Darach Miller

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Education

PhD Biology, New York University, New York, NY, USA
  Genomics and Systems Biology track, dissertation adviser David Gresham

September 2012
- February 2018

B.S. Genetics, University of California at Davis, Davis, CA, USA
  Minor in Quantitative Biology and Bioinformatics

September 2007
- December 2011

Publications

Steady-state and dynamic gene expression programs in response to variation in environmental nitrogen

April 2016

Molecular Biology of the Cell

Edoardo Airoldi, **Darach Miller**, Rodoniki Athanasiadou, Nathan Brandt, Farah Abdul-Rahman, Benjamin Neymotin, Tatsu Hashimoto, Tayebeh Bahmani, David Gresham

> We explored the transcriptome reponses of budding yeast to changes in environmental nitrogen. I used mRNA dynamics modeling and 4-thiouracil pulse-chase labeling with qPCR to identify and confirm some mRNA subject to destabilization upon a re-feeding of nitrogen.

Growth Rate-Dependent Global Amplification of Gene Expression

Preprint, pending

Pre-print on bioRxiv   Revising for resubmission

Niki Athanasiadou, Benjamin Neymotin, Nathan Brandt, **Darach Miller**, Daniel Tranchina, David Gresham

> We explored the scaling of the yeast transcriptome with growth rate, using a novel statistical normalization method for using spike-ins with RNAseq. To confirm these results, I designed, optimized, and used a flourescent poly-dT probe flow cytometry assay as orthoganol confirmation.

Presentations

Accelerated mRNA Degradation Contributes to Gene Expression Remodeling During a Nitrogen Upshift

August 2017

Workshop talk @ 2017 International Conference of Yeast Genetics and Molecular Biology

Darach Miller, David Gresham (NYU)

High-throughput Genetics of mRNA Dynamics using FISH, FACS, and Sequencing

August 2017

Talk @ New York Area Meeting in Quantitative Biology

Darach Miller, David Gresham (NYU)

Genetic factors controlling accelerated mRNA degradation during a nitrogen upshift (video)

July 2016

Platform talk during yeast community's main session @ GSA's TAGC16 in Orlando

Darach Miller, David Gresham (NYU)

Screening and Investigating Interactions Between Haloarchaeal Species

April 2011

Talk @ UCDavis Undergraduate Research Conference

Darach Miller, Marc Facciotti (UC Davis)

Posters

mRNA stability regulation accelerates functional reprogramming of the yeast transcriptome during a nitrogen upshift
Poster @ CSHL Eukaryotic mRNA processing meeting
Darach Miller, David Gresham

August 2017

Accelerated mRNA degradation contributes to gene expression remodeling during a nitrogen upshift
Poster @ ICYGMB annual meeting.
Darach Miller, Benjamin Neymotin, David Gresham

September 2015

Teaching

Quantitative Methods in Human Genetics
Undergraduate-level course

Spring 2015,
Spring 2016

Designed and taught introductory R to explore examples of relevant statisical methods

Applied Genomics: Intro. to Bioinf. & Network Modeling
Graduate-level course

Fall 2013

Designing and running practice in the analysis of genomics datasets using techniques such as network clustering and transcript dynamics modeling.

Principles of Biology
Undergraduate-level course

Fall 2012

Coordinate exercises in benchwork and data analysis of basic molecular biology and genetics.

Students

Daniel Pham, Undergraduate at North Park University
Mentored as part of 2017 Summer Undergraduate Research Program
Finishing undergraduate studies

Summer 2017

Alex Ferrena, Undergraduate at New York University
Former student, mentored his transition into bioinformatics
Starting MS Bioinformatics program at Columbia

Fall 2016

Stephen Nyarko, Student at Stuyvesant High School
Mentored design of a yeast genetic screen for a science competition
Starting undergraduate studies at Harvard

Fall 2015,
Summer 2016

Awards

NYU Departmental Kopac Teaching Award
For the best TA (after the first year), here for work on the graduate-level Applied Genomics course

2013-2014

NYU Departmental Kopac Service Award
For making a contribution to the department's academic environment, in organization of peer-to-peer skills workshops and social events.

2014-2015

Training

CSHL Yeast Genetics and Genomics Course   Summer 2015

Three-week intensive course on the fundamental methods and practices of yeast genetics, instructed by Brown, Dunham, and Gartenberg.

The Art & Craft of Teaching   Fall 2015

Semester-long course on the theory and practice of university teaching, especially focused on engaging students in active learning and using assesment effectively.

Experience, skills

Budding yeast methods
- General handling, culturing in batch and chemostat, genetics, crossing and dissection
- mRNA FISH, specific (Stellaris and Affymetrix) and general (poly-A homebrew)

Molecular biology
- Nucleic acids from extraction to sequencing, primarily mRNA using a lab-homebrew RNAseq protocol
- Developed a low-input amplicon library preparation protocol
- 4-thiouracil metabolic-labeling experiments
- RT-qPCR

Flow cytometry
- Designed (poly-dT hybridization) and optimized several assays (mRNA FISH, FITC, SytoxGreen)
- Experienced with a BD Accuri C6; trained but not independently approved to solo a BD Aria

Other wet-bench
- Haloarchaea culturing and genetic manipulation
- Parafilm and araldite embeding and sectioning of mouse tissue

Scripting/programming languages
- **R** is my primary working language for analysis. Very familiar with `ggplot`, familiar with `tidyverse` packages. Modeling experience, using `lm()` and `mle()` for transcript dynamics, growth phenotypes, flow cytometry & Sort-seq
- **Python** used to develop a combination UMI-extractor and amplicon-splitter using `BioPython` and `multiprocessing` queues
- **Perl** was first language, took an introductory comptuer science course in **C**.

Linux/Unix systems, bioinformatics
- Used a HPC system with PBS and SLURM scheduler to develop and run pipelines for sequencing quantification and modeling. Used *in silico* benchmarking simulations to optimize tools for RNAseq alignment, amplicon barcode calling, and for extracting and using UMIs.
- Using Linux-only as personal system since 2010: Ubuntu 10.04, then Crunchbang, then Arch for the last five years

Other computational
- LaTeX, `pandoc` (this), `git`, `Makefiles`
- Basic ImageJ batch scripting, some `EBimage`

Research experience

Doctoral research, Gresham lab, New York University

<div style="text-align: right">Summer 2013 - current</div>

mRNA stability changes can be used to effect rapid changes in gene expression during enivronmental changes. I used transcript dynamics modeling to infer candidate mRNAs that are destabilized during a nitrogen upshift, and adapted 4-thiouracil labelling methods to demonstrate that the destabilization occurs using a pulse-chase qPCR experiment. I then scaled the method up to use RNAseq and made some analytical advances to demonstrate that the destabilization is more general than the Nitrogen-Catabolite-Repression regulon. To determined the *trans* genetic factors of this, I redesigned a Fluorescent In-Situ Hybdridization protocol to measure mRNA FISH with flow cytometry, then redesigned barcode-sequencing protocols to more robustly handle low-input fixed cell samples with a more advanced error-correcting amplicon design, then combined these approaches with Sort-Seq modeling to estimate mRNA abundance dynamics for 3,300 mutants in a pooled library. This assay confirmed the role of previously known mRNA synthesis control, the central role of the Lsm1-7p/Pat1p complex in eukayrotic mRNA degradation, and pointed towards translation initation events mediated by elements in the 5' UTR as contributing to the destabilization.

Summer internship, Baliga Lab, Institute for Systems Biology

<div style="text-align: right">Summer 2011</div>

I worked to develop a high-throughput forward-genetic transposon-sequencing screen for Halobacterium salinarum. My contribution was improving the efficiency of haloarchaea transformation, so I adapted lipofection reagents from mammalian cell-culture systems to improve transformation efficiency, and characterized the efficiency of the *in-vitro* transposition reaction.

Undergradaute research, Facciotti Lab, University of California at Davis

<div style="text-align: right">Fall 2010 - Spring 2012</div>

Haloarchaea express genes that facilitate competition via secreted anti-microbial compounds. I designed and carried out a 60x60 all vs. all inhibition screen via spot assays, to characterize the network of pair-wise interactions. I then used BLAST on their recently completed genome assemblies to identify homologs and identified one genetic factor that explained some profiles of growth inhibition.

Other experience

Social media coordinator, Yeast Course, Cold Spring Harbor Laboratory

<div style="text-align: right">2017 - current</div>

Working to build a social media presence for the the CSHL Yeast Course. Building an alumni list and connecting alumni across years to help attendees and boost recruitment of new attendees from outside the community.

Research technician, van Winkle Lab, UC Davis

<div style="text-align: right">2008 - 2009</div>

Microscopy sample preparation (mouse disection via microtome).

Bike mechanic/instructor, Davis Bike Collective

<div style="text-align: right">2007 - 2012</div>

Volunteer mechanic/instructor and shift supervisor at community bike shop. Lots of teaching and reconciling bicycle theory with the extensive natural variation in design and function. Never met a seatpost I couldn't extract.

Note: This document's content is written in YAML and typset by Pandoc into HTML and PDF. Source code of YAML and pandoc templates available on github.