detected in the viral population of a HIV-negative patient  
172 under PrEP. Interestingly, a switch of virus from GT1a to GT4d was observed by Sanger  
173 sequencing in this patient two years later. The comparison among anterior minority GT4d  
174 sequences obtained from UDS with posterior GT4d sequence obtained from Sanger sequencing  
175 showed a 2% of minimum genetic distance among these sequences. At the time of HCV GT4d  
176 infection diagnosis, the patient was treated by 12 weeks of sofosbuvir and ledipasvir and  
177 obtained an undetectable HCV viral load after 2 months. However, the patient did not continue  
178 his follow-up in the hospital so we could not obtain more details about the SVR post-treatment.

179 An example of phylogenetic tree constructed from viral sequences of a mixed infection between  
180 predominant GT4d and minority GT1b virus is shown in figure 1 (the second patient). This  
181 patient was possibly infected with multiple minority transmitted GT1b viruses.

## 182 **DISCUSSION**

183 In our study, a low prevalence (4.4%) of mixed HCV GT infections was observed in a  
184 population of MSM with high-risk behaviors who were recently diagnosed with HCV infection.  
185 The prevalence of mixed HCV GT infections varies depending on the study population and the  
186 technique sensitivity. Indeed, a study using UDS showed the low prevalence of mixed HCV  
187 GT infection at 1.7% in 76 seronegative, HCV-RNA positive blood donors while a higher  
188 prevalence ranging from 14%-39% of mixed HCV GT infections was reported in people who  
189 inject drugs with both chronic and acute hepatitis C [4,17]. In our study, the prevalence of mixed  
190 HCV GT infections was investigated by UDS in a population of patients at high risk of multiple  
191 HCV exposures, HIV+ and HIV- MSM at high risk of HIV acquisition. Among 68 patients  
192 enrolled, only three (4.4%) were infected with HCV of mixed GTs involving GT4 and GT1  
193 with frequencies of minority viral populations ranging from 0.32% to 10.7%. Interestingly, a  
194 switch from GT1a to GT4d virus (based on Sanger sequencing) after 2 years was observed in a  
195 patient previously infected by predominant GT1a and minority GT4d virus (based on UDS).  
196 However, the actual 2% minimum genetic distance among the previous minority GT4d  
197 sequences obtained from UDS and the later GT4d sequence from Sanger sequencing could not  
198 distinguish if the same virus emerged, or a different virus was contracted.

199 Of note, two patients were HIV co-infected and the other was included in a PrEP program (the  
200 IPERGAY trial). A concurrent mixed HCV GT infection is associated with faster  
201 immunological progression and faster clinical progression in patients co-infected with HIV if  
202 they are not treated effectively with antiretrovirals [5]. Moreover, mixed HCV GT infections

203 possibly impact the treatment outcome of GT-specific DAAs [18,19]. However, in this study,  
204 the three patients with mixed infections obtained virological success under anti-HCV treatment.  
205 It is not surprising because the minority GT and the predominant GT viral populations involving  
206 GT1 (GT1a and GT1b) and GT4 virus have equivalent susceptibility to anti-HCV treatment  
207 (either by sofosbuvir/ledipasvir or peginterféron alfa-2a/ribavirine). Indeed, a study on 335  
208 patients co-infected with HIV-1 and HCV GT1 (GT1a and GT1b) or GT4 who received  
209 sofosbuvir/ledipasvir showed similar SVRs across different HCV GTs [20]. It is probably the  
210 reason why no deleterious impact on treatment response has been expressed in the three cases  
211 of mixed GT infections in this study.

212 In this study, a strict cut-off of 3% of genetic distance was used to eliminate contamination  
213 from PCR or sequencing steps. Only sequences of a sample with genetic distance greater than  
214 3% compared to sequences of other samples in the same experiment were considered as mixed  
215 infections. This cut-off is quite strict, which may underestimate the mixed GT infection rate in  
216 our study. Indeed, another mixed GT infection between predominant GT3a and minority GT1a  
217 virus was detected if using a cut-off less strict at 1% of genetic distance. In this study, we  
218 identified only mixed infections of different GT viruses while mixed infections of different  
219 subtype viruses in the same GT are possible. Therefore, further studies using different analysis  
220 approaches will be interesting to address this question.

221 In conclusion, we observed a low prevalence of 4.4% of mixed HCV GT infections in a  
222 population of MSM at high-risk behaviors with recent HCV infection. Determining HCV  
223 genotype becomes less clinically significant with the introduction of pan-genotypic DAAs.  
224 However, these treatments are still not globally available and affordable, especially in resource-  
225 limited countries. The impact of mixed HCV genotype infections has not been established in  
226 this study. It should be noted that the study population involved a small group of MSM in a  
227 specific area (Paris) and treatment success of patients with mixed HCV GT infections was

228 limited to only three patients. From a public health perspective, the MSM population engaging  
229 in high-risk behaviors still requires special attention in terms of mixed infections as pointed  
230 above compared to the general HCV-infected population with a regular monitoring of anti-HCV  
231 treatment response particularly when pan-genotypic treatment is not used.

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- 299

301 **CONFLICT OF INTEREST**

302 All authors do not have any conflicts of interest to declare.

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310

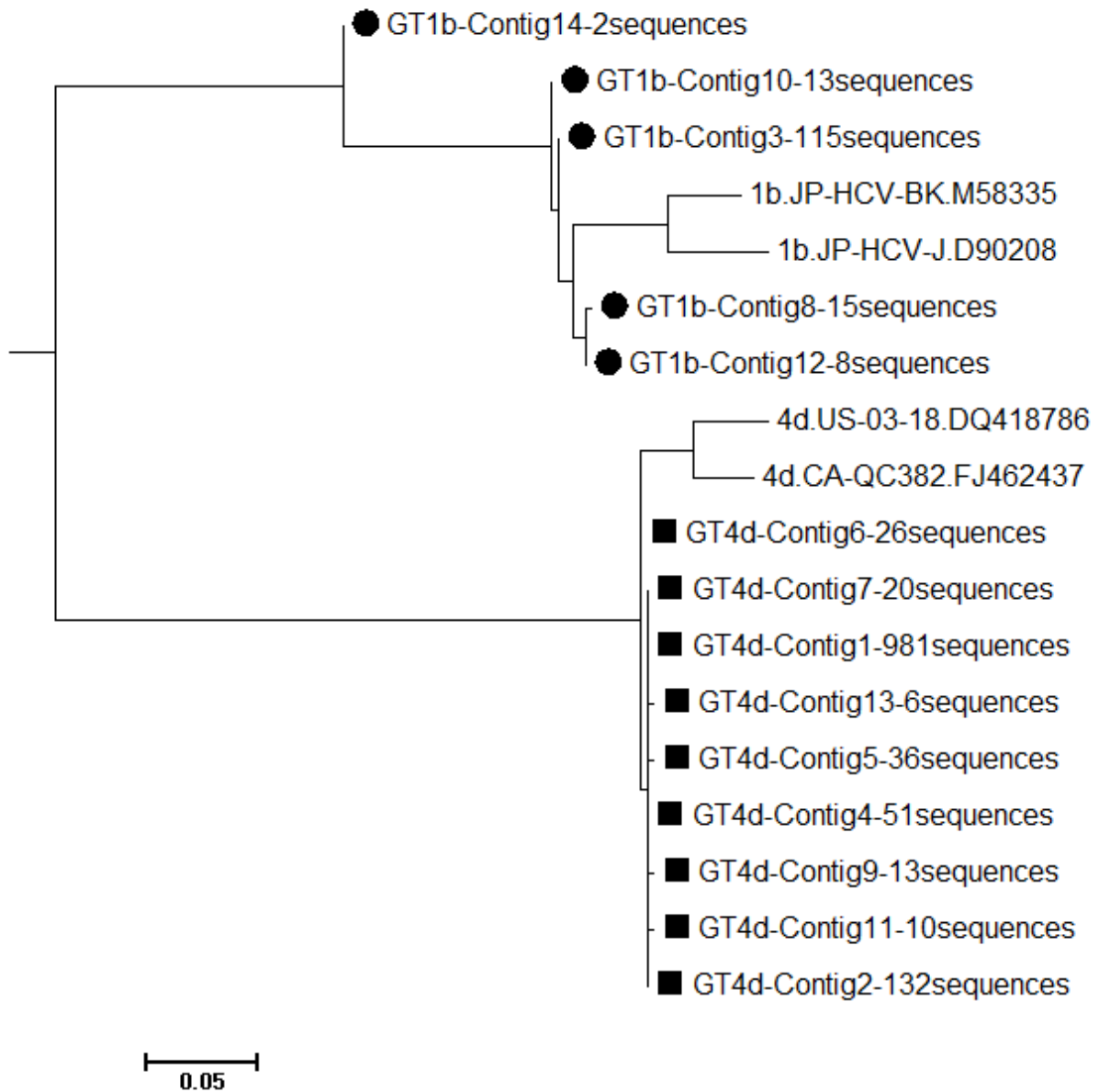
311 **Table 1:** Patient characteristics

<b>Characteristics</b>	<b>Total (n=68)</b>	<b>HIV-positive patients (n=50)</b>	<b>HIV-negative patients (n=18)</b>
Age (years), median (IQR)	38.5 (30.5-46.0)	42.5 (34.5-46.0)	32.0 (27.5-35.8)
Men having sex with men, n (%)	58 (85.3)	43 (86.0)	15 (83.3)
Unknown sexual orientation, n (%)	10 (14.7)	7 (14.0)	3 (16.7)
HCV viral load, log IU/ml, median (IQR)	5.9 (5.3-6.7)	5.9 (5.3-6.9)	5.5 (5.3-5.6)
HCV genotype			
➤ Genotype 1a, n (%)	32 (47.1)	24 (48.0)	8 (44.4)
➤ Genotype 4d, n (%)	28 (41.2)	20 (40.0)	8 (44.4)
➤ Genotype 3a, n (%)	6 (8.8)	5 (10.0)	1 (5.6)
➤ Genotype 2k, n (%)	2 (2.9)	1 (2.0)	1 (5.6)
ALAT (IU/L), median (IQR)	320.0 (146.5-535.5)	315.0 (144.8-480.8)	467.0 (234.0-647.0)
HIV co-infection (%)	50 (73.5)	50 (100.0)	0 (0.0)
Number of patients with detectable HIV-RNA, n (%)	N/A	5 (10.0%)	N/A
CD4 count (cells/mm <sup>3</sup> ), median (IQR)	N/A	673.0 (531.0-873.0)	N/A
Number of patients with STIs*, n (%)	15 (22.1)	10 (18.2)	5 (27.8)
HCV reinfection (%)	15 (22.1)	14 (28.0)	1 (5.6)

312 IQR: Interquartile range, ALAT: ALanine AminoTransferase, \*: sexually transmitted infections

313 detected less than 1 month before recent hepatitis C diagnosis, N/A: not applicable





314

315

316 **Figure 1:** Phylogenetic tree constructed from UDS contig sequences of individual with mixed  
 317 HCV genotype (GT) infection between predominant GT4d and minority GT1b and reference  
 318 sequences of GT4d and GT1b virus from Los Alamos HCV database (accession number in their  
 319 names). Viral sequences of patients are marked with shape (black square for GT4d and black  
 320 circle for GT1b virus). Number of sequences assembled in each contig is also presented in the  
 321 taxon's name.