PERSONAL BACKGROUND: From the complex genital morphology exhibited in ducks, to cooperative sperm trains in mice, down to bacteria capable of hijacking host reproduction, I am fascinated by how reproduction influences evolution and speciation. However, my desire to pursue my Ph.D. was not always as clear. For my undergraduate education I attended SUNY Oswego, which as a relatively small, rural college does not have many of the same resources to provide many opportunities for undergraduate research as larger universities may. Additionally, I was not confident that I would have the experience or financial means necessary to support my goal of pursuing graduate school. Despite these obstacles, my junior year at SUNY Oswego I discovered my passion for reproductive evolutionary biology when I took a class called "Sexual Diversity and Evolution." Exposure to topics like pre- and post-copulatory sexual selection, sexual antagonism, and the Red Queen hypothesis, intrigued me and fueled a desire to pursue research. They are now fundamental to my Ph.D. studies in the Center for Reproductive Evolution at Syracuse University. The research community at Syracuse integrates ecology, microbiology, bioinformatics, and evolutionary biology within one department, providing a unique environment to foster my research interests while strengthening my personal and professional development as a scientist.

INTELLECTUAL MERIT: Inspired by his class, I approached Dr. Chris Chandler, who taught "Sexual Diversity and Evolution," about helping to analyze his latest next-generation sequencing data from an isopod species *Trachelipus rathkei*. While strong theoretical and experimental work exists describing allosome evolution, it is often restricted to a small subset of model organisms. Isopods are an emerging model for sex chromosome evolution due to their remarkable variation in sex determination mechanisms; within the group both XY and ZW sex determination can exist. Furthermore, their allosomes are young and homomorphic. By utilizing the potentially co-existing XY and ZW systems in *T. rathkei*, we aimed to understand the underlying mechanisms shifting autosome to allosome. First, analyzing *T. rathkei* genomic and transcriptomic data was essential. With no prior bioinformatics training, I had a steep learning curve, but the captivating and challenging nature of the field made me eager to persevere. I independently worked on identifying Z-linked genes. Similar to the X chromosome, the Z chromosome has been shown to harbor genes essential for both sexes, however far less is known about the ZW system. By identifying putative Z-linked genes I planned to explore their function and compare their GO terms with other ZW models but I was unable to resolve any definitive genes. Contrary to expectations, we hypothesized based on these results that extensive recombination between allosomes in *T. rathkei* is still occurring.

To learn more specialized techniques, Dr. Chandler funded my travel to the University of Poitiers in France to collaborate with Dr. Richard Cordaux and the Ecology, Evolution and Symbiosis (EES) team. The EES primarily studies the effect of *Wolbachia* on isopod evolution. In isopods, *Wolbachia* can induce feminization, which causes genetic males to develop as functioning neo-females. Since isopod allosomes are homomorphic, cytogenetic methods or fluorescent *in situ* hybridization is not a viable option to characterize their sex determination mechanism. To do so, first, *Wolbachia* infection status must be ruled out via negative PCR and second, crosses between neo-males and true females must be completed. Surgical sex-reversal in isopods is accomplished by microdissection of the androgenic gland and subsequent injection into a juvenile female. Within a few molts, the successfully sex-reversed female (neo-male) will function as a male, but genotypically remain female. By crossing a neo-male and true female, we use F1 sex ratio to determine whether the parental population has ZW or XY sex chromosomes.

Additionally, sex-reversal is a powerful tool for examining sex differentiation and development between individuals of the same genotype yet vastly different phenotypes. The EES taught me the techniques for microdissection and surgical sex-reversal, in addition to molecular diagnostics of *Wolbachia*. I helped establish neo-male cohorts, both in France and Oswego, for long-term collaborative projects based on monitoring transgenerational sex ratio distortion.

When I returned to New York, my main task was to establish lab populations free of *Wolbachia* infection, however while surveying wild individuals, I found that the prevalence of *Wolbachia* greatly differed depending on species despite collecting sites in the same geographic region. This was a significant discovery because differences in *Wolbachia* prevalence between species suggests that each species has a different evolutionary history with the endosymbiont despite the long evolutionary history between terrestrial isopods and *Wolbachia*. Interspecific horizontal acquisition of *Wolbachia* is thought to be uncommon. I presented this work on wild populations at the RISE Scholarly & Creative Activities Symposium in Oswego, NY and the 2017 Society for Integrative and Comparative Biology conference in New Orleans, LA.

Wolbachia infection can be difficult to detect via PCR due to primer specificity and sensitivity issues, and as the most abundant reproductive endosymbiont, it is important to have an efficient diagnostic test capable of strain level resolution. Therefore, I focused my Honors Thesis on developing a bioinformatic pipeline to screen archived arthropod data for the presence of *Wolbachia*. I discovered eight novel host-*Wolbachia* associations and for each putative infection I assembled a draft genome. To explore the distribution and relationship of strains over the range of host taxa, I used these genomes to construct a phylogeny capable of assigning supergroup taxonomy. I spoke on this research at QUEST, where I was awarded the Sigma Xi Award for excellence in experimental design and execution, and published this work in PeerJ[1].

After graduating from SUNY Oswego in 2017 with my B.Sc. in Zoology, I decided to explore other areas of evolutionary biology to solidify my decision to pursue my Ph.D. I joined Dr. Suzanne Edmands' lab as a research technician at the University of Southern California (USC). At USC, I investigated incipient speciation through mito-nuclear incompatibilities and sex-biased gene expression in the copepod species *Tigriopus californicus*. *T. californicus* have stable, long-term polygenic sex determination and populations can have up to 12% mitochondrial (mt) divergence yet remain capable of hybridization. They are an ideal model for studying sex-specific mt effects and the uneven accumulation of deleterious mt mutations (Mother's Curse). I created twelve cybrid lines by fully introgressing six mt haplotypes onto two isogenic nuclear backgrounds. Additionally, I established a technique for dissecting the reproductive tract of *T. californicus*. I discovered that males have a paired reproductive tract rather than the previously reported single-sided morph. Using single cell RNA-seq, we identified putative sex-specific genes by comparing expression of gonadal and carcass tissue of each sex. I presented this work at the 2018 GSA Population, Evolution, and Quantitative Genetics conference in Madison, WI.

While my work at was USC intriguing, I could not stop thinking about the complex dynamics of host and microbes. The Center for Reproductive Evolution (CRE), led by Drs. Steve Dorus and Scott Pitnick, is the ideal setting to return to reproductive biology and host-microbe interactions. The CRE is innovative and highly integrative, combining comparative genomics, molecular evolution, and coevolutionary phylogenetics. Joining the lab under the co-advisement of Drs. Dorus and Pitnick has already proven invaluable to the development of my ideas. My knowledge of reproductive endosymbionts synergizes with Dr. Dorus's expertise in bacterial genomics, virulence and molecular reproductive evolution and Dr. Pitnick's extensive knowledge of reproductive phenotypes and comparative phylogenetics.

BROADER IMPACTS: Since the genomic revolution, decreased cost in NGS technology and advances in metagenomics have revealed previously underappreciated microbiome diversity and complexity. My research on reproductive endosymbionts will lead to a deeper understanding of the influence of variation in microbial community structure on host evolution. Furthermore, characterizing the relationship between host and microbe as a complex biomolecular network rather than binary, has the potential to advance many fields, specifically pathology and epidemiology. I aspire to integrate genomics, microbiology, bioinformatics, and phylogenetics to expand our knowledge of the nuanced and intimate relationships between host and microbe.
EDUCATIONAL OUTREACH: I am enthusiastic about integrating my proposed work with opportunities for community educational outreach. "Genomes and Society" is an established educational initiative created by the CRE, already with great success. Through this program the CRE develops teaching modules that are freely disseminated online for teachers to utilize in their own classrooms and provides opportunities to host students in the lab for a more personalized learning and mentoring experience. I will add to this online resource by developing my own lesson plans, focused on the topics of metagenomics and bioinformatics. After visiting local high schools to implement and assess my modules, I will recruit groups of high school students to spend the summer in the lab with me working on experimental crosses, data collection, and analysis to in order to teach them both wet-lab and dry-lab techniques.
OPEN SCIENCE APPROACH: I believe in the concept of open science, which means more to me than accessibility to my data and methodological transparency. Fundamentally, it represents a core set of values based on inclusivity and representation in the scientific community that has historically been lacking in the field. I plan on not only upholding this belief by disseminating my findings through open access journals, depositing data to permanent online repositories and developing code on open-source platforms, but more importantly, actively seeking the engagement and participation of undergraduates, especially by members of underrepresented groups. Likewise, I plan on supporting their retention in STEM fields. As an undergrad, I found it intimidating to be one the few, if not the only, female in my computational biology courses. However, as I began to develop my skills independently with the help of free resources like Stack Overflow or R-bloggers, I was pleasantly surprised to find that the community of bioinformaticians willing to welcome newcomers greatly outweighs the antiquated stereotype of elitist programmers. In my experience, bioinformatics-based projects allow low-cost opportunities for undergraduate participation while providing the potential to produce high quality, publishable results. There is so much public data available that is waiting to be explored in creative ways. I want to capitalize on these resources by mentoring undergraduates, specifically women, to help them to explore their hypotheses while developing increasingly valuable bioinformatic skills, which are applicable far beyond evolutionary biology. Programs at Syracuse like WiSE and McNair Scholars will aid in my recruitment of driven undergraduates.
PERSONAL DEVELOPMENT: The support of my mentors has been integral to my success thus far. By continuing to personally develop qualities of enthusiasm and approachability, I intend to be a successful mentor. To accomplish this, I will participate in the Future Professoriate Program, which emphasizes the teaching dimension of graduate education as fundamental to a successful academic career. Additionally, I will continue to attend mentoring workshops hosted by WiSE.
FUTURE GOALS: Following the completion of my Ph.D., I aim to continue a career in academia that combines my passion for research, teaching, and advocating for open and inclusive science.

[1] **Pascar** & Chandler. (2018) A bioinformatics approach to identifying *Wolbachia* infection in arthropods. *PeerJ*.