Association between single nucleotide polymorphisms in the PI3K/AKT/mTOR pathway and bladder cancer risk in a sample of Iranian population

Article - PDF

Article - HTML

Article - XML

Published Jan 2, 2018

DOI https://doi.org/10.17179/excli2017-329

Fatemeh Bizhani
Cellular and Molecular Research Center, Zahedan University of Medical Sciences, Zahedan, Iran; Department of Clinical Biochemistry, School of Medicine, Zahedan University of Medical Sciences, Zahedan, Iran

Mohammad Hashemi
Cellular and Molecular Research Center, Zahedan University of Medical Sciences, Zahedan, Iran; Department of Clinical Biochemistry, School of Medicine, Zahedan University of Medical Sciences, Zahedan, Iran

Hiva Danesh
Department of Clinical Biochemistry, School of Medicine, Zahedan University of Medical Sciences, Zahedan, Iran

Akbar Nouralizadeh
Urology and Nephrology Research Center; Department of Urology, Shahid Labbafinejad Medical Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Behzad Narouie
Urology and Nephrology Research Center; Department of Urology, Shahid Labbafinejad Medical Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Gholamreza Bahari
Department of Clinical Biochemistry, School of Medicine, Zahedan University of Medical Sciences, Zahedan, Iran

Saeid Ghavami
Department of Human Anatomy and Cell Science, College of Medicine, Faculty of Health Sciences, University of Manitoba, Winnipeg, MB R3E 0J9, Canada; Health Policy Research Center, Shiraz University of Medical Sciences, Shiraz, Iran

Abstract

In the past few years several investigations have focused on the role of PI3K/AKT/mTOR pathway and its deregulations in different cancers. This study aimed to examine genetic polymorphisms of this pathway in bladder cancer (BC). In this case-control study, 235 patients with pathologically confirmed bladder cancer and 254 control subjects were examined. *PIK3CA*, *AKT1* and *mTOR* variants were analyzed using polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP). The findings proposed that the *PIK3CA* rs6443624 SNP significantly decreased the risk of BC (OR=0.44, 95 % CI=0.30-0.65, p<0.0001 CA vs CC; OR=0.35, 95 % CI=0.16-0.78, p=0.0107, AA vs CC; OR=0.60, 95 % CI=0.46-0.79, p=0.0002, A vs T). The *AKT1* rs2498801 variant is associated with a decreased risk of BC (OR=0.57, 95 % CI=0.39-0.82, p=0.003, AG vs AA; OR=0.74, 95 % CI=0.56-0.97, p=0.032, G vs A) while, AKT1 rs1130233 polymorphism considerably increased the risk of BC (OR=3.70, 95 % CI=2.52-5.43, p<0.0001, GA vs GG; OR=5.81, 95 % CI=1.53-21.97, p=0.010, AA vs GG; OR=2.71, 95 % CI=1.98-3.70, p<0.0001, A vs G). Additionally, mTOR rs2295080 variant notably increased the risk of BC (OR=2.25, 95 % CI=1.50-3.38, p<0.0001, GT vs GG; OR=4.75, 95 % CI=2.80-8.06, p<0.0001, TT vs GG; OR=3.10, 95 % CI=2.34-4.10, p<0.0001, T vs G). None of the other examined polymorphisms (*AKT1* rs1130214, *AKT1* rs3730358, *mTOR* rs1883965) revealed significant association with BC. In conclusion, our findings suggest that *PIK3CA* rs6443624, *AKT1* rs2498801, *AKT1* rs1130233, as well *mTOR* rs2295080 polymorphism may be related to bladder cancer development in a sample of Iranian population. Validation of our findings in larger sample sizes of different ethnicities would provide evidence on the role of variants of PI3K/AKT/mTOR pathway in developing BC.

How to Cite

Bizhani, F., Hashemi, M., Danesh, H., Nouralizadeh, A., Narouie, B., Bahari, G., & Ghavami, S. (2018). Association between single nucleotide polymorphisms in the PI3K/AKT/mTOR pathway and bladder cancer risk in a sample of Iranian population. *EXCLI Journal*, *17*, 3-13. https://doi.org/10.17179/excli2017-329

More Citation Formats

Issue

Vol 17 (2018)

Section

Original articles

This work is licensed under a Creative Commons Attribution 4.0 International License.

Authors who publish in this journal agree to the following terms:

- The authors keep the copyright and grant the journal the right of first publication under the terms of the Creative Commons Attribution license, CC BY 4.0. This licencse permits unrestricted use, distribution and reproduction in any medium, provided that the original work is properly cited.
- The use of general descriptive names, trade names, trademarks, and so forth in this publication, even if not specifically identified, does not imply that these names are not protected by the relevant laws and regulations.
- Because the advice and information in this journal are believed to be true and accurate at the time of publication, neither the authors, the editors, nor the publisher accept any legal responsibility for any errors or omissions presented in the publication. The publisher makes no guarantee, express or implied, with respect to the material contained herein.
- The authors can enter into additional contracts for the non-exclusive distribution of the journal's published version by citing the initial publication in this journal (e.g. publishing in an institutional repository or in a book).

Most read articles by the same author(s)

- Mohammad Hashemi, Batool Sharifi-Mood, Azam Rasouli, Shadi Aminia, Mohammad Naderi, Mohsen Taheri, Macrophage migration inhibitory factor -173 G/C polymorphism is associated with an increased risk of pulmonary tuberculosis in Zahedan, Southeast Iran , EXCLI Journal: Vol 14 (2015)

Powered by

LEIBNIZ RESEARCH CENTRE FOR WORKING ENVIRONMENT AND HUMAN FACTORS

Make a Submission

USER

Username

Password

Remember me

Login

JOURNAL CONTENT

Search

Search Scope

All

Search

BROWSE

- By Issue
- By Author

EXCLI Journal has been added to

- Directory of Open Access Journals (DOAJ)
- Electronic Journals Library (EZB)
- Web of Science
- SCOPUS
- Pubmed Central
- Pubmed
- EBSCO Academic Search
- SCImago
- LIVIVO
- BASE

Impact Factor

- *2013: 0.728*
- *2014: 0.857*
- *2015: 1.292*
- *2016: 1.462*
- *2017: 2.424*

EXCLI Journal is a platinum open access journal. There are neither fees for authors submitting their papers nor fees for readers accessing PDFs of the published papers.

Articles published in EXCLI Journal are licensed under a Creative Commons Attribution 4.0 International License.