Creating a genetic database of herpetofauna to aid future eDNA studies, Ecuador.

In September of 2022, I spent two months in the eastern Andes of Ecuador, assisting an organisation in creating a genetic database of the local herpetofauna – amphibians and reptiles. The reserve in which this project took place was located on the edge of the Llanganates-Sangay Ecological Corridor (LSEC). The LSEC was designated by the World Wildlife Fund (WWF) as "a gift from the Earth" in the year 2002 due to the great floral and faunal biodiversity it contains in a small area, especially true of herpetofauna, being the most biodiverse place on Earth for herpetofauna. Furthermore, many species found here are not found anywhere else on Earth.

Herpetofauna, especially amphibians, have been widely used as ecological indicators across tropical studies, outperforming mammals in this respect. Nonetheless, in comparison to mammals and birds which receive significant conservation attention, herpetofauna are often understudied within the Tropics despite being some of the most threatened taxa globally. In general, many tropical areas are largely understudied when it comes to herpetofauna, making it an exciting field to work in if you enjoy discovering new species. Herpetofauna, however, are sensitive (especially amphibians) to changes in their environment making them vulnerable to anthropogenic impacts and diseases, and their vibrant colours, make them ideal candidates for the illegal trade of wild animals. For these reasons, their populations are drastically decreasing increasing the need for conservation efforts.

Before a conservation strategy can be put into place, however, we need information with regards to the number of species, and the number of individuals, we are dealing with in an area, in order to maximise the effect of the available resources. To do this, we need to monitor herpetofauna – assess their population size and richness. Some of the most common methods employed to do this are cost-and-time-consuming methods, demanding the need for alternatives. This is where eDNA comes in. With the onset on new technology, conservation biologists are now able to detect the DNA of a species sampled from an environmental source (e.g., the surface of a leaf) in the absence of the intended organism. This means that the organism does not even have to be there for scientists to be able to detect it, hence the term environmental DNA (eDNA). But before an identification of the DNA can be made, a database needs to be created. A reasonable analogy for this is when you scan items at a supermarket. For the scanner to know what product is attached to a particular barcode, the barcode needs to be in the system, so that each time you run that particular barcode over a

scanner, the item attached to that barcode pops up on the screen, e.g., barcode 25068533 refers to peanut butter. Similarly, to know the name of the species to which the sampled DNA belongs to, we need a database with genetic references. This is what I was helping with. This mainly involves walking 3-4 hours in the night, taking genetic samples from herpetofauna and sequencing them in the lab. The use of DNA in conservation is a rapidly developing field that makes the future of conservation pretty exciting and bright!



Figure. A.





Pictures of some of the herpetofauna genetic samples were taken of during my project. Look how beautifully detailed these animals are. The colours and patterns are magnificent, **Figure A (top most set of pictures)**.: (Top left) Dendropsophus sarayacuensis; (top right) Bothrocophias microphthalmus; (bottom left) Chimerella mariaelenae; (bottom right) Rhinella festae. **Figure B**: (Top left) Enyalioides praestabilis; (top right) Boana almendarizae; (middle) Anolis sagrei; (bottom left) Pristimantis katoptroides; (bottom right) Pristimantis quaquaversus. Photo credits – Armen Keuylian.