

Spring Semester Research Experience (SSRE)

Program Overview

Administered through UNLV's Dr. William W. Sullivan Center for Academic Enrichment and Outreach (CAEO), the AANAPISI STEM 2024 Spring Semester Research Experience (SSRE) offers eligible undergraduates in CAEO's AANAPISI STEM, project the opportunity to conduct research under the guidance of a faculty mentor. The SSRE program, lasting the duration of the entire Spring semester, provides students with a series of training activities and assignments designed to help students gain insight into research at UNLV. By participating in undergraduate research, students are exposed to the process of scholarly inquiry and will develop a host of skills related to critical thinking, academic writing, and presenting research.

Program Guidelines

1. There are no set hourly requirements for student-faculty research—each academic discipline lends itself to unique research hours. Hourly commitments are established through student-faculty agreements. However, if a SSRE student has concerns about the hours he or she is asked to commit to research work, the student should discuss the matter with Terri Bernstein, CAEO's Assistant Director for Undergraduate Research.
2. Each SSRE student will receive a stipend of **\$2,800** to support research activities during the Spring semester. Stipends are disbursed by the UNLV Financial Aid and Scholarships Office in two equal payments (\$1,400 each) to students' MyUNLV accounts. Payments are issued on 3/1/24 and 6/7/24 (approx. dates). **Students who have not completed the required assignments by the specified due dates may have their payments discontinued.**
3. Each SSRE mentor will receive funds totaling \$750 to support supplies and/or travel purchases relevant to their research. Note: These funds are transferred to a Nevada System of Higher Education (NSHE) account designated by faculty mentors. Only persons currently employed by the NSHE are eligible to receive funds for serving as a SSRE faculty mentor. While a SSRE student can be mentored by a non-NSHE faculty member, that faculty member will not receive incentive funds.

SSRE Student Expectations

1. Each student must prepare a **research poster*** to be presented at the Office of Undergraduate Research (OUR) undergraduate research symposium.
2. Each student must submit a one-page, **structured abstract*** detailing the research conducted during the Spring semester. **The structured abstract must be approved by the student's faculty mentor.**
3. Each student must complete the **training activities** and **assignments** specified in the *Program Handbook*.

SSRE Faculty Mentor Expectations

1. Faculty mentors are expected to meet regularly with their mentees to discuss their research projects.
2. Faculty mentors are expected to ensure that their mentees receive proper guidance and supervision to successfully meet the outcomes described in the students' application/project descriptions.


Program Support

In addition to faculty mentors, the following staff are available to provide support for students involved in research:

CAEO Undergraduate Research
Terri Bernstein <i>Asst. Director for Undergraduate Research</i> Contact: terri.bernstein@unlv.edu Hours: Available by appointment

*Upon completion of the research and structured abstract, students' final assignments may be posted in UNLV's Digital Scholarship Repository with permission from all authors involved with the project. To learn more, visit <https://digitalscholarship.unlv.edu/>

**Spring Semester Research Experience (SSRE)
Timeline & Activities****

	Training Activities	Assignments
January	<u>SSRE Orientation Meetings</u>	Participant Confirmation (due by 1/16/24)
February	<p style="text-align: center;"><u>Introduction to Library Databases</u> Dr. Xan Goodman Date: Friday, February 2 Time: 4:30 pm to 5:15 pm Location: Virtual Zoom Link</p> <p style="text-align: center;"><u>Meet your Subject Librarian</u> <i>Library Database Meeting</i></p> <p style="text-align: center;"><u>How to Create a Structured Abstract</u> Dr. Rafael Oganessian Date: Thursday, February 15 Time: 1 pm to 2 pm Location: Virtual</p>	<p style="text-align: center;">Subject Librarian Form (If necessary, due 2/26/24.)</p> <p style="text-align: center;">Structured Abstract Draft I: <i>Introduction & Objectives</i> Resource (due by 2/23/24)</p>
March	<p style="text-align: center;"><u>Mandatory Check-in Meeting</u> <i>(Schedule meeting with Terri by end of March)</i></p> <p style="text-align: center;"><u>Mentor Interview</u> <i>Research Questions & Methods</i></p> <p style="text-align: center;"><u>Making a Research Poster</u></p> <p style="text-align: center;">Use the link below to find the dates this topic will be offered: Link</p>	<p style="text-align: center;">Mentor Interview Form (due by 3/18/24)</p> <p style="text-align: center;"> Mentor Interview.docx.pdf</p> <p style="text-align: center;">Structured Abstract Draft II: <i>Methods</i> (due by 3/29/24)</p>

April	<p><u>Mandatory Check-in Meeting</u> <i>(Schedule meeting with Terri by end of April)</i></p> <p><u>Making a Research Poster</u> Use the link below to find the dates this topic will be offered: Link</p>	<p>Structured Abstract Draft III: Results & Conclusion (due by 4/19/24)</p> <p>Poster Presentation <i>Poster Rough Draft</i> (due by 4/26/24)</p>
May	<p><u>Must Attend THREE Workshops conducted by UNLV's Office of Undergraduate Research***</u></p>	<p>Final Poster & Structured Abstract (both due by 5/17/24)</p> <p>Post-survey (due by 5/17/24)</p>

Assignments should be emailed to terri.bernstein@unlv.edu by 11:59 pm of the due date.

Select and attend **three workshops** conducted by UNLV's Office of Undergraduate Research during the Spring 2024 semester. For each workshop attended, verify your attendance by completing [this google form](#).

[View the workshop calendar here.](#)

Example of a Structured Abstract***

Crystal Wu

Earth and Environmental Science

David Kreamer, Ph.D., Professor, Department of Geoscience

Review of the Ecological Impacts of Selenium in the Grand Canyon

Introduction

The Grand Canyon supplies water to over six million visitors annually. The springs are a natural habitat and water source for aquatic and avian organisms in the southwestern United States (Walters et al. 2015). However, the Grand Canyon is contaminated by various chemicals. Selenium, a chemical element, and nutrient to all living organisms is toxic in high levels (Tan and Nancharaiyah 2016). The contaminant has been traced throughout the food web (Walters et al. 2015). Although the water in the Grand Canyon has been studied and sampled for decades, no current, comprehensive database stores the information in one location. The lack of a database hinders the ability to analyze the water quality accurately. The development of a compiled database can provide a comprehensive source of water quality samples, verified data sources, and a uniformed format. The database is significant since it supplies information to study the impact of various chemicals to the ecosystem, mining contamination, and sustainability of native tribes.

Objective

The primary objective is to compile data on the water quality of the Grand Canyon into one comprehensive database.

Methods

We are composing collected data from different agencies such as the U.S. Geological Survey, EPA's Storage and Retrieval system, Natural Park Service, and Arizona Department of Environmental Quality into a comprehensive database. We also included data from published books, peer-reviewed scientific journal articles, and verified field notebooks. The database we are composing divides the different contaminants sampled from springs, creeks, and rivers. Various chemicals and water measurements have already been tested and documented in the field. Chemical

elements such as Selenium, Uranium, and Arsenic are incorporated in the database. Also, turbidity, pH, and the temperature are included in the hydrologic measurements. After entering all of the data, we will be creating different graphs, data trends, and comparisons to analyze chemical concentrations, data gaps, and comparing maximum contaminant levels.

Preliminary Findings

Within the Grand Canyon, there are water quality regulations to preserve the environment. The maximum contaminant level (MCL) determines the allowed amount of contaminants in the water. Various chemicals have exceeded the maximum contaminant level in the Grand Canyon. Selenium with a maximum contaminant level of 50ug/L has been surpassed in approximately seven springs. The maximum contaminant level for freshwater organisms is 5ug/L. The high levels of Selenium have a potential to impact the ecosystem of different springs (Luoma and Presser 2009). Also, Selenium has only been analyzed 8.3% of the time. Each time the chemical has been tested, it exceeded the MCL standard.

Discussion and Implications

Since contaminants have surpassed the maximum contaminant level in various locations in the Grand Canyon, monitoring and remediation are necessary. There is a need for further fish and wildlife sampling to determine the negative implications to the food web. Ecosystems can be permanently altered with high levels of contaminants (Walters et al. 2015). With a comprehensive database, areas with high Selenium levels can be identified and adequately treated. The database will be a critical device to facilitate research.

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***Note: Your structured abstract does not have to strictly follow this example. Consult with your mentor to determine the appropriate headers and writing style for your structured abstract. Also, many SSRE projects follow timelines that are significantly longer than the Spring semester. If your project is in progress (i.e., no results), it is acceptable to remove the "Results" header and provide a larger "Discussion" section—the final structured abstract is a reflection of the progress you have made during the Spring semester. Also, citations are required within your structured abstract.

Examples of Research Posters

THE TESH-KTASH CHILD: EVOLUTIONARY MONTAGE DURING THE MIDDLE PALEOLITHIC

Nirosh Moodley & Alesha Pettit
Department of Anthropology & Ethnic Studies, University of Nevada-Las Vegas



Background
Discovered in 1938 in the Tashkent district of southern Uzbekistan, Teshik-Tash 1 represents a juvenile Homo sapiens, aged between nine and eleven years old. He was classified as *Homo neanderthalensis*. The pertinent characteristics of the find in this context provided the backdrop for this classification. Firstly, the Teshik-Tash child was buried with associated grave goods reminiscent of Middle Paleolithic assemblage which has been described as "Mousterian-like" (Gentry et al. 2009: 48). Secondly, the very location of the find was the earliest known site of hominin occupation outside of the Levant. Recent research, however, challenges this boundary by questioning whether Teshik-Tash 1 truly is a Neanderthal specimen (Gentry, 2010). The Teshik-Tash juvenile is thus an important fossil to understand the dynamic and possible cultural links between the hominins of the Near East and those of Central Asia.

The Site


- Single, deliberate burial
- Three cultural layers?
- Middle Paleolithic assemblage
- Mousterian-like lithics
- Ritual artefacts: grave goods?
- Neanderthal burial?

The Cranium


- Severely crushed, possible animal attack
- Original reconstruction flawed
- Mosaic morphology (Gentry, 2009)
- Not wholly Neanderthal
- Neanderthal, early modern human or transitional?

Methods

- Thirty-three craniofacial measurements: Bulikire and Uebelaker (2004)
- Comparison to
 - Qafzeh 11 juvenile early modern human
 - Juvenile modern human
 - Adult modern human
 - La Chapelle Neanderthal
 - La Ferrassie Neanderthal



Teshik-Tash 1



Qafzeh 11 early modern human
La Chapelle-aux-Saints 1 Neanderthal

Results

- Mosaic craniofacial anatomy
- Close similarity to Qafzeh 11, La Chapelle-aux-Saints 1
- Larger than modern human sub-adult
- Close similarity to adult modern human
- Dental eruption = same as modern human

Conclusions

- Clear example of mixed traits
- Illustrates variability in Late Pleistocene hominin record
- Cannot be termed wholly Neanderthal or wholly modern human

Implications

- Challenging for comparison: scarcity of Central Asian finds
- More research necessary to draw further conclusions
- Valuable study for phylogenetic tree


Further References

Gentry, A., & Uebelaker, T. (2009). Is Central Asia the Eastern Outpost of the Neanderthal Range? A Reassessment of the Teshik-Tash Child. *Journal of Human Evolution*, 56(2), 45-50.

Clark, J., Vile, S., Vireo, S., Chikidze, T., Demirewa, A., Sironomov, A., Sironov, T. (2008). New hominin remains from Dagestan. *Journal of Human Evolution*, 55(5), 523-527.


Bolomeev, S. and Uebelaker, T. (2004). Discovery of the Teshik-Tash Child in southern Uzbekistan. *Central Asian Archaeological Journal of Physical Anthropology*, 2(2), 181-183.

Wardlewell, S. (2004). The Neanderthal Child from the Teshik-Tash. *Case in southern Uzbekistan*. *Central Asian Archaeological Journal of Physical Anthropology*, 2(2), 181-183.



CENTER FOR ACADEMIC ENRICHMENT & OUTREACH

This research was conducted with the generosity of the UNLV Center for Academic Enrichment and Outreach, the UNLV AANAPISI Program and the kind support of Dr. Brian Villacres, PhD (UNLV Department of Anthropology)



Interactions between T-Cell Death Associated Gene 51 (TDAG51) and Tubby Proteins

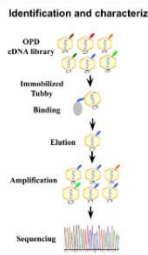
Christopher D. Williams, Lorena P. Samentar, and Nora B. Caberoy, Ph.D.
School of Life Sciences, University of Nevada, Las Vegas

INTRODUCTION

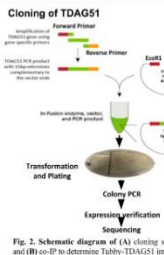
- Mutations within Tubby protein
- Responsible for retinal degeneration, hearing loss, and obesity
- Mechanisms of disease pathogenesis are not fully understood
- The Caberoy Lab used an open-reading frame (ORF) phage display to identify proteins that interact with Tubby
- Protein interactions can reveal pathways
- Tubby is involved in
 - TDAG51 or Pleckstrin-Homology Like Domain Family A member 1 (PHLDA1)
 - conserved proline-histidine rich nuclear protein responsible for apoptotic effects in T cells
 - putative Tubby binding partner
 - shares pathways shown to be affected by mutations in Tubby
- **Project goal:** To demonstrate the interaction of Tubby and TDAG51

METHODS

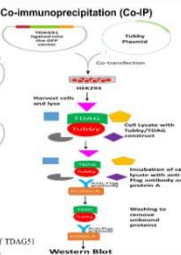
Identification and characterization of TDAG51 as Tubby-binding protein



Cloning of TDAG51



Co-immunoprecipitation (Co-IP)



SUMMARY

- TDAG51 was identified as a putative Tubby-binding protein by ORF phage display
- TDAG51 and TDAG51:PH were successfully cloned into universal GFP vector and expressed in HEK293 cells
- Tubby-TDAG51 interaction was independently validated by co-immunoprecipitation
- PH domain of TDAG51 is necessary for its binding with Tubby.

Future Directions

- Determination of Tubby domain that binds to TDAG51
- Co-IP of TDAG51 with Tubby N and Tubby C terminal only
- Protein pull-down assay using purified proteins
- Characterization of Tubby-TDAG51 co-localization using immunohistochemistry and confocal microscopy
- Cellular model – Neuro2A
- Animal model – brain and retina of WT and Tubby mice

References

1. Caberoy, N. B. et al. (2010). *J. Mol. Neurosci.* 25, 74-83.
2. Nagar, M. (2016). *Biochem. Biophys. Res. Commun.* 476, 1039-1046.
3. Carroll, K.J. et al. (2004). *Nat. Rev. Mol. Cell Biol.* 5, 55-64.
4. Caberoy, N. B. et al. (2010). *The EMBO Journal*, 29(23), 3898-3910.

Acknowledgements

I am thankful to the Caberoy Lab for letting me work alongside them to help me with my research project. I would like to thank Lorena Samentar for working patiently alongside me and always finding better methods. And I would like to give a special acknowledgment to Dr. Nora Caberoy for her wisdom and guidance throughout the entire project. I would also like to thank LSAMP for providing me a great opportunity to expand my scientific knowledge and gain in-depth research experience.

This project was supported by NIH/NEI grant R01EY020665-R01EY020665 Pathway to Independence Award to NIC.

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RESULTS

Figure 2: 816 base pairs (bp) TDAG51 and 495 bp TDAG51:PH were amplified by PCR. Agarose gel electrophoresis results, visualized under UV light, of PCR amplification using gene specific primers.




Figure 3: pGFP1-N In-Fusion Ready Vector was linearized after digestion with EcoRI and HindIII restriction enzymes. A. Schematic diagram of the GFP vector. B. Agarose gel electrophoresis results showing the GFP vector after digestion with the endonuclease as control.

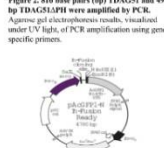


Figure 4: Two positive clones yielded the expected size of ~740 and 690bp (enclosed in red boxes during PCR screening of the colonies). Agarose gel electrophoresis of 10 colonies using sequence specific primers.

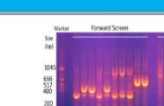


Figure 5: GFP was expressed by HEK293 cells transfected with purified plasmids from PCR positive clones. Brightfield and fluorescence photomicrographs of HEK293 cells transfected with GFP only, TDAG-GFP and TDAG:PH-GFP. Bright-field images are shown for comparison.

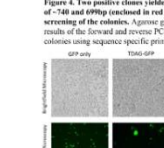


Figure 6: GFP bound Ha-TDAG51 (~68kDa) and Ha-TDAG51:PH (~45kDa) proteins were expressed by HEK293 cells. HEK293 cells were transfected with purified plasmids, harvested, and lysed. Western blot analysis using mouse anti-Ha mAb antibody detected TDAG51 and TDAG51:PH. Ha-GFP (~25kDa) was used as control.

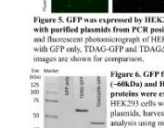


Figure 7: The sequence of TDAG51 and TDAG51:PH is identical to the target sequence. Portion of the ClustalW 2.1 multiple sequence alignment results showing the sequence of the TDAG51 clone with the target sequence for TDAG51, and the upstream and downstream regions with deletion of the PH domain for TDAG51:PH.

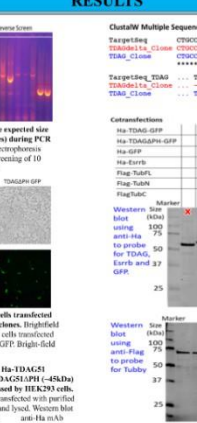


Figure 8: Both Tubby and TDAG51 proteins were expressed by HEK293 cells upon co-transfections. HEK293 cells were co-transfected with Tubby and TDAG51 plasmids, harvested, and lysed. Mouse anti-Ha mAb antibody was used to detect TDAG51, Earth, and GFP for Western blot analysis. Earth and GFP co-transfections were used as controls. These successful co-transfections were then used for Co-IP.

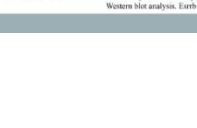


Figure 9: Flag-Tubby interacts with Ha-TDAG51 but not with Ha-TDAG51:PH *in vivo*. Co-immunoprecipitation with anti-Flag antibody and probed a blots was done using lysate of cells that expressed both Tubby and TDAG51. Western blot analysis was done using both anti-Flag and anti-Ha antibodies to detect Tubby and TDAG51, respectively. Earth which was used in the positive control did not show a prominent band in the lysate but displayed a prominent band in the co-IP. Whole cell lysate was also loaded as reference.

