Reagent and Data Resources for Investigation of RNA Binding Protein Functions in Drosophila melanogaster Cultured Cells

Stephanie E. Mohr,*† Yanhui Hu,* Kirstin Rudd,* Michael Buckner,* Quentin Gilly,* Blake Foster,* Katarzyna Sierzputowska,* Aram Comjean,* Bing Ye,*† and Norbert Perrimon*‡

*Drosophila RNAi Screening Center, Department of Genetics, Harvard Medical School, Boston, Massachusetts 02115, †Life Sciences Institute, University of Michigan, Ann Arbor, Michigan 48109, and ‡Howard Hughes Medical Institute, Boston, Massachusetts 02115

ABSTRACT RNA binding proteins (RBPs) are involved in many cellular functions. To facilitate functional characterization of RBPs, we generated an RNA interference (RNAi) library for Drosophila cell-based screens comprising reagents targeting known or putative RBPs. To test the quality of the library and provide a baseline analysis of the effects of the RNAi reagents on viability, we screened the library using a total ATP assay and high-throughput imaging in Drosophila S2R+ cultured cells. The results are consistent with production of a high-quality library that will be useful for functional genomics studies using other assays. Altogether, we provide resources in the form of an initial curated list of Drosophila RBPs; an RNAi screening library we expect to be used with additional assays that address more specific biological questions; and total ATP and image data useful for comparison of those additional assay results with fundamental information such as effects of a given reagent in the library on cell viability. Importantly, we make the baseline data, including more than 200,000 images, easily accessible online.

High-throughput cell-based RNA interference (RNAi) screening, including in Drosophila cultured cells, provides a format for large-scale interrogation of gene function. RNAi technology has significantly improved over time and the approach now serves as a robust method for functional genomics discovery (Mohr et al. 2014). Many advances have helped limit false discovery (i.e., false-positive and false-negative results) in high-throughput screens in general and RNAi screens specifically. Nevertheless, RNAi screens remain associated to some degree with false discovery, including sequence-specific off-target effects (OTEs) (Kulkarni et al. 2006; Moffat et al. 2007). Additional factors that impact false discovery and thus affect overall primary screen data quality include the quality of gene annotations used for RNAi reagent design, the rules and filters applied to design of the reagents, the number of unique reagents per gene in the primary screening library, the layout of control and experimental reagents on screen assay plates, the number of replicates performed in a given screen, and the types of analyses performed with the primary data (Birmingham et al. 2009; Boutros and Ahringer 2008; DasGupta et al. 2007; Mohr et al. 2014).

For some projects, it is more appropriate to screen a subset of genes rather than to perform a genome-wide screen (Boutros and Ahringer 2008). A focused approach can reduce costs, allow for rapid follow-up on results from other omics studies, provide focus to follow-up assays, help establish positive controls (i.e., when done prior to a full-genome screen), and/or help address false-negative discovery (i.e., when done after a full-genome screen). In addition, when the target gene number is reduced, it becomes easier to include more unique reagents per gene, include a generous number of positive and negative controls, and apply optimal plate layouts (e.g., avoid the use of edge wells, which are subject to position-dependent effects or "edge effects") (Boutros and Ahringer 2008; Mohr 2014). Potential disadvantages of screening with a focused library include missing unexpected results and the fact that gene set enrichment analyses, which can be highly informative when applied to genome-wide screen data, might not be as informative or appropriate because the initial library is biased.

KEYWORDS Drosophila RNA binding protein RNAi data sharing high-throughput screen

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†Corresponding author: Harvard Medical School, 77 Avenue Louis Pasteur, New Research Building Room 336D, Boston, MA 02115. E-mail: stephanie_mohr@hms.harvard.edu
The usefulness of a library, small or large, improves when researchers know priori which reagents in the library affect general cell health (e.g., compromise cell division, growth, and/or viability), because this can impact interpretation of results obtained with more sophisticated assays (DasGupta et al. 2007). Thus, obtaining "baseline" data and making these data freely available are important for establishing a reagent library as a high-quality and useful resource. Additional factors that influence the usefulness and quality of an RNAi reagent library can include the number of unique reagents per gene and effectiveness of the reagents.

RNA binding proteins (RBPs) are of special interest because they are involved in a broad range of fundamental cellular activities, including RNA editing, localization, stability, translation, transcription, and transport (Gamberi et al. 2006; Glisovic et al. 2008) as well as DNA damage responses (Dutertre et al. 2014). RBPs also regulate cellular processes such as pluripotency (Ye and Blelloch 2014) and senescence (Wang 2012), and have demonstrated relevance to human diseases, including inherited diseases, neuronal diseases, and cancer (Castello et al. 2013; Fredericks et al. 2015; Gerstberger et al. 2014; Kim et al. 2009; Lenzken et al. 2014). Notably, many of these processes can be studied using cultured cell assays, making the gene set particularly relevant for development of a high-quality cell-based RNAi screen library. We curated a list of genes that encode RBPs, synthesized a corresponding Drosophila cell-based RNAi reagent library, performed an initial characterization of the library, and, importantly, made raw and analyzed data from this initial characterization, including more than 100,000 images, available online. Thus, studies utilizing this resource should help our understanding of RBPs in Drosophila and other species.

MATERIALS AND METHODS

Bioinformatics analysis and curation of Drosophila melanogaster RBPs

We generated a list of known and putative Drosophila RBPs using a combination of literature and database mining and expert curation. The major resources we explored are gene ontology annotation (http://www.ncbi.nlm.nih.gov/) (Harris et al. 2004), UniProt protein annotation (http://www.uniprot.org/) (Apweiler et al. 2004), and protein domain annotation of InterPro (http://www.ebi.ac.uk/interpro/) (Apweiler et al. 2001). The target gene list contains 427 unique genes that code for proteins binding to mRNA, rRNA, tRNA, and other non-coding RNAs.

In vitro synthesis of dsRNA for RNAi

We used UP-TORR (http://flyma.org/up-torr) (Hu et al. 2013) to identify appropriate reagent templates in our collection. As needed for two reagents per gene coverage, we designed additional dsRNAs using SnapDragon (http://www.flyma.org/cgi-bin/RNAi_find_primers.pl). We used standard protocols to prepare dsRNAs (Mohr 2014; see http://www.flyma.org/DRSC-PRR.html for protocol). In brief, we used liquid handling automation to individually select PCR templates for double-stranded RNA (dsRNA) synthesis based on our existing collections. Next, we quality-analyzed the dsRNAs, used a Multiprobe liquid handling robot (PerkinElmer) to normalize dsRNA concentrations, and used an Agilent Bravo liquid handling robot to array normalized dsRNAs into a final 384-well "assay-ready" format.
Table 1 Genes for which two of two unique dsRNA designs each confer good statistical significance (Z-score ≥1.5 or ≤−1.5 for 2 of 2 dsRNAs) in the total ATP levels assay

| FlyBase ID    | Gene Symbol | DRSC Reagent ID | Z-score | Expressed† |
|---------------|-------------|-----------------|---------|------------|
| FBgn0262739   | AGO1        | DRSC30762       | 3.06    | Yes        |
|               |             | DRSC39159       | 3.38    |            |
| FBgn0027873   | Cpsf100     | DRSC34503       | 1.60    | Yes        |
|               |             | DRSC14146       | 1.71    |            |
| FBgn0016978   | snRNP-U1-70K| DRSC28803       | 1.79    | Yes        |
|               |             | DRSC34940       | 2.05    |            |
| FBgn0087035   | AGO2        | DRSC40785       | −2.07   | Yes        |
|               |             | DRSC31769       | −1.86   |            |
| FBgn0015393   | hoip        | DRSC303546      | −2.82   | Yes        |
|               |             | DRSC31857       | −2.75   |            |

† Evidence of expression in untreated S2R+ cells based on modENCODE data and queried using the DRSC cell expression tool http://www.flyrnai.org/cellexpress.

Cell culture and RNAi knockdown
All studies were performed using S2R+ cultured cells and standard methods for culture. Cells and reagents were dispensed into 384-well assay plates using a WellMate (Thermo) or Mantis (Formulatrix) liquid handling robot. For RNAi, cells were dispensed into assay plates containing dsRNAs at a standard concentration for the “bathing” method (passive uptake; see http://www.flyrnai.org/DRSC-PRR.html for a step-by-step protocol).

High-throughput screening
We used the Cell Titer Glo reagent (Promega) and a Spectramax Paradigm automated luminometer ( Molecular Devices) to measure total well levels of ATP following RNAi knockdown (protocol at http://www.flyrnai.org/DRSC-Protocol-atp-levels.html). The data were analyzed using standard statistical approaches. For imaging, we used an Opera automated confocal imaging system (PerkinElmer) to image cells stained with DAPI and FITC-Phalloidin following RNAi knockdown (http://www.flyrnai.org/DRSC-Protocol-cellfich.xml for protocol). Images were obtained using 20x or 60x water immersion lenses and confocal fluorescence imaging.

Data availability
Raw and analyzed data from the total ATP screen assay are available for view or download at our FlyRNAi.org web site (Flockhart et al. 2012). Specifically, data can be exported from FlyRNAi as comma-separated values (CSV) files or searched and viewed online using the Gene Lookup or Screen Summary graphical user interfaces at http://www.flyrnai.org (Flockhart et al. 2012). To create the visualization of the total ATP data set shown in Figure 1, we exported the raw and analyzed data from our database, uploaded the data to Plotly (https://plot.ly/), and used tools at Plotly to generate the scatter plot and labels. An interactive view of the graph of Z-scores shown in Figure 1 as well as the underlying data are freely available at Plotly (https://plot.ly/~semohr/60). The data are also available at PubChem BioAssays https://pubchem.ncbi.nlm.nih.gov assay. cgi?aid=1159508. Data files from the PerkinElmer Opera confocal microscope are captured in the proprietary FLEX file format. Images were converted from FLEX format to TIFF format using Acapella software. Raw images (.jff) or minimally processed images (.jiff) are available on request for automated analysis. For online search and view, we uploaded scaled TIFF image files at Flickr (Yahoo, Inc.), where they are made available in JPEG format. The images were made public under a Creative Commons license. They are associated with the user account “dsrc_lab” and can be viewed at https://www.flickr.com/photos/132735911@N05/. The Opera image file naming system separates the following with an underscore: plate ID; well location; position within the well; channel; and position in the Z-axis. For example, the file 100B225_F24_S25_W1_Z1 corresponds to plate 100B225 ("100") indicates the test plate layout; “B” indicates that dsRNAs were present at the concentration appropriate for the bathing method of dsRNA uptake; and “225” reflects the aliquot number for the specific plate used), well F24, position S25, and channel W1 (in this case, FITC-Phalloidin staining) at a single plane of focus (Z1). The “gene list” file for the RBP library downloadable at http://www.flyrnai.org/DRSC-SUB.html can be used to associate specific wells with specific DRSC reagents and target genes. A searchable lookup table linking specific reagents and genes to image data at Flickr is available at http://www.flyrnai.org/DRSC-RBP_data.php. At the Flickr account, subsets of control images have been organized into “albums” (folders). We also assigned some key words to all images (e.g., “confocal”) or subsets of images (e.g., “hoip”), and others were automatically assigned by Flickr (e.g., “blackandwhite”).

RESULTS AND DISCUSSION

A Drosophila RNAi library targeting RNA binding domain-containing proteins
The Drosophila RNAi Screening Center (DRSC) and others have developed robust approaches for RNAi reagent and library design (Mohr 2014). We applied these approaches to production of a focused library targeting genes that encode RNA binding domain-containing proteins. To do this, we first generated a list of known and predicted Drosophila RBPs using a combination of literature and database mining and expert curation, and then generated the reagent library (see Materials and Methods). Features of the dsRNA library include: design of dsRNAs with minimal predicted OTEs using SnapDragon (http://www.flyrnai.org/snapdragon); coverage with two or more unique dsRNAs per gene; tracking of dsRNA production and quality analysis in our database; and inclusion of standard dsRNA controls on each 384-well assay plate. To minimize edge effects (i.e., reduced viability or other data anomalies frequently observed at assay plate edges), dsRNAs were excluded from the outermost two wells of each plate. We included two positive controls: dsRNA targeting thread (Diap1), which results in cell death, and dsRNA targeting Rho1, which leads to the appearance of large, binucleate cells. We also included three negative controls, dsRNAs targeting GFP and LacZ, neither of which is present in wild-type Drosophila cells, and wells with an equal volume of water (no dsRNA). The layout of control dsRNAs on each plate can be viewed at http://www.flyrnai.org/DRSC-LAY.html and the layout of all dsRNAs in the library can be downloaded from http://www.flyrnai.org/DRSC-SUB.html.
Screen for changes in total ATP levels using the RBPs library

We next used Promega Cell Titer Glo to measure total ATP levels after 5 days of incubation of S2R+ cultured cells in three replicates of each unique assay plate in the library. Full raw and analyzed data are available at the DRSC FlyRNAi.org database (Blockhart et al. 2012). The distribution of Z-scores for dsRNAs in the screen is shown in Figure 1. An interactive view of the graph as well as the data are freely available at https://plot.ly/~semohr/60. Genes that might be considered primary screen "hits" (positive results) from the total ATP levels screen based on commonly applied criteria are summarized in Table 1, Table 2, and Table 3. By Z-score, the strongest hit for "high ATP levels" is Agarnaut-1 (AGO1), an Argonaught family protein required for miRNA maturation (Okamura et al. 2004). The strongest hit for "low ATP levels" is hoi-palloi (hoip), which encodes a ribosomal protein and has been associated with neuronal mutant phenotypes in Drosophila (Prokopenko et al. 2000). The opposing results obtained with dsRNAs targeting AGO1 and AGO2 (Table 1) are consistent with the distinct roles of AGO1 and AGO2 in small RNA biogenesis (Okamura et al. 2004; Okamura and Lai 2008; Zhou et al. 2008). The result with AGO1 suggests that one or more microRNAs (miRNAs) might normally dampen growth and/or viability of S2R+ cells, consistent with roles identified for some miRNAs in signaling and cancer (Hagen and Lai 2008; Jackstadt and Hermeking 2013). In the case of AGO2, suppression of the AGO2-mediated endogenous small interfering RNA (siRNA) pathway might result in increased mobilization of transposons (Czech et al. 2008), perhaps accounting for the observed compromise in cell viability, and/or might result in detrimental changes to metabolism or stress responses (Lim et al. 2011).

Table 1 comprises a conservative list of high-confidence hits; Table 2 and Table 3 add additional lower-confidence hits that might be interrogated in follow-up studies and/or compared with other screen data. Each of the reagents in Table 3 has no predicted off-targets and is predicted to target all isoforms of the gene (Hu et al. 2013). Moreover, modENCODE cell expression data for S2R+ cultured cells suggest that most of these genes are normally expressed in S2R+ (Booher et al. 2011; Lee et al. 2014). Thus, we predict that most of these are "primary hits" due to a false-negative result with the other dsRNAs targeting the same genes rather than due to false-positive discovery with the positive dsRNA. To further improve library quality, we plan to add additional unique dsRNAs for those cases in which different dsRNAs targeting the same gene do not give comparable results (i.e., for a subset of genes in Table 2 and all genes in Table 3). The complete set of Z-scores as well as modENCODE results regarding expression in S2R+ cells (Booher et al. 2011; Lee et al. 2014) are available in supporting information, Table S1. Moreover, we have made raw and analyzed data available via a variety of online repositories as summarized at http://www.flyrnai.org/DRSC-RBP_data.php.

High-throughput imaging using the RBPs library

To further characterize the RBPs library, we stained cells with DAPI and FITC fluorescence-conjugated Phalloidin to visualize nuclei and actin filaments, respectively. The result with hoi-palloi is presented in Figure 2. Moreover, the data are freely available at https://plot.ly/~semohr/60. As with the total ATP levels screen, we focused on those genes for which one of the two dsRNAs for each gene confers a high Z-score (≥1.5 or ≤−1.5) in the total ATP levels assay.
filamentous actin, respectively, in paraformaldehyde-fixed S2R+ cells. The cells were then imaged at 20x and 60x using a fluorescence confocal imaging system. As expected, Rho1 serves as an effective positive control for image-based assays, as treatment with Rho1 dsRNA results in a binuclear phenotype readily detectable using a DNA dye and any marker that defines the cell body. These cells also appear larger. Also as expected, few cells are detected in images corresponding to thread (Diap1) dsRNA control wells. Consistent with the total ATP assay results (Table 1), few cells are detected in images corresponding to wells treated with dsRNA targeting AGO2 or hoip.

Availability of RNAi screen data in the form of text or numbers is facilitated by public databases including FlyRNAi, GenomeRNAi, and NCBI PubChem BioAssays (Flockhart et al. 2012; Gilsdorf et al. 2010; Wang et al. 2014). Ideally, researchers will also be provided with access to baseline image data, e.g., to help identify reagents with gross effects on cell morphology. However, high-throughput, high-content image data sets are large both in total size and in terms of the total number of individual images, presenting significant challenges to image data management. As a result, making images easily available for search and view online has been seen as a significant challenge. Although solutions arising from within the biological community such as the Online Microscopy Environment OMERO platform (Allan et al. 2012) hold strong promise for making image data public online, the solutions offered to date are not easy to implement and support, requiring significant expertise and infrastructure. As a result, although it is relatively easy to share complete sets of screen image data, such as for automated analyses (e.g., because an entire image data set can be shared using a file transfer protocol or on an external hard drive), making it possible for researchers to easily view images associated with a specific subset of reagents has remained a barrier. To find a near-term, feasible solution to making a set of baseline image data publically searchable and viewable online, we chose to make images available at flickr.com. Advantages of flickr include that the site has been around for more than 10 years, it offers 1 terabyte of free image storage, and it is additionally supported in part by the Dana Farber/Harvard Cancer Center, which is supported in part by NCI Cancer Center Support Grant NIH 5 P30 CA06516. N.P. is an Investigator with the Howard Hughes Medical Institute.

CONCLUSION

The DRSC has a longstanding commitment to building high-quality functional genomics reagents and making large-scale screen data publically available through its own database, FlyRNAi (Flockhart et al. 2012), as well as at meta-databases such as GenomeRNAi (Gilsdorf et al. 2010) and PubChem BioAssays (Wang et al. 2014). Here, we have shown that established and new media solutions can be utilized effectively for public data availability. The baseline data sets for the RBPs library help provide a measure of overall library quality and will aid the interpretation of results obtained using other assays. The DRSC has and continues to generate other focused libraries based on community input. Analysis of other libraries to the same extent as that presented in this study would add value to existing and new libraries. Moreover, because a large proportion of the genes represented in the RBP and other DRSC focused libraries have been conserved, the results of screens using these libraries are likely to have impact beyond Drosophila.

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