ABSTRACT

The receptor for advanced glycation end products (RAGE), soluble RAGE (sRAGE) and its ligands are involved in the pathogenesis of cancer. Glyoxalase I (GLO1) is an enzyme which detoxifies advanced glycation end product (AGE) precursors. Four polymorphisms of RAGE (rs1800625 RAGE -429T/C, rs1800624 -374T/A, rs3134940 2184A/G, rs2070600 557G/A (G82S), and GLO1 rs4746 419A/C(E111A)) were determined by PCR-RFLP in 214 patients with ccRCC. A group of 154 healthy subjects was used as control. We found significant differences in the allelic and genotype frequencies of GLO1 E111A (419A/C) SNP between patients and controls—higher frequency of the C allele in ccRCC—58.6 vs. 44.5 % in controls, OR (95 % CI) 1.77 (1.32–2.38), p=0.0002 (corrected p=0.001); OR (95 % CI) CC vs. AA 2.76 (1.5–4.80), p=0.0004 (corrected p= 0.002); and AC+CC vs. AA 2.03 (1.23–3.30), p=0.0034 (corrected p=0.017). The values of sRAGE in a subgroup of 132 patients were evaluated before and three weeks, three and six months after surgery and in cancer relapse. According to relapse of the cancer, the patients were divided into two groups. The postoperative elevation of sRAGE was seen in group of ccRCC without relapse. Stable postoperative sRAGE were in group with relapse. We have not detected the difference between sRAGE in ccRCC group and control group. Our results demonstrate the link of E111A GLO1 SNP to the presence of the tumor and the significance of sRAGE in follow-up of localised renal cancer after surgery.

Key words: RAGE, sRAGE, glyoxalase I, renal cell cancer, polymorphism