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MOLECULAR EVIDENCE OF NOSOCOMAL TRANSMISSION OF HEPATITIS C VIRUS (HCV) IN A HEMODIALYSIS UNIT

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BACKGROUND

Nosocomial infection is still relevant in hepatitis C virus (HCV) transmission in patients submitted to hemodialysis (HD). There is a great concern that this vulnerable patient population continues to be at risk for iatrogenic HCV transmission that might be facilitated through undiagnosed infections. The failure to completely adhere to established safety guidelines can lead to transmissions of HCV since this infection can remain undiagnosed because of relatively minor ALT changes and a significant delay in HCV seroconversion in some patients. The aim of this study was to evaluate by sequence analyses the occurrence of HCV transmission in a HD unit in the state of Rio de Janeiro, Brazil, which reported anti-HCV seroconversion in 4 previously negative patients.

METHODS

A total of 130 patients and 56 staff from a hemodialysis unit were prospectively followed between December, 2016 and March, 2017.

HCV-RNA DETECTION AND QUANTIFICATION

- **Quantitative Real-Time PCR Abbott plataform**
- **Detection limit: 12 UI/mL**

NUCLEOTIDE SEQUENCING AND PHYLOGENETIC ANALYSIS

- **NS5B RT-PCR amplification**
- **Phylogenetic analysis: Sequences were compared to reference and Brazilian non related sequences.**
- **Maximum Likelihood, bootstrap 1000 replicates (MEGA software, v7)**

RESULTS

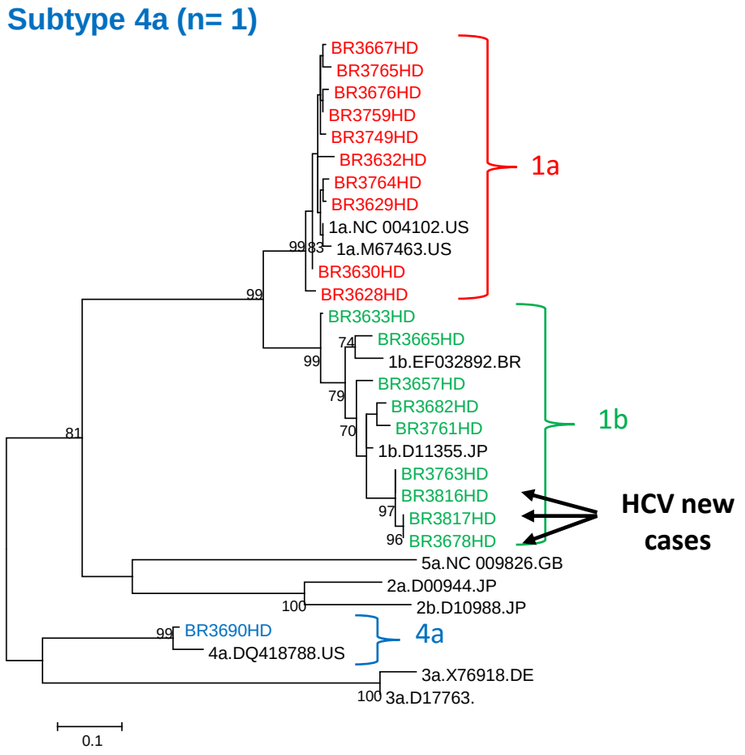
- **HCV-RNA was detected in 23 HD patients (17,7%)**
- **Viral loads ranged from <12 - 1 2.324,983 IU/mL**
- **Genotypes 1a (n = 10), 1b (n-9) and 4a (n = 1) were detected.**
- **Three patients were not sequenced/genotyped due to low viral load, including one case of recent infection.**
- **Phylogenetic analysis revealed that 4/9 (44.4%) genotype 1b samples formed a highly related group, 3 of them from cases of recent infection and one from a chronic case (index case) demonstrating the existence of a common source of infection.**
- **Transmission in patients with genotypes 1a and 4a was discarded due to the low similarity among the sequences.**
- **All staff were negative for HCV-RNA.**

HCV viral loads from chronic carriers and acute cases

	SAMPLE	VIRAL LOADS	LOG
HCV CRONIC CARRIERS FROM HD UNIT	BR3761HD	53.696	4,75
	BR3682HD	69.931	4,84
	BR3628HD	1.517.050	6,18
	BR3690HD	185.780	5,27
	BR3632HD	60.441	4,78
	BR3676HD	1.061.288	6,03
	BR3764HD	152.047	5,18
	BR3749HD	213.386	5,33
	BR3765HD	165.250	5,22
	BR3704HD	ND	0
	BR3663HD	ND	0
	BR3763HD	34.922	4,54
	BR3672HD	ND	0
	BR3629HD	504.468	5,7
	BR3630HD	1.420.692	6,15
	BR3665HD	910.312	5,96
	BR3667HD	11.686.021	7,07
	BR3633HD	917.276	5,96
	BR3631HD	ND	0
	BR3657HD	2.436.875	6,39
	BR3634HD	ND	0
	BR3759HD	ND	0
	BR3636HD	ND	0
HCV NEW CASES FROM HD UNIT	BR3817HD	147.885	5,17
	BR3816HD	110.635	5,04
	BR3678HD	920	2,96
	BR3818HD	1.339	3,13

Phylogenetic analysis of HCV-RNA positive samples

Subtype 1a (n = 10)
Subtype 1b (n = 9)
Subtype 4a (n= 1)

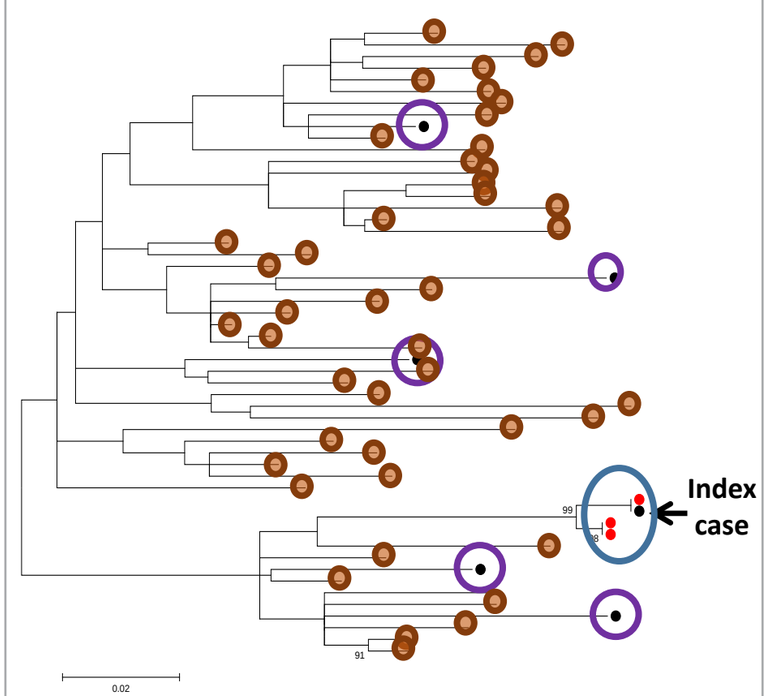


*Three samples could not be amplified due to low viral loads

Genetic distances:

Brazilian 1b / other HD sequences: d=0,07
HD sequences linked to the outbreak: d=0,006

HCV Genotype 1b phylogenetic tree



CONCLUSIONS

- **HCV infection in the HD setting is a serious problem that has persisted despite the adoption of biosafety measures and improved diagnostic tools;**
- **Twenty-three chronic cases and 4 new cases were detected in the HD unit;**
- **Genotypes 1a (n = 10), 1b (n-9) and 4a (n = 1) were detected;**
- **Evidence of nosocomial transmission among HD patients were provided by phylogenetic analyzes;**
- **The index case, as a source of HCV transmission, was identified;**
- **The introduction of molecular diagnostic methods in health system is a top priority for preventing and controlling the risk of transmitting bloodborne viruses in the HD scenario.**

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CONFLICTS OF INTEREST

No conflits of interest

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