

As the world's "6th Mass Extinction" continues due to anthropogenic change, more and more species are driven to endangerment and become susceptible to the risks associated with small population sizes. One such species recently discovered in 2015, the Conception Bank Silver Boa (*Chilabothrus argentum*), is classified as Critically Endangered on the IUCN Red List, with an estimated census population of 128 individuals (95% confidence interval of 78-246). Unfortunately, recent (2020) legislative changes in the Bahamas have made it highly untenable to continue most externally-funded ecological research, including fulfilling critical recommendations made by the IUCN in 2019 for conservation actions to protect the Silver Boa. To prevent a full shutdown of conservation efforts, we will perform whole genome sequencing of all currently existing samples taken from Silver Boas to assess the species' population size and genomic health. Using Illumina short read sequencing, we have successfully obtained reads for 12 individuals out of only 20 existing specimen samples, each at an estimated 30X coverage. To obtain a closely-related reference for haplotype calling, we are assembling a high-quality reference genome from the Turks and Caicos Boa (*Chilabothrus chrysogaster*), the closest living relative of the Silver Boa. Using these genomes, we will begin by analyzing the Silver Boa population's level of heterozygosity and degrees of relatedness between individuals. We then aim to determine the demographic history of the population, and whether the population experienced recent decline or has been at a small size for a longer time. With this information, we hope to evaluate whether the Silver Boa population is suffering from or at risk of inbreeding depression, or has had the fortune of undergoing purging of deleterious alleles and is genetically stable at a small population size. Besides contributing to our eventual goal of sequencing every living Silver Boa, our work will allow us to gain insights into the population's genomic health and evolutionary history and thus better inform outstanding plans that include conservation management and a breeding program