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INTRODUCTION

The interleukin-1 receptor antagonist (IL-1RA) is a protein that in humans is encoded by the IL1RN gene.

Previous epidemiological studies have presented evidence regarding associations between IL1RN polymorphisms and sepsis susceptibility.

The role of this polymorphism in predisposition to infection has not been explored in heart recipients.

OBJETIVES

- ✓ In the present study the potential role of IL-1RN genotypes was evaluated as a potential risk factor of severe infection in heart recipients.

METHODS

We evaluated 57 heart transplant recipients and 208 healthy controls.

Genomic DNA was extracted from peripheral blood and amplified by PCR-SSP.

Allelic and genotypic frequency of 86-bp variable number of tandem repeats (VNTR) sequence in intron 2 of IL-1RN gene was determined.

Alleles were allele 1 (410 pb) having 4rp, allele 2 (240 pb) 2rp, allele 3 (500 pb) 5rp, allele 4 (325 pb) 3rp and allele 5 (595 pb) 6rp.

The genotypes were classified as AA, BB, and AB.

The associations between IL-1 polymorphisms and distinct clinical outcome risk were estimated by calculating ORs and 95%CI.

Overall infections were defined as all infection that required IV antimicrobial therapy after transplantation.

Catheter related infection and superficial surgical infection were not considered as infectious outcomes in this study.

RESULTS

The distribution of genotypes was as follows: AA 24 (40.7%), AB 27 (45.8%), BB 7 (11.9%).

Genetic model BB + AB vs. AA was not associated with overall infection risk during the first 3 months after transplantation, OR 0.71; 95% confidence interval (95%CI) 0.23-2.19, $p=0.55$.

AB vs AA + BB was not associated with overall infection risk, OR 2.06, 95% CI 0.69-6.25, $p=0.20$.

AB vs AA + BB was a significant risk factor of death during long term follow-up: 7 out of 8 patients who died were genotype AB, OR 10.84, 95% CI 1.24-94.95, $p=0.03$.

CONCLUSIONS

IL-1RN genotypes were not associated with infectious outcomes in this pilot study performed in heart recipients.

The potential relationship of AB genotype with death risk warrants further exploration in future studies with greater number of patients.