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Data in Brief

Data Article

A comprehensive dataset of microRNA misexpression phenotypes in the *Drosophila* eye

Fernando Bejarano, Eric C. Lai*

Developmental Biology Program, Sloan Kettering Institute, 1275 York Ave, Box 252, New York, NY 10065, USA

A B S T R A C T

microRNAs (miRNAs) are a broad class of ~22 nucleotide regulatory RNA, which collectively have broad effects on the transcriptome and are involved in diverse biology, from development and adult physiology, and from homeostasis to disease and pathology. We investigated the effects of systematically expressing microRNAs (miRNAs) during the development of the *Drosophila* compound eye using the *GMR-Gal4* driver. The objective was to determine what fraction of miRNAs were capable of inducing aberrant morphology that was easily and reproducibly scored by visual inspection under a dissecting microscope. We assayed multiple independent insertions of 166 miRNA transgenes (536 lines), comprising solo miRNAs, miRNA operons and individual constituent miRNAs from operons. We find a substantial number reproducibly altered normal eye development and a smaller number induced lethality in most or all progeny. We provide the comprehensive results of this screen, documenting numerous miRNA transgenes that interfered with normal eye development when activated using *GMR-Gal4*. These data can be mined by the *Drosophila* community to query the in vivo effects of any individual miRNA of interest in the eye, as well

https://doi.org/10.1016/j.dib.2021.107037

as utilized as a foundation for more complex genetic perturbations that involve miRNA misexpression in the eye.

Specifications Table

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Subject	Biology
Specific subject area	Genetic screen data, microRNA, *Drosophila* eye
Type of data	Table
	Figure
How data were acquired	Visual inspection and iPhone photography.
Data format	Raw
	Analyzed
Parameters for data collection	*Drosophila* crosses performed at 25°C and 60% humidity on cornmeal-molasses food.
Description of data collection	Adult progeny bearing *GMR-Gal4* and a *UAS-miRNA* transgene were inspected under a dissecting microscope and eye phenotypes were recorded using a controlled vocabulary and supplemented with additional descriptive notes. The eyes from a subset of animals were photographed.
Data source location	Institution: Sloan Kettering Institute
	City/Town/Region: New York
	Country: USA
Data accessibility	With the article
Related research article	F. Bejarano, C.-H. Chang, Kailiang Sun, Joshua W. Hagen, Wu-Min Deng and Eric C. Lai, A comprehensive *in vivo* screen for anti-apoptotic miRNAs indicates broad capacities for oncogenic synergy, Developmental Biology (2021) https://doi.org/10.1016/j.ydbio.2021.02.010 [1].

Value of the Data

- This is the first comprehensive genetic screen of in vivo miRNA activities in the developing eye.
- Any *Drosophila* researcher will be able to use these data to assess if a miRNA of interest can affect eye morphology when overexpressed.
- These data can be used to check if any individual miRNA of interest has in vivo impact in the powerful eye model. In addition, these data can be used as a pre-screen for other followup studies. For instance, one can take the miRNAs that induce phenotypes in the eye and compare them to other tissue-specific screens. In addition, one might use these miRNA data to discover synthetic phenotypes with other genetic perturbations, or conduct modifier screens in sensitized backgrounds.

1. Data Description

Fig. 1. Montage of adult *Drosophila* eyes expressing different *UAS-DsRed-miRNA* transgenes under control of the *GMR-Gal4* driver. All images are from adult females. *Canton-S* and *GMR-Gal4* (heterozygous transgene) exhibit normal eyes with crystalline ommatidial patterning. Activation of representative miRNAs during eye development yields diverse classes of adult eye defects. Examples of eye phenotypes include rough eyes of varying degrees, larger or overgrown eyes, necrosis, interommatidial bristle defects, glazing, or altered pigmentation.

Supplementary Table 1. Complete screen results of *UAS-miRNAs* tested against *GMR-Gal4*. We describe the results of the miRNA misexpression screen in the developing eye. We utilized a controlled vocabulary to describe phenotypes, and also included descriptive phenotypes as appropriate. The collection initially started with often multiple independent insertions of each transgene.
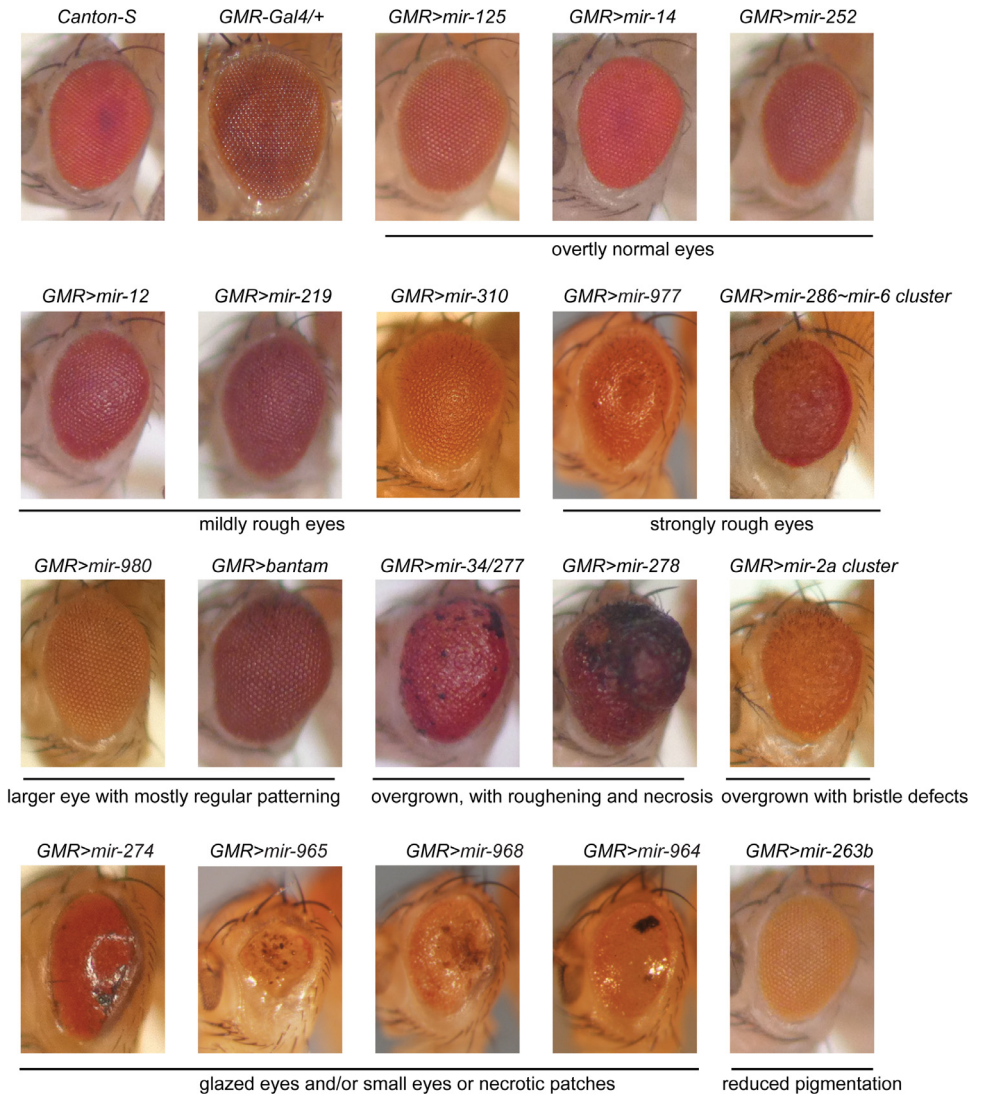
Fig. 1. Montage of adult *Drosophila* eyes expressing different *UAS-DsRed-miRNA* transgenes under control of the *GMR-Gal4* driver. All images are from adult females. *Canton-S* and *GMR-Gal4* (heterozygous transgene) exhibit normal eyes with crystalline ommatidial patterning. Activation of representative miRNAs during eye development yields diverse classes of adult eye defects. Examples of eye phenotypes include rough eyes of varying degrees, larger or overgrown eyes, necrosis, interommatidial bristle defects, glazing, or altered pigmentation.

Note that most of the transgenes contain DsRed in the backbone, although some do not carry a fluorescent marker (see information in the "transgene-internal stock name" column). Also note that many miRNA operons are represented as the full operon (or as a transgene with multiple members), but also often as individual members of the cluster. We considered those phenotypes that were qualitatively similar amongst two or more insertions to be due to the misexpressed miRNA, as opposed to a transgenic position effect. We selected up to two independent insertions as representative for that miRNA transgene for subsequent studies (e.g., see Bejarano, Developmental Biology 2021).

Supplementary Table 2. Summary of *Drosophila* miRNAs that induced eye phenotypes.

In total, we analyzed 544 *UAS-miRNA* transgenic lines comprising 166 different constructs. activated by *GMR-Gal4*. Of these 100 constructs did not induce overt phenotypes (or the defects were not reproducible across insertions), while 66 generated phenotypes (eye defects or lethality) that were reproducible amongst two or more individual insertions of the miRNA construct.

2. Experimental Design, Materials and Methods

2.1. Drosophila *genetic screen of miRNA activities in the eye*

We previously described a genomewide collection of conditionally inducible *Drosophila* miRNA transgenes [2]. We used these to examine the consequences of systematically activating these in the developing eye. To do so, we crossed *UAS-DsRed-miRNA* lines to the *glass multimer reporter-Gal4* (*GMR-Gal4*) driver, which is predominantly active in cells posterior to the morphogenetic furrow of the developing eye [3]. The screen assayed 536 transgenes covering 166 distinct miRNA constructs. These typically comprise multiple independent insertions of each construct, and included both solo miRNA loci and miRNA clusters, as well as individual miRNA constructs extracted from the clusters [2]. Crosses were maintained on standard cornmeal-molasses media at 25°C and 60% humidity and the relevant progeny were examined under a dissecting microscope.

The regular crystalline structure of the wildtype *Drosophila* eye facilitates identification of various defects in exterior patterning. Phenotypes recorded included rough eyes, smooth eyes, pigmentation defects, necrosis, small or large eyes. Although the eye is not needed for viability *per se*, some miRNAs induced lethality. This can be accounted for by the spatially broader expression of *GMR-Gal4* outside of the eye [4,5]. Phenotypes that were qualitatively reproducible across independent insertions were considered to represent activities of the miRNA *per se*, as opposed to chromosomal position effects. The miRNA phenotypes are described using a controlled vocabulary and supplemented with additional descriptions. On the basis of these data, we were able to define two functionally representative insertions of each of *UAS-DsRed-miRNA* construct, which were saved as part of the transgenic collection.

Ethics Statement

No human subjects were studied and no vertebrate animals were studied.

CRediT Author Statement

Fernando Bejarano: Experimental execution. **Eric Lai:** Conceptualization, Manuscript preparation.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships which have or could be perceived to have influenced the work reported in this article.

Acknowledgments

Supplementary Materials

Supplementary material associated with this article can be found in the online version at doi:10.1016/j.dib.2021.107037.

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