Published online 2014 December 25.

Letter

## Association of Arg462Gln Polymorphism in RNASEL Gene With the Risk of Prostate CancerAmong Iranian Population

Roshni Roy<sup>1,\*</sup>; Bidyut Roy<sup>1</sup>

<sup>1</sup>Unit of Human Genetics, Indian Statistical Institute, Kolkata, India

\**Corresponding author*: Roshni Roy, Unit of Human Genetics, Indian Statistical Institute, 203, B.T. Road, Kolkata-700108, India. Tel: +91-3325753241, E-mail: roshniroy16@gmail.com **Received:** September 18, 2014; **Revised:** October 12, 2014; **Accepted:** October 14, 2014

Keywords: Prostate Cancer, Familial; 2-5A-Dependent Ribonuclease; Polymorphism, Genetic

## Dear Editor,

In the July issue of "Gene, Cell and Tissue", R462Q Mutation in Prostate Cancer Specimens 1 investigated the effect of Arg462Gln polymorphism in sporadic prostate cancer patients among Iranian population. The study samples comprised of formalin fixed paraffin embedded specimen obtained from 51 histopathologically confirmed specimens from patients with prostate cancer and 70 from control individuals with non-cancerous prostate (prostatitis, hyperplasia). RNASEL Arg462Gln or G1385A polymorphism analysis performed using ARMS (Amplification Refractory Mutation System) PCR with allele specific primers were used to detect single-base substitution. This was followed by the association analysis between RNASEL genotype and prostate cancer. The authors could not find any significant association between the polymorphism and risk of disease.

Few years back a worldwide epidemiological survey on prostate cancer revealed that it is the third leading causes of death in developed countries such as United States and emphasized that it is becoming a growing health concern in the developing nations as well 2. Like any other complex neoplastic disorder both genetic and non genetic factors interact in its development and progression 3. Age, ethnic background and family history are the three main epidemiological risk factors for this disease out of which family history is the strongest contributor. Based on family history, prostate cancer can be classified into sporadic, familial and hereditary. Hereditary predispositions are guite rare and contribute to less than 5% of the cases while familial cases account for 10-20% of cases. The rest are sporadic cases with typically only one person in their family who were diagnosed with the disease 4.

Numerous studies have been conducted to identify the prostate cancer susceptibility genes using linkage analysis. Smith et al. identified the first susceptibility locus, designated as HPC1, which mapped to the long arm of chromo-

some 1 (1q24-25) (5), few years later, Carpten et al. reported RNASEL gene as one of the candidate for HPC1 (6). RNASEL is an endonuclease involving in apoptotic and antiviral activities of interferons. Along with truncating mutations in this gene, several missense variants were reported by Rokman et al. by screening the entire coding sequence of RNASEL using Single-strand conformation polymorphism (SSCP) (7). The Arg462Gln variant has a significant role in hereditary prostate cancer as the variant has three times less enzymatic activity compared to the wild genotype (8). They also reported that heterozygous individuals had double the risk of prostate cancer compared to the noncarrier cases with hereditary prostate cancer, but at the same time various studies did not find any association between sporadic prostate cancer and this variation in Caucasian and African American population (8,9).

The statistical analysis has been limited to unadjusted risk calculation. The risk calculation after adjustment to the age and clinical parameters would be a better approach. The control DNA was taken from hyperplastic prostate tissue so this tissue may not represent as a proper control sample. It is better to use DNA samples obtained from healthy individuals as the healthy control. Moreover the sample size is very small for any association study thus; a larger sample size is certainly warranted in future. Sometimes, ARMS PCR may produce incorrect genotypes, especially in homozygotes, so, it is better to recheck the genotypes by alternate sequencing methods. The authors did not find any association between Arg-462Gln polymorphism and the risk of sporadic prostate cancer. Despite the limitations, this study is important as it may be first of its kind among Iranian population.

## **Authors' Contributions**

Roshni Roy: interpretation of data and drafting of the manuscript; Bidyut Roy: critical revision of the manuscript for important intellectual content.

Copyright @ 2015, Zahedan University of Medical Sciences. This is an open-access article distributed under the terms of the Creative Commons Attribution-Non-Commercial 4.0 International License (http://creativecommons.org/licenses/by-nc/4.0/) which permits copy and redistribute the material just in noncommercial usages, provided the original work is properly cited.

## References

- Muendlein A, Lang AH. R462Q Mutation in Prostate Cancer Specimens. Gene Cell Tissue. 2014;1(3).
- Haas GP, Delongchamps N, Brawley OW, Wang CY, de la Roza G. The worldwide epidemiology of prostate cancer: perspectives from autopsy studies. *Can J Urol.* 2008;15(1):3866–71.
- Lessick M, Katz A. A genetics perspective on prostate cancer. Urol Nurs. 2006;26(6):454–60.
- Ostrander EA, Markianos K, Stanford JL. Finding prostate cancer susceptibility genes. Annu Rev Genomics Hum Genet. 2004;5:151–75.
- Smith JR, Freije D, Carpten JD, Gronberg H, Xu J, Isaacs SD, et al. Major susceptibility locus for prostate cancer on chromosome 1 suggested by a genome-wide search. *Science*. 1996;274(5291):1371-4.
- 6. Carpten J, Nupponen N, Isaacs S, Sood R, Robbins C, Xu J, et al. Germline mutations in the ribonuclease L gene in families showing linkage with HPC1. *Nat Genet.* 2002;**30**(2):181–4.
- Rokman A, Ikonen T, Seppala EH, Nupponen N, Autio V, Mononen N, et al. Germline alterations of the RNASEL gene, a candidate HPC1 gene at 1q25, in patients and families with prostate cancer. *Am J Hum Genet.* 2002;**70**(5):1299–304.
- Casey G, Neville PJ, Plummer SJ, Xiang Y, Krumroy LM, Klein EA, et al. RNASEL Arg462Gln variant is implicated in up to 13% of prostate cancer cases. *Nat Genet.* 2002;**32**(4):581–3.
- Robbins CM, Hernandez W, Ahaghotu C, Bennett J, Hoke G, Mason T, et al. Association of HPC2/ELAC2 and RNASEL non-synonymous variants with prostate cancer risk in African American familial and sporadic cases. *Prostate*. 2008;68(16):1790–7.