MiRProvide: a comprehensive database of predicted and validated microRNA-target interactions

Mohammad Hasan Jafari Najaf Abadi [a], Seyed Hamid Aghaee Bakhtiari[a,b *]
a Mashhad University of Medical Sciences, Faculty of Medicine, Department of Medical Biotechnology, Mashhad, Razavi Khorasan, Iran
b Mashhad University of Medical Sciences, Biotechnology Research Center, Mashhad, Razavi Khorasan, Iran
*aghaeibh@mums.ac.ir

Abstract: MicroRNAs are a class of non-coding RNAs that control numerous genes by targeting their mRNAs. Experimental validation is the gold standard method for finding gene targets. Considering the difficulties of experimental biological validation, it is essential to develop computational methods that can identify and prioritize potential miRNA targets. The main problem of these algorithms is high rate of false positives. On this basis, there are muitiple databases that integrate the results of different prediction algorithms as well as laboratory confirmed results. However, the need to improve the performance of these databases is completely sensed due to some problems and shortcomings. Some problems of these databases are outdated algorithms, absence of a user-friendly interface, the low number of prediction algorithms and validated databases, and lack of appropriate filters on the result page to achieve desired results. The miRProvide (miRNA Prediction and Validation Database) is developed to address these issues. miRProvide classifies the results into four tabs of information, predict, validate and combine and uses the latest version of miRNA target prediction algorithms. For the first time, this database has collected most of the validated data from the relevant databases including miRecords, miRTarBase and miR2Disease. The miRProvide interface is in accordance with researchers requirements and is completely user-friendly. Users can perform their search by any number of miRNA or gene and selection of desired prediction algorithms and validated method type. The information tab provides the appropriate statistics of the results and therefore users in each of four tabs can drag and drop each column of the result table to group the results according to that column. This grouping does not has any limitation and the user can classify according to another parameter, while in other databases, users should manually check the large numbers of results. In validation tab, users can visit the results of all validated databases together and there is a papers column that provide the number of articles which report the relationship between a specific mir and gene. Moreover, there is a module that user can fill any number of mir and gene to view the existing mir-gene links as graphs. Also in this module in order to achieve better results, due to the complexity of communication, there are filters that can filter the results based on numbers of supporting databases and articles for each mir-gene link. Bestmir is another miRProvide useful module that researchers can use it to obtain best miRNA that targets several genes simultaneously.

Keywords: microRNA; target prediction; mir-gene links; validated database; prediction database

References

[1] Thomson, D. W., Bracken, C. P., & Goodall, G. J. (2011). Experimental strategies for microRNA target identification. Nucleic acids research, 39(16), 6845-6853.
[2] Li, L., Xu, J., Yang, D., Tan, X., & Wang, H. (2010). Computational approaches for microRNA studies: a review. *Mammalian Genome*, *21*(1-2), 1-12.
[3] Dweep, H., Gretz, N., & Sticht, C. (2014). miRWalk database for miRNA–target interactions. *RNA Mapping: Methods and Protocols*, 289-305.