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miRNA Database: A database on miRNA expressions in cell lines

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Abstract

miRNAs are small non-coding RNA molecules which regulate the gene expression at translational and post-transcriptional level by targeting mRNA. In today's world miRNA have enormous role in various functions which involves vertebrates, invertebrates, plants and viruses etc., to know the importance of each miRNA candidates in human and mice, we designed this database called as miRNA Database, which integrate the data from various sources and explain functions of each miRNA candidate and their expressions in cell lines. Currently miRNA Database gives the information of 100 miRNA lists and expression in different cell types. Future approach: We are going to incorporate some of the remaining miRNAs and also update the existing miRNAs list.

Availability: http://162.144.119.64/database/

Keywords*:* miRNA; HTML; database

1. Introduction

In 1993, MicroRNAs were first discoved by Victor Ambros, in *Caenorhabditis elegans*. MicroRNAs (miRNAs) are small, non-coding single-stranded endogenous RNA molecules approximately 22-25 nucleotides in length, which regulate the gene expression at post-transcriptional levels. miRNA form complementary binding region to target mRNA at the 3' untranslated region (UTR) that inhibit the gene expression by cleavage or translational repression[1,2]. In general, miRNA play an important role in numerous kinds of cells including stem cells[3], also involved in proliferation, apoptosis, cell differentiation, signaling cascade and in various cancers[4,5] etc.,

The main strategy of this database is mainly to help for research purposes, this database contain a list of 100 miRNAs, each miRNA list have a collection of sufficient literature data that explain the expression of miRNA in cell lines of different types of cell. The research in miRNA is fast moving in today's world. This database will provide a platform for some of the R&D organizations to interconnect each miRNA in the form of network; it might be used for discovery of drugs to cure some of the incurable diseases by using small RNA.

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2. Methods

2.1 Data Collection:

The database was constructed by writing script in HTML and php following the method of Usha et al.[6]. This database contains home page, list of miRNA candidates, download request, publication and contact, which can be accessed at http://162.144.119.64/database/. Data were collected from various literature sources such as PubMed (http://www.ncbi.nlm.nih.gov/pubmed/), Science Direct (http://www.sciencedirect.com/), knimbus(http://www.knimbus.com/), Google scholar (http://scholar.google.co.in/), Mary Ann Liebert (http://www.liebertpub.com/), Ingenta Connect (http://www.ingentaconnect.com/), Bentham Publishers (http://benthamscience.com/), Scribd (http://www.scribd.com/) etc., the main keywords were used to select the required articles in all the above literature sources and searched repeatedly with the same keywords but with an additional keyword source to pull maximum literature articles. The resulted data searches were downloaded. Further each miRNA article are reviewed twice by pulling the information of miRNA expression with the following headlines: titles of the article, abstract, organism name, miRNA name, target mRNA, cell line, cell type, Type of Interaction, Effect of miRNA, PubMed ID etc., the tabulation contains all this information. For each miRNA the above data is tabulated and stored in Microsoft Excel. This data is available for the public for research purposes.

The complete list of miRNAs can be found at https://www.karnataka.gov.in/bangaloreuniversity/mirnadatabase/Download.html. A snapshot of the database is given in Fig I. These miRNA databases give the basic idea of expression of each miRNA which can be further used for the discovery of the drug for the treatment of various diseases.

2.2 Description of the evidence

100 miRNAs are considered in the preparation of this Database, for which more than 3000 articles were searched and gathered all the information of each articles from different sources of literature to cover maximum available data of each miRNA. The published articles from different sources of literatures were downloaded and stored, individual articles are reviewed, then pulled out important points and tabulated. Each and every miRNA data were tabulated and is available in our database. There are several databases existing but this is the first database which curates the information of individual miRNA expression in different cell types. Further, we are planning to upload some of the remaining miRNAs.

2.3 Utility:

miRNA database is available for research purpose to know the function of each miRNAs involvement in gene regulation and also provids a quick review of all the literature curated data of individual miRNA from various journals. By using this database, the molecular signaling networks of diabetes nephropathy was found that some of the miRNAs have a role in controlling the regulation to prevent diseases[7], and also found the regulatory network of miRNA-125 in causing leukemia[8]. The molecular signaling pathways of miRNA could play a role as a biomarker to prevent the incorrect regulation of genes. It is also useful to cure the diseases by identifying regulation of miRNA in various pathways, further it gives the clue for future research development.

2.4 Future development:

Today miRNA expression is recognized as an important function in several biological processes. miRNAs which have a role in different regulatory network will be incorporated. Continuous updates of remaining miRNAs from recent published articles will be carried out.

3. Acknowledgement

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***Conflict of interest*:** The author's declares none.

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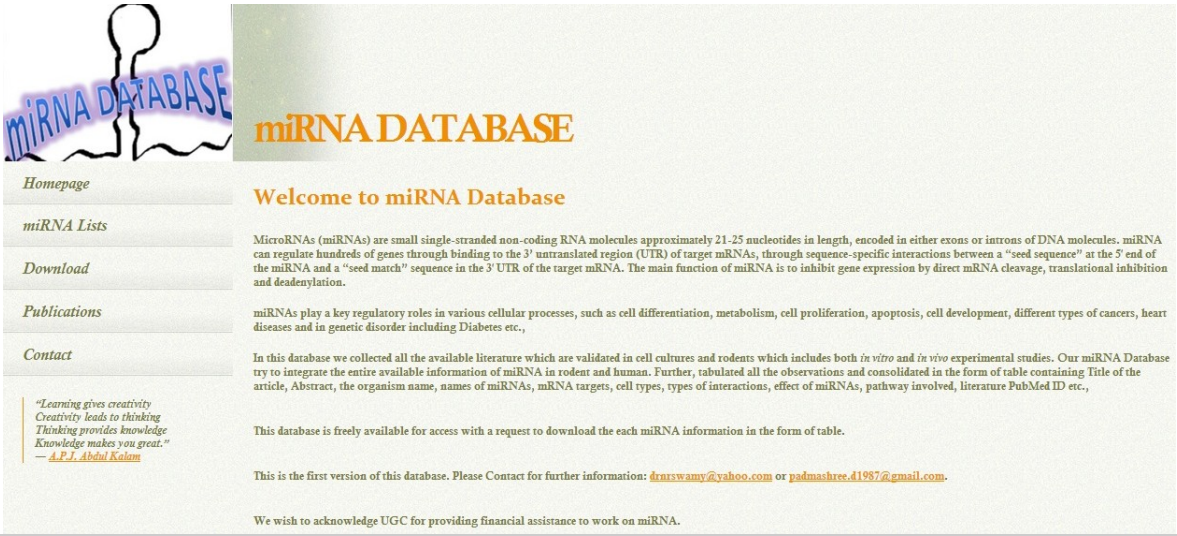

Figure I: Snapshot of miRNA homepage