Heart transplantation is performed in patients with end-stage heart failure, in whom all other methods of treatment failed. The most common causes of end-stage heart failure are dilated cardiomyopathy and coronary artery disease. The destiny of these patients is highly variable. Prediction of long term survival in patients after heart transplantation is not satisfactory and up to now has not been found reliable marker. Most of the patients die after heart transplantation due to cardiovascular disease.

This thesis is focused on molecular genetics and statistical analysis of four single nucleotide polymorphisms, namely rs17817449 (16q12.2, FTO gene), rs2943634 (2q36.3; intergenic region), rs6922269 (6q25.1; MTHFD1L gene), and rs10757274 (9p21.3; intergenic region). According to genome wide association studies are these SNPs assosiated with cardiovascular diseases. We genotyped DNA samples of 364 heart donors and 364 heart recipients. The results were statistically compared (using OR and Pearson's $\chi 2$ test) with the control group, which consisted of samples of individuals from the general population MONICA study. We examined the genotype in patients whose hearts failed due to dilated cardiomyopathy or coronary artery disease and then in patients with cardiac allograft vasculopathy. Furthermore, we focused on the genotypes of patients who died within 10 years after transplantation due to cardiovascular disease.