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IntmiR: a complete catalogue of intronic miRNAs of human and mouse

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Abstract:
IntmiR is a manually curated database of published intronic miRNAs of Human and Mouse genome. Each entry in the database, aims at providing a complete resource of intronic miRNA with their target gene and deregulation in various diseases with related tissues and pathways. The current release contains 426 intronic miRNA loci from human and 76 from mouse, expressing distinct target mRNA sequences. Database gives information on an intronic miRNA-disease relationship, including miRNA ID, pathaway connected and related tissues. All entries can be retrieved by miRNA ID or target gene. *IntmiR* is freely available at rgcb.res.in/intmir.

Keywords: MicroRNA, intronic miRNAs, Database Organization

Availability: rgcb.res.in/intmir.

Background:
MicroRNA (miRNA) is a short (about 21 to 23 nucleotides) single stranded RNA molecule that playing an important role in gene regulation **[1].** Thousands of miRNAs have been identified in nematodes, insects, birds, amphibians, fishes, plants, mammals, and even viruses using molecular cloning and bioinformatics prediction **[2].** MicroRNAs have been implicated in processes and pathways such as development, cell proliferation, apoptosis, metabolism and morphogenesis, and in diseases including cancer **[3].**

Intronic microRNA is a class of miRNAs belongs to intronic regions of protein-coding genes. About 50% of these intronic miRNAs reside in introns whose length is longer than 5,000 bps **[4].** It is likely that intronic miRNAs can have their own independently regulated transcription units, which can be regulated by RNA polymerase II (Pol II) or RNA polymerase III (Pol III). It was recently demonstrated that RNA Pol III could transcribe human miRNAs through associated repetitive elements **[5].** Although the intronic miRNAs and their host genes could be regulated independently, it is possible that intronic miRNA can still down-regulate its own host protein-coding gene by targeting the untranslated region (UTR) of the host gene **[6].** Another biological implication is that intronic miRNAs could play an important role as negative feedback regulators.

IntmiR contains a database of published intronic miRNAs which enables to retrieve necessary information regarding miRNAs. The database has provides intronic miRNA sequence data, references and links to other resources for all published miRNAs **[7].** It currently links the intronic miRNAs to their targets, corresponding pathways with each target, associated diseases and related tissues **[8, 9, 10].** The pathway maps depict molecular relationships from areas of active research. Towards this end '*IntmiR*'- provides a comprehensive package of information associated with intronic miRNAs.

Database Organization:
IntmiR provides a simple search and retrieval interface and database search can be by the intronic miRNA or its sequence. It provides all the target genes (symbol and name) corresponding to the intronic miRNA or sequence and also the pathways associated with each target gene if any. It also retrieves all the intronic miRNAs and associated pathways given a target gene if any intronic miRNA corresponds to that gene. It also accepts intronic miRNA or its sequence and retrieves all the diseases and tissues associated along with the corresponding Pubmed ID **(Figure 1).** There is also facility to submit new additions which are added after validation and approval. *IntmiR* thus provides an open access platform which enables an easy and comprehensive retrieval of all the necessary information about intronic miRNAs and aims to help strengthen the bridge between database developers, curators, and users **(Figure 2).**

Architecture of IntmiR:
IntmiR has a MySQL relational database as the back-end. The Web pages are dynamically generated by the PHP scripts hosted on Apache server. Along with PHP scripts, JavaScript and AJAX was also used to facilitate continuous site navigation, efficiency and validations. *IntmiR* can be accessed by the users from a standard web browser on any operating system. The complete database used to construct *IntmiR* can be downloaded as a flat file or in the Microsoft excel format and *IntmiR* also provides researchers to upload data on new intronic miRNA observed in human and mouse.

Conclusion:
IntmiR provides a user-friendly interface, a convenient search option, allowing efficient recovery of sequence, regulatory target genes, related diseases and pathways and other information. We hope *IntmiR* provides the first comprehensive view of intronic miRNAs and associated regulons in Human and Mouse.

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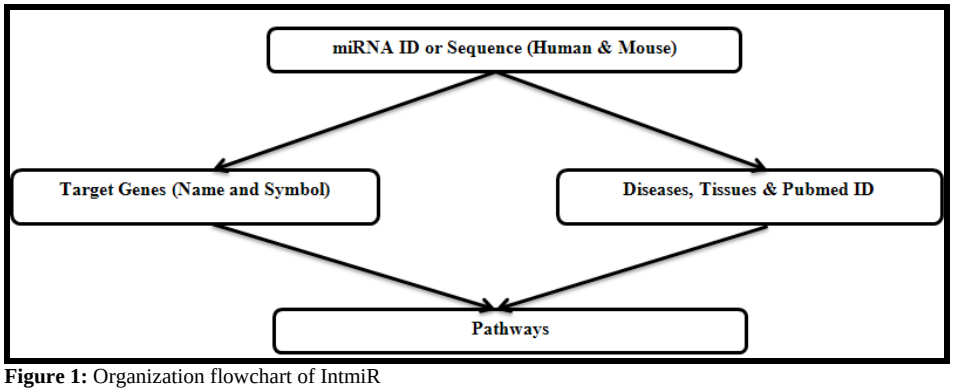

Figure 1: Organization flowchart of IntmiR

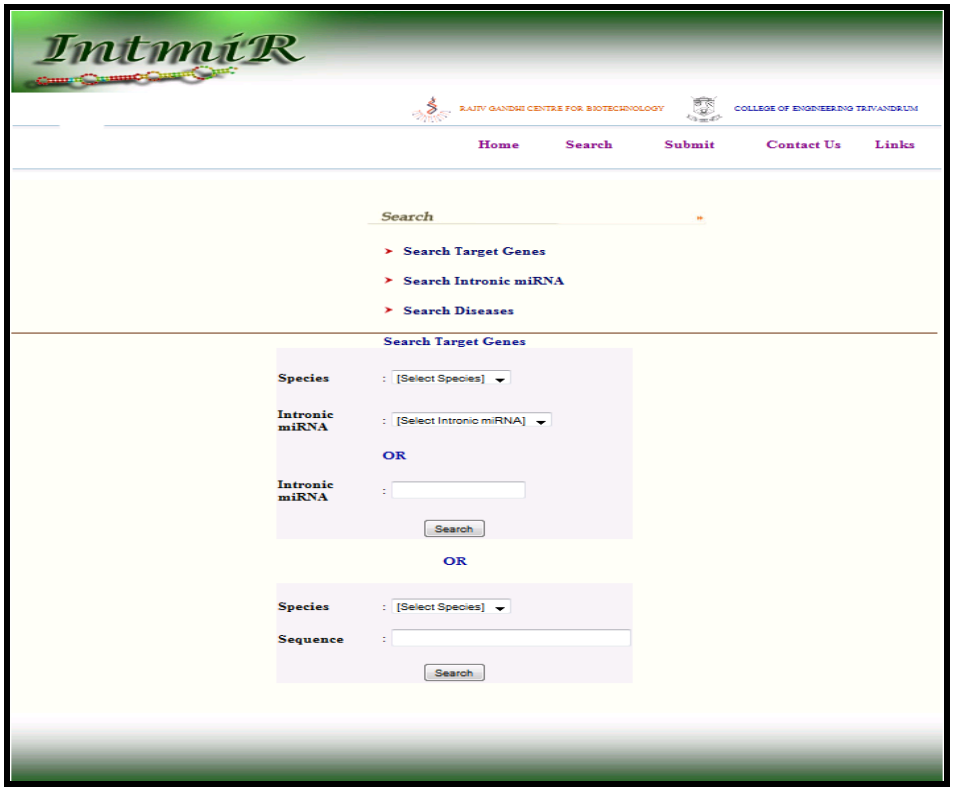

Figure 2: Screen capture of IntmiR showing search option

Future Developments:

The *IntmiR* is being constantly developed and supplemented with new experimental data from the available literature sources. We are planning to update the database annually. Concurrently, its integration with the existing databases and its search capabilities are being constantly improved.

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