

Abstract

Analyse of the French livestock of the Honeybee *A.mellifera* using molecular markers: Implication to genetic conservatories set up.

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The honey bee (*Apis mellifera* L.) exhibit a natural biodiversity very well structured into four evolutionary lineages and 26 geographical subspecies. Its interest in agronomy, and use as a producing species lead the beekeeper to exchange subspecies and strains all over the world. These artificial migrations events tend to blot out the natural structure of the species, and if it is to important, can endanger the survival of some of the natural subspecies.

In order to understand the impact of queen importations in France, we studied a total of 5247 colonies, belonging to 52 French populations covering most of the French administrative regions. Using mitochondrial DNA, our study show that 73 % of the colonies belong to the local western Mediterranean lineage. The level of introgression due to queen importations is very irregular and range from 0.5% to 96% according to the location. Observations of local haplotypes seem to point out that France is divided into three different areas: Corsica, Southern and Northern populations.

The use of microsatellite markers shows that the level of population differentiation is very low. When differentiated, this is mostly due to the level of within population introgressions.

Mapping our results lead us to define putative areas where conservation protocols can be considered.

Key words: '*Apis mellifera mellifera*', mtDNA, Microsatellites loci, genetic conservation.