Rochester Academy of Science™

BULLETIN

"An organization of people interested in the Natural Sciences"

December 2023 January 2024; Vol. 77, #11

President's Message

2023 Scientific Paper Session

Did you get to our 49th annual Fall Scientific Paper Session at RIT this past November 4th? It was an exciting time. The faculty at RIT's School of Physics and Astronomy, led by our own Dr. Michael Richmond, did an excellent job in planning and delivering this program and provided a small army of competent student volunteers to help with every aspect. It was a pleasure to work with them.

The leading purpose of this society is and always has been to promote scientific study and research. We provide public outreach programs and we have many opportunities to serve our members. However, I believe that our greatest contribution to the advancement of science is in nurturing young scientists and encouraging them to continue their careers in the sciences. The Scientific Paper Session is our flagship program in this area. For many students, this is their first time publicly presenting a poster or oral report on their research.

We had more than 270 people attend, to see the 79 posters and hear the 30 oral presentations – substantially more in each than last year. Attendees came from 19 Upstate New York schools – Corning Community College, Finger Lakes Community College, Hobart & William Smith Colleges, Houghton University, Ithaca College, Keuka College, Nazareth University, Niagara University, Rochester Institute of Technology, St. John Fisher University, SUNY Brockport, SUNY Buffalo State University, SUNY Corning Community College, SUNY Environmental Science and Forestry, SUNY Geneseo, SUNY Oswego, University of Rochester, and Wells College.

You will see articles in the next few Bulletins high-lighting a few of the research projects presented.

The Astronomy and Fossil Sections ran outreach display tables for attendees. We also had a table with past issues of *Proceedings of the Rochester Academy of Science*, with issues going back to 1892.

After lunch, we reconvened in the 1250 Auditorium where Michael Richmond and I welcomed all. We introduced our two keynote speakers Roger Easton, Jr. of RIT's Carlson Center for Imaging Science partnered with Dr. Jeyhan Kartaltepe of RIT's School of Physics for the Annual Larry King Memorial Lecture. This was well attended.

A video was made of the two talks. It is available at https://rasny.org/paper-session.

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Renew Your Membership

Unless you are a Life Member, note that your membership will expire on December 31, 2023. Please renew your membership at your earliest convenience. Use this link to renew. https://rasny.org/how-to-join.

If you are a Life Member, consider making a donation to the RAS.

2024 Eclipse Watch

On December 1st, 2023, it will be just **128** days until the total solar eclipse passes through Rochester on Monday, April 8, 2024. I noted last month that one unusual spectacle to watch for is the moon's shadow speeding across the earth's surface.

Yes, I'm bein' followed by a moonshadow, Moonshadow, moonshadow. – Cat Stevens

There is an interesting simulation of the moon's shadow moving from Sinaloa Mexico, where it comes in from the Pacific Ocean, to Eagle Pass, TX, where it crosses the US border, and the across the United States. If you start it at 2:15, you can follow it from western Ohio as it approaches Buffalo and Rochester. https://www.greatamericaneclipse.com/april-8-2024. For each locality on the center line, it gives the time of totality, duration of totality, speed of the Moon's shadow across the earth's surface, and the width of the path of totality. For Buffalo, totality starts at 3:18PM and lasts 3 minutes and 45 seconds. The moon's shadow is speeding at 2,254 MPH and the width of the shadow is 111.1 miles. For Rochester, totality starts at 3:20PM and lasts 3 minutes and 40 seconds. The moon's shadow is speeding at 2,315 MPH and the width of the shadow is 110.6 miles.

On another note, people have asked if they can reuse their eclipse glasses left over from previous events. The American Astronomical Society says modern eclipse glasses do not expire. If the glasses were compliant with the ISO 12312-2 standards (in effect from 2015 on) and have no punctures, scratches or tears, they should be fine as long as the filters/lenses remain

attached to the frames. In other words, if you stored them carefully, you can use them again. On the other hand, glasses are so cheap and eyes so valuable, that I will be using new glasses even though I still have mine from 2017.

Jim Seidewand in an ASRAS discussion noted that that you should keep in mind to buy your glasses from a valid source. Rainbow Symphony and American Paper Optics are the two main manufacturers, close to the astronomy community, and those are tested and approved by the American Astronomical Society. Note that many of the glasses sold on Amazon were found by the AAS to be counterfeit, although most tested ok. If you get your glasses from RAS/ASRAS or the RMSC, you will have the good ones.

Student Grants program

We have announced the 2023-2024 Student Grants program run by the RAS to all the local area colleges.

This past January, the RAS Grants Committee awarded a total of $5750 for ten research projects. The maximum amount of each grant is $700 for research, plus a $50 unrestricted grant to the author of our top submission. Last year's grant financing was permanently increased by the RAS Board and ranged from $400 to $750. We were able to give ten awards due to the generosity of our members.

Five of these were featured in articles in the Bulletin this past year. I hope that you enjoyed these. In June, you saw the report on **Amaya Bechler's** research (Cornell University) on whether the gut microbiome and diet is modulated to meet the energetic demands of reproduction and molt in migratory songbirds, using black-throated blue warblers.

In July, the research project of **Noor Zamamiri** (Syracuse University) was examined. She studied whether an inserted gene (β-glucosidase) in poplar plants was weakening the cellulose in the cell wall, which would make poplar more useful as a biofuel source.

Gabriella Orfanides is developing a reliable methodology to assess chronic physiological stress of songbirds using heat shock proteins. She was featured in our August issue.

In September, we reported on **Charly Campanella** (St. John Fisher University) and her research into TET2 (Ten-Eleven Translocation-2) and whether this human gene is necessary for the creation of red blood cells (erythropoiesis) with a goal of contributing to development of treatment for diseases such as anemia and myelodysplastic syndrome (MDS).

Lastly, in October we had the study of male black-throated blue warblers by **Braeden Thomson** at Cornell University to see if increased metabolic demands during reproduction caused oxidative stress through the over-production of reactive oxygen that can damage lipids, proteins, and DNA.

We ran these articles to show you the type of cutting edge research that is being done at our local colleges and universities by undergraduate students working with talented advisors. The RAS grants are important not only because they support research by developing young scientists, but also because they are given significant weight in qualifying these scholars for graduate schools and scholarships. A grant from the RAS is a prestigious award for them.

If you would like to help sponsor an additional award, please contact me to set up a donation.

No part of our annual dues is used to make these awards. We can only make an additional award with the donations made by members by December 15. I invite you to join me in contributing, however small, to the Rochester Academy of Science Student Grants program.

* * *

Thanks for all the help!

My thanks for helping at the RAS Paper Session to members Noveera Ahmed, Frank Bov, Jutta Dudley, Tony Golumbeck, Helen Haller, Santosh Kurinec, John Handley, Larry Hirsch, Dan Krisher, Logan Kusher, Theodore Lechman, Elizabeth Pixley, Michael Richmond, Linda Saalman, Alex Smith, Tim Tatakis, James Zollweg, Karen Wolf, and Kevin Zwiebel. Between them they covered poster frame set–up and take-down, moderating oral sessions, greeting and registration, food service monitoring, photography, and outreach tables. Wow!

* * *

Volunteers Wanted for RMSC Program

On December 30 and 31, the Rochester Museum and Science Center will be having their closing weekend of their school break week special program, STEAM through the Eras. (STEAM is STEM plus art. The fields are the areas of science, technology, engineering, the arts, and mathematics.) They would like volunteers who have experience with microscopes to work with kids looking through microscopes at slides and objects from our education department and found on our grounds. If you can help, let me know at mgrenier@frontiernet.net. ASRAS (Astronomy) and Fossil Sections will also have interactive display tables set up and could use help there. The programs run from 11AM to 3PM, and any hour or more that you can come would be appreciated.

Michael Grenier, President RAS

Events for December 2023, January 2024

NOT MEETING IN DECEMBER:
Mineral
Herbarium
RAS Board

NOT MEETING IN JANUARY:
Fossil

DECEMBER, 2023 EVENTS

Dec. 6 Wed: ASRAS Board meeting
7:00 p.m. At U of R. ASRAS members are welcome. Contact: Anthony Golumbeck at semp@use.startmail.com.

Dec. 1 Fri: Astronomy Members Meeting
6:30 p.m. – 9:45 p.m. Annual holiday extravaganza at the Planetarium, 697 East Avenue, Rochester. Bring an appetizer, dessert or dish to pass. Contact: Anthony Golumbeck at semp@use.startmail.com.

Dec. 5 Tue: Fossil Section Meeting
7:30 p.m. Meeting will be held in the community meeting room at the NEQALS building, 1030 Jackson Rd., Webster 14580. The meeting will feature the return of our annual Show-n-Tell and Pizza party. The section will provide Pizza and drinks while members are asked to bring some of their choice fossil finds from the past couple of years. For meeting details and login info see the *FossiLetter* or contact Michael Grenier at paleo@frontier.com. It will not be broadcast on Zoom.

JANUARY, 2024 EVENTS

Jan. 5 Fri: Astronomy Members Meeting
7:30 p.m. – 9:30 p.m. RIT, Carlson Building, room 1125. The speaker will be Jeff Heavy from L3 Harris who will speak about the Chandra X-Ray Observatory. Contact: Anthony Golumbeck at semp@use.startmail.com.

Jan. 10 Wed: Herbarium
1:00 p.m.-4:00 p.m. The Life Sciences section will hold a workshop at the RAS Herbarium, located in the basement of the Rochester Museum and Science Center (RMSC). We will be continuing to organize plant specimens in preparation for digitizing the collection. If you plan to attend, please send an RSVP to Elizabeth Pixley. At RMSC go to the front desk to meet other participants. For more information, contact Elizabeth Pixley, herbarium curator (334-0977 or eypixley@gmail.com).

Jan. 17 Wed: RAS Board Meeting
7:00 p.m. – 9:00 p.m. Church of the Ascension. Contact: Michael Grenier, mgrenier@frontiernet.net

Jan. 23 Tues: Mineral Section Virtual Meeting
7:00 p.m. Zoom only. Program to be determined. Contact: Jutta Dudley, juttasd@aol.com.

ONGOING EVENTS EVERY MONTH:

STRASENBURGH OBSERVATORY
ASRAS will operate the telescope at Strasenburgh Planetarium on mostly clear Saturday nights. Contact: Jim Seidewand (585) 703-9876.

Rochester Research in Review.

(These are Hot Links which when clicked lead to the press release on the Science Daily website.)

Keeping a human in the loop: Managing the ethics of AI in medicine. University of Rochester

Familiarity breeds contempt for moral failings. Cornell University

Microplastics' shape determines how far they travel in the atmosphere. Cornell University

With unprecedented flares, stellar corpse shows signs of life. Cornell University

Temperature variability reduces nesting success. Cornell University

Paleoclimatologists use ancient sediment to explore future climate in Africa. Syracuse University

The Goldilocks Effect: Researchers establish framework for protein regulation. Syracuse University

M33 by John Larysz

2022-2023 Undergraduate Student Research Grant Award Winner

By Derek Emrich, Rochester Institute of Technology.

Derek Emrich; photo provided by author.

Abstract

Transcriptomics is the study of the complete set of transcribed RNA from genomic DNA in an organism. Transcribed DNA produces mRNA in all life forms. In eukaryotes, most mRNA molecules have a poly(A) tail added at their 3' end. Biomedical research uses the transcriptome to study gene expression and regulation in cells. There are only a limited number of ways to purify these tailed RNA from total RNA. These methods inherently have limitations in selectivity and sensitivity, leaving a gap in our understanding of transcription and regulation.

Introduction

Transcriptomics is the study of all RNA transcripts produced by the genome under different conditions or in different cell types. Messenger RNA (mRNA) is single stranded RNA produced by genomic DNA which is then used for protein synthesis. In eukaryotes, mRNA often contains a long polyadenylated tail called the poly(rA) tail. These mRNAs represent gene expression and can change in different cell types, including different cellular disease states. Researchers often use these tails as targets to isolate the mRNA from total RNA. The traditional method for capturing the poly(rA) tail involves using short strands of thiamine with a DNA backbone called oligo(dT). The poly(rA) tail of mRNA binds to the oligo(dT) strands forming an antiparallel duplex. The non tailed RNA is washed off leaving the mRNA behind.

We have been using strands of locked nucleic acids (LNA) with adenine nucleotides, (i.e. poly(LNAA)). These strands of poly(LNAA) form parallel duplexes at pH 5.5 and may form in high ammonium concentrations. Under these conditions poly(LNAA) binds strongly to the poly(rA) tail of the mRNA and the poly(LNAA)–poly(rA) interaction exceeds the melting temperature of the oligo(dT)-poly(rA) bond. Our new method could potentially improve the capture of low abundance mRNA, giving a better understanding of a cell's transcriptome.

See Figure 1 on page 6.

Methods

Total RNA Extraction

This is the protocol we are currently using for total RNA extraction from Saccharomyces cerevisiae, aka bakers yeast.

Buffers

P1

- 50 mM Tris-HCl pH 8.0
- 10 mM EDTA

P2

- 200 mM NaOH
- 1% SDS

N3

- 4.2 M Gu-HCl
- 0.9 M potassium acetate
- pH 4.8

RW1- RNA Wash- Originally we used RNA Wash From Monarch RNA Cleaning Kit

- 20% Ethanol
- 900 mM GITC
- 10 mM Tris-HCl pH 7.5

Binding Buffer

- 5 M GuHC
- 30% Isopropyl Alcohol

Methods

First prepare an overnight culture of Saccharomyces Cerevisiae in YPD broth. We used 50mL of a 300mL culture for each extraction, but 25 mL of overnight growth at 30*C should be sufficient. Pellet cells and pour off supernatant.

Then resuspend the cells in 400uL of P1 buffer and transfer to a 1.5mL tube. Then add 10uL of RNAse IN. Then add 150uL 10X solution of DTT. Add approximately 200mg of glass beads. Vortex the mixture horizontally at max speed for 10 minutes in 4*C.

After vortexing, add 400uL of P2 buffer, invert tube to mix. Let the tube incubate for no more than 5 minutes. (A longer incubation time increases the risk of genomic DNA shredding and staying in solution). Neutralize the P2 buffer using the N3 buffer. Invert the tube multiple times in order to mix, do not vortex. Incubate on ice for 5 minutes. Centrifuge the mixture at 15000 RPM for 20 minutes. Collect 750uL of supernatant and transfer to fresh 1.5mL tubes. Discard the tube with the pellet. Then add 750uL of absolute ethanol to the collected supernatant and immediately mix. Prepare the silica matrix by adding 50uL of binding buffer. Add up to 850uL of sample to the column. Spin at 9000 RPM for 30 seconds, discard flowthrough. Repeat this step until all of the solution has been passed through the column. Then wash the column with 500uL of RNA wash buffer twice. Centrifuge for 30 seconds between each wash. Discard flowthrough after each wash. After the two washes then centrifuge for 3 minutes to remove the residual wash buffer. Transfer the column to fresh 1.5 mL tubes. Add 100uL of nuclease free water to the center of the silica matrix, do not run the water down the walls of the column. Incubate at room temperature for 1.5 minutes. Then centrifuge at 9000 RPM for 1.5 minutes. Columns can be saved and cleaned if desperate, but otherwise discard the column and collection tube. Store the eluted RNA at -80*C until future use. The total RNA concentration and purity was measured using a Nanodrop 2000. The quality of the extracted RNA was determined using gel electrophoresis.

See Figure 2 on page 6.

Performance

Image Lab Analysis

After reverse transcription and pcr, the samples were analyzed using gel electrophoresis. We used final concentrations of 2% Agarose, 1X Tris-Acetate EDTA, (TAE), and 0.5X Gel Red per gel. The gels were run in 1X TAE buffer at 100V until the loading dye was about ¾ total distance. The gels were imaged using Bio-Rad Gel Imager and analyzed using the Image Lab software. The software is able

to measure the intensity of each band present in the gel. For each trial we set the trials input as one and the other samples were a ratio of sample to input. Finally we adjusted the ratio for the volume of each sample in the same manner, using the input volume. Our initial trials were showing that the unbound was higher band intensities than the input. We never conclusively determined the cause of this, but as our competence increased we stopped seeing this problem in qPCR.

See Figure 4 on page 6.

In figure 4 we compare mRNA isolation trials using the LNA probe at pH 4.5 and oligo(dT) at pH 7. We can see that the Unbound is higher than the input sample. The LNA samples were eluting tailed target mRNA. There did appear to be more non-tailed targets in the LNA elution than the oligo(dT) elution. This could be due to the inherent limitations of this analysis method. The results of figure 5 show that we were able to form the parallel duplex using 1M ammonium sulfate in the SSC buffer. Future trials with qPCR did not show the same results. More testing would need to be done in order to draw conclusions.

Quantitative PCR analysis

Quantitative PCR is able to measure the starting quantity of a template. This is possible by creating a standard curve using standards of known concentration. In order to quantify the cDNA in the samples, I first needed to generate standards of the PCR template. I did this by purifying the PCR product and normalizing the concentrations to 10.0ng/Ul. Then I made one tenth serial dilutions to 1fg. I was able to do qPCR thanks to Dr. Osgood, who generously let me use his Bio-Rad CFX 96 real time quantitative PCR machine. I made two replicates of the standard reactions per primer. The software then uses the linear regression to quantify the quantity of the unknown samples. The first thing we noticed was that the oligo(dT) samples had extremely high starting quantities in the input with probe and the unbound. We researched the observation and realized that it most likely is caused by the selective priming of poly(A) tailed mRNA by the oligo(dT) probe. This was observed multiple times and it is known that poly(a) tailed mRNA can be primed for reverse transcription by the oligo(dT). Figure 6 shows the high signal from the input and unbound samples of oligo(dT) after the probe is added. In Figure 7 we removed the Input with probe sample in order to compare the elutions. The elutions are within error of each other and more testing will be needed in order to produce the most accurate analysis.

See Figures 7, 8 on page 6.

We also measured the ribosomal 18 subunit RNA, 18s rRNA, as a measure of enrichment. Since 18s rRNA does not have a poly(a) tail, the starting quantity of the elution should be much less than the input. In Figure 8 we see the rRNA target produces much less signal in the elution than in the input. We noticed that the LNA unbound sample has less signal than the oligo(dT), which suggests there was more rRNA removed from the input. The elution shows that it did not carry over. Our previous experiments suggested that the rRNA may be non selectively binding to the plastic tube and the beads under low pH conditions.

Practical Application

A common use of oligo(dT) purified mRNA is to measure expression levels of mRNA of interest. Heat shock proteins are well studied and are overexpressed in many different organisms. We chose to do an expression analysis of heat shock protein 42, HSP42, in the yeast. In order to do the experiment we first needed to find housekeeping genes which are used as a non changing reference which to measure the change of expression against. We decided that ubiquitin conjugating enzyme 6, UBC6 would be a good reference gene. I grew two liquid overnight cultures of S. cerevisiae at 30*C. I then incubated one culture at 42*C for two hours and the other at 30*C for two hours. I performed the total RNA extraction of each culture and used qPCR to determine the Ct values of each sample, then used the Bio-Rad software to calculate the 2–ΔΔCt to determine normalized expression levels of HSP42 in both cultures. In Figure 9 we see the results of the expression analysis, which shows oligo(dT) and LNA performing similarly.

See Figure 9 on page 6.

Conclusion

Our initial observations provided evidence that LNA-A could be used as a probe for mRNA isolation. After receiving funding from the Rochester Academy of Science we were able to explore this possibility further and perform a more quantitative experiment. Our results suggest that the LNA-A probe is forming a parallel duplex with the poly(a) tailed mRNA, and we are able to enrich poly(a) tailed mRNA from non tailed mRNA. When compared to oligo(dT) our results showed that they were almost identical in the quantities and expression of the targets we chose. Initially using ammonium sulfate at a neutral pH seemed to be promising, but then the qPCR experiments revealed that may not be the case. The higher melting point of the LNA parallel duplex led us to hypothesize that shorter tailed mRNA, which otherwise could be missed by oligo(dT), would be captured by the LNA probe. We already have future experiments planned, using poly(a) polymerase, to test the minimum tail lengths that each probe can capture. With more funding, we will also be able to get RNA sequencing of each sample from both probes. This will allow us to extensively analyze the similarities and differences in the outcomes. Our team believes that there are ways to optimize the method to provide a unique insight on future transcriptome profiling, and a better understanding of nucleic acid interactions in general.

(*Edited for brevity*)

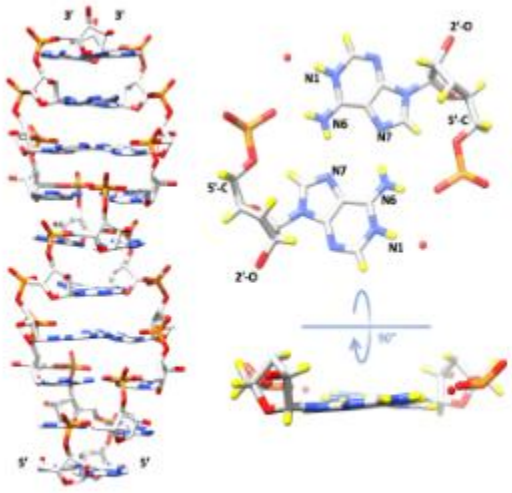


Fig 1. 3D representation of the LNA duplex. This image is directly from (Pickard, 2020)

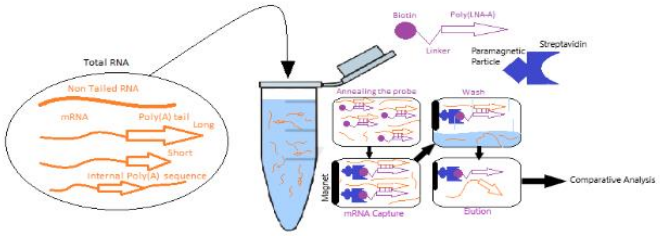


Figure 2- A depiction of the mRNA isolation procedure.

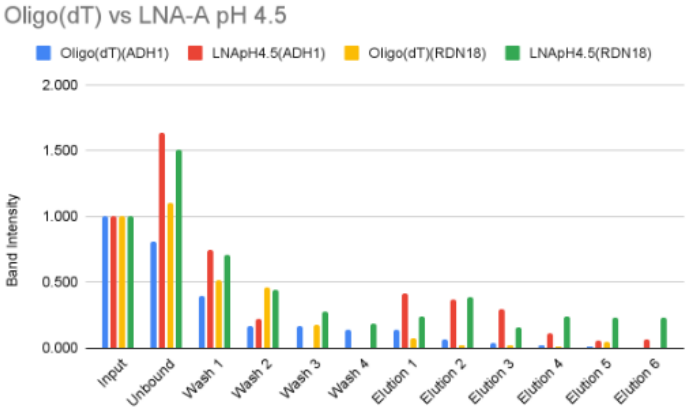


Figure 4- Histogram showing the quantity of cDNA per sample relative to the Input. This is comparing the LNA-A probe to the Oligo(dT) probe for tailed target(ADH1) and untailed(RDN18)

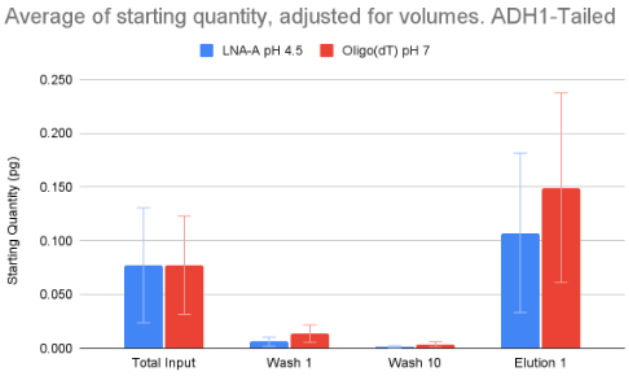


Figure 7- Using the qPCR standard curve we were able to estimate the starting quantity of our target in each sample. This histogram omitted the input with probe.

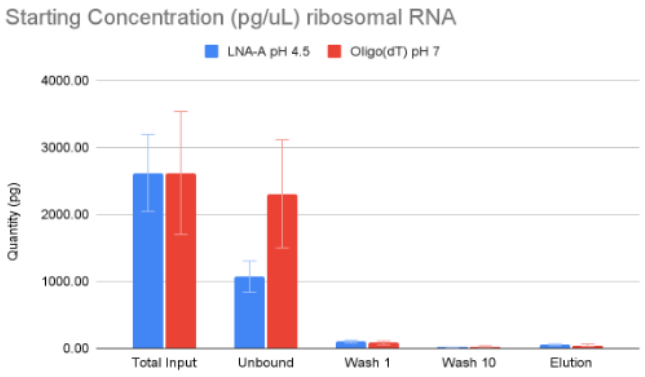


Figure 8- This histogram shows the starting quantity, using the standard curve method, of ribosomal RNA in each sample.

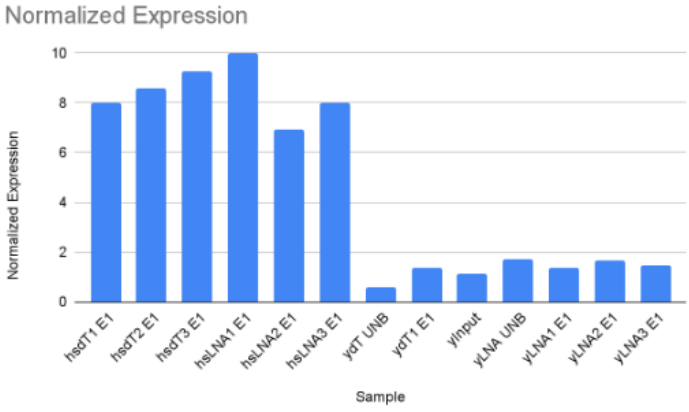
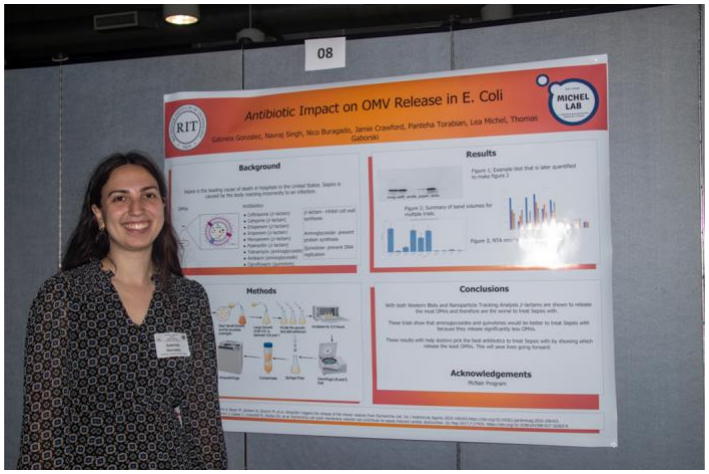
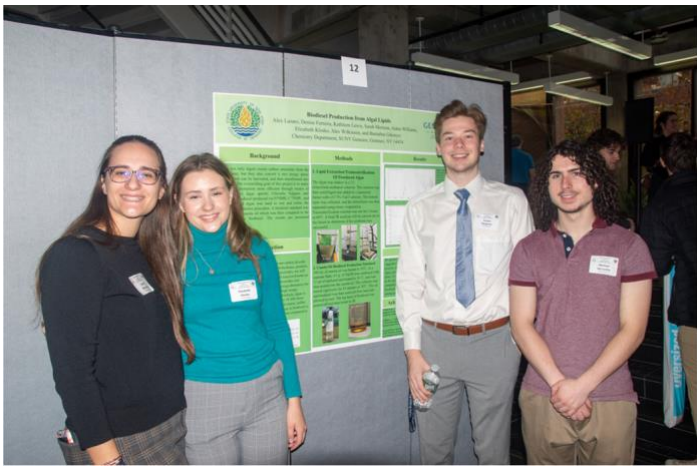


Figure 9- Using the $2^{-\Delta\Delta Ct}$ method, we determined the normalized expression of HSP42 when the yeast culture is heat shocked vs un-shocked. Hs designates heat shocked, y designates non shocked.

Fall Paper Session Poster Presentations
The following are a few posters from the November, 2023 Fall Paper Session held at RIT.



Gabriela Gonzalez of RIT. Photo: R. Crumrine



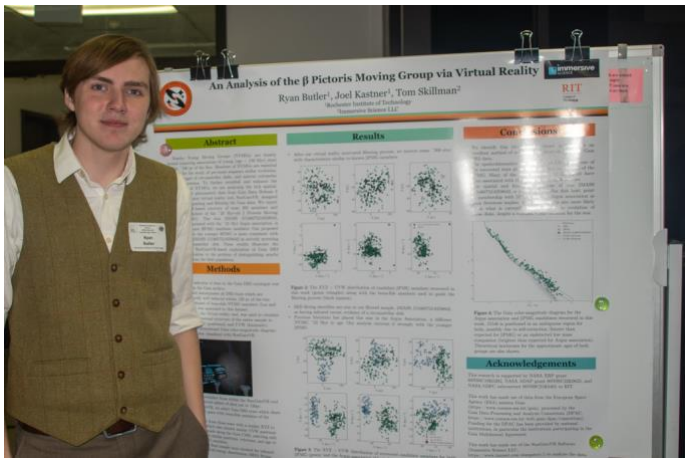
Sarah Mertson, Elizabeth Klosco, Daniel Bergman and Michael McCarthy of SUNY Geneseo. Photo: R. Crumrine

Antibiotic Impact on the Release of Outer Membrane Vesicles in E. Coli
by Gabriela Gonzalez, RIT

Abstract:
Sepsis is currently the leading cause of deaths in hospitals in the United States. Antibiotics are an important part of sepsis treatment, but may contribute to the over-exuberant inflammatory response that is the hallmark of sepsis due to its trigger of the release of outer-membrane vesicles (OMVs) from bacteria. We tested nine different antibiotics from three different antibiotic families, for their effect on OMV release from *Escherichia coli* bacteria. Following incubation of the bacteria with individual antibiotics, we isolated the OMVs using ultracentrifugation and quantified the OMVs using immunoblotting and nanoparticle tracking analysis. Our results show that several commonly used beta-lactam antibiotics significantly enhance the release of OMVs from E. coli, while aminoglycoside and quinolone antibiotics kill the bacteria without significantly enhancing OMV release. These results suggest that the selection of antibiotics may have a significant impact on bacterial OMV production, which could in turn contribute to sepsis-related inflammation.

Biodiesel Production of Algal Lipids
by Sarah Mertson, Elizabeth Klosco, Daniel Bergman and Michael McCarthy, SUNY Geneseo

Abstract:
In the age of climate change, the most important research must go towards finding green energy sources. Algae not only ingest excess carbon emissions from the atmosphere, but they also convert it into energy dense lipids which can be harvested, and then transformed into biodiesel. The overarching goal of this project was to make algal lipid extraction more efficient through means of culturing the algae species *Chlorella vulgaris* and evaluating biodiesel produced via H1NMR, C13NMR, and IR. Powdered algae was then used to test and refine the biodiesel production procedure. A biodiesel standard was created from canola oil which was then compared to the powered algae biodiesel.



Ryan Butler of RIT. Photo: R. Crumrine

An Analysis of the Beta Pictoris Moving Group Via Virtual Reality
by Ryan Butler, Joel Kastner and Tom Skillman, RIT

Abstract:
Nearby Young Moving Groups (NYMGs) are loosely bound comoving associations of young (age < 150 Myr) stars within ~100 pc of the Sun. Members of NYMGs are essential subjects for the study of premain sequence stellar evolution, the late stages of circumstellar disks, and nascent extrasolar planetary systems. To further establish and enhance the membership of NYMGs, we are analyzing the rich spatial, kinematic, and photometric data from Gaia Data Release 3 (DR3) with a new virtual reality tool, StarGateVR, designed for efficiently parsing and filtering the Gaia data. We report a StarGateVRbased recovery of some 200 members and candidate members of the ~20 Myr-old Beta Pictoris Moving Group (BPMG). The star 2MASS J15460752- 6258042, previously associated with the ~55 Myr Argus association, is among these new BPMG candidate members. Our proposed membership in the younger BPMG is more consistent with the status of 2MASS J15460752-6258042 as actively accreting from a circumstellar disk. These results illustrate the potential for StarGateVR-based exploration of Gaia DR3 data in application to the problem of distinguishing nearby young stars from the field population. This research is supported by NASA XRP grant 80NSSC19K0292, NASA ADAP grant 80NSSC22K0625, and NASA/GSFC subcontract 80NSSC21K0401 to RIT.

ABOUT THE ACADEMY

The Rochester Academy of Science™, Inc. is an organization that has been promoting interest in the natural sciences since 1881, with special focus on the western New York state region. Membership is open to anyone with an interest in science. Dues are minimal for the Academy and are listed in the membership application online. Each Section also sets dues to cover Section-related publications and mailings. We are recognized as a 501(c)3 organization.

For information, contact President Michael Grenier at (585) 671-8738 or by email paleo@frontier.com.
The Academy Internet website is http://www.rasny.org or see us on Facebook at https://www.facebook.com/Rochester-Academy-of-Science-792700687474549.

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