Personal Statement- Jazlyn Mooney

I made the decision to pursue evolutionary anthropology and population genetics, because it gave me an integrative framework for understanding biology. Population genetics gave me the ability to view biology from an anthropological perspective. For example, how did geographic populations become genetically distinct groups? Alternatively, what happens when previously outbred groups homogenize? These questions pertain directly to my research and to my life. Being a multi-ethnic individual, I often wonder how relevant my filling out a form that asks for ethnicity at the doctor's office is. Does it mean that I get a better diagnosis because I marked Hispanic, African American, and Native American? Should my ethnicity play a role in my treatment? In anthropological terms, I am an admixed individual and potentially carry genes associated with Native Americans, Africans, and Europeans. If this is true, then how is it beneficial for a physician to ask what my ethnicity is, unless they know exactly which genes I carry? Questions like this have sparked my interest in studying genomics and anthropology. I want to study admixed populations during my graduate school career because admixed populations can answer many questions about human evolutionary history. Additionally, admixture has occurred in many modern populations and many individuals carry genes from more than one geographic population. During my undergraduate career, I had the opportunity to pursue population genetics research projects. My mentor, Dr. Jeffrey Long has guided me and helped me to conduct creative research projects. I have also been able to participate in lab meetings alongside Dr. Long and his graduate students, which has been invaluable.

One of the first steps for many new researchers, myself included, is downloading publicly available data. Data acquisition became my first research project. I worked with a group that developed and wrote a protocol for downloading and working with sequence data from the UCSC Genome Browser. The purpose of this protocol was to guide someone who did not have any previous knowledge about the UCSC Genome Browser interface. We demonstrated how to search for and download each sequence. Then, the protocol showed the user how to load and run simple tasks with the data in MEGA 5. I personally wrote the portion of the protocol pertaining to loading the data into MEGA 5, compare the sequences, and create a simple phylogenetic tree. Upon finishing this project, I moved on to working with larger data sets. I worked on assembling genomic data from a nosocomial antibiotic resistant form *Klebsiella pneumoniae*. Next, I explored summer research programs where I could study genetics in a medical setting. I chose the University of Chicago because I would be able to combine my interests in anthropology and biology by working in a physician's laboratory.

I had the opportunity to spend a summer at the University of Chicago conducting research through the PSOMER program, exclusively for prospective MD/ PhD students. I was in the Maitland lab, where I worked specifically on assembling haplotypes, using PHASE, for assessing sensitivity to an angiogenesis inhibitor, Sorafenib. Angiogenesis inhibitors work by blocking the Vascular Endothelial Growth Factor (VEGF) pathway. The VEGF signaling pathway post-transcriptionally activates endothelial Nitric Oxide Synthase (eNOS). Both VEGF

and eNOS have previously been associated with increases in blood pressure. Adrenergic β-2 receptor (ADRB2) is a G-protein coupled receptor that causes heart contractility. Previous studies on ADRB2 have shown that its sensitivity is genetically variable. Therefore, we hypothesized that ADRB2 was responsible for the decreased heart rate seen in patients taking Sorafenib. The decrease in heart rate may have occurred to compensate for the increased blood pressure experienced by patients taking Sorafenib. In order to test this hypothesis, patients were haplotyped and had an ambulatory blood pressure cuff that measured both blood pressure and heart rate. We concluded that there was a significant association between increased diastolic blood pressure and multiple VEGF haplotypes, as well as a single eNOS SNP. We also found that there was a trend toward significance for ADRB2 haplotype category A and the observed decrease in heart rate. I was able to present my research at the *Chicago Summer Research Forum and Poster Session*. I spoke about my project to both my peers and current faculty at the University of Chicago. Having the opportunity to work intensively with pharmacogenomics marker haplotypes prepared me well for my honors thesis, which also involved haplotype generation.

Upon returning to New Mexico, I began the culmination of my undergraduate work, my honors thesis, titled "Inferring Evolutionary History from AIMs". My honors thesis was part of a larger project where I was able to collaborate with one of the graduate students in lab, Sara Niedbalski. She had identified a series of ancestry informative markers (AIMs) and classified each AIM as African or non-African. Then, she classified the AIMs as ancestral or derived. Serial Founder Effects predicts that the expansion out of Africa results in non-African populations carrying a subset of common variation previously found in Africans. Interestingly, there exists a small amount of ancestral AIMs observable in non-Africans. My thesis examined the implications of the presence of these ancestral AIMs observed in non-Africans. In order to do this, I filtered HapMap genome data in two African populations and two Non-African populations in search of target African and Non-African AIMs. Next, I constructed multiple-locus haplotypes to compare the homozygosity of derived AIMs and of ancestral AIMs observed in Africans versus non-Africans. I wrote the majority of the programs that I used for file filtering and organizing in C++. I found that all of the African AIMs had a lower homozygosity than the non-African AIMs, which is consistent with the Serial Founder Effects Model. I was also able to identify two interesting ancestral Non-African AIMs on chromosome five. These AIMs had a relatively low homozygosity and the amount of haplotype backgrounds that contained these two AIMs appeared to be suggestive of either admixture or diversity preservation.

After working on multiple computational research projects, I became interested in the process of collecting sequence data. I decided to take a half a year course on techniques in molecular biology. During this course, I processed raw sequence data from both plants and animals. I processed DNA and RNA sequences from Sycamore species, *Platanus wrightii*, and snail species, *Biomphalaria glabrata*. I learned basic purification techniques that are required for collecting sequence data. These techniques included enzymatic manipulation, hybridization,

molecular cloning, primer construction and gel electrophoresis. I read and analyzed the raw sequence data in Sequencher. Then, I used our generated sequence data to construct phylogenetic trees in FigTree. Finally, I submitted novel sequence data for publication on GenBank.

During my time at the University of New Mexico, I acquired degrees in Biology (B.S. degree) and Evolutionary Anthropology (B.S. degree). Because of my commitment to my education, I maintained the Presidential Scholarship at UNM and was on the Dean's List every semester, achieving a 3.9 cumulative GPA. I graduated with honors from both the University and Anthropology departments. Conducting research throughout my undergraduate career greatly improved my data management, organization, and implementation skills. I became an efficient programmer in C++ and gained some experience in R as well. I learned how to write programs for mathematical calculations, file filtering, file generation, and searching within a file. Programming is an important skill for graduate school, because some graduate programs are moving toward whole genome sequencing. Whole genome sequencing leaves the user with a large amount of data to be processed. Proficiency in programming greatly improves my ability to sort through and utilize large amounts of sequence data in a reasonable amount of time. Additionally, I was able to present my project, which allowed me to become more comfortable with public speaking.

The NSF Graduate Research Fellowship would provide me with the funding to conduct a project that involves multi-disciplinary training in genetics and bioinformatics, as well as interact with persons of diverse cultural backgrounds, both within the surrounding community and academia. I will utilize my academic, research, and personal experiences to become a well-rounded graduate student. I believe I can use my multi-ethnic background as a way to connect with, and mentor, minority high school students and undergraduates entering the STEM field, particularly women. During graduate school, I want to study the evolutionary history of modern humans and human genetic variation. I plan to explore these topics by improving upon research techniques in population genetics that I learned during my undergraduate career. For my graduate research, I will take an anthropological approach that uses European ancestry in African Americans as a tool to identify the fitness consequences of nonsynonymous mutations associated with the out of Africa migration. I will present my findings to persons within the fields of biology, anthropology, and medicine. Being a multi-ethnic individual allows me to better understand and communicate my results to both the academic and minority communities. Therefore, I would also like to make my results publicly available through an online supplement. My research may benefit epidemiologists as well, as results potentially improve disease treatment and genetic screening for specific harmful alleles.