

A common CCK-B receptor intronic variant does not predict risk for or survival in pancreatic adenocarcinoma

Anita Balázs¹, Balazs Nemeth², Balazs Ordog³, Eszter Hegyi⁴, Istvan Hritz¹, Laszlo Czako¹, Jozsef Czimmer⁵, Szilard Godi⁵, Adrienn Csiszko⁶, Zoltan Rakonczay Jr.¹, Andrea Parnicky⁷, Ferenc Izbeki⁸, Adrienn Halasz⁸, Zsuzsanna Kahan⁹, Peter Hegyi^{1,10}, Miklos Sahin-Toth² on behalf of Hungarian Pancreatic Study Group

¹First Department of Medicine, University of Szeged, Szeged, Hungary, ²Department of Molecular and Cell Biology, Boston University Henry M. Goldman School of Dental Medicine, Boston, MA 02, United States, ³Department of Pharmacology and Pharmacotherapy, Faculty of Medicine, University of Szeged, Szeged, Hungary, ⁴2nd Department of Pediatrics, Comenius University Medical School, University Children's Hospital, Bratislava, Slovakia, ⁵First Department of Internal Medicine, University of Pécs, Hungary, ⁶Institute of Surgery, University of Debrecen, Clinical Center, Debrecen Hungary, ⁷Heim Pál Childrens Hospital, Budapest, Hungary, ⁸First Department of Medicine, Szent György Teaching Hospital of County Fejér, Székesfehérvár, Hungary, ⁹Department of Oncotherapy, University of Szeged, Szeged, Hungary, ¹⁰MTA-SZTE Translational Gastroenterology Research Group, Szeged, Hungary

Introduction: Cholecystokinin-B receptor (CCKBR) is often over-expressed in pancreatic ductal adenocarcinoma; stimulation of the receptor promotes tumor growth. Single nucleotide polymorphism c.811+32C>A in intron 4 of *CCKBR* was previously reported to correlate with higher cancer risk and poorer survival. The variant was suggested to induce retention of intron 4, resulting in a new spliceform with enhanced receptor activity.

Aims: Our objective was to validate the c.811+32C>A variant as an emerging biomarker for pancreatic cancer risk and prognosis.

Patients & methods: We genotyped variant c.811+32C>A in 122 pancreatic adenocarcinoma cases and 106 controls by sequencing and examined its association with cancer risk and patient survival. To test the functional effect of variant c.811+32C>A on pre-mRNA splicing, we constructed minigenes, harboring the *CCKBR* coding sequence and intron 4 with or without the variant. Transcription and splicing of *CCKBR* was evaluated in transiently transfected HEK 293T cells.

Results: We found the intronic variant in 35 heterozygous and 5 homozygous cases and in 32 heterozygous and 3 homozygous controls (allele frequency 18.4% and 17.9%, respectively). Survival analysis showed no significant difference between median survival of patients with the C/C genotype (266 days) and patients with the A/C or A/A genotypes (257 days). *CCKBR* minigenes with or without variant c.811+32C>A exhibited no difference in expression of the intron-retaining splice variant.

Conclusion: These data indicate that variant c.811+32C>A in *CCKBR* does not have a significant impact on pancreatic cancer risk or survival in a Hungarian cohort.