

Poster presentation

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MicroRNA sequence and expression database

Koray Dogan Kaya*¹, Gokhan Karakulah², Cengiz Yakicier¹ and Ozlen Konu¹

Address: ¹Department of Molecular Biology and Genetics, Bilkent University, Ankara, Turkey and ²Department of Medical Informatics, Institute of Health Sciences, Dokuz Eylul University, Izmir, Turkey

Email: Koray Dogan Kaya* - kkaya@bilkent.edu.tr

* Corresponding author

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Background

MicroRNAs, which are small ribonucleic acids that bind to 3'UTR regions of mRNAs by base complementation, play crucial roles in regulation of development and differentiation [1]. Herein we report on development of a web interfaced database, *Bilkent University miRNA Sequence and Expression database* [Figure 1; <http://139.179.97.62/~koray>] that integrates the species-specific mature miRNA sequence information and a set of associated public

microarray data as tabular and graphical summaries supplemented with statistical analyses <http://www.bioconductor.org>. The database also makes use of GO annotation data of miRNAs targets to determine the significance of GO term enrichment in a subset of miRNAs.

Data and methods

Bilkent University miRNA sequence and expression database was constructed using Mysql version 14.7 on Suse

Bilkent University

miRNA sequence and expression database

This database is constructed for observing the miRNA functions from the systems point of view. The database is comprising human, zebrafish, *C. elegans* and mouse mature miRNA data. Current combines mature miRNA dinucleotide properties to the public miRNA expression data and it links this relation to ontology data of their targets. The dinucleotide frequencies may reflect the genomic position function. After the selection of a dataset you may choose the set of miRNAs that bear the selected dinucleotide or the reverse set, or you may choose a completely different set by manual checkboxes. Submission of this job will give the mean expression values as a graph for the conditions defined by the selected dataset. You may then retrieve ontology data related to the targets which statistically significant ontology terms. Or you can just deal with ontology of the targets just by selecting an absent dinucleotide and an organism from sequence properties section.

Sequence Properties :

None Select the absent dinucleotide in region nucleotides 2-7 other than 2-7 full sequence
Select the organism(s) Human Zebrafish Mouse C. elegans

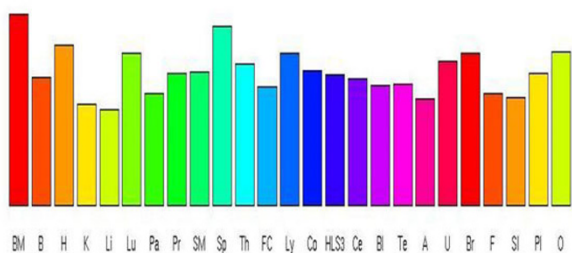
Sequence Properties : Dinucleotide Abundance Tables

Select the organism(s) Human Zebrafish Mouse C. elegans

miRNA Microarray Data Analysis

Figure 1

The interface of miRNA sequence and expression database.



Annotation	Repetition Number
ous system development	2
lopment	2
ulation of transcription, DNA-dependent"	2
apoptosis	2
ral immune response	2
tive regulation of cell proliferation	2
lation of apoptosis	2
lation of progression through cell cycle	2
use of cytochrome c from mitochondria	2
lation of transcription from RNA polymerase II promoter	1

Annotation	p Value
ous system development	0.07191535
lopment	0.07191535
ulation of transcription, DNA-dependent"	0.2750636
apoptosis	0.009287366
ral immune response	0.001299214
tive regulation of cell proliferation	0.01126062
lation of apoptosis	0.004439473

Figure 2

Left: Bar graph of microarray expression data for Hsa-mir-15a and Hsa-mir-16. Right: miRNA target GO annotation distribution and significantly enriched GO terms reported. One of the annotated targets were found to be BCL-2, a well known anti-apoptotic protein [5].

Linux 10.0 server; the web interface implemented in HTML 4.0 combined with PHP version 4.4.0. Statistical calculations were performed using R package version 2.2.1. miRNA mature sequences from *Homo sapiens*, *Mus musculus*, *Danio rerio* and *Caenorhabditis elegans* were downloaded from miRBase of Sanger Institute database <http://microrna.sanger.ac.uk/> version 8.2. Two independent microarray data sets [3,4] were associated with human and mouse miRNA dinucleotide motif frequency, respectively. Human miRNA targets were extracted from Argonaute Database of Heidelberg <http://www.ma.uni-heidelberg.de/apps/zmf/argonaute/interface/>. GO ontology data were linked with Argonaute gene symbols and alias data from Entrez Gene Database <http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?DB=gene>.

Results and conclusions

The database allows for selection of miRNAs based on their dinucleotide properties and reports expression pattern of this particular set of sequences (Figure 2).

High expression of hsa-mir-15a and hsa-mir-16, known to be deleted in chronic lymphocytic leukemia, was detected in bone marrow and spleen (Figure 2a). Analysis of these miRNAs in terms of their targets resulted in significant representation of antiapoptosis and humoral immune response GO terms, both attributable to BCL-2 (Figure 2b). Although BCL2 is well known for its role in cell survival, there is no known direct relation of BCL-2 with immune response. Future studies involve integration of multiple species-specific gene expression data sets and implementation of correspondence analysis tools for multivariate analysis of sequence and expression data. The presented database will help understand miRNAs in a sys-

tems biology context via integration of the sequence, expression, and functional attributes.

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