The revolution of new genetic tools for the study of the ecology of rare or elusive species, using non-invasive approaches.

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Since the last decade, the development of new molecular biology technologies and particularly the Next Generation Sequencing methods have revolutionized the study of biodiversity. Using non-invasive approaches (collect of faeces, hairs, urine, saliva..), these methods presently allow to detect the existence of cryptic species, to estimate gene flow among isolated populations, their population sizes but also to study the ecology of rare or elusive species, like their diets, their microbiomes, their sex ratio, their daily movements or their putative niche overlapping or hybridations with closely related species. More particularly, these new genetic methods are interesting for the study of threatened species, in order to propose the best management measures for them.

Using different examples developed in my laboratory, I will enhance the interest of such studies, as complementary tools to other methodologies developed in the fields. As an example, these studies evidenced the most precise information concerning the diets of the Polar bear populations living in northern Canada, the European otter living in France, the Pyrenean Desman, the aquatic shrew or different African and Asian primate species, like the apes and the gorillas. These informations are of a prime interest to better understand the impact of habitat destruction on the food availability, and how these threatened species can adapt themselves to survive to global changes. On a more fundamental aspect, these studies evidenced how species having a close ecological niche, like the Pyrenean desman and the aquatic shrew can live in a same area, by shifting their diets, in order to avoid competition.

Keywords :

Next Generation Sequencing methods, metabarcoding, non invasive approaches, threatened species, diet.