

Project Update: July 2010

Preliminary results

This project was very important because it was the first one that studies the genetic population structure in *Ctenomys magellanicus* in Tierra del Fuego to protect this endemic species.

We make 3 campaigns in October 2009, December 2009 and February 2010 and we trapped 40 individuals, 20 of each subpopulation (Figure 1). We traveled a total of 2150 km between the three campaigns. These field campaigns were useful to update the current and ancestral distribution of the species in Tierra del Fuego, which is very important if we want to preserve the species. The subpopulation of 34 chromosomes located north of Tierra del Fuego, is distributed more evenly and has a more limited distribution while the subpopulation of 36 chromosomes has many isolated demes which make the distribution of the species in this area more widely (Figure 1). Because this type of distribution, it is expected that the subpopulation with the highest number of isolates have a greater number of haplotypes (wahlund effect), while in the other subpopulation, we expect to find fewer haplotypes.

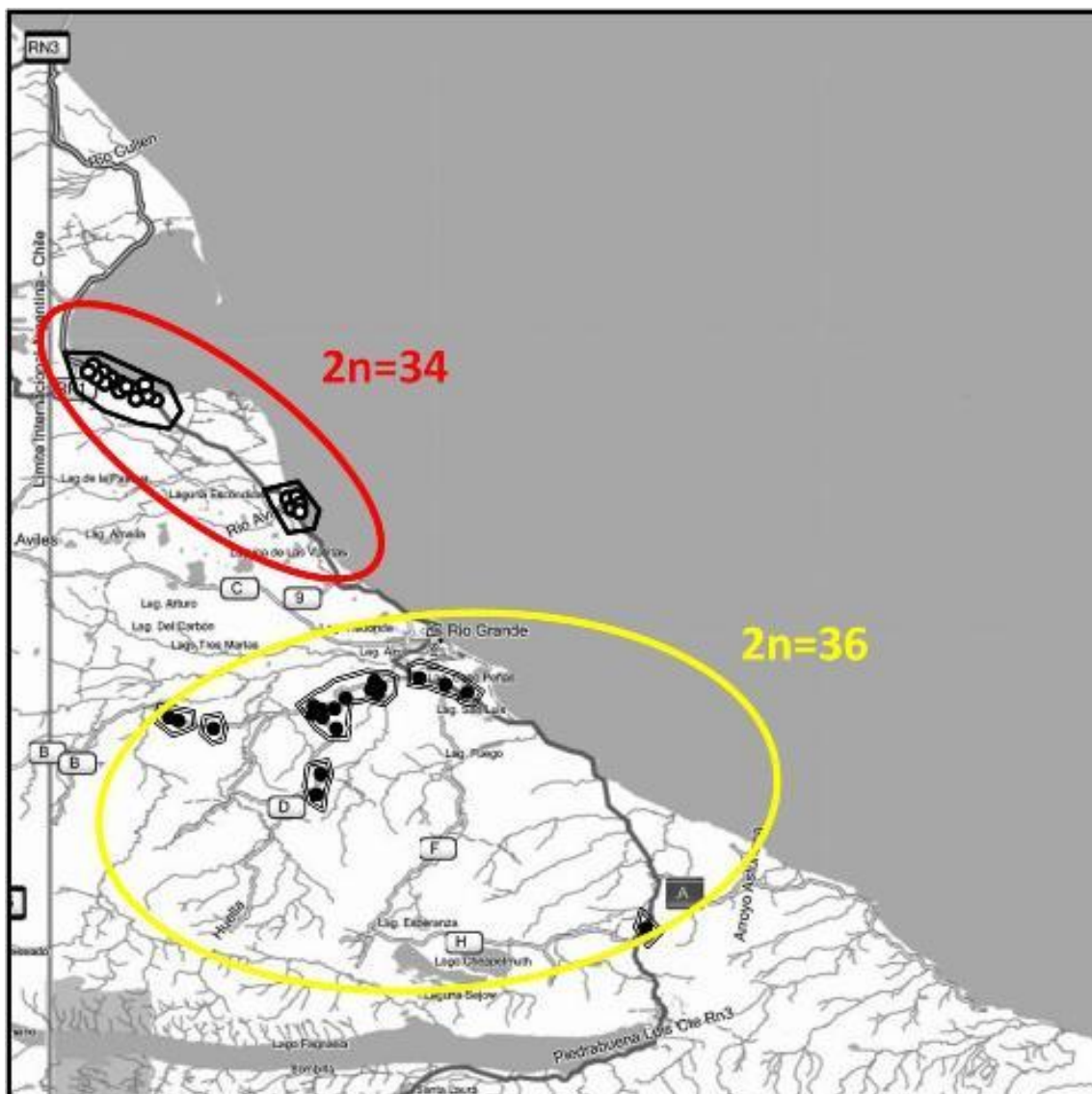


Figura 1. Samples distribution in Tierra del Fuego. The two subpopulations are highlighted in red ($2n=34$) and yellow ($2n=36$).

At the laboratory, we extract DNA from the 40 samples (Figure 2 left) and we amplify a fragment of mtDNA (D-loop) to study the genetic variation (Figure 2 right). We have some troubles in the amplification of 7 samples, but we keep trying to amplify these samples.

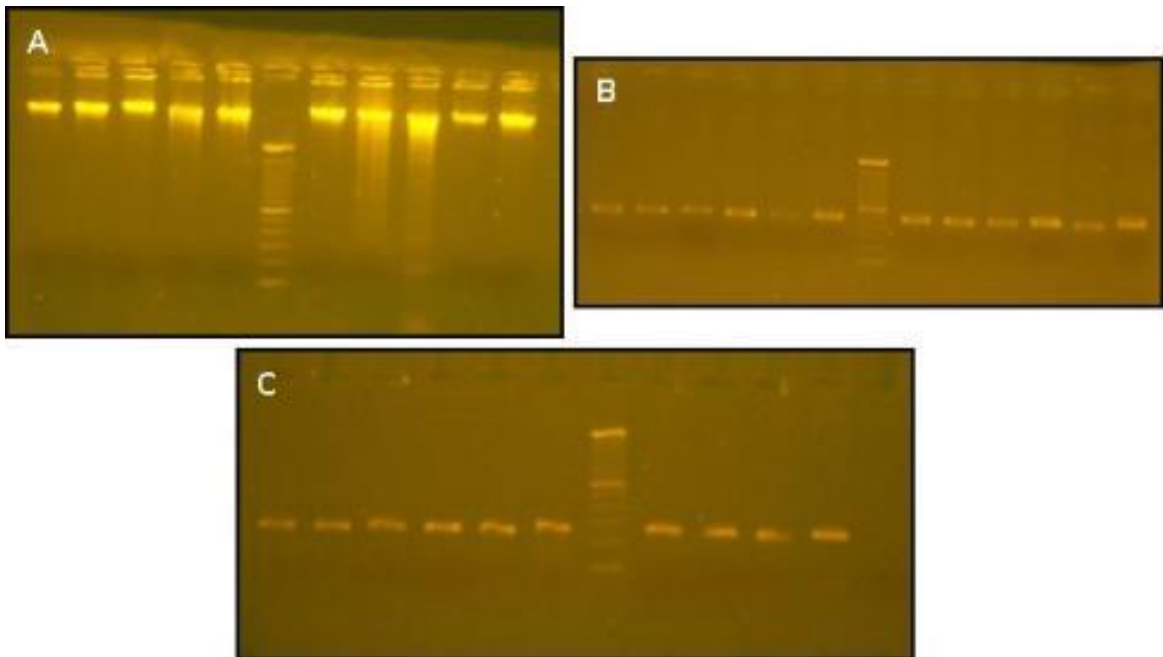


Figure 2. A) DNA quantification; B) D-loop quantification (approx. 420 bp); C) Microsatellites quantification (approx. 250 bp).

For the moment, we found 10 haplotypes. In the Figure 3 we can see that there are no common haplotypes between subpopulations; the north subpopulation has only 3 haplotypes (A, E and G) and the south have 7 haplotypes (B, C, D, F, H, I and J).

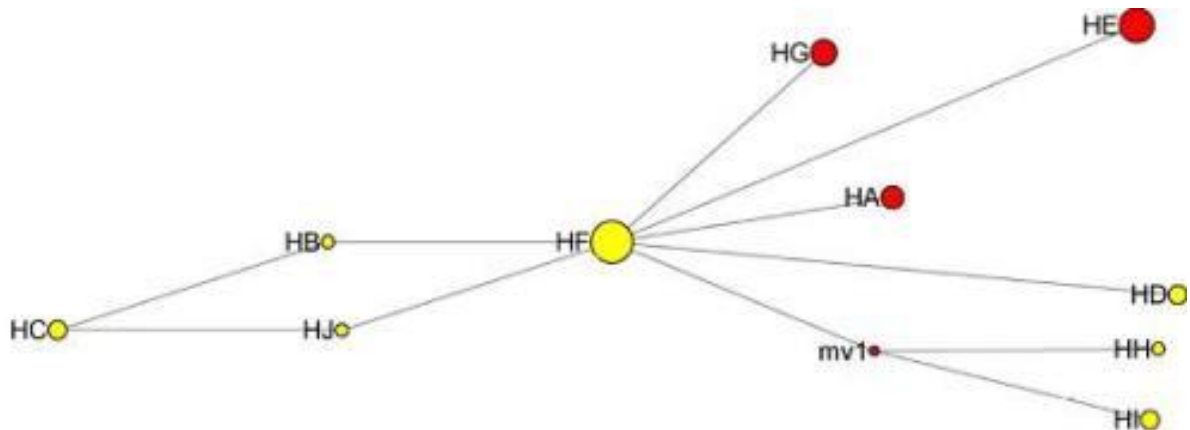


Figure 3. Haplotype network.

These results are what we expected, so now we want to study the nuclear markers (microsatellites) because it can help us to study the gene flux between subpopulations and intra-population. At the moment, we amplify 5 microsatellites of a total of 10 in almost all the samples. Once we have the 10 microsatellites amplified in the 40 samples, we could analyze the gene flux and then, of course, we will use this information to design the management plan of the species.



Figure 4. A) *Ctenomys magellanicus* cave; B) *Ctenomys magellanicus* individual; C) Capture of one individual; D) *Ctenomys magellanicus* in his natural habitat.

Another person from the lab is studying the morphological aspects in these 2 subpopulations so with both morphological and molecular analysis we could conclude if these two subpopulations are in a process of active speciation or not. Finally, in few months we want to make a field exploration to find the species north of this distribution because we have some evidences that the species is also in the southern of Santa Cruz (continental Argentina). If we confirm this information (that there are two different species and the new distribution in the continental Patagonia) the conservation status of the species will change and so the management plan.