Background: Several polymorphisms of the dimethylarginine dimethylaminohydrolase (DDAH) genes have been studied in cardiovascular diseases. These molecules play an important role in the regulation of nitric oxide synthesis and release. The aim of the present study was to establish the role of DDAH gene polymorphisms in the risk of developing myocardial infarction (MI) in a well-characterized clinical cohort of Mexican patients.

Methods: One polymorphism (rs1498373) in the DDAH1 and three in the DDAH2 (rs805304, rs3131383, and rs805305) genes were analyzed by 5´ exonuclease Taqman genotyping assays in 289 patients with MI and 289 healthy unrelated controls. The differences between patients and healthy controls were evaluated by X2, Fisher's exact test, and Woolf method for odds ratio (OR). P values were corrected (pC) multiplying by the number of comparisons made. The analysis of linkage disequilibrium was done by Haploview versión 4.1. Observed and expected frequencies in the studied polymorphic sites were in Hardy-Weinberg equilibrium.

Results: Similar distribution of DDAH1 and DDAH2 polymorphisms was observed in MI patients and healthy controls. The three DDAH2 polymorphisms were in linkage disequilibrium and were included in five haplotypes: H1 (ACC), H2 (CGC), H3 (CGA), H4 (CCC), and H5 (AGC). MI patients showed decreased frequencies of the H4 (P < 10-4) and H5 (P = 0.004) haplotypes when compared to controls.

Conclusions: Our results suggest that the DDAH gene polymorphisms are not associated with risk of developing MI when they are analyzed independently. However, when the polymorphisms were analyzed in blocks (haplotypes), it was possible to distinguish two protective uncommon haplotypes for developing MI.