2025

UNDERGRADUATE
RESEARCH FORUM

April 3, 2025

The Ohio State University

LIMA

Purpose

The **Lima Campus Undergraduate Research Forum** is designed to showcase the research performed by our students on the Ohio State Lima campus. Lima students also present their research at the Denman Undergraduate Research Forum, the Spring Undergraduate Research Festival and at many discipline-specific events.

THANK YOU

We thank the Dean's Office for supporting the Lima Campus Forum.

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The Ohio State University at Lima Undergraduate Research
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ABSTRACTS

Agapé Anderson
Research Advisor: Ryan W. Norris

Investigating the evolutionary history of the Kashmir voles in the genus *Hyperacrius*

The voles in the genus *Hyperacrius* are restricted to the alpine regions of Northern Pakistan and Kashmir. Two species of *Hyperacrius* are recognized based on morphological and ecological differences. The Murree vole *(Hyperacrius wynnei)* is the larger species and is found in forest habitats. True's vole *(Hyperacrius fertilis)* is a smaller species from a more open subalpine environment. Five subspecies are recognized from these two species, including three from *H. fertilis* and two from *H. wynnei*. Our objective is to assess the evolutionary history of this genus using genetic data. We sequenced the cytochrome *b* gene from specimens of *Hyperacrius* throughout the known range. We constructed phylogenetic trees using PAUP and BEAST and compared our *Hyperacrius* data to a dataset of mountain voles *(Alticola)* from the same region. *Hyperacrius* exhibits substantial genetic variability and deep divergence times. Our results suggest that current taxonomy underestimates the number of species in this genus.

Leah Beraki
Research Advisor: Ryan W. Norris

Reconciling taxonomy with phylogeny in zokors, root rats, and bamboo rats (Myospalacinae and Rhizomyinae: Spalacidae)

Muroid mole-rats (family Spalacidae) are a group of burrowing rodents from the Old World. Norris (2017) divided Spalacidae into the subfamilies Myospalacinae (zokors), Rhizomyinae (root rats and bamboo rats), and Spalacinae (blind mole rats, which are not part of my study). Norris (2017) recognized six species in Rhizomyinae and eleven species in Myospalacinae; however, he argued that there are additional unrecognized species. The focus of my project is to use available genetic data to determine the number of species present in Rhizomyinae and Myospalacinae and the boundaries between these species. I analyzed a large dataset of the cytochrome b gene downloaded from GenBank that consisted of Rhizomyinae individuals (n=87) and Myospalacinae individuals (n=46). I constructed a phylogenetic tree using BEAST. I evaluated the different taxonomic hypotheses with regard to monophyly, genetic distance, divergence time, and formal species delimitation analyses. The existing taxonomy of bamboo rats, *Rhizomys* and *Cannomys*, and zokors, *Myospalax* and *Eospalax*, appears to align with my results. I resolved the inconsistency of the phylogeny of root rats *(Tachyoryctes)*. Norris (2017) recognized two species, *T. macrocephalus* and *T. splendens*, but my results indicate there should be at least four. I recognize *T. splendens* s.s. from northwest Ethiopia, *T. macrocephalus* from the Bale Mountains, *T. somalicus* from northeast Ethiopia and Somaliland, and *T. annectens* from southern Ethiopia and other East African countries. The Ethiopian highlands appear to be the cradle of diversity in this genus.

Blessy Christian
Research Advisor: Ryan W. Norris

Reconstructing the evolutionary history of the Great Markhor *(Capra falconeri)* in Pakistan

The Markhor *(Capra falconeri)*, a wild goat found in the mountains of Pakistan, has been categorized as endangered and nearing extinction since 1994 due to threats to survival, like habitat loss, illegal hunting, and climate change. Using data available on GenBank, I analyzed mitochondrial DNA sequences from cytochrome oxidase 1 *(Cox1)* and cytochrome b *(Cytb)* genes to look at the evolutionary history of this species and other members of the genus. Phylogenetic trees were constructed to look at the markhor and related species in the genus *Capra*, including Siberian ibex *(Capra sibirica)* and wild goat *(Capra aegagrus)* from neighboring areas. Unfortunately, the markhor samples in GenBank were either not sourced to a specific location or limited in geography sampling, with only three verifiable localities represented. Due to this, inferences were made based on limited data. The samples that came from Torghar Hills and southern Pakistan formed a distinct clade, which appears to be the straight-horned markhor *(Capra falconeri megaceros s.l.)* or the Suleiman markhor *(C. f. jerdoni)*. Samples from the Hindu Kush and Himalayan mountains *(C. f. falconeri s.l.)* showed little genetic differentiation even across the Indus River valley, which has been shown to be a major geographic barrier in small mammals. Contrary to my hypothesis, markhor do not show the same pattern of biogeographic structure as montane rodents from these mountains.

Aubrey Gerten, Anthony Gerten and Isabella Salem
Research Advisor: Robin K. Bagley

Evaluating parasitoid flies associated with *Neodiprion* sawflies

In the process of understanding the mechanisms and origins that create diversity in the living world, one potentially under-explored area of evolutionary biology is what role parasites can play in generating biodiversity. Parasites form symbioses with their hosts, such that they benefit while the host is harmed. One system where this occurs frequently are *Neodiprion* sawflies, which are attacked by a wide range of parasitoids, or lethal parasitic insects. The sawflies are agricultural pests, and because of this, information has been compiled on their parasitoids in hopes of discovering a method of biological control. Most of the work, however, has been done on the wasp parasitoids, and substantially less work has been done on their fly parasites (Order Diptera, Family Tachinidae). These parasitoids have the ability to lay their eggs on or inside of sawfly larvae and then consume them from the inside out after the fly pupates. It is currently uncertain how many and which species of fly parasites are able to attack *Neodiprion*, but here we report the results of an initial survey of tachinid flies reared as by-catch from ~20 years of sawfly collections. This work, which continues from that of a past student, has currently identified fourteen putative species on the basis of morphological differences. We plan to follow up on these initial identifications using genetic barcoding of a mitochondrial DNA region, as well as through the use of more diagnostic keys, to further identify these specimens to the genus or species level. This will ultimately allow us and future researchers to evaluate their ecologies and evolutionary history.

Jesse Gunsett

Research Advisor: Ryan W. Norris

Uncovering relationships among Central Asian white-toothed shrews in the genus *Crocidura*

The genus *Crocidura*, commonly known as white-toothed shrews, is one of the most species-rich genera in all mammals with over 180 currently recognized species. However, these shrew species are very difficult to tell apart without the help of genetic data, and the relationships among the species in Asia are not entirely clear. This project aims to discover more about the relationships among *Crocidura* species in and around Pakistan. I compiled publicly available genetic samples of these species from GenBank and generated a phylogeny using the computer program PAUP. These phylogenies clarify the relationships among *Crocidura* species and when different clades diverged from one another. Future plans for this project are to retrieve genetic data from tissue samples of Pakastani shrews and learn how they fit into the newly constructed *Crocidura* phylogeny.

Ariel S. Kline
Research Advisor: Zachery T. Beres

Plant Species of the Tecumseh Interpretive Nature Preserve on the Ohio State Lima Campus

Revitalization and conservation efforts have been ongoing at the 2-acre northeastern corner of the Ohio State Lima campus. The Tecumseh Interpretive Nature Preserve was established at this site circa 2017 to maintain and study the biodiversity of this ecological system. Investigating the identity of the plants found within this prairie is a crucial foundational step for future research at this location. A multi-faceted identification process, including AI-based plant recognition software, field photography, a prior list of seeded plants, and traditional field guides, was used to make accurate identifications. By cross-referencing these methods, a growing catalog of 60 plant species has been developed so far. Moving forward, this research will shift focus to the relationship between Lepidoptera (butterfly and moth) species and their specific host plant species. Seven of the eight host plants for these previously identified lepidopterans have already been identified, and the next step after confirming the final identification will be a population-level study of the aforementioned host plants. By comparing the two population data sets of lepidopterans and their host plants, an assessment of their ecological dependencies can be made, further contributing to conservation efforts that support both plant and pollinator communities.

Elizabeth C. Mahler
Research Advisor: Robin K. Bagley

Comparison of traditional keys and genetic barcodes for two morphologically indistinct *Colias* butterflies

An ongoing mission of evolutionary biology is to gain a more thorough understanding of current biodiversity. One important key to that is how to properly distinguish between species. Identifying species, especially Lepidopterans (butterflies), can be as simple as looking at the pattern and color variation of said species. On the other hand, some species have a close enough resemblance, especially to a non-expert eye, that genetic barcodes are necessary to provide a definitive identification. A case where this might be necessary is the distinction between Orange Sulphurs *(Colias eurytheme)* and Clouded Sulphurs *(Colias philodice)*. These butterflies are similar in size, shape, and pattern but differ in the quantity of orange on the dorsal wing surface. Guides suggest if there is any visible amount of orange on the wings it is an Orange Sulphur. Based on the large range of color observed between these species and difference in human color perception, I hypothesize these field guides' recommendations are not accurate. To this end, this study tests the accuracy of this identification method by comparing the amount of orange on *Colias* butterfly wings to their species identity as confirmed by their DNA sequence at a standard identification gene. To do this, we collected and identified a quantity of both species from the Tecumseh Interpretive Nature Preserve and the Cottonwood Trail Access using the guides methods. The percentage of orange on the dorsal surface of the wings were then quantified using microscopic imaging and computer softwares. To cross check the guides' methods, the species were then identified with genetic barcoding by DNA sequencing.

Arshia Mani and Harshjot Kaur
Research Advisor: Ryan W. Norris

Investigating the molecular evolution of the hypoxia-associated *Epas1* and *Hbb* genes in superfamily Muroidea with regard to altitude and lifestyle

The *Epas1* gene controls the production of hypoxia-inducible factor 2-alpha (HIF-2α) protein and has been shown to vary among human populations in response to high altitudes. The Hemoglobin β *(Hbb)* gene is responsible for providing the instructions for the production of beta-globin, a component of hemoglobin. Studies in several mammals such as deer mice have shown adaptations in *Hbb* related to elevation. The Plateau Zokor *(Eospalax baileyi)* is a species of subterranean rodent found at very high elevations. The combination of high elevation and subterranean environment subjects these animals to extreme hypoxia. We compared amino acid changes (which lead to changes in proteins) with nucleotide changes across the evolutionary history of the superfamily Muroidea for each of these genes. We downloaded, from GenBank, both the amino acids and nucleotide sequences for *Epas1* and *Hbb* for 10 species of muroid rodents. These rodents were categorized based on elevation into three lifestyle categories: terrestrial, subterranean, and aquatic habitats. We examined the molecular evolution of these genes across phylogenies to identify shifts in rates of protein evolution that potentially relate to elevation and lifestyle.

Keerthi Merugu and Alayna Welch
Research Advisor: Zachery T. Beres

Campus Canopy: A Study of the Tree Species on the Ohio State Lima Campus

Our study focused on the identification and classification of trees located on The Ohio State University at Lima campus. This project aims to contribute to a comprehensive campus tree inventory serving as a valuable resource for future ecological studies, campus planning, and sustainability initiatives. Throughout this study, we identified 74 trees to species across the campus but heavily focusing on the North Quad and around the Science Building. Trees were identified using Peterson's A Field Guide to Eastern Trees. Some of the species identified included Chinese Elm, Pin Oak, Yellow and Ohio Buckeye, Sweetgum, Shagbark Hickory, and Red Maple. Ohio is home to approximately 125 native tree species, and our inventory included a significant number of these. After identifying each tree, we measured their diameter at breast height (DBH). These baseline measurements can be used to calculate carbon sequestration of each tree on campus to better understand differences in secondary growth among species in combatting climate change. Tree DBH measurements ranged from 4 cm (Eastern Redbud) to 87 cm (Bur Oak). The GPS location of each tree was also recorded to aid in future identification and tracking each tree over time. We intend to create an updated walking tree guide for campus to be used and enjoyed by students and visitors. By learning more about the trees around them, students can gain a better appreciation for campus biodiversity and better understand the important role these trees play in supporting local ecosystems by providing habitat for wildlife, enhancing campus green spaces, and mitigating our carbon footprint. We also hope that this can foster a deeper connection to the natural environment for students.

Rachel Ryan
Research Advisor: Nancy Risner

Secrets of the Canal: Screening microorganisms of the Miami-Erie Canal

Water is a large part of everyday life across the world and is essential for all living things on Earth. For many, contact with water comes from more than just drinking or bathing, it also comes in the form of entertainment and leisure with things such as fishing, swimming, and simply enjoying the view. For me, this contact came from a body of water running through my hometown of Delphos, Ohio. A portion of the Miami-Erie Canal is of utmost importance to Delphos and its rich history, but it also has a secret: it is notorious for being “dirty” and is rumored to have an abundance of mutated animals. This led to curiosity if there were any microorganisms present that would pose a risk to the health of our community. In this study, grab samples were collected from three locations in the littoral zone of the canal and one from the littoral zone of a chemically treated pond for comparison. To screen for the presence of microscopic organisms in these samples, a grid-based screening method was used. From this, I have classified the identifiable organisms, to the best of my ability, into potential species based on their morphological appearance and created a diversity index using the collected data. Here I will discuss my initial findings and implications of some charismatic organisms that I have identified thus far.

Gavin Schimpf, Ethan Silva and Taylor Turner
Research Advisor: Robin K. Bagley

Crushing Bugs for Fun (and Science)

For many years beetles were thought to be the kings of genetic diversity, but more recently that estimate has shifted towards wasps, with estimates of parasitic wasps alone ranging from 400,000 to 1.1 million. While this uncertainty in estimates might seem surprising, in reality it is not feasible to think that humans will be able to individually categorize every species on Earth. Many species are difficult to describe because of their size or lifestyle (e.g., parasitic mites and nematodes that live inside of other organisms). One way we propose to circumvent this issue is by using molecular tools to gain the relative abundance of many different taxa and then extrapolate that ratio to estimate a range of global species richness. Here we describe our approach, which leverages passive Malaise traps to gather large quantities of the 5 major insect orders: Coleoptera (beetles), Hemiptera (true bugs), Hymenoptera (bees, ants, wasps, and sawflies), Lepidoptera (butterflies and moths), and Diptera (flies). Each specimen collected is then photographed and identified to the lowest taxonomic level possible. The insects are then crushed and their DNA is obtained, along with that of any symbionts on or inside of them. We will then use blocking primers to selectively amplify 18s rRNA, a marker present in all eukaryotes, from the symbionts, allowing us to assess how many associate with each specimen.

Sophia Walker
Research Advisor: Ryan W. Norris

Reconstructing the evolutionary history of blind mole rats (Spalacinae)

Blind mole rats (subfamily Spalacinae) are a group of rodents that are subterranean and completely blind. They have the most degenerate eyes among placental mammals. Blind mole rats are native to Eastern Europe, Western Asia, and the Middle East, divided into two genera: *Spalax* and *Nannospalax*. Norris (2017) recognized eight species within *Spalax* and three within *Nannospalax*. Historically many more species have been recognized within the subfamily and Norris (2017) argued that 11 species is an underestimate. This study aims to refine the classification of Spalacinae by analyzing molecular data. Using cytochrome *b* gene sequences from GenBank (n=183), I assessed genetic relationships among individuals within the subfamily. Latitude and longitude coordinates were plotted to visualize geographic distributions, and a phylogenetic tree was constructed using BEAST to infer evolutionary relationships. The phylogenetic analysis indicated that the species *Spalax* generally aligns with the taxonomy of Norris (2017), whereas *Nannospalax* contains substantial diversity that extends beyond the three species recognized by Norris (2017). These findings support the need for reassessment of taxonomy within the genus *Nannospalax*.

Carter Welch
Research Advisor: Zachery T. Beres

Bioassessment of the Lost Creek on the Ohio State Lima Campus Using Micro Invertebrates

Flowing between the Tecumseh Interpretative Nature Preserve and the Ohio State Lima Regenerative Farm, the Lost Creek flows through the northern portion of the Ohio State Lima campus. This creek has been the focus of our research for the past three years. During that time, we have assessed habitat quality, monitored the chemical composition of the water, and explored the biodiversity of macroinvertebrates. A holding pond was added to the Ohio State Lima farmland with the goal of reducing chemical runoff. The chemical tests performed on the water have been informative, but some of the tests have low sensitivity. One way to remedy this is by indirectly assessing water quality with the microscopic organisms living in the creek. Compared to the macroinvertebrates previously sampled, these organisms will respond to chemical changes in the water significantly faster. The same two portions of the Lost Creek previously monitored were used again. Between August 2024 and December 2024, we collected water samples and filtered them to capture these micro invertebrates. The organisms were then suspended in a 90% acetone solution. We measured the fluorescence of these samples which gives an estimate of chlorophyll concentrations. Notably, neither of our two sites showed a significant difference in fluorescence [204.99 nm vs. 224.21 nm, respectively; *t*-test ($p = 0.899$)]. However, our sample size was rather low and over a broad period of time. This data will allow future research opportunities to monitor biodiversity changes and habitat alterations while additional changes are made to the surrounding farmland. Future students are expected to continue this work with more vigorous sampling efforts to capture seasonal fluctuations in the micro invertebrate populations. These patterns will be especially important to determine whether agricultural run-off is impacting our local waterway.

2025 Students of Bio 1114E: Subah Auhona, Blessy Christian, Aaron Hutchins, Madison Linder, Salah Mohammed, Brittany Pitts, Malachi Talbert and Enki White
Research Advisors: Robin K. Bagley and Zachery T. Beres

From Rotting Fruits to Lab Tables

This research project was completed as part of our Biology 1114E lab experience. Our study examined the genetics of *Drosophila melanogaster*, the common fruit fly. *D. melanogaster* is a model organism in biology for understanding the genetics behind biological processes and diseases often mirrored in humans. This research aims to explore the evolutionary relationships between eleven varieties of fruit flies obtained from four different suppliers. We targeted the barcoding region of the cytochrome oxidase I (COI) region within the mitochondrial genome of these fruit flies. This region of DNA encodes the final enzyme used in the electron transport chain in cellular respiration. Because of the importance of this enzyme, this region of DNA is the standard for identifying animals using DNA barcoding. During one of our labs, we extracted the DNA from our fruit flies and prepared the DNA samples to be amplified using polymerase chain reaction (PCR). This allowed our instructors to run the PCR and clean the remaining DNA outside of the confines of our lab schedule. The DNA samples were sequenced using a MinION for ~72 hours. Using this sequenced DNA, we will compare the genomes of our fruit flies using an online supercomputer during another lab session. This project is ongoing, and we are currently waiting for the genetic data to complete our analysis. This project accomplished several learning outcomes of Biology 1114 including to enhance our understanding of genetics and aid us in learning how DNA can be used to compare organisms. This research project is novel to Biology 1114 across all Ohio State campuses and provided us with an opportunity to learn about population genetics and phylogenies firsthand using a very real-world experience.

Kris Fields
Research Advisor: Virginia Tompkins

The Relation Between Narrative Comprehension Question Type (Inferential vs. Literal) and Preschoolers' Theory of Mind Development

Theory of mind (ToM) refers to the ability to understand our own and others' beliefs, emotions, and intentions. ToM is related to narrative comprehension because making inferences about characters' mental states and how they motivate behavior is critical to understanding stories. Thus, researchers argue that ToM might be more strongly related to inferential narrative comprehension questions. However, research on the correlation between ToM and literal vs. inferential questions has been inconsistent thus far. One study found a significant correlation between ToM and inferential question comprehension and no correlation with literal question comprehension (Dicataldo et al., 2023). Other studies focused specifically on literal comprehension have found a strong relationship between preschoolers' ToM and their ability to answer literal questions regarding characters, setting, initiating event, problem, and outcome (Altun, 2020, 2021). A recent meta-analysis, averaging across studies, found no difference in the relation between ToM and literal vs. inferential comprehension questions (Tompkins et al., 2024). These inconsistent findings between studies highlight the complexity of the relationship between ToM and narrative comprehension and emphasize the need for further research. No studies have reported on individual question types; ToM may play different roles depending not only on inferential vs. literal questions, but also specifically what content is being recalled (e.g., character names, setting). My prediction is that inferential question comprehension will correlate with greater ToM comprehension in the participants than literal questions because of the demand for the use of critical thinking and analysis of the text. Our research is an ongoing longitudinal study and currently consists of 125 preschoolers assessed on ToM and narrative comprehension (12 questions). Not surprisingly, ToM is significantly correlated with narrative comprehension, $r = .32$, $p < .01$. We will also present the relations between ToM and literal vs. inferential questions and specific question types.

Adam Jmiai
Research Advisor: Joseph Green

Excessive Smartphone Usage Patterns and General Suggestibility

Olson and colleagues (2020) found a small positive correlation (r=.17) between hypnotic suggestibility and heavy smartphone usage patterns. A subsequent investigation secured an even stronger correlation (r=.48) between non-hypnotic suggestibility and scores on a brief smartphone addiction scale (J. Olson, personal communication, September 9, 2024). In the current study, we administered the Smartphone Addiction Scale (SAS-SV; Kwon et al., 2013) to N=112 (81 females; 31males; M age = 20.54; SD=5.18) undergraduate students at The Ohio State University at Lima, along with measures of suggestibility, absorption, interpersonal anxiety, need to belong, dissociation, attitudes about hypnosis, and the expectancy of being a good hypnotic subject. Participants estimated the amount of time they spent on their phones and their sleeping patterns. Consistent with our prediction, we obtained a r=.58 between suggestibility and smartphone usage. Individuals who reported obsessing about their phones to the point of struggling to concentrate on other tasks and feeling great anxiety when not able to access their phones tended to also score high on a general trait of suggestibility. The suggestibility measure included items assessing the ease of being persuaded by others, the influence of advertising, and the importance of fitting in socially. As expected, additional measures of getting highly absorbed in tasks, time distortion, social anxiety, and the desire be socially accepted also positively correlated with both smartphone usage and with suggestibility. We conducted an exploratory step-wise regression analysis to examine the ability of our variables (including participants' gender) to predict smartphone addiction. Only suggestibility was retained in the final predictive model (Adj. R^2=.33). Our male and female participants scored similarly on the smartphone scale.

Students at high risk of smartphone addiction (n=49) scored higher on every item of the SAS-SV, relative to those classified as low risk (n=63). We discuss the implications of our findings.

Victoria Sibert
Research Advisor: Virginia Tompkins

Parents' Mental State Talk and Children's Executive Functioning

The development of executive functioning skills in early childhood is crucial for milestones such as academic success, sociocognitive development, theory of mind, social and moral competence, and emotion regulation (Clark, Pritchard, & Woodward, 2010; Dilworth-Bart, 2012; Carlson, Mandell, & Williams, 2004; Hughes & Ensor, 2011; Kochanska, Murray, & Coy, 1997). Executive functioning includes essential skills like working memory, cognitive flexibility, and inhibitory control. Several studies have confirmed that there is a relationship between parents' mental state talk (i.e. talk about cognition, beliefs, emotions) with children and children's theory of mind (i.e., the understanding of mental states) However, parents' mental state talk may also play a role in children's executive functioning, particularly cognitive flexibility, which involves flexibly shifting between two role sets. This is because parents' mental state talk often involves contrasting perspectives (e.g., the difference between thought and reality.) This study is part of a larger longitudinal project examining early environmental predictors of children's cognitive skills. Specifically, it investigates the relationship between parents' mental state talk and children's executive functioning. In this study, we code parents' mental state talk by asking how they would respond in different storybook scenarios involving conflict and varying perspectives. We coded by making note of how many 'mental state talk' words are used in their response. Mental states can refer to the mom, child, or book character and includes words that fall into these categories: cognitive, desire, emotion, modulations of assertion, and perception. The ongoing longitudinal study involves 125 participants, primarily 4-year-olds, with data collected over three waves. This presentation focuses on data from wave one. I hypothesize that there will be a significant relationship between parents' (mothers' and fathers') mental state talk and preschoolers' cognitive flexibility.

STEP PROGRAM

SECOND YEAR
TRANSFORMATIVE EXPERIENCE

Kyira Knous

STEP Program Advisors: Ian Breidenbach and Alyssa Brown

Argentinian for a Month

In July of 2024, I had the wonderful opportunity through the Second-year Transformational Experience Program (STEP) to travel abroad and live with a host family in Cordoba, Argentina for a month. During this time, I attended classes at Oníx International School and I held an apprenticeship at Hospital Tránsito Caceres de Allende. At this placement, I shadowed social workers, psychiatrists and psychologists so I could see how their practices to treat mental health and addiction differ from ours in the United States. I was able to assist in translating between doctors and English-speaking patients which was a valuable role I upheld and took pride in.

Outside of my apprenticeship and school, I grew close with Argentine natives and other exchange students in my program. Together, we experienced the night life and traveled to recommended destinations to see what all Argentina had to offer. We went horseback riding in the mountains, learned about Cordoba's history at their local art museum and made friends with everyone we saw. Never in my life have I experienced so much love from people I barely knew. The genuine human connection and the professional networking I experienced was irreplaceable.

Argentina is different from the United States in the way it is considered a "Third World" country. However, I believe it is truly a blessing that they are in a different state of development than the United States. Lack of technology, presence of public transport as a primary mode of transportation, and the use of cash really boosted the morale of the people I interacted with. Relationships are heavily valued in Argentina, and I do not know if I will ever be able to experience anything like this ever again. Overall, this experience has enhanced my education and cultural competence.

Lydia Wilson

STEP Program Advisors: Ian Breidenbach and Alyssa Brown

Discovering Toronto through MUNDO

My STEP Project was the *MUNDO's May Experience*. MUNDO (Multicultural Understanding through Nontraditional Discovery Opportunities) is an organization through Ohio State that supports Ohio State students in becoming active, socially conscious, resilient change makers who serve, learn and lead in ways that respect and advocate for themselves and others. This was an 8-day international educational road trip in Toronto, Ontario. I learned about the multicultural histories and legacies of one of Canada's most diverse and multicultural urban communities. I learned history through exposure and went to places like the Royal Ontario Museum, the Ontario Black History Society, Native Canadian Centre of Toronto, Niagara Falls, Kensington Market, St. Lawrence Market and more.

The main reason why I chose the *MUNDO May Experience* is because I wanted to have a study abroad experience. This gave me the freedom and flexibility to travel outside of the country but with a group. I was able to stick with the group during pre-planned events, but then I was able to have independence without the group. This allowed me to go to places that weren't a part of the itinerary, like the Aquarium.

I also was looking to build a community at main campus before I moved and this was the perfect opportunity. Since this trip last May, I've had two other experiences with Mundo.

I volunteered at the H*uman Impact Services organization* and was able to give back to an entire community. This organization housed families while also providing food to the entire neighborhood. I met with other college students and learned about the different experiences and hardships they have gone through.

My favorite parts of my trip were going to Niagara Falls, Kensington Market, St. Lawrence Market, visiting the Toronto Islands, going to Chinatown, going to a comedy club and going to the aquarium.

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