Clinical Infectious Diseases

BRIEF REPORT

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Transcontinental Dissemination of the L2b/D-Da Recombinant *Chlamydia trachomatis* Lymphogranuloma venereum (LGV) Strain: Need of Broad Multi-Country Molecular Surveillance

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Previously, we identified a *Chlamydia trachomatis* lymphogranuloma venereum (LGV) recombinant strain possessing a non-LGV *ompA* genotype. Here, culture-independent genome sequencing confirms its circulation in Europe, Middle East, and North America, and unveils emergence of antibiotic resistance. Broad surveillance is needed.

Keywords. *Chlamydia trachomatis*; lymphogranuloma venereum (LGV); recombination; intercontinental dissemination; fluoroquinolones resistance.

Lymphogranuloma venereum (LGV), a sexually transmitted infection (STI) caused by *Chlamydia trachomatis*, raises current public health concern particularly due to its common clinical presentation as ulcerative proctitis and its circulation among men who have sex with men (MSM) [1]. Global LGV infection rates are not known because most countries lack comprehensive LGV surveillance systems, or do not generate data that are considered representative at national levels. Still, LGV cases are believed to be substantially underdiagnosed [2] and to be increasing in several European countries [1] and North America [3, 4]. LGV is caused by *C. trachomatis* strains from L1-L3 *ompA* genotypes, with the ongoing proctitis-associated epidemics being primarily caused by L2b strains (although several countries have reported increasing frequencies of the ancestral L2 genotype) [3, 5, 6]. Recently, we reported an LGV outbreak in Portugal, mostly affecting human immunodeficiency virus (HIV)-positive MSM engaging in high-risk sexual practices, caused by a novel LGV strain with a recombination-driven non-LGV *ompA* genotype [7]. This recombinant strain retains greater than 99% of the genome sequence of the epidemic L2b clone, but exhibits a hybrid main antigen (MOMP, encoded by the typing gene *ompA*) with the typical epitope repertoire of noninvasive and prevalent non-LGV strains (genotype D-Da) [7]. Its detection was possible due to the application of rapid LGV discriminatory commercial nucleic acid amplification tests (NAATs), followed by classical *ompA* genotyping as nonconcordant typing results were obtained by the 2 approaches (LGV and non-LGV, respectively) [7]. Still, the scarce usage of classical *ompA* typing or multi-loci sequence typing (MLST) techniques for the molecular surveillance of *C. trachomatis* around the world jeopardizes a proper knowledge of the real dissemination landscape of the recombinant L2b/D-Da LGV strain.

METHODS

After the identification and genome characterization of the recombinant L2b/D-Da strain in Portugal [7], the Portuguese National Reference Laboratory (NRL) for Curable STIs was contacted by NRL counterparts from Canada (National Microbiology Laboratory, Public Health Agency of Canada, PHAC) and Israel (Chlamydia National Reference Laboratory, National Public Health Laboratories) as these countries detected LGV strains with the same hybrid L2-L2b/D-Da *ompA* sequence (NCBI accession MN094864). The PHAC performs genotyping on all clinical specimens collected nationwide from patients suspected clinically of having an LGV infection. The PHAC LGV molecular surveillance strategy relies on a first screening by qPCR (LGV/non-LGV) [8], subsequent *ompA* sequencing, and additional *pmpH* sequencing to resolve recombinants and variants. In turn, Israel NRL applies an in-house MLST based on the scheme of Bom et al [9]. In short, the loci

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Nonstandard Abbreviations. ENA, European Nucleotide Archive; HIV, human immunodeficiency virus; LGV, lymphogranuloma venereum; MLST, multi-loci sequence typing; MOMP, major outer membrane protein; MSM, men who have sex with men; NAAT, nucleic acid amplification test; NRL, National Reference Laboratory; PHAC, Public Health Agency of Canada; ST, sequence type; STI, sexually transmitted infection.

Human Gene: lymphogranuloma venereum (LGV) *ompA*.

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of the scheme [*hctB* (CT046), *CT058*, *CT144*, *CT172*, *pbpB* (CT682)] and *ompA* (CT681) are amplified and sequenced, and the MLST database of Uppsala University, Sweden (http://mlstdb.bmc.uu.se/) is used to assign the sequence type (ST). Similar to the originally described recombinant L2b/D-Da strain [7], the isolates detected in Israel belong to ST58.

In order to confirm the presence of this recombinant LGV strain in these 2 countries, subsets of positive DNA samples from Israel (obtained using MagNA Pure Compact, ROCHE) (n = 2) or lysates (in APTIMA Hologic buffer) from Canada (n = 5) were sent to the Portuguese NRL for *C. trachomatis* culture-independent targeted genome sequencing and bioinformatics analysis, as previously described [7]. One representative L2b/D-Da positive sample detected in 2019 from Portugal was also sequenced. The phylogenetic analysis of the newly sequenced strains (n = 6) (Supplementary Table 1) was performed in combination with genome sequence data of 5 hybrid L2b/D-Da strains from Borges et al, (2019) [7]. The tree was constructed using IQ-TREE (version 1.6.12) based on 23 core variant sites (Supplementary Table 2) detected after mapping quality-controlled reads against the parental-like strain L2b/UCH-1/proctitis (NCBI accession numbers: AM884177.2/NC_010280.2 for chromosome and AM886279.1 for the plasmid; used as outgroup in the tree) using Snippy (version 4.6.0; https://github.com/tseemann/snippy; parameters: --mapqual 20 --mincov 4 --minfrac 0.9 --basequal 20). The analysis included strains with >70% of the genome covered by at least 4-fold coverage, and excluded any variant site falling within the *ompA*-containing recombinant region (NC_010280; approximate positions 55221–59461) or low coverage regions (<4-fold coverage) observed in any of the compared genomes. The phylogenetic placement of ISR02 strain, which does not meet the 70% threshold (Supplementary Table 1), was inferred after confirmation of its SNP profile through visual inspection of the mapping reads in the 23 core variant sites using IGV (https://igv.org/app/).

Chlamydia. trachomatis-specific reads generated in this study were deposited in the European Nucleotide Archive (ENA) (https://www.ebi.ac.uk/ena/data/view/PRJEB32243) (accession numbers listed in Supplementary Table 1). A representative genome sequence of the recombinant strain and the chimeric *ompA* were previously deposited in ENA/NCBI (CAAKND010000000/CAAKND01) and NCBI (MN094864), respectively [7].

RESULTS

Partial or near-complete *C. trachomatis* genome data were collected directly from 6 clinical samples representative of the novel hybrid non-LGV *ompA* genotype detected in the 3 countries (Canada, Israel, and Portugal) (Supplementary Table 1). All strains clustered together at genome-scale level and revealed the expected unique L2b/D-Da recombinant fingerprint (ie, exchange of ~75% of the *ompA* gene and 4 complete neighboring genes with a genotype D/Da strain (Figure 1A; Supplementary Table 1) [7]. Notably, 2 clinical strains (CAN04 and PT26) exhibited a Ser83Ile amino acid change in DNA gyrase subunit A (GyrA) (Supplementary Table 2) that most likely mediates fluoroquinolone resistance [10]. Figure 1B summarizes the proportion the novel hybrid L2b/D-Da genotype in the total number of *ompA*-genotyped confirmed LGV cases *per* country and year. Although the proportion in Portugal decreased in 2019 (3.1%) in comparison with 2017 (12.5%) and 2018 (16.5%) [7], a progressive and considerable increase has been observed in Canada in last years, with this recombinant strain accounting for 26.3% (143/543) of all LGV cases in 2019 (Figure 1B). In Israel, the NRL receives suspected cases according to voluntary physician's requests. One L2b/D-Da case was detected per year in 2018 and 2019, out of the 11 and 17 confirmed LGV cases, respectively (Figure 1B).

DISCUSSION

In this study, we confirm the circulation of the novel recombinant LGV strain (with a hybrid L2b/D-Da *ompA* genotype) in Europe, Middle East, and North America. Two clinical isolates collected in different continents were found to carry a *bona fide* genetic determinant of fluoroquinolone resistance. This strong genetic evidence for antibiotic resistance in circulating strains supports that more efforts are needed to investigate resistance traits in *C. trachomatis* [10, 11]. In fact, little is known about antibiotic resistance (and its potential relation with treatment failures) in clinical settings, since resistance phenotyping and genome screenings are hardly applicable for routine surveillance of obligate intracellular bacteria [10, 11]. In another perspective, we cannot anticipate the clinical implications of the emergence of fluoroquinolone-resistant strains, since these antibiotics are not first-line drugs for *C. trachomatis* treatment. Resistance might have been triggered by the common prescription of fluoroquinolones to treat co-infections. The novel recombinant LGV strain is circulating among MSM (most of them co-infected with HIV and other STI agents) often reporting risky sexual behaviors and involvement in international sexual networks [7]. These trends seem not to differ from the ones exhibited by the epidemic L2b clone [1, 5, 7]. Still, the rather atypical character of the recombinant L2b/D-Da strain, marked by a hybrid *ompA* (coding the main antigen) and neighbor genes with mutational signatures typical of highly prevalent genotypes (E, F, and D), led us to hypothesize that this strain may display modified transmission (or even tissue tropism and pathogenic) capabilities [7]. The transcontinental spread of the novel strain, and its marked increase in the prevalence in Canada during the last years, may favor this hypothesis. Concordantly, a significant increase in L2-L2b/D-Da cases since 2018 was also recently

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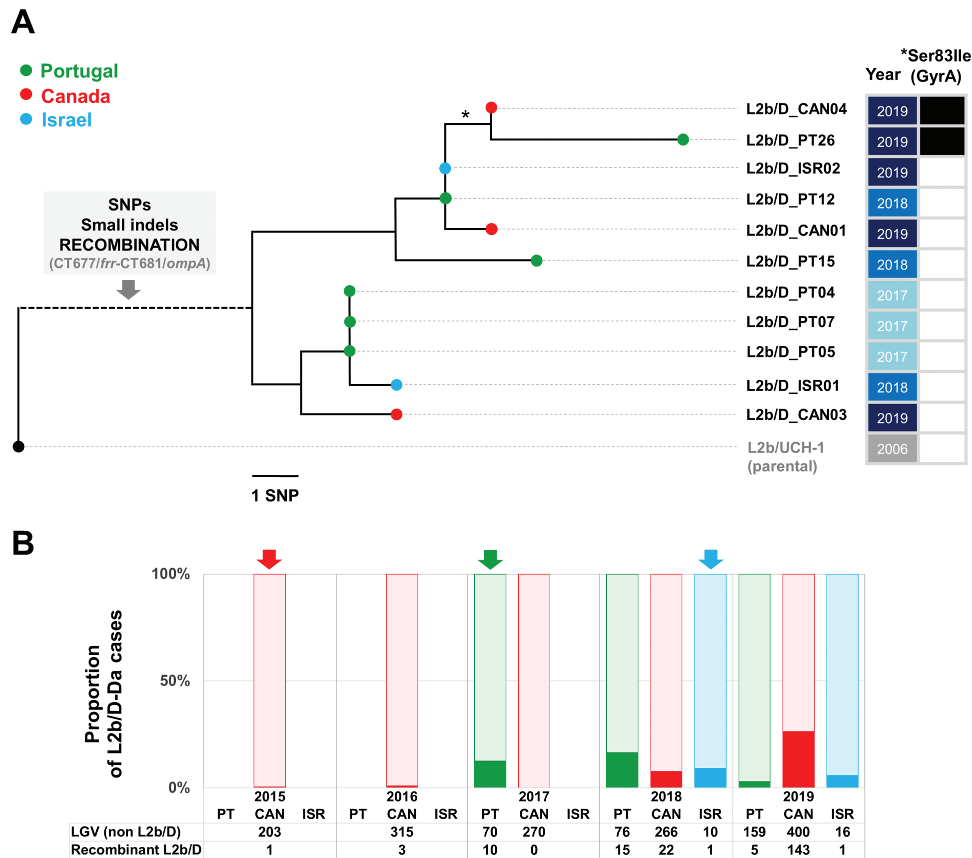

Figure 1. *A*. Genome-based phylogenetic reconstruction of *Chlamydia trachomatis* L2b/D-Da recombinant clinical isolates detected in Portugal, Canada, and Israel. The phylogenetic tree includes 11 hybrid L2b/D-Da clinical strains: 5 strains with nearly complete genome data from Borges et al, 2019 [7] and the 6 strains analyzed in the present study (Supplementary Table 1) (details in Methods section). The metadata blocks near the strains designations denote the year of collection and the detection (in 2 clinical strains) of a SNP (asterisk) leading to a Ser83Ile amino acid change in DNA gyrase subunit A (GyrA) (Supplementary Table 2) that was previously shown to mediate *C. trachomatis* resistance to fluoroquinolones in vitro [10]. Apart from the recombination event leading to the genetic transfer of *ompA* and 4 neighboring genes from a serovar D/Da strain to a L2b strain, the diversification of the hybrid LGV strain has been marked by discrete SNP and small indels accumulation (see Table S2 in Borges et al, 2019 and Supplementary Table 2 of the present study). The tree branch in dashed line reflects the genetic distance in the core-alignment (see Methods section), and not the real distance of the L2b/D-Da most recent common ancestor to the parental-like strain L2b/UCH-1/proctitis (used as outgroup in the tree). L2b/D-Da complete genomes analyzed so far differ by ~20 SNPs from L2b/UCH-1, with 10 of them being shared by all recombinant strains. PT, Portugal. CAN, Canada. ISR, Israel. *B*. Proportion of L2b/D-Da strains among *ompA*-typed confirmed LGV cases *per* country since the year of collection of the first L2b/D-Da-associated sample (indicated by arrows). CAN, Canada; ISR, Israel; PT, Portugal.

reported in Italy [12], also suggesting the broad circulation of this recombinant strain. Taking into account the estimated substitution rate of 0.2 SNPs per genome *per* year for the LGV lineage [11] and the observed lack of phylogenetic clustering by country within the L2b/D-Da sub-lineage, we speculate that this recombinant strain has been circulating undetected for several years. Importantly, its detection could only be possible because the 3 NRLs apply LGV molecular surveillance approaches relying on more than 1 genome locus (including the historical *ompA*). Of note, a few cases have been reported in France [13, 14] where *ompA* sequencing matched genotype Da, whereas *pmpH* amplification was positive for L2b. Although these data suggest that another potentially relevant LGV recombinant strain is circulating, genome sequencing is still needed to confirm the LGV genomic background.

In summary, we anticipate that a better knowledge of the worldwide circulation landscape of the hybrid L2b/D-Da strain (and other clinically relevant variants/recombinants) will be hard to achieve, giving the current scarce application of classical *ompA* typing and MLST around the world. A multi-country systematic molecular surveillance of *C. trachomatis* (LGV) infections, based on rapid multi-loci typing (ideally including *ompA*), is needed to track the emergence of novel variants towards an enhanced monitoring and control of this prevalent STI.

Supplementary Data

Supplementary materials are available at *Clinical Infectious Diseases* online. Consisting of data provided by the authors to benefit the reader, the posted materials are not copyedited and are the sole responsibility of the authors, so questions or comments should be addressed to the corresponding author.

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Notes

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Potential conflicts of interest. The authors: No reported conflicts of interest. All authors have submitted the ICMJE Form for Disclosure of Potential Conflicts of Interest. Conflicts that the editors consider relevant to the content of the manuscript have been disclosed.

References

1. European Centre for Disease Prevention and Control. Lymphogranuloma venereum. In: ECDC. Annual epidemiological report for 2017. Stockholm: ECDC, **2019**.
2. Cole MJ, Field N, Pitt R, Amato-Gauci AJ, et al. Substantial underdiagnosis of lymphogranuloma venereum in men who have sex with men in Europe: preliminary findings from a multicentre surveillance pilot. Sex Transm Infect **2020**; 96:137–42.
3. Totten S, MacLean R, Payne E, Severini A. *Chlamydia* and lymphogranuloma venereum in Canada: 2003–2012 summary report. Can Commun Dis Rep **2015**; 41:20–5.
4. Pathela P, Jamison K, Kornblum J, et al. Lymphogranuloma Venereum: an increasingly common anorectal infection among men who have sex with men attending New York City sexual health clinics. Sex Transm Dis **2019**; 46:e14-e17.
5. Thomson NR, Holden MT, Carder C, et al. *Chlamydia trachomatis*: genome sequence analysis of lymphogranuloma venereum isolates. Genome Res **2008**; 18:161–71.
6. Peuchant O, Touati A, Sperandio C, et al. Changing pattern of *Chlamydia trachomatis* strains in lymphogranuloma venereum outbreak, France, 2010–2015. Emerg Infect Dis **2016**; 22:1945–7.
7. Borges V, Cordeiro D, Salas AI, et al. *Chlamydia trachomatis*: when the virulence-associated genome backbone imports a prevalence-associated major antigen signature. Microb Genom **2019**; 5:e000313.
8. Chen CY, Chi KH, Alexander S, et al.. A real-time quadriplex PCR assay for the diagnosis of rectal lymphogranuloma venereum and non-lymphogranuloma venereum *Chlamydia trachomatis* infections. Sex Transm Infect **2008**; 84:273–6.
9. Bom RJ, Christerson L, Schim van der Loeff MF, Coutinho RA, Herrmann B, Bruisten SM. Evaluation of high-resolution typing methods for *Chlamydia trachomatis* in samples from heterosexual couples. J Clin Microbiol **2011**; 49:2844–53.
10. Sandoz KM, Rockey DD. Antibiotic resistance in *Chlamydiae*. Future Microbiol **2010**; 5:1427–42.
11. Hadfield J, Harris SR, Seth-Smith HMB, et al. Comprehensive global genome dynamics of *Chlamydia trachomatis* show ancient diversification followed by contemporary mixing and recent lineage expansion. Genome Res **2017**; 27:1220–9.
12. Marangoni A, Foschi C, Tartari F, et al. Lymphogranuloma venereum genovariants in men having sex with men in Italy. Sex Transm Infect **2020**; doi: 10.1136/sextrans-2020–054700.
13. Touati A, Peuchant O, Hénin N, et al. The L2b real-time PCR targeting the pmpH gene of *Chlamydia trachomatis* used for the diagnosis of lymphogranuloma venereum is not specific to L2b strains. Clin Microbiol Infect **2016**; 22:574.e7-9.
14. Peuchant O, Touati A, Laurier-Nadalié C, et al. Prevalence of lymphogranuloma venereum among anorectal *Chlamydia trachomatis*-positive MSM using pre-exposure prophylaxis for HIV. Sex Transm Infect **2020**; 96:615–7.

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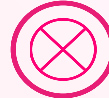
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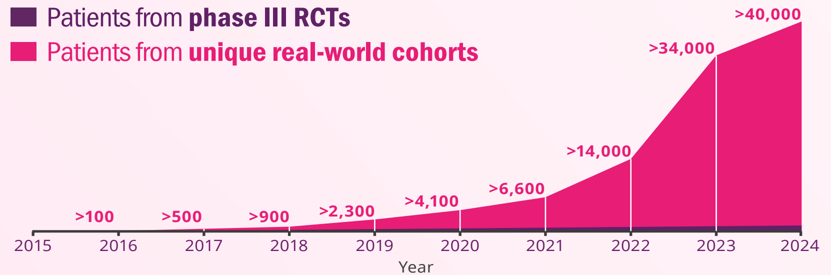

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REFERENCES

1. Maggiolo F et al. BMC Infect Dis 2022; 22(1): 782.
2. Taramasso L et al. AIDS Patient Care STDS 2021; 35(9): 342–353.
3. Cicculło A et al. JAIDS 2021; 88(3): 234–237.
4. ViiV Healthcare. Data on File. REF-223795. 2024.
5. Cahn P et al. AIDS 2022; 36(1): 39–48.
6. Rolle C et al. Open Forum Infect Dis 2023; 10(3): ofad101.
7. Cordova E et al. Poster presented at 12th IAS Conference on HIV Science. 23–26 July 2023. Brisbane, Australia. TUPEB02.
8. De Wit S et al. Slides presented at HIV Glasgow. 23–26 October 2022. Virtual and Glasgow, UK. M041.
9. Llibre J et al. Clin Infect Dis 2023; 76(4): 720–729.
10. ViiV Healthcare. Data on File. REF-220949. 2024.
11. Rolle C et al. Poster presented IDWeek. 11–15 October 2023. Virtual and Boston, USA. 1603.
12. Slim J et al. Abstract presented IDWeek. 11–15 October 2023. Virtual and Boston, USA. 1593.
13. DOVATO. Summary of Product Characteristics. June 2023.

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ABBREVIATIONS

3TC, lamivudine; **CD4,** cluster of differentiation 4; **DTG,** dolutegravir; **FDA,** United States Food and Drug Administration; **FTC,** emtricitabine; **HIV,** human immunodeficiency virus; **ITT-E,** intention-to-treat exposed; **NRTI,** nucleoside/nucleotide reverse transcriptase inhibitor; **RCT,** randomised controlled trial; **RNA,** ribonucleic acid; **TAF,** tenofovir alafenamide fumarate; **TDF,** tenofovir disoproxil fumarate; **XTC,** emtricitabine.

FOOTNOTES

*Data extracted from a systematic literature review of DTG+3TC real-world evidence. Overlap between cohorts cannot be fully excluded.
**The reported rate reflects the sum-total of resistance cases calculated from GEMINI I and II (n=1/716, through 144 weeks), STAT (n=0/131, through 52 weeks), and D2ARLING (n=0/106, through 24 weeks).[5-7]
†GEMINI I and II are two identical 148-week, phase III, randomised, double-blind, multicentre, parallel-group, non-inferiority, controlled clinical trials testing the efficacy of DTG/3TC in treatment-naïve patients. Participants with screening HIV-1 RNA ≤500,000 copies/mL were randomised 1:1 to once-daily DTG/3TC (n=716, pooled) or DTG + TDF/FTC (n=717, pooled). The primary endpoint of each GEMINI study was the proportion of participants with plasma HIV-1 RNA <50 copies/mL at Week 48 (ITT-E population, snapshot algorithm).[13]
‡STAT is a phase IIIb, open-label, 48-week, single-arm pilot study evaluating the feasibility, efficacy, and safety of DTG/3TC in 131 newly diagnosed HIV-1 infected adults as a first line regimen. The primary endpoint was the proportion of participants with plasma HIV-1 RNA <50 copies/mL at Week 24.[6]
§D2ARLING is a randomised, open-label, phase IV study designed to assess the efficacy and safety of DTG/3TC in treatment-naïve people with HIV with no available baseline HIV-1 resistance testing. Participants were randomised in a 1:1 ratio to receive DTG/3TC (n=106) or DTG + TDF/XTC (n=108). The primary endpoint was the proportion of participants with plasma HIV-1 RNA <50 copies/mL at Week 48.[7] Results at week 24 of the study.
||The reported rate reflects the sum-total of resistance cases calculated from TANGO (n=0/369, through 196 weeks) and SALSA (n=0/246, through 48 weeks).[8,9]
¶TANGO is a randomised, open-label, trial testing the efficacy of DOVATO in virologically suppressed patients. Participants were randomised in a 1:1 ratio to receive DOVATO (n=369) or continue with TAF-containing regimens (n=372) for up to 200 weeks. At Week 148, 298 of those on TAF-based regimens switched to DOVATO. The primary efficacy endpoint was the proportion of subjects with plasma HIV-1 RNA ≥50 copies/mL (virologic non-response) as per the FDA Snapshot category at Week 48 (adjusted for randomisation stratification factor).[8,13]
#SALSA is a phase III, randomised, open-label, non-inferiority clinical trial evaluating the efficacy and safety of switching to DTG/3TC compared with continuing current antiretroviral regimens in virologically suppressed adults with HIV. Eligible participants were randomised 1:1 to switch to once-daily DTG/3TC (n=246) or continue current antiretroviral regimens (n=247). The primary endpoint was the proportion of subjects with plasma HIV-1 RNA ≥50 copies/mL at Week 48 (ITT-E population, snapshot algorithm).[9]

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