BMC Systems Biology

Poster presentation

MicroRNA sequence and expression database

Koray Dogan Kaya*[1], Gokhan Karakulah[2], Cengiz Yakicier[1] and Ozlen Konu[1]

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

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

* Corresponding author

from BioSysBio 2007: Systems Biology, Bioinformatics and Synthetic Biology
Manchester, UK. 11–13 January 2007

Published: 8 May 2007

BMC Systems Biology 2007, **1**(Suppl 1):P29 doi:10.1186/1752-0509-1-S1-P29

This abstract is available from: http://www.biomedcentral.com/1752-0509/1?issue=S1

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 suplemented 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

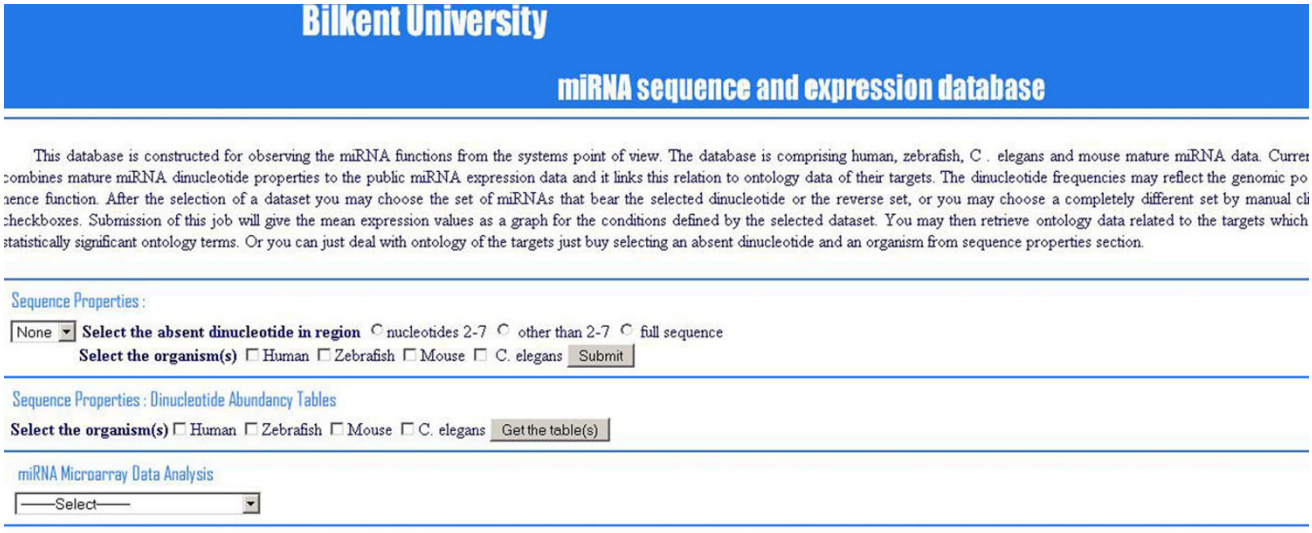
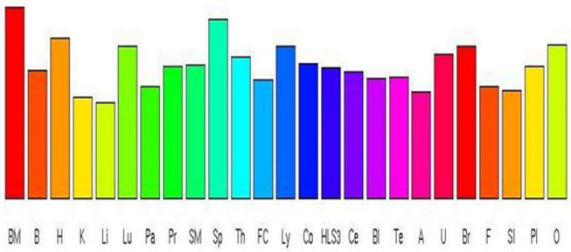


Figure 1
The interface of miRNA sequence and expression database.



Annotation	Repetition Number
ous system development	2
lopment	2
ulation of transcription, DNA-dependent"	2
apoptosis	2
oral immune response	2
tive regulation of cell proliferation	2
lation of apoptosis	2
lation of progression through cell cycle	2
se 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
oral 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 Heildelberg http://www.ma.uni-heidelberg.de/apps/zmf/argonaute/interface/. GO ontology data were linked with Argaonaute 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 systems biology context via integration of the sequence, expression, and functional attributes.

References

1. Bartel DP: **MicroRNAs: genomics, biogenesis, mechanism and function.** *Cell* 2004, **116:**281-297.
2. Koray DK: **Evaluation of microRNA sequence composition and expression.** In *M.Sc. thesis of Bilkent University Molecular Biology and Genetics Department, Ankara, Turkey*; 2005.
3. Baskerville S, Bartel DP: **Microarray profiling of microRNAs reveals frequent coexpression with neighboring miRNAs and host genes.** *RNA* 2005, **11(3):**241-7.
4. Thomson JM, Parker J, Perou CM, Hammond SM: **A custom microarray platform for analysis of microRNA gene expression.** *Nat Methods* 2004, **1(1):**47-53.
5. Carney DA, Wierda WG: **Genetics and molecular biology of chronic lymphocytic leukaemia.** *Curr Treat Options Oncol* 2005, **6(3):**215-25.