

**Determining Mountain Tapir Population structure in the Colombian Andes
using DNA markers**

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The mountain tapir (*Tapirus pinchaque*) is considered the most endangered tapir species in the world. Its distribution is restricted to the high lands of the Andean region of northern Peru, Ecuador and Colombia. The entire remaining population is probably less than 3000 individuals, mainly distributed in Colombia. Unfortunately the necessary information for its conservation is still lacking. It is necessary to get up-to-date data about recent distribution, habitat fragmentation and population structure to be able to take key actions for its long term conservation. Recent advances in technology and genetics have opened the door to new strategies for mountain tapir conservation. Using molecular markers to monitor mountain tapirs is a first step to understanding its population structure. When combined with Geographic Information Systems, this knowledge will permit us to manage mountain tapir populations in a convenient manner in order to conserve them for the long term. The main objective of my project is to determine mountain tapir population structure in the central mountain chain of the Colombian Andes using molecular markers. In other words, I want to identify how the remaining mountain tapir populations are grouped in the study area and if the identified aggregation patterns are due to recent or historical isolation. This knowledge is very important to avoid incorrect management decisions such as joining mountain tapir populations that historically have not been in contact, or to avoid leaving populations separated that can in fact be joined to solve inbreeding problems.

A series of field trips will be performed in order to collect mountain tapir DNA samples within national parks and unprotected habitats along the central mountain chain of the Colombian Andes. Samples will mainly consist of hairs and droppings left by the animals in the field, so it will be not necessary to handle the animals, thus preventing any risk for them. The coordinates of each collection place will be taken using a GPS device. DNA will be extracted from the collected samples at the Population Genetics Lab at Javeriana University in Bogotá, Colombia. PCR and sequencing procedures will be performed for a series of molecular markers. As a result I will be able to discriminate between individuals, so I can determine a minimum population size. As all of the genetic samples will be georeferenced I'll be able to locate each animal on a digital map showing the remaining habitat fragments. I will then be able to assign each animal to its corresponding habitat fragment. By seeing how the individuals in one fragment are related to individuals inhabiting contiguous or isolated fragments, I'll be able to determine how the mountain tapir population inhabiting the study area is structured from a genetic perspective. A series of complementary analyses will be performed to see if genetic results are supported by ecological or morphological data. For ecological data, habitat characterization will be performed in the DNA collection places and for morphological data I'll use camera traps to observe basic morphological differences.

Results of this study will be used to begin a long term mountain tapir monitoring program using molecular tools as a permanent low-cost strategy to keep information up to date for population management by Colombian environmental authorities. If successful, the procedure will be replicated along the entire mountain tapir range in the eastern mountain chain of the Colombian Andes, as well as in Ecuador and Northern Peru.