Workshop on “*Wildlife, parasites and pathogens:*

*from barcoding to disease ecology*”

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**Interest of genetic barcoding approaches for the study of biodiversity and epidemiology**

Johan Michaux

Conservation Genetics Unit, Institute of Botany (Bat. 22), University of Liège Belgium

CIRAD Animal et Gestion Intégrée des Risques (AGIRs), Campus de Baillarguet,

F-34093 Montpellier Cedex 5, France.

Until recently, biological specimens were mainly identified using morphological features like the shape, size and colour of body parts. However, these methods were not always the most appropriate and many misidentifications happened according to the expertise of the researchers.

Since several years, the development of sequencing technologies as well as the phylogenetic species concept led to the appearance of a new identification approach called “DNA barcoding”. This method identifies species using a very short genetic sequence from a standard part of the genome. The gene region that is being used as the standard barcode for almost all animal groups is a small region of the mitochondrial cytochrome c oxidase 1 gene (“CO1”). COI is proving highly effective in identifying mammals, birds, butterflies, fish, flies and many other animal groups.

The same approach was also developed in bacteria’s, using fragments of the 16S rRNA region and led to the identification of a large panel of prokaryotes species.

These approaches have recently been improved by the settlement of Next Generation Sequencing technologies, allowing easily the identification of a large number of species within a short period of time.

The aim of my presentation will be to present the interest but also the limitations of such barcoding approaches, in the field of conservation biology as well as epidemiology.