Introduction: Type 2 diabetes mellitus (T2DM) is a worldwide spread disease of affluence which prevalence has been growing. Although, the probability of its manifestation is being linked above all with environmental factors, genetic susceptibility plays an important role too. The aim of this thesis was to find out the association of four polymorphisms with the risk of T2DM manifestation in Czech population. Polymorphisms rs10203174 *THADA*, rs6819243 *MAEA*, rs849135 *JAZF1* and rs1552224 *ARAP1* (*CENTD2*) were chosen based on their risk in British population.

Methodology: We studied groups of 712 Czech patients with T2DM and 752 healthy controls selected as a random sample of Czech population in the post-MONICA study. For a genotypisation rs10203174 and rs6819243 we used the PCR–RFLP method. For an analysis of genotypes rs849135 and rs1552224 was used the real-time PCR method. The results were analysed via odds ratio (OR) a chi-square test.

Results: In case of the rs1552224 variant, the risk was proved with statistical significance (P = 0,01). The value of OR for the risk allele T is 1,37 (95% CI 1,07-1,75). In case of the polymorphisms rs10203174, rs6819243 and rs849135 no significant association with the disease was proved. For rs10203174 the value of OR of the allele C is 1,20 (95% CI 0,91-1,56, P = 0,20), OR of the allele T polymorphism rs6819243 is 1,12 (95% CI 0,71-1,77, P = 0,61) and for rs849135 the OR of allele A is 1,03 (95% CI 0,76-1,38, P = 0,86).

Conclusions: In contrast to British population, the variants rs10203174, rs6819243 and rs849135 in Czech population do not significantly influence risk of the manifestation of T2DM. Rs1552224 TT homozygotes have a 1,4times heightened probability of the disease occurrence.