Polymorphism rs3729825 of MHRT predicts worse cardiac prognosis in Chagas disease

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Chagas disease (CD), caused by *Trypanosoma cruzi*, may progress to chronic cardiac involvement, the most severe form. Single-nucleotide polymorphisms (SNPs) in regulatory genes may influence disease outcome. We investigated the association of SNP rs3729825 (C > T) in the lncRNA myosin heavy chain-associated RNA transcript (MHRT) with cardiac parameters in patients with chronic CD. Genotyping was performed using polymerase chain reaction–restriction fragment length polymorphism (PCR-RFLP), and echocardiographic data were analysed. Carriers of CT/TT genotypes exhibited larger atrial and ventricular diameters, as well as a reduced left ventricular ejection fraction, indicating a poorer prognosis. These findings suggest that rs3729825 may serve as a prognostic genetic marker in CD.

Keywords: Chagas disease, genetic polymorphism, long non-coding RNA, prognosis, single-nucleotide polymorphism.

Materials and methods

Study design

The present cross-sectional study employed purposive sampling, involving 210 patients with confirmed CD, as determined by positive serology in at least two of three diagnostic tests (ELISA, indirect hemagglutination, and indirect immunofluorescence). All patients were in the chronic phase and were clinically followed at the Chagas Disease Outpatient Clinic, Faculty of Health Sciences, University of the State of Rio Grande do Norte (UERN), Mossoró-RN, Brazil.

Participants were informed about the study objectives and procedures and provided written informed consent. Peripheral blood samples (4 ml) were collected for DNA extraction at the Molecular Biology Laboratory of UERN. Patient data were coded and stored in a secure database accessible only to the research team. The study was approved by the Ethics Committee of UERN (CEP/UERN – Protocol 1.160.553, CAAE: 43783915.3.0000.5294).