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Molecular characterization of Trypanosoma cruzi in four Chagas disease patients who acquired the infection by different routes of transmission

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Background: *Trypanosoma cruzi*, the etiological agent of Chagas disease (CD) is characterized by a tremendous genetic diversity. Different typing methods have made it possible to classify the parasite into six genetic groups (discrete typing units, DTUs), named TcI to TcVI. Beyond the vectorial transmission, limited to endemic areas, other routes of transmission are blood transfusion, organ transplantation, and congenital transmission. In Spain, screening for CD in all blood and organ donors coming from endemic areas has been mandatory since 2005. However, in relation to mother to child transmission, not all the communities have established an official prevention program. The aim of this study was to determine the *T.cruzi* genotype of four patients with different immune status and infected by different routes of transmission.

Material/methods: Samples from four patients with CD were investigated: two congenital transmission cases from Bolivian *T. cruzi* seropositive mothers, one HIV co-infected patient from Bolivia, and one recipient who received platelet transfusion from a Brazilian donor. DNA was obtained from a clinical sample (one congenital case), and culture (three other cases). DNA from reference control strains were simultaneously analysed. Molecular characterization was performed combining PCRs of the intergenic region of the mini-exon gene, the 24Sα and 18S regions of rDNA and A10 repetitive sequence.

Results: Genotyping characterization was successfully carried out in all samples. TcV DTU was identified in three patients: both congenital cases, and HIV co-infected patient. On the other hand, Tc II was detected in the platelet transfusion recipient. The size of amplified products in base pairs (bp) from characterization PCRs are summarized in table 1.

Table 1. Size of amplified products (bp) from characterization PCRs.

CD Case	Mini-exon gene	rDNA			A10	DTU
		24s		18s V1-V2		
		D71-D72	D71-D76			
Congenital C_1	300 bp	110 & 120 bp	140 & 125 bp	165 bp	210 bp	**Tc V**
Congenital C_2	300 bp	110 & 120 bp	140 & 125 bp	165 bp	210 bp	**Tc V**
HIV co-infected	300 bp	110 & 120 bp	140 & 125 bp	165 bp	210 bp	**Tc V**
Platelet transfusion recipient	300 bp	125 bp	140 bp	165 bp	225 bp	**Tc II**

Conclusions: Molecular characterization can be successfully performed in clinical samples with high parasite load. TcV was identified in all cases with a common Bolivian origin as source of infection. In contrast, TcII DTU was characterized in the recipient who received platelet transfusion from a Brazilian donor. DTUs distribution in migrant population seems to be similar to that observed in the patients' countries of origin.