Extrait du metabarcoding.org

http://metabarcoding.org/spip.php?article38

Second Metabarcoding Spring School in Crete (13-17 May 2013)

- Events - Metabarcoding spring school in Crete (13-17 May 2013) -

Date de mise en ligne : Thursday 17 January 2013

metabarcoding.org

In the context of the European project <u>MARBIGEN</u>, the Institute of Marine Biology, Biotechnology and Aquaculture (former Institute of Marine Biology and Genetics) of the <u>Hellenic</u> <u>Centre for Marine Research</u>, organizes the 2nd DNA Metabarcoding Spring School in Crete, Greece.

The advances in next-generation sequencing (NGS) technologies have revolutionized many fields of the biological sciences, including that of biodiversity studies. Many ecological questions rely on the knowledge of the list of species involved in the studied process. Tackling this demand using standard methods of taxonomical identification, is often a difficult task that relies on highly qualified persons. DNA barcoding has introduced the use of short standardized genomic sequences (barcode) as a character in taxonomical identification. DNA metabarcoding uses the same principle that associates DNA sequences to taxa for estimating biodiversity of an environmental sample. Metabarcoding approaches use total and usually degraded DNA from environmental samples to analyze biotic assemblages and can be potentially carried out for any kind of organisms in an ecosystem. These analyses rely on specific genetic markers, called metabarcodes, which should be optimized for taxonomic resolution, minimal bias in amplification of the target organism group and short sequence length. As all living organisms spread cells in their environment, a PCR amplicon obtained with adequate primers from the total DNA extracted from an environmental sample, can be consider as a mirror of the biodiversity present in the environment. The pertinent choice of the primer pair allows to focus on a specific group as, for example, plants. Then the sequencing of a large number of individual DNA molecules of the PCR amplicon using NGS technologies allows establishing a list of taxa present in the sample. Metabarcoding can be applied to many ecological studies such as plant community analysis, plankton and benthic community analysis, past ecosystem reconstruction, or diet assessment.

After the success of the <u>1st DNA Metabarcoding Spring School in French Alps</u>, we organize the 2nd one in Crete, which includes lectures and bioinformatic practical sessions on metabarcoding. The School is open for 20 participants (post-graduate students or researchers) that will attend both lectures and practicals, and for 30 additional participants that will follow only the lectures.

The focus will be mainly on marine biodiversity, however people from all fields of metabarcoding are encouraged to participate.

Main lecturers

- Antony Chariton (CSIRO, Australia)
- Eric Coissac (LECA, CNRS, France)
- François Pompanon (LECA, CNRS, France)
- Xin Zhou (BGI, China)
- Lucie Zinger (EDB, CNRS, France)
- ...

Provisional program

	Monday 13	Tuesday 14	Wednesday 15	Thursday 16	Friday 17				

9h -	Welcome	Eric Coissac: In silico selection and	Eric Coissac: Basic	Antony Chariton: Can metabaroding be used to routinely	Lucie Zinger: DNA
10h		design of barcodes for DNA	analysis of DNA	monitor and assess estuarine environments?	metabarcoding in
		metabarcoding	metabarcoding data		community ecology
10h -	François Pompanon:	Xin Zhou: Using standard barcode	Lecture	Antony Chariton: Environmental monitoring of marine and	Xin Zhou: A PCR free
11h	Introduction to DNA	for DNA metabarcoding		estuarine sedimentary environments: wins, losses and	approach of DNA
	metabarcoding			considerations.	metabarcoding
	Coffee break	Coffee break	Coffee break	Coffee break	Coffee break
11h00					
-					
11h30	Four participant	Four participant presentations	Four participant	Four participant presentations	Four participant
11h30	presentations		presentations		presentations
- 12h					
	Lunch	Lunch	Lunch	Lunch	Lunch
12h30					
-					
14h30	Metabarcoding marker	Experimental design	Metabarcoding data	Metabarcoding data analysis II	Excursion
14h30	design in silico		analysis I		
-					

Second Metabarcoding Spring School in Crete (13-17 May 2013)

17h30

Application

The number of participants will be limited to 20 that will attend both lectures and practical sessions. Thirty (30) more participants will follow only the lectures. Applications including a short CV and a short motivation letter should be sent to spring2013 at metabarcoding.org, with subject: "MARBIGEN DNA Metabarcoding School 2013" no later than 1 March 2013.

Workshop venue

The workshop will be held in the premises of the Hellenic Centre for Marine Research in Crete, Greece in the main building of Thalassokosmos complex (former US base at Gournes, Heraklion).

Accommodation

Accommodation will be provided in hotels in the area of the workshop venue, in special prices for the participants.

Workshop Costs

There are no registration fees for the workshop. Participants will have to pay for their accommodation, meals and travel expenses. The average cost for accommodation and meals for 6 days is not expected to exceed 350 euros.