

Bioinformatic Evaluations for Locating the microRNA Suppressing PI3K/AKT Pathway and Analysis in Prostate Cancer Cell Lines

Seyed Hamid Aghaee-Bakhtiari¹, Ehsan Arefian^{2,3}, Masoud Soleimani⁴, Siamak Mirab Samiee⁵, Farshid Noorbakhsh⁶, Reza Mahdian^{7*}, Pezhman Fard-Esfahani^{8**}

- 1- PhD Candidate, Department of Molecular Medicine, Biotechnology Research Center, Pasteur Institute of Iran, Tehran, Iran
- 2- Assistant Professor, Department of Microbiology, School of Biology, College of Science, University of Tehran, Tehran, Iran
- 3- Researcher, Department of Molecular Biology and Genetic Engineering, Stem Cell Technology Research Center, Tehran, Iran
- 4- Associate Professor, Department of Hematology, Faculty of Medical Sciences, Tarbiat Modares University, Tehran, Iran
- 5- Assistant Professor, Food and Drug Laboratory Research Center, Ministry of Health and Medical Education, Tehran, Iran
- 6- Assistant Professor, Department of Immunology, Faculty of Medicine, Tehran University of Medical Sciences, Tehran, Iran
- 7- Assistant Professor, Department of Molecular Medicine, Biotechnology Research Center, Pasteur Institute of Iran, Tehran, Iran
- 8- Assistant Professor, Department of Biochemistry, Pasteur Institute of Iran, Tehran, Iran

*Corresponding Address: P.O.Code: 1316943551, Department of Molecular Medicine, Biotechnology Research Center, Pasteur Institute of Iran, Tehran, Iran
Email: mahdian@pasteur.ac.ir

** Corresponding Address: P.O.Code: 1316943551, Department of Biochemistry, Pasteur Institute of Iran, Tehran, Iran
Email: fard-esfahani@pasteur.ac.ir

Received: 25/Jun/2014, Accepted: 05/Nov/2014

Abstract

Objective: Prostate cancer is the fifth most common cancer. In 2012, it was the second leading cause of cancer death for men worldwide. The PI3K/AKT pathway plays an essential role in pathogenesis of prostate cancer; the key role of this pathway in cancer progression makes it an attractive target for prostate cancer therapy. MicroRNAs (miRNAs) that regulate gene expression have a special ability to simultaneously control multiple genes and pathways which make them candidates for therapeutics. This study aims to determine miRNAs which target the PI3K/AKT pathway and evaluate them in prostate cancer cell lines.

Methods: In order to determine an effective miRNA for the PI3K/AKT pathway, we assessed six genes from this pathway which have been proposed as drug targets in ten different prediction algorithms. Next, the candidate miRNAs were analyzed in expression profile and pathway analysis databases. Expression of candidate miRNAs in control and prostate cancer cell lines were subsequently evaluated.

Results: According to bioinformatics, the miR-29 family could target the most genes from this list. Other bioinformatic estimates confirmed these results. The miR-29 family showed significant downregulation in prostate cancer cell lines LNCAP, PC3 and DU-145 compared to control samples.

Conclusion: These results propose the possibility of using the miR-29 family to inhibit the PI3K/AKT pathway in prostate cancer.

Keywords: Prostate Cancer, PI3K/AKT Pathway, Bioinformatics Prediction, miR-29 Family

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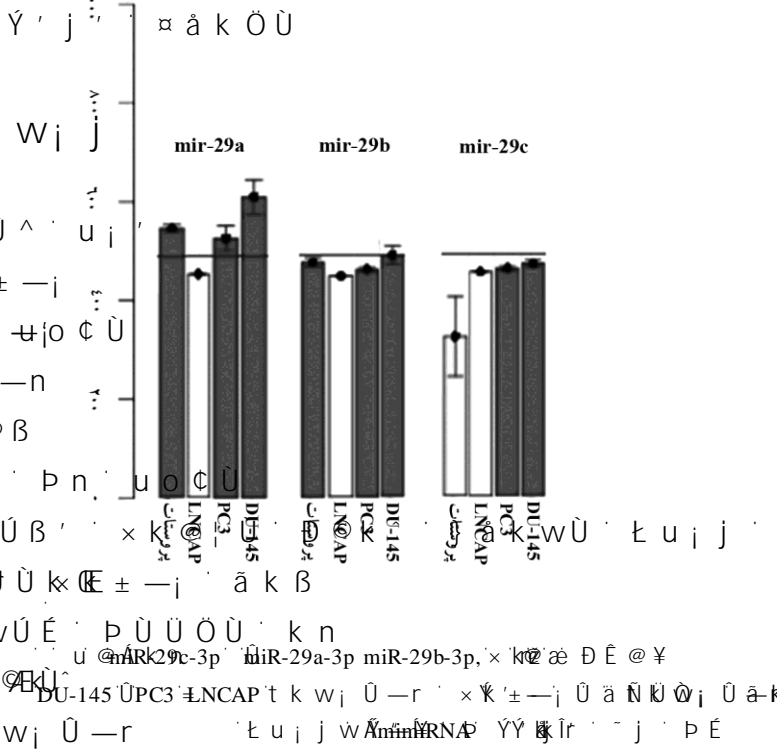
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Real Time qPCR miRNA



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