m$^5$C-Atlas: a comprehensive database for decoding and annotating the 5-methylcytosine (m$^5$C) epitranscriptome

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ABSTRACT

5-Methylcytosine (m$^5$C) is one of the most prevalent covalent modifications on RNA. It is known to regulate a broad variety of RNA functions, including nuclear export, RNA stability and translation. Here, we present m$^5$C-Atlas, a database for comprehensive collection and annotation of RNA 5-methylcytosine. The database contains 166 540 m$^5$C sites in 13 species identified from 5 base-resolution epitranscriptome profiling technologies. Moreover, condition-specific methylation levels are quantified from 351 RNA bisulfite sequencing samples gathered from 22 different studies via an integrative pipeline. The database also presents several novel features, such as the evolutionary conservation of a m$^5$C locus, its association with SNPs, and any relevance to RNA secondary structure. All m$^5$C-atlas data are accessible through a user-friendly interface, in which the m$^5$C epitranscriptomes can be freely explored, shared, and annotated with putative post-transcriptional mechanisms (e.g. RBP intermolecular interaction with RNA, microRNA interaction and splicing sites). Together, these resources offer unprecedented opportunities for exploring m$^5$C epitranscriptomes. The m$^5$C-Atlas database is freely accessible at https://www.xjtlu.edu.cn/biologicalsciences/m5c-atlas.

INTRODUCTION

To date, >170 ribonucleotide modifications have been identified in various RNA types. These modifications affect transcript functions and regulate gene expression, in part by influencing the intramolecular interaction of RNA with RNA binding proteins through changing the local RNA 3D structures (1). Although a large number of RNA modifications have been identified, the underlying molecular mechanisms remain largely unclear. As one of the most common post-transcriptionally modified bases, 5-methylcytosine (m$^5$C) is a dynamic RNA marker found in most eukaryotes, prokaryotes and archaea (2). High throughput and biochemical studies have shown that m$^5$C is widely distributed over all RNA species and plays essential roles in RNA biology. For example, m$^5$C regulates ribosome synthesis and processing by altering the conformation of rRNA (3), thereby affecting translation fidelity (4). m$^5$C sites on tRNA are evolutionarily conserved and contribute to maintenance of tertiary structure (5,6). m$^5$C has also been reported to function in mRNA, influencing its turnover (7,8), export from nucleus (9) and translation (5,10). Additionally, aberrant levels of RNA cytosine methylation are implicated in various disease states and conditions (11). Thus, there is a clear need for comprehensive databases that provide the necessary tools and information for further exploration of m$^5$C epitranscriptomes.

The m$^5$C-Atlas database offers a unique opportunity for researchers to gain a more comprehensive understanding of m$^5$C biology by providing a comprehensive collection of m$^5$C sites and quantitative condition-specific methylation levels. This database also presents several novel features, such as the evolutionary conservation of a m$^5$C locus, its association with SNPs, and any relevance to RNA secondary structure. All m$^5$C-atlas data are accessible through a user-friendly interface, in which the m$^5$C epitranscriptomes can be freely explored, shared, and annotated with putative post-transcriptional mechanisms (e.g. RBP intermolecular interaction with RNA, microRNA interaction and splicing sites). Together, these resources offer unprecedented opportunities for exploring m$^5$C epitranscriptomes.
Figure 1. The design of m\textsuperscript{5}C-Atlas. m\textsuperscript{5}C-Atlas features a high-confidence collection of m\textsuperscript{5}C sites and quantitative profiles in multiple species. Through a rigorous filtering process, most potential false positive sites analyzed by pipeline were removed. It also provides conservation information among three vertebrate species and the disease-association of individual m\textsuperscript{5}C sites.

High-throughput technologies for RNA m\textsuperscript{5}C detection

With recent advances in high-throughput sequencing (HTS) technology, the amount of data on RNA methylation is huge and continues to grow. Several HTS technologies have been developed to detect RNA m\textsuperscript{5}C methylation, including m\textsuperscript{5}C immunoprecipitation sequencing (m\textsuperscript{5}C-RIP-seq) (7,14), m\textsuperscript{5}C RNA bisulfite sequencing (m\textsuperscript{5}C BS-seq) (15), m\textsuperscript{5}C methylation individual nucleotide resolution crosslinking immunoprecipitation (m\textsuperscript{5}C-miCLIP) (16,17), 5-azacytidine-mediated RNA immunoprecipitation (5-Aza-IP) (18) and TET-Assisted peroxotungstate oxidation sequencing (TAWO-Seq) (19). Among them, m\textsuperscript{5}C-RIP-seq applies anti-m\textsuperscript{5}C antibodies to enrich the methylation-containing fragments, yielding low resolution methylation peaks (from 50 bp to 150 bp). Similar to the design of RIP-Seq, 5-Aza-IP incorporates cytidine nucleoside 5-azacytidine into RNA, and uses antibodies to capture the methyltransferase that is covalently linked with 5-azacytidine residues. m\textsuperscript{5}C-miCLIP and photo-crosslinking-assisted m\textsuperscript{5}C sequencing (PA-m\textsuperscript{5}C) are technologies that permit the detection of m\textsuperscript{5}C at single nucleotide resolution (20). A key limitation of 5-Aza-IP, miCLIP and PA-m\textsuperscript{5}C lies in the requirement for overexpression of methyltransferases in the cell to interact with the modified bases, restricting detection to only a subset of sites targeted by the specific writer. RNA bisulfite sequencing (RNA BS-seq) has been a gold standard technique in the detection of cytosine methylation. We have therefore constructed m\textsuperscript{5}C-Atlas (Figure 1), the first comprehensive database exclusively for RNA 5-methylcytosine, to help decipher the m\textsuperscript{5}C epitranscriptomes.

Construction of m\textsuperscript{5}C-Atlas

To date, several publicly available databases, such as MODOMICS and RMBase, have been curated for epitranscriptomics. Among them, MODOMICS is a database of RNA modification with a focus on the chemical structures of modified ribonucleotides, corresponding biosynthetic pathways and RNA modification enzymes (1). RMBase is an epitranscriptome database that contains 1 397 000 modification sites detected by HTS techniques, covering multiple types of modifications such as m\textsuperscript{6}A, pseudouridine and m\textsuperscript{5}C (23). Both databases contain information on m\textsuperscript{5}C with different biological and technical perspectives. However, these databases are not specifically developed for m\textsuperscript{5}C and only contain a fraction of the available information on RNA cytosine methylation. We have therefore constructed m\textsuperscript{5}C-Atlas (Figure 1), the first comprehensive database exclusively for RNA 5-methylcytosine, to help decipher the m\textsuperscript{5}C epitranscriptomes.

Compared with the existing epitranscriptome databases, m\textsuperscript{5}C-Atlas features a high-confidence collection of reliable m\textsuperscript{5}C sites from single base resolution technologies (see Table 1). Relative to other low-resolution technologies (eg. MeRIP-Seq), the base-resolution methods offer superior accuracy and reliability. The methylation levels of the putative m\textsuperscript{5}C sites were further quantified from various BS-Seq samples derived from different cell lines and tissues. The collected methylation sites span diverse species, including animal, plant, microorganisms and viruses (see Table 2). Besides basic gene annotations, m\textsuperscript{5}C-Atlas also provides a rich set of functional annotations, such as the evolutionary conservation of the modification sites between vertebrates (human, mouse and zebrafish), overlap with RNA binding protein (RBP), miRNA and splicing junctions, and any single nucleotide polymorphism (SNP) associated with the loss of the m\textsuperscript{5}C methylation locus. In addition, the stem region introduced by different filtering methods during data processing. Overall, these HTS technologies have their own unique sets of advantages and shortcomings in RNA m\textsuperscript{5}C detection.
ing samples were obtained and analyzed for filtering high-

Moreover, in order to report the m5C sites on tRNA and

The other positional information was also down-

available with meRanTK version 1.2.1b (28). The unique

BS-seq alignment tool with default parameters, meRanGh

Clean reads were mapped to reference genomes by an RNA

Adaptor contaminations from the NCBI GEO database (25), covering 13 species, such

As human, mouse, zebrafish, fly, Arabidopsis, yeast and

viruses. The other positional information was also down-

loaded from original articles or relevant GEO datasets.

rRNA, the processed data were download from the NCBI

GEO database (18), supplementary material (26) and pre-

duced to infer the secondary structure of the region where the m5Cs i
tes were identified by this optimized pipeline are available for download

on the download page.

Secondary structure annotation

RNA secondary structures are essential for RNA stability and function. The high temperature during bisulfite treatment during DNA BS-Seq can cause severe RNA degradation. Thus, the temperature of the treatment process for RNA is lower than DNA, so that incomplete conversion is a major issue of the technique. We used the RNA sec-

ondary structure prediction software RNAfold to infer the secondary structure of the region where the m5C sites were

located (MEA 0.1, -T 70). This information was annotated to suggest potential thermal stable stem structure for user, since the hybridized regions of nucleic acids are often resistant to bisulfite conversion (21,22).

Quantitative profiles of putative m5C sites

The coverage number and cytosine count were recorded from candidate m5C site files as calculated by meRanCall. The methylation levels of m5C sites in different conditions, treatments, cell lines or tissues were also calculated and recorded. In addition, the gene expression levels in different samples were quantified from BAM files of the aligned BS-Seq by StringTie (gene expression levels in TPM).

Conservation of m5C sites in vertebrates

In the cross-species comparative analysis, we used the LiftOver tool from the UCSC genome browser to map the m5C locus of a single species to the homologous coordinates of the target species (30,31). If the mapped sites also have m5C modifications in the target species, then these methylation sites will be considered to have methylation conservation between the two species. In addition, for the human m5C sites, the conservation level of putative sites was calculated and shown in m5C-Atlas. Two types of conservation scores, phastCons (32) and fitCons (33), were used to represent the degree of evolutionary conservation under the genomic region of the corresponding RNA methylation site.

Basic annotation for m5C sites

In addition to basic gene and transcript annotation information (34), splice sites, miRNA target sites and RNA binding protein (RBP) binding sites were also integrated into m5C-Atlas to help understand the potential functions and regulation of m5C in various aspects (see Supplementary Table S2). The miRNA target sites and RBP intermolecular interaction with RNA information were obtained from star

Base (35) and POSTAR (36) respectively. The splicing site information were obtained from the UCSC database (37).

Potential involvement of individual m5C sites in pathogenesis

By comparison with previous databases (RMVar (38) and RMDisease (39)), it is assumed that the disease caused

Table 1. Comparison of m5C-Atlas with other databases

| High-confidence m5C sites | m5C-Atlas More Complete | MODOMICS Limited Volume | RMBase Incomplete |
|---------------------------|-------------------------|-------------------------|------------------|
| Detection methods & species | 6 & 13 | LC-MS | 1 & 3 |
| Quantitative methylation profiles | Yes | - | - |
| Matched gene expression profiles | Yes | - | - |
| Conservation in vertebrates | Yes | - | - |
| Viral m5C sites | Yes | - | - |
| RNA modification pathways | - | Yes | - |
| Condition-specific m5C profiles | Yes | - | - |
| Putative secondary structure | Yes | - | - |
| Post-transcriptional annotations | Yes | - | Yes |
by single-base mutation may be induced by the loss of m^5^C methylation, the instability of RNA structure, function changes or changes in downstream interactions due to the changes in cytosine position caused by mutation. Therefore, the analysis of diseases caused by modified cytosine can implicate the potential involvement of a single m^5^C site in pathogenesis. The site mutation and disease data used in this analysis were obtained from dbSNP database (40).

**Database and web interface implementation**

MySQL was used to store and manage metadata in m^5^C-Atlas. Hypertext Markup Language (HTML), Cascading Style Sheets (CSS) and Hypertext Preprocessor (PHP) were used to build the displayed Web interface. The Jbrowse genome browser was used for interactive exploration and visualization of related records (41).

**RESULT**

m^5^C-Atlas aggregates a total of 166,540 high-reliability sites (see Table 2 and Supplementary Table S2). The coverage of each site is greater than 30 and high-stringency filtration was performed through stringent pipeline and other methods. These sites cover 13 species, including human (134,649 sites), mouse (16,279 sites), zebrafish (7,846 sites), fly (5421 sites), Arabidopsis (684 sites), Saccharomycyes cerevisiae (1,539 sites), Brassica rapa (21 sites), Caenorhabditis elegans (4 sites), Ginkgo biloba (5 sites), Nannochloropsis oceanata (39 sites), Triticum turgidum subsp (17 sites) and two viruses, Human immunodeficiency virus (31 sites), Murine leukemia virus (5 sites). For human m^5^C data, three distinct techniques were used to support it, including MeRIP-seq, Aza-IP-seq, and BS-seq.

Quantitative profiles were estimated over 206 experimental conditions (different cell lines, tissues or experimental treatments), which were gathered from 351 high-throughput sequencing samples including the methylation level of sites, the number of cytosines, and the coverage number. Among them, there are 177 human m^5^C modification high-throughput sequencing samples, including 22 cell lines/tissues, and 91 different experimental treatments or conditions. For 69 mouse high-throughput sequencing samples, 17 cell lines/tissues and 13 different experimental treatments or conditions were provided in m^5^C-Atlas (for the other 11 species, please refer to Table 2). The BAM files of high-throughput samples are used to obtain gene expression through StringTie, and are matched to each site according to the condition, cell line and treatment, providing a reference for the user's analysis and processing.

Basic annotations for 11 species, including gene annotation information for 11 species, RBP information for five species, splicing site information for four species, and miRNA information for three species were all generated (Supplementary Table S2). Disease association information (SNP) caused by single m^5^C site mutation was also analyzed and displayed in 5 species. Moreover, conservation analysis was performed among human, mouse and zebrafish to identify the conserved m^5^C sites between two vertebrate species (see Table 2).

The main function of Atlas is to collect, reprocess, and display high-quality location information for users. Users can search the gene/gene interval of interest on the homepage to obtain the m^5^C methylation data of this gene/gene interval. Users can also click on different modules (mRNA, tRNA, rRNA), select different species, organelles, and annotation information under different modules to perform range screening to view m^5^C methylation site information. In addition, all information can be downloaded from the download module.

**Case study on lncRNA: XIST**

XIST is a long non-coding RNA (lncRNA) expressed in the X inactivation center (XIC). After transcription, XIST is not translated into protein, but instead silences gene transcription on one of the two X chromosomes of female mammals (42,43). Previous studies have identified m^5^C on functionally important region of XIST, which can regulate the interaction between XIST and the chromatin-associated protein complex, PRC2 (44). Searching by gene name, XIST, at the front page of m^5^C-Atlas database, returns 147 m^5^C sites and statistical graphs (Figure 2A and B). The field of species and tissue/cell line allows users to select organisms and the supporting cellular conditions. Meanwhile, users can query the specific m^5^C sites and then filter the associated RBP, miRNA, splicing site or SNP to investigate on specific functional annotation. Detailed in-

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### Table 2. Contents of m^5^C-Atlas database

| Species | Site number (mRNA) | Cell line/tissue | condition/treatment | Quantitative profiles | Basic annotation | Disease association | Conservation in vertebrates |
|---------|-------------------|------------------|--------------------|-----------------------|-----------------|-------------------|--------------------------|
| Homo sapiens | 124 105 | 22 | 91 | Yes | Yes | Yes | Yes |
| Mus musculus | 16 279 | 17 | 13 | Yes | Yes | Yes | Yes |
| Danio rerio | 7846 | 1 | 7 | Yes | Yes | Yes | Yes |
| Drosophila melanogaster | 5421 | 2 | 3 | Yes | Yes | Yes | Yes |
| Arabidopsis thaliana | 684 | 6 | 22 | Yes | Yes | Yes | Yes |
| Saccharomycyes cerevisiae | 1539 | 1 | 2 | Yes | Yes | Yes | Yes |
| Brassica rapa | 21 | 1 | 2 | Yes | Yes | Yes | Yes |
| Caenorhabditis elegans | 4 | 1 | 1 | Yes | Yes | - | - |
| Ginkgo biloba | 5 | 1 | 2 | Yes | Yes | - | - |
| Murine leukemia virus | 5 | 1 | 1 | Yes | Yes | - | - |
| Triticum turgidum subsp | 17 | 1 | 2 | Yes | Yes | - | - |
| Nannochloropsis oceanata | 39 | 1 | 2 | - | - | - | - |
| Human immunodeficiency virus | 31 | 2 | 1 | - | - | - | - |
Figure 2. The m$^5$C site of lncRNA XIST and related information. (A) The bar chart showing the number of m$^5$C sites on the XIST gene, RBP, miRNAs target, splicing site, SNP diseases, and conservation site. (B) 147 m$^5$C sites records of XIST were detected and statistic in different conditions and cell lines/tissues. (C) Basic information of m$^5$C hg19 59672 site on XIST. (D) Different experimental conditions that can detect the m$^5$C site. (E) RNA binding protein part provides the information that the RBP interaction region covers this m$^5$C site. (F) miRNA target part provides the information that the miRNA interaction region covers this m$^5$C site. (G) Jbrowse of m$^5$C hg19_59672 site.

formation of the sites will be displayed after clicking on one of the site ID (m$^5$C hg19_59672 for example). The basic information section includes the site ID number, chromosome, position, strand, gene, gene region, transcript ID, 41 bp reference sequence, secondary structure and data source information (Figure 2C). The experimental condition section reports one or more biological samples under which the site is m$^5$C modifiable. For our example (m$^5$C hg19_59672), the table shows that the site was observed to be m$^5$C modifiable under two experimental conditions (Figure 2D). The GSE number, cell line, condition, cytosine count, coverage, TPM and methylation level of each experimental condition are all listed in the table. Other annotation information is listed after the experimental condition part, including RBP, miRNA-RNA interaction, splicing site, SNP and multi-technical support (the number of technologies that can detect this site). For site m$^5$C hg19_59672, the database shows that it lies within the interaction range of 39 RBPs and 3 miRNAs (Figure 2F and E, respectively). These information, in turn, can be used to evaluate the interaction between m$^5$C sites and other post-transcriptional regulators. User can also click ‘Visualize in genome browser’ (Figure 2C) to display the Jbrowse (Figure 2G).

Case study on protein-coding gene: NECTIN2

NECTIN2 is an immunoglobulin-like molecular protein. It plays a fundamental role in the formation of adhesion and tight junctions between epithelial cells and fibroblasts (45). As an immune molecular ligand, NECTIN2 is upregulated on the surface of virus-infected cells and cancer cells, thereby activating CD226 to mediate the recogni-
tion of toxic lymphocytes and the killing of abnormal cells (46). A total of five records related to `NECTIN2' are returned after querying its gene name at the front page of the m^5C-Atlas. These records can be further selected by filtering the associated RBP, miRNA, splice site, and SNP information. Detailed information will be returned after clicking the specific m^5C sites. The website will be redirected to the source page of the GEO database after selecting the samples under specific cellular conditions. In addition, it is convenient to find that the selected site was identified in 93 different-condition experiments under the experimental condition section. The query page provides users a summary of m^5C status on NECTIN2, suggesting that cytosine methylation may have a potential role in regulating the function of the mRNA transcripts of NECTIN2, since >90 experimental conditions were found this m^5C site. In the section of technique annotation, the site has also been reported as m^5C-modifiable under certain conditions of the RBS-seq technology which increases confidence that the locus is truly m^5C modifiable. After examining its associated post-transcriptional regulation for RBP and splicing site, three RBPs and one splicing site were found to overlap or be close to this m^5C site. Interestingly, the m^5C formation at this site is silenced by a known disease-related SNP, which might indicate that the site is involved in the pathogenesis of uterine corpus endometrial carcinoma.

**Case study on protein-coding gene: HDGF**

Hepatoma-derived growth factor (HDGF) is a hairpin-binding growth factor associate with several cancer types including breast, lung and pancreatic cancers (47–49). As an oncogene, HDGF was identified that relates to metastatic tumour progression by stabilizing the mRNA through the binding of m^5C modified sites at 3' UTR to YBX1 and NSUN2 (8). Searching for the gene name 'HDGF' at the front page of the m^5C-Atlas database, a total of 84 records related to 'HDGF' are returned. These records can be further filtered by RBP, miRNA, splice site, and SNP information. After clicking m^5C sites (here we choose site m5C_hg19_67285), more information of this site will be provided. Under experiment condition part, the site is identified to appear in 45 different-condition experiments with high coverage. In the conservation annotation part, this site has been identified to conserve with the site of mouse (chr3:87914991+). Moreover, the phastCons and fitCons of this site has also been calculated and displayed. In post-transcriptional regulation for RBP and splicing site parts, 16 RBPs and one splicing site were found to be associate with this m^5C site.

**CONCLUSION**

With recent advances in HTS technologies, the transcriptomic profiles of RNA modifications under different biological conditions have been revealed. As one of the most prevalent post transcriptional modifications on RNA, 5-methylcytosine has received much attention during the last few years. Many biological processes, including cell development and carcinogenesis (8), have been linked to both the topology and dynamics of RNA m^5C. Despite its important roles in RNA biology, a database for RNA m^5C is still lacking. Here, we utilized advanced pipelines, secondary structure annotation, IVT, multiple technologies overlapping and stringent method which put forward previously to analyze the data to present m^5C-Atlas, a new and comprehensive knowledgebase for deciphering the m^5C transcriptome.

We collected quantitative data of m^5C methylation sites from 13 species and re-processed the RNA bisulfite sequencing datasets using two protocols: a classic pipeline and a stringent pipeline. The reference sites are merged from Aza-IP, miCLIP and RBS-seq, enabling exploration of the consistency between different techniques. In addition, m^5C-Atlas provides insights into the functions of individual m^5C sites via functional annotations such as conservation in vertebrate species and the association with the diseases-related SNPs. Other transcriptomic data, such as RBP, miRNA, and splicing sites were all incorporated into the m^5C-Atlas, and are available both as results tables and as tracks on a genome browser. These resources will provide researchers with new opportunities to study the function of m^5C transcriptomes.

Although the m^5C-Atlas is a comprehensive database for 5-methylcytosine, there are still some limitations should be improved in the current version, 1), the data quality for each samples or species is unequal, for example, the raw data for Brassica rapa, Caenorhabditis elegans, Ginkgo biloba, Nannochloropsis oculata and Triticum turgidum subsp contained rRNA information, which reduced the mRNA information in sequencing, resulting the less m^5C sites were reported on mRNA; 2), the current pipeline for tRNA m^5C calling is still a challenge, the sequences of tRNA isodecoders are highly similar, and the current BS-seq is difficult to map m^5C sites to exact tRNA; 3), The annotation information of some species, such as Nannochloropsis oculata, are incomplete.

**SUPPLEMENTARY DATA**

Supplementary Data are available at NAR Online.

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Author’s contributions: K. Chen and Z. Wei conceived the idea; J. Ma processed the epitranscriptome datasets and implemented the functional annotations; B. Song, constructed the web interface; J. Ma drafted the manuscript. All authors read, critically revised and approved the final manuscript. We thank for the Jianheng Liu from Sun Yat-sen University for his help in the data processing and the discussion for tRNA m^5C BS-seq.

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