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LETTER

ncRNA2MetS v2.0: a manually curated database for metabolic syndrome-associated ncRNAs

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1 Introduction

Metabolic syndrome (MetS) and its five characteristic diseases (central obesity, type 2 diabetes, hypertension, hypertriglyceridemia, reduced high-density lipoprotein cholesterol) pose a serious threat to human health [1]. A large number of studies have demonstrated that non-coding RNAs (ncRNAs) are instrumental in the pathogenesis of diseases related to metabolic syndrome [2]. Therefore, there is an urgent need to develop a database for storing MetS-associated ncRNAs. In recent years, scholars have established several metabolic diseases-associated biomolecules databases [3,4], but they are not specifically used for storing MetS-associated ncRNAs and lack the latest data. To provide the most comprehensive MetS-associated ncRNA data, we constructed the ncRNA2MetS v2.0 database. We hope that it can facilitate researchers to study on mechanism of ncRNA in metabolic syndrome.

2 Materials and methods

The goal of the ncRNA2MetS v2.0 is to collate and integrate ncRNAs (microRNAs, lncRNAs, and circRNAs) associated with metabolic syndrome and its characteristic diseases. The data comes from relevant literature published as of August 2024. Firstly, we used “miRNA”, “microRNA”, “lncRNA”, “long non-coding RNA”, “circRNA”, “circular RNA”, “non-coding RNA”, or “ncRNA” and “metabolic syndrome” or its five characteristic diseases as keywords to query the PubMed database by the title/abstract search strategy. Consequently, over 4000 articles published since 2007 were obtained. After manual screening, only 2750 articles that truly focused on MetS-associated ncRNAs were retained. Secondly, we read each article in detail and extracted the MetS-associated ncRNA information within it. These information includes the name, identifier and category of ncRNA, the name, identifier and ICD-11 classification of disease, species, tissues, verification methods, expression pattern, the name of gene regulated by ncRNA, the reference article, and a succinct description of the association in the reference article. Throughout this procedure, we exclusively collected MetS-associated ncRNA information that had been verified by various biological experiments. To guarantee the authenticity and reliability of each association, all data has been checked and confirmed by three researchers. As a result, 1505 associations between metabolic syndrome and its five characteristic diseases and three types of ncRNAs were included in the ncRNA2MetS v2.0 database, involving six species.

3 Database interface

The ncRNA2MetS v2.0 database provides useful resources for researchers to explore the mechanism of ncRNA in metabolic syndrome and its characteristic disease. For the convenience of users, we have developed a specialized website that provides users with a straightforward and friendly interface. This website consists of eight parts, including the HOME, BROWSE, SEARCH, SUBMIT, STATISTICS, INTERACTION NETWORK, DOWNLOAD, and HELP page, as shown in Fig. 1. The website of biomed-bigdata.online is freely.

4 Conclusion

In this paper, we introduced a MetS-associated ncRNA database, ncRNA2MetS v2.0. It is anticipated that the database can promote the exploration of mechanism of ncRNAs in metabolic syndrome.

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Special Column—Code & Data

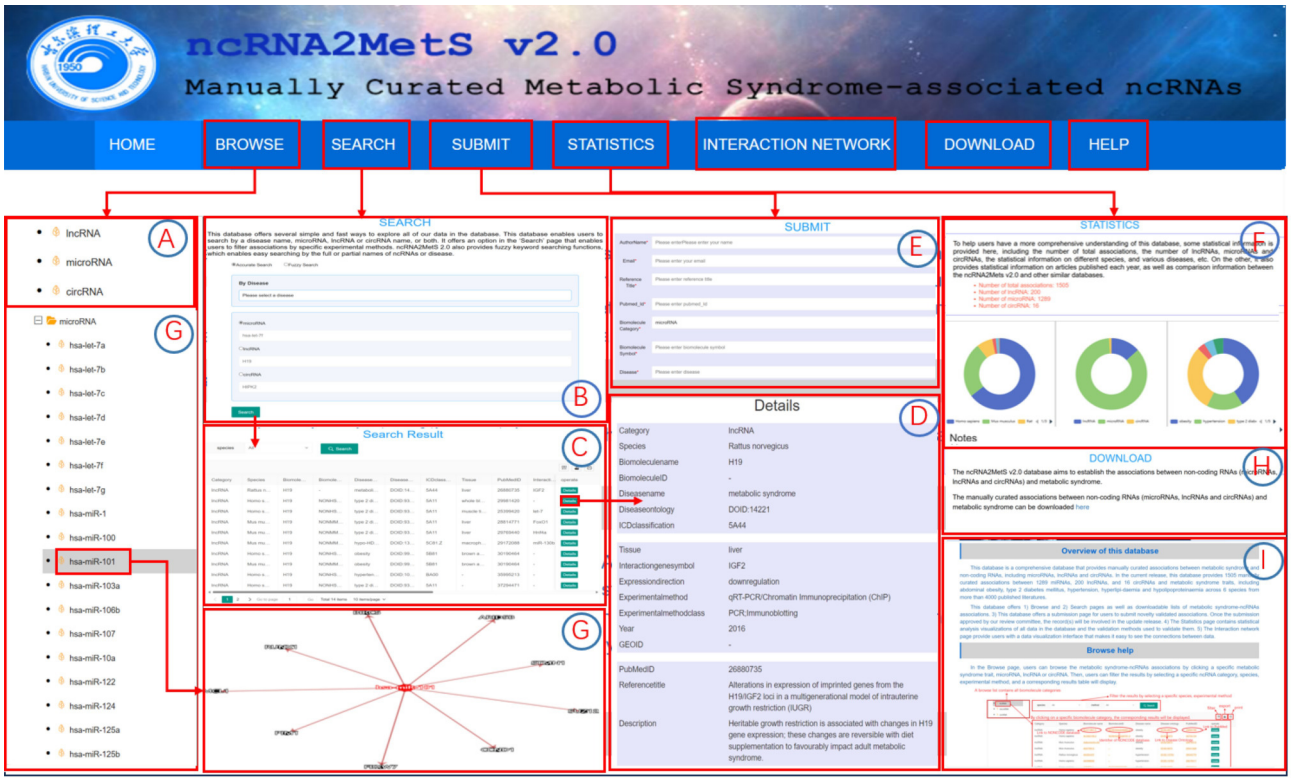

Fig. 1 The interface of ncRNA2Mets v2.0. (A) Browsing data; (B) searching data; (C) displaying results; (D) details page; (E) submit page; (F) statistics page; (G) interactive network display; (H) download page; (I) help page

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