Review Article

Identification and Discovery of Novel microRNAs in the Human Genome

Sadat Dokanehiifard[1], Bahram Mohammad Soltani[2*]

1- Ph.D. Candidate, Department of Molecular Genetics, Faculty of Biological Science, Tarbiat Modares University, Tehran, Iran
2- Assistant Professor, Department of Molecular Genetics, Faculty of Biological Science, Tarbiat Modares University, Tehran, Iran

**Corresponding Address: P.O.Code: 1411713116, Department of Molecular Genetics, Faculty of Biological Science, Tarbiat Modares University, Tehran, Iran*
Email: soltanib@modares.ac.ir

Received: 21/Jun/2014, Accepted: 05/Nov/2014

Abstract

Although more than 98% of the human genome is transcribed, most of these transcripts are not translated into proteins. Rather, they are considered as non-coding RNAs. MicroRNAs (miRNAs) are very short non-coding RNAs approximately 22 nucleotides in length which regulate many key processes of cells such as growth, proliferation, differentiation, cell cycle, apoptosis (programmed cell death) and metabolism. On the other hand, it is known that these small regulatory molecules are involved in many human diseases such as different cancers and cardiovascular disorders. Therefore, discovery and functional characterization of novel miRNAs is a prominent achievement. Low abundance and spatiotemporal expression of these mediator molecules make their discovery difficult by conventional methods. Therefore, bioinformatics software have been designed for the prediction of stem-loop structures capable of producing miRNA precursors in the human genome. On the other hand, there are several bioinformatics tools for prediction of miRNA target genes. Prediction of miRNA target genes helps to characterize the function of a miRNA. In this paper, we have reviewed some of the common efficient bioinformatics tools and experimental approaches used for prediction and identification of the miRNA genes and their target genes.

Keywords:miRNA, miRNA target genes, Bioinformatics

Modares Journal of Medical Sciences: *Pathobiology*, Vol. 18 (2015-2016), No. 1, Pages: 1-21

[illegible] miRNA [illegible]

[illegible]

[illegible]

[illegible]
Email: soltanib@modares.ac.ir

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

non coding [illegible] ncRNA [illegible] non-protein-coding RNA [illegible] functional [illegible] non-messenger-RNA [illegible] tRNA [illegible] snoRNA [illegible] ribosomal RNA [illegible] Transfer RNA [illegible] small interfering [illegible] small nucleolar RNA [illegible] lncRNA [illegible] interacting [illegible] piRNA [illegible] non coding RNA [illegible]

[illegible]

[illegible] *Caenorhabditis elegans* [illegible]

[illegible] www.mirbase.org [illegible]

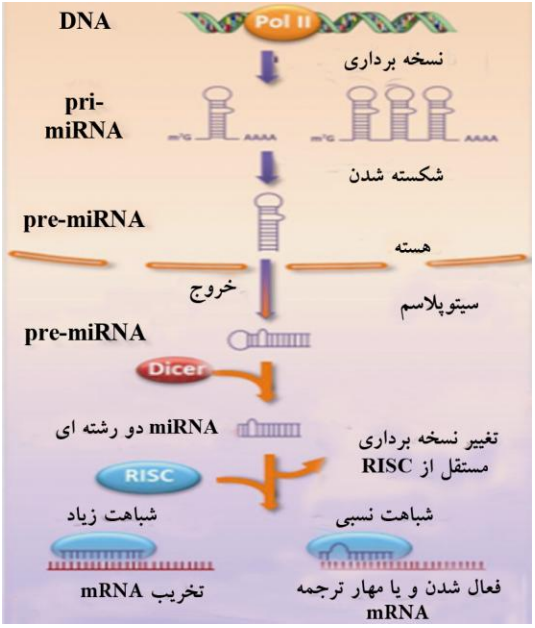
[illegible]

[illegible]

[

[illegible]

[illegible] Induced Silencing Complex (RISC) [illegible] miRNA [illegible] PhenomiR [illegible] http://mips.helmholtz-muenchen.de/phenomir/ [illegible] Human miRNA and Disease Database (HMDD) [illegible] http://202.38.126.151/hmdd/mirna/md/ [illegible]



[illegible]

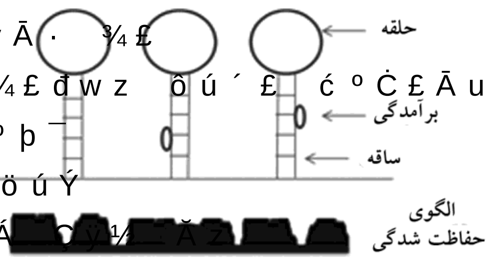
[illegible]

[illegible]

microRNA

miRNA

Positional Cloning



stem

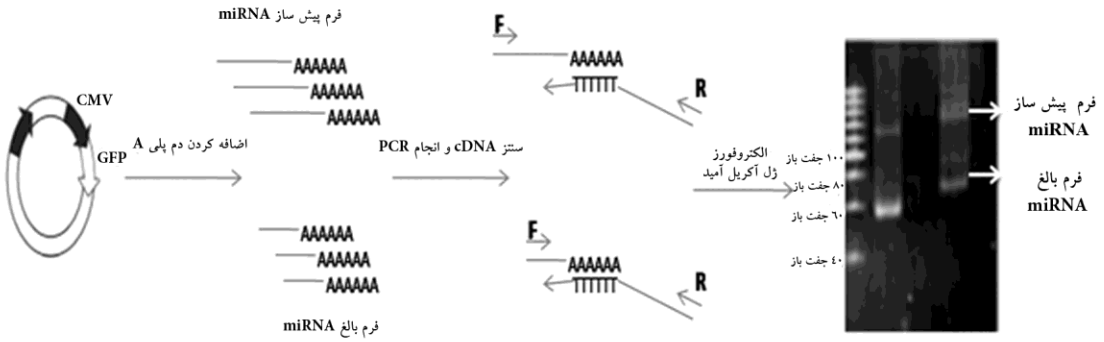
Bulge

Redundancy

Deep Sequencing

cDNA

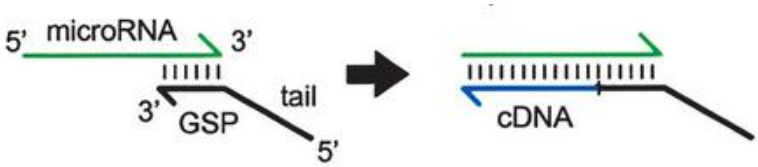
[illegible] ATP [illegible] Polyadenylate [illegible] Polymerase [illegible] Oligodeoxythymidine Primer [illegible] miRNA [illegible] Anchored [illegible] cDNA [illegible] Oligodeoxythymidine [illegible] PCR [illegible] Polyadenylate [illegible]



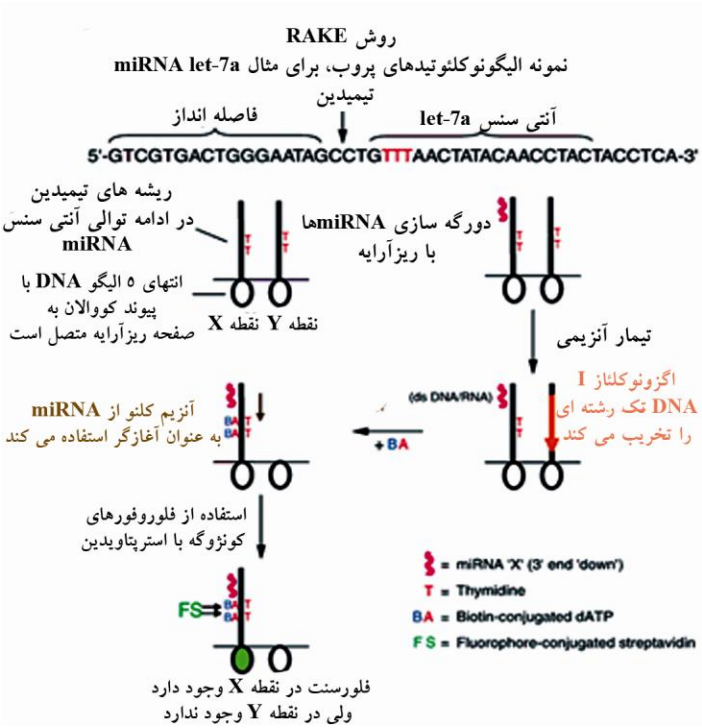
[illegible] PCR [illegible] miRNA [illegible]

[illegible] **Northern Blot** [illegible] miRNA [illegible]

[illegible] **Primer Extension** [illegible] **miRNA** [illegible] Probe [illegible] cDNA [illegible]



Gene Specific Primer: GSP



RNA-primed, Array-based Klenow Enzyme (RAKE)

miRNA

qRT-PCR

miRNA

Biotin-conjugated

Streptavidin

miRNA

In Situ

anti-miRs

Tough Decoy (TuD) miRNA sponges antagomiRs

miRNA

[illegible] miRNA [illegible]

[illegible] miRNA [illegible]

[illegible] miRNA [illegible]

[illegible] miRNA [illegible]

[illegible] miRNA [illegible]

[illegible] miRNA [illegible]

[illegible] miRNA [illegible]

[illegible] high-throughput $HITS-CLIP [illegible]

sequencing of RNA isolated by crosslinking

photoactivatable- $PAR-CLIP immunoprecipitation

ribonucleoside-enhanced crosslinking and

Biotin tagged miRNA immunoprecipitation

[illegible] PCR [illegible]

[illegible] miRNA [illegible]

[illegible] miRNA [illegible]

[illegible] miRNA [illegible]

[illegible] miRNA [illegible]

[illegible] miRNA [illegible]

miRNA [illegible]

[illegible] miRNA [illegible]

[illegible] miRNA [illegible]

[illegible] miRNA [illegible]

[illegible] miRNA [illegible]

[illegible]

[illegible]

miRNA [illegible]

URL	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
http://mima.imbb.forth.gr/SSCprofiler.html	[illegible]	[illegible]	Hidden Markov Models (HMM)	[illegible]	[illegible]	SSC profiler	1
http://tagc.univ-mrs.fr/mireval/	2013	[illegible] miRBase [illegible]	triplet-SVM support vector machines (SVM)	[illegible]	[illegible]	MirEval 2.0	2
http://www.bioinf.seu.edu.cn/miRNA/	2007	[illegible]	random forest (RF)	[illegible]	[illegible]	MiPred	3
http://demo1.interagon.com/miRNA/cgi-bin/MicroprocessorSVM.cgi	[illegible]	[illegible]	support vector machine (SVM)	[illegible]	[illegible]	Microprocessor	/
http://mima.jnu.ac.in/cidmirna/	[illegible]	[illegible]	stochastic context free grammar	[illegible]	[illegible]	CID-miRNA	0

[illegible] **SSC profiler** [illegible] miRNA [illegible] (http://mima.imbb.forth.gr/SSCprofiler.html)