The use of molecular data for the management of the Baiji and Finless porpoise populations 'River dolphins genotyping' - BL/11/C27

(Geographic) study area: China (Yangtse River)

Data used: DNA data

Context and objectives

This project consisted in initiating a collaboration project with the Department of river dolphin research, at the Chinese academy of science, to investigate the Baiji and finless porpoise populations in the Yangtze River, in order to **determine the best management conditions for these endangered species**. The project was divided in two main parts:

(1) validation of statistical methods used in population/conservation genetics, using data sets from experimental laboratory populations of a model organism, Caenorhabditis remanei (WP 1) and

(2) isolation of microsatellites for the two species, and genotyping samples from both populations in order to infer their genetic structure for management purposes (WP 2)

Methodology

- DNA microsatellite loci were isolated for C; remanii and experimental laboratory populations of this model organism were set up. We implemented (i) constant size populations which experienced one bottleneck event (drastic temporary size reduction) as well as (ii) three populations of constant size exchanging different proportions of migrants at each generation. We then genotyped the worms at the end of the experiment and used the microsatellite data to detect bottlenecks with the program "Bottleneck". The principle of the method is that, in bottlenecked population, rare alleles have a higher probability of being lost than more frequent alleles. We analyzed the microsatellite data in order to test the robustness of the method to violation of its assumptions. We also attempted to detect migration using the programs "Migrate", "IM", and "BayesAss+".
- 40 microsatellite loci were isolated for Neophocaena phocaenoides and 50 microsatellite loci for and Lipotes vexillifer.

Results

BayesAss+ appears to be a powerful program to infer recent migration rates. Evaluating the performances of the program Bottleneck was more difficult: in the replicates in which the laboratory-reared populations were in an equilibrium state, i.e., when the number of loci featuring a heterozygosity excess was not significantly high in the control population, a bottleneck event was detected only in 4 experiments out of 6 from data collected in bottlenecked populations. In addition, in two cases out of four, a bottleneck was not far from being detected in the control population (replicate 5, i.e., a deviation from equilibrium was probably already present in both populations before the bottleneck event), and one other case was close to the statistical limit of detection (replicate 4, bottleneck 2). An article describing the results of these experiments is in preparation.

We also isolated 40 microsatellite loci for Neophocaena phocaenoides and 50 microsatellite loci for and Lipotes vexillifer. Sequences from these loci, as well as sequences of primer pairs for amplifying them were sent back to professor Wand Ding. These loci were used by the Chinese partner of the project to genotype samples from finless porpoise populations.

The first collaborative manuscript, in preparation, will be submitted **before November 2007 to an international peer-reviewed journal.**

Products and services

Two articles are in preparation and will be submitted soon to peer-reviewed journals.

The markers will be used for the objective management of finless porpoises in China.

- Website:
- Articles :

Execution

Period: 2004-2007

Laboratory/network:

- Laboratory of Evolutionary Genetics- **Prof. Milinkovitc** (IBMM, ULB)
- Wang Ding Laboratory (Chinese Academy of Science)

Discipline

Hydrology & freshwater resources
Biodiversity
Evolutionary Genetics