ATTENTION
HORAIRE MODIFIÉ !

Vendredi 30 octobre 2015, 14:00
Grande salle de réunion

METAGENOME SKIMMING AND LARGE-SCALE COMPARATIVE GENOMICS OF COMPLEX ARTHROPOD COMMUNITIES

par

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- The broad potential offered by shotgun sequencing to the exploration of biodiversity is overcoming past paradigms of biology. Today, shallow sequencing of samples representing complex arthropod communities can be used to explore a wide variety of questions, places and communities which remained inaccessible until now. Such "metagenomic skimming" has already been used as an alternative approach for building large-scale phylogenies or explore soil arthropod microfauna (1-3) and shows potential for biodiversity analysis and biomonitoring (4,5).

- Our previous works also showed that shallow sequencing of insect gut content or bulk extracted specimens can recover diet remnants and bacterial symbiotic patterns (6,7) and first, I will briefly discuss the potential of metagenomic symbiont reads either to reveal dynamics of interactions between predator/prey or to build exploratory food webs.

- Strikingly, these studies generally involve the use of ethanol as a preserving media, but few attempts were made to exploit this resource (8). In a second part, I aim to raise awareness about the potential of preserving ethanol. We realized an extensive multi-level biodiversity profiling of the ethanol used for collecting insects from different communities. I will discuss the species recovery made from the preserving media and why concomitant DNAs also appear to be an exploration of symbiotic/parasitic interactions and gut content. It appears that neglecting the preserving media is misusing a source of genetic material which could strengthen evolutionary, ecological and biodiversity studies.

1) **Andújar C. *et al.*** – Phylogenetic community ecology of soil biodiversity using mitochondrial metagenomics. – *Mol. Ecol.*
2) **Crampton-Platt A. *et al.*** – Soup to tree: the phylogeny of beetles inferred by mitochondrial metagenomics of a Bornean rainforest sample. – *Mol. Biol. Evol.*
3) **Gómez-Rodríguez C. *et al.*** – Validating the power of mitochondrial metagenomics for community ecology and phylogenetics of complex assemblages. – *Methods Ecol. Evol.*
4) **Zhou X. *et al.*** – Ultra-deep sequencing enables high-fidelity recovery of biodiversity for bulk arthropod samples without PCR amplification. – *Gigascience.*
5) **Tang M. *et al.*** – High-throughput monitoring of wild bee diversity and abundance via mitogenomics. – *Methods Ecol. Evol.*
6) **Paula D.P. *et al.*, 2014.** – Detection and decay rates of prey and prey symbionts in the gut of a predator through metagenomics. – *Mol. Ecol. Resour.*
7) **Linard B. *et al.*, 2015.** – Metagenome skimming of insect specimen pools: potential for comparative genomics. – *Genome Biol. Evol.*
8) **Hajibabaei M. *et al.*, 2012.** – Assessing biodiversity of a freshwater benthic macroinvertebrate community through non-destructive environmental barcoding of DNA from preservative ethanol. – *BMC Ecol.*