






Dissecting earthworm biodiversity patterns in tropical rainforests through the use of DNA barcoding

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Rationale
Soil invertebrate functions

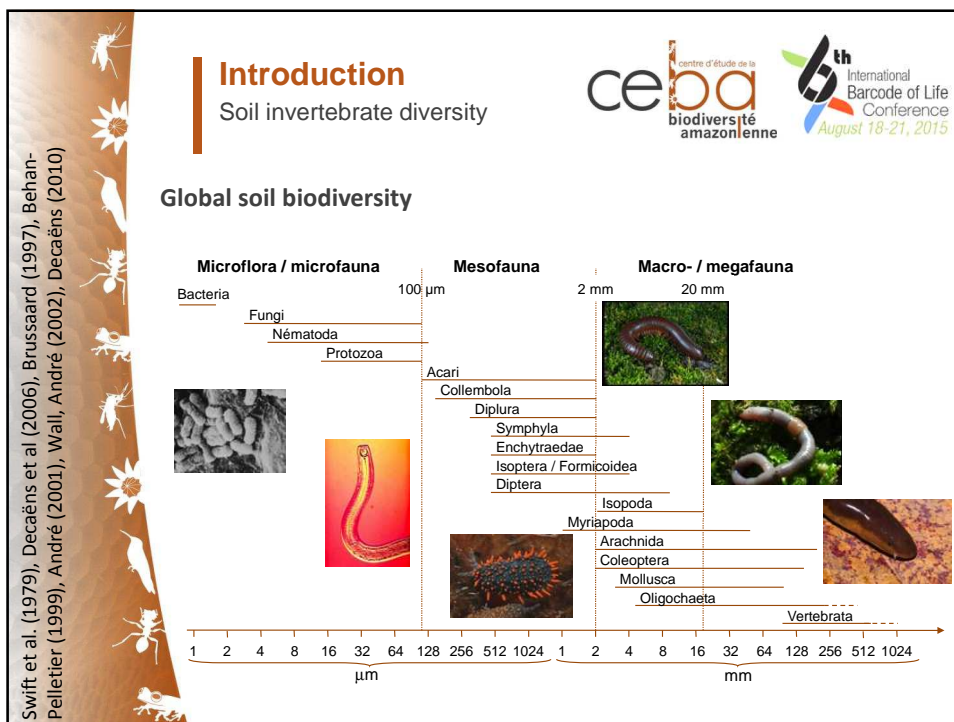
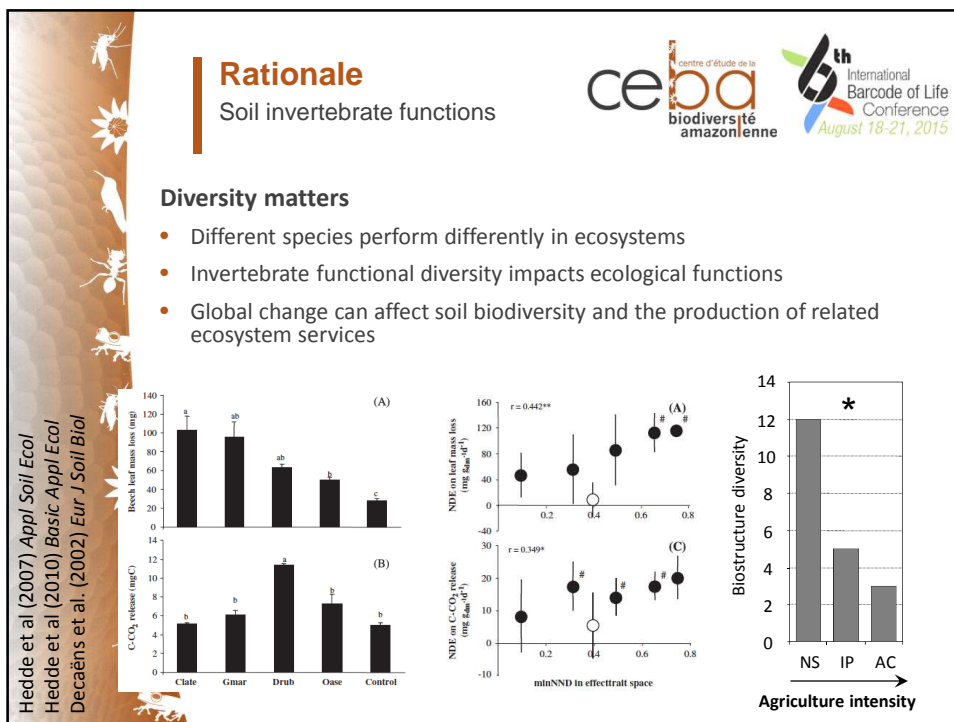
The values of soil invertebrates

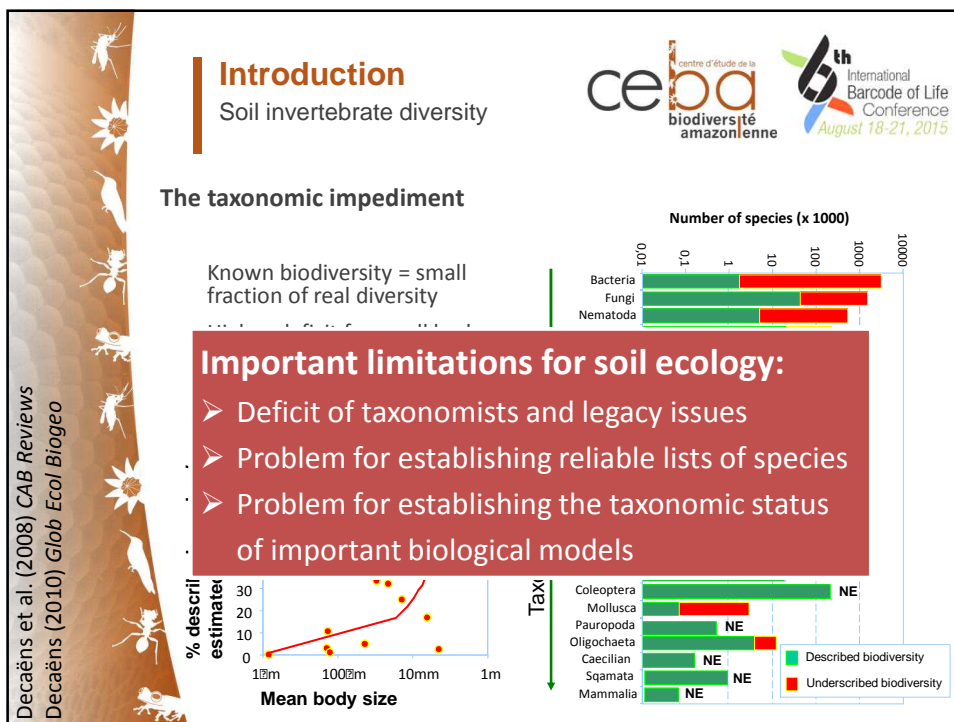
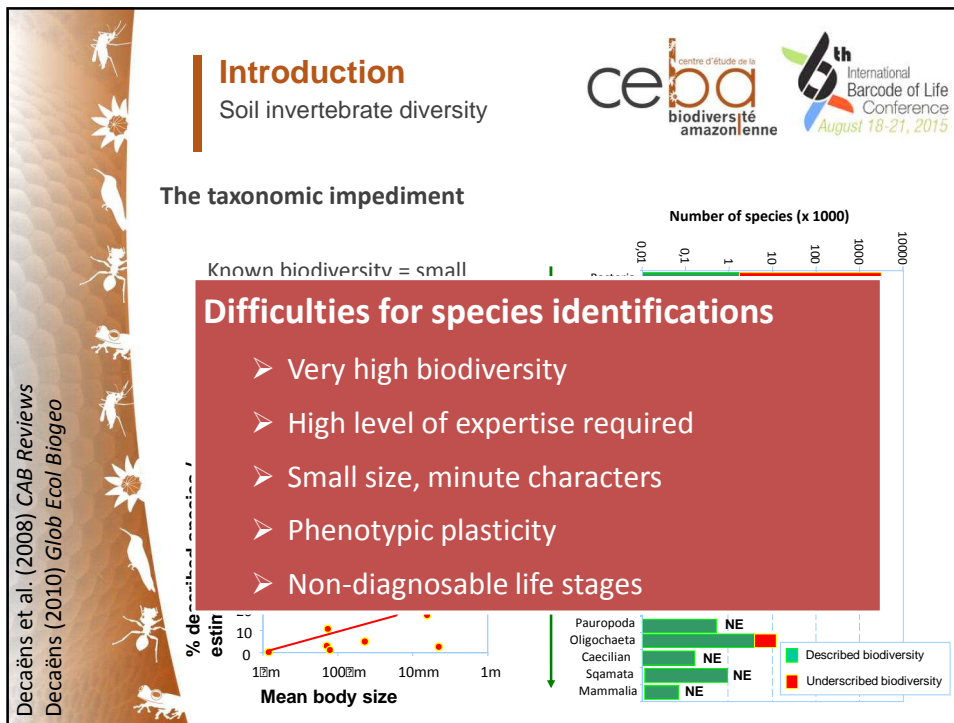
- Ecological importance: regulators of soil processes
- Economic importance: maintenance of soil fertility
- Strategic importance: highly diverse communities
- Strategic importance: invasive species
- Practical importance: used as bioindicators of soil quality or pollution





Decaëns et al. (2006) Eur J Soil Biol






Lavelle & Lapiéd 2003, Rougerie et al. (2009),
James et al. (2010), Richard et al. (2010),
Novo et al. (2011), Decaëns et al. (2013)

Rationale

Earthworms






Earthworm global patterns

- Are present in most soils of the world
- Represent the dominant component of soil faunal biomass in many ecosystems
- 5500 species described to date

DNA barcoding

- Rapid identifications, species discrimination
- Juveniles identification
- Cryptic diversity

- **Molecular operational taxonomic units (MOTUs)**
- Community scale barcoding to describe diversity patterns in regions where taxonomy is mostly unresolved
- **Useful tool in soil ecology, macroecology, biogeography...**

Rationale

Earthworm diversity patterns in tropical rainforests

Context



- Earthworm communities are poorly studied when compared to other groups
- We still know very few about earthworm diversity and distribution in tropical rainforests
- For example: only 22 sp listed from French Guiana (Pavlicek & Csuzdi, 2012)

The WormBank project:

- To build a library of DNA barcodes (COI) for earthworms of French Guiana
- To use the data to explore community patterns at different spatial scales

Funding

: CEBA, CNRS (APEGE, Nouragues), ANR, iBOL


Material and methods
Sampling design

ceba centre d'étude de la biodiversité amazonienne

6th International Barcode of Life Conference
August 18-21, 2015

Study sites in French Guiana:

Material and methods
Sampling design

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- A range of selected habitats in each site
- At least 3 replicates / habitats
- In each replicate:
 - Hand sorting of 3 soil blocks of 25x25cm
 - 2 hours (2 people) of qualitative sampling on a 1ha area
 - Soil, litter, decaying trunks, epiphytic soils...

Material and methods

Sampling design



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Laussat white sands



Paracou station



Cacao



Saül





Kaw mountain



Mitaraka inselbergs




Nouragues Pararé station




Nouragues Inselberg station

Material and methods

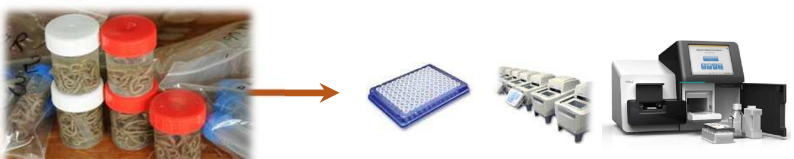
Sample processing



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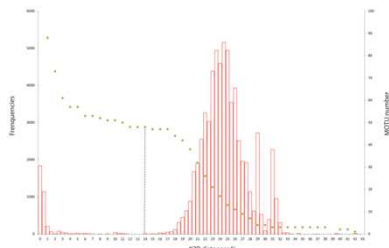


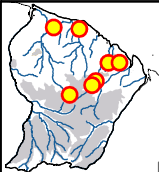
DNA barcoding

- Specimens fixed in 100% ethanol, separated into morphospecies
- Up to 5 specimens / morpho sp / sample for individual-based barcoding
- COI sequencing using Sanger (iBOL funding) or MiSeq technology (APEGE funding)

Barcode gap identification



- Identification of the barcode gap at 14% (Nouragues data)
- MOTU → species richness and community structure





Results


Regional diversity

New results for seven study sites

- 2561 specimens barcoded in seven different locations

Neighbour joining tree



Year	# specimens	# of MOTUs	
Inselberg	2010	440	38
Pararé	2010	213	27
Kaw	2013	227	29
Paracou	2013	389	45
Laussat	2014	97	11
Cacao	2011-13	793	36
Saul	2013-14	402	36
Total	2561	148	

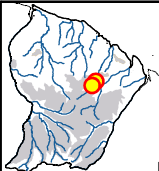
→ Total of 148 MOTUs

→ Good match with morphology (Nouragues data)

→ Most are sp new for science



→ Dramatic increase compared to the 22 species checklist (Pavliček & Csuzdi, 2012)

→ Highlight a strong deficit




Results

Regional diversity

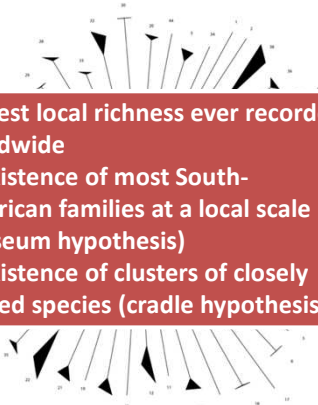
Focus on Nouragues' communities

- 650 specimens barcoded in two different locations (Pararé and Inselberg)
- 5 families, 12 genera, 48 species level MOTUs
- Good match with morphology, except in a few cases



Decaëns et al. (2016) Soil Biol Biochem

Neighbour joining tree

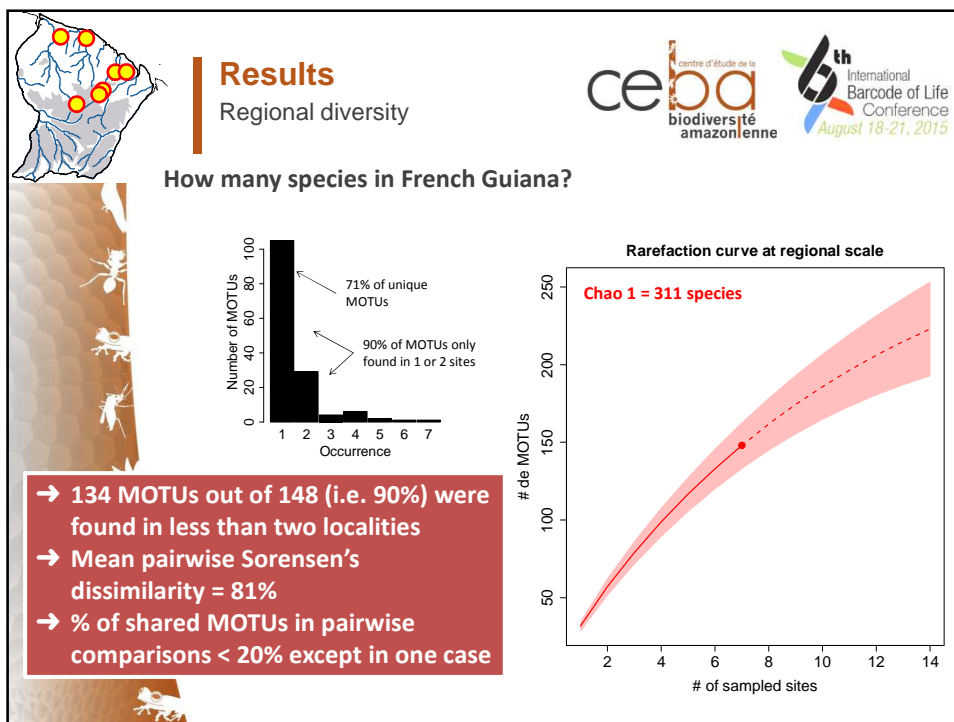
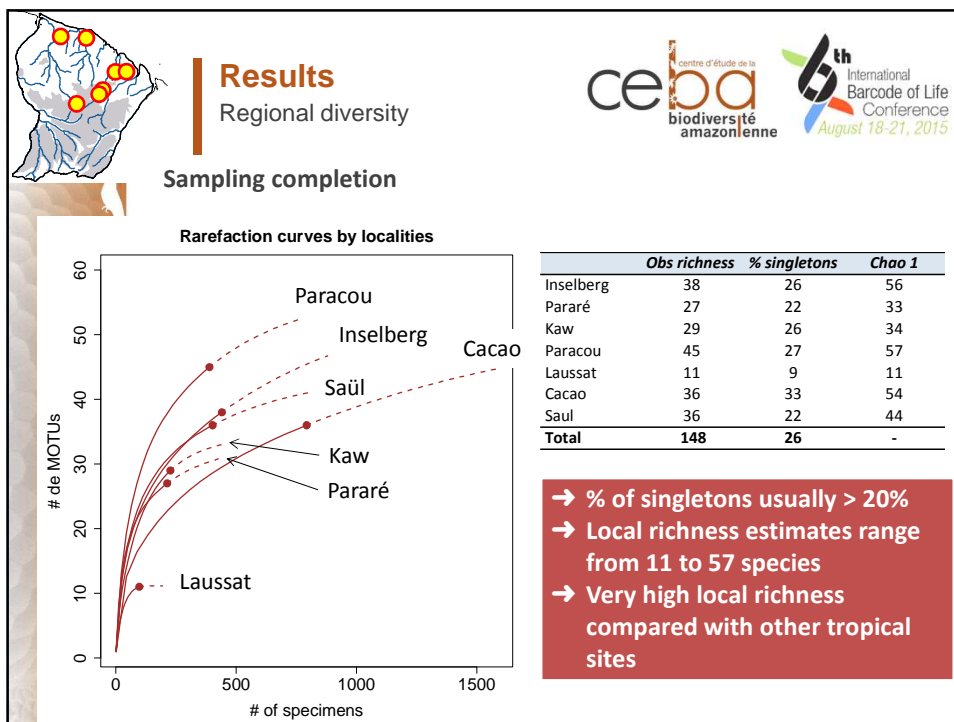


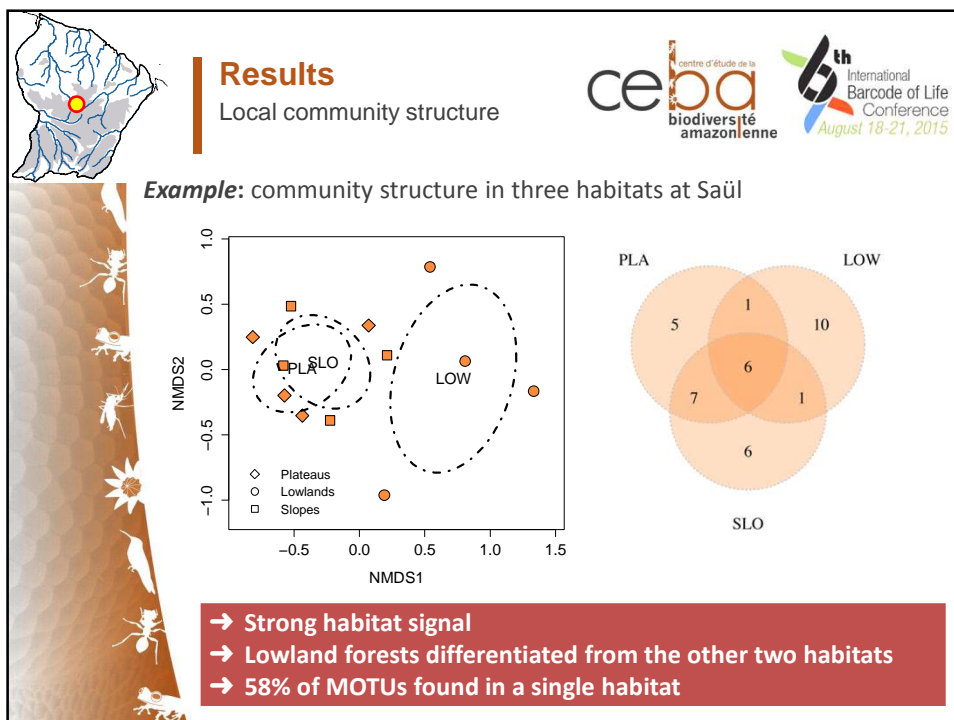
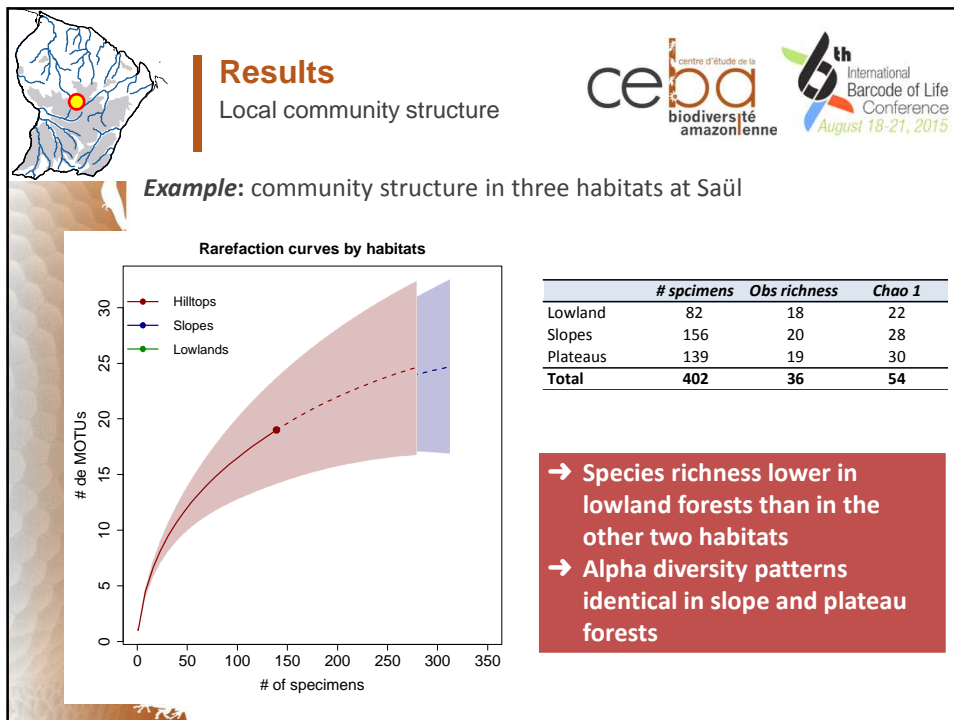
→ Highest local richness ever recorded worldwide

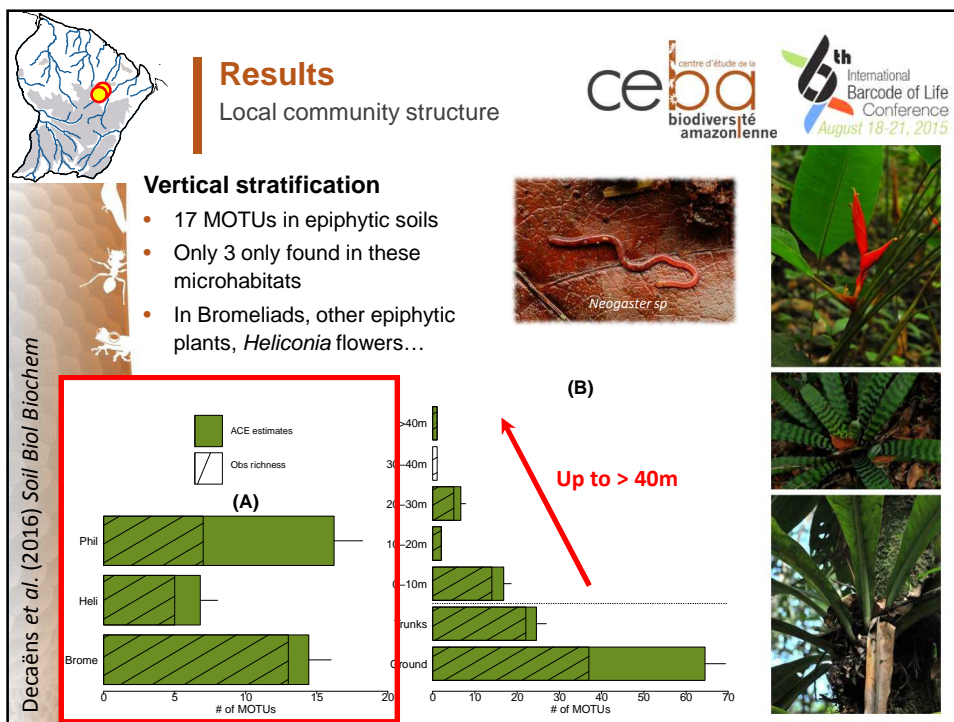
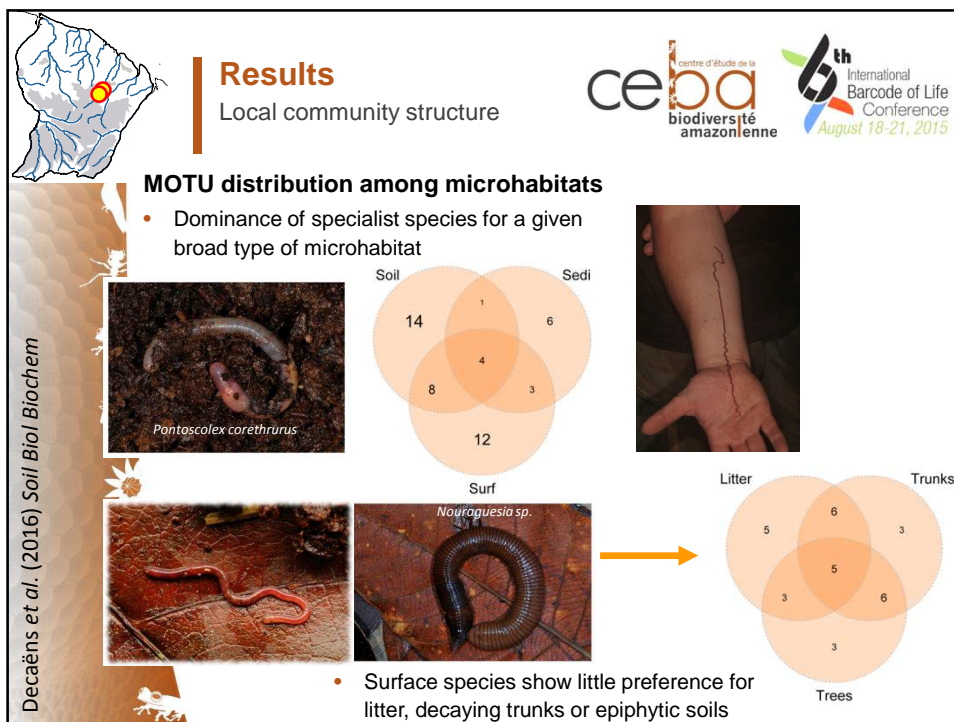
→ Coexistence of most South-American families at a local scale (museum hypothesis)

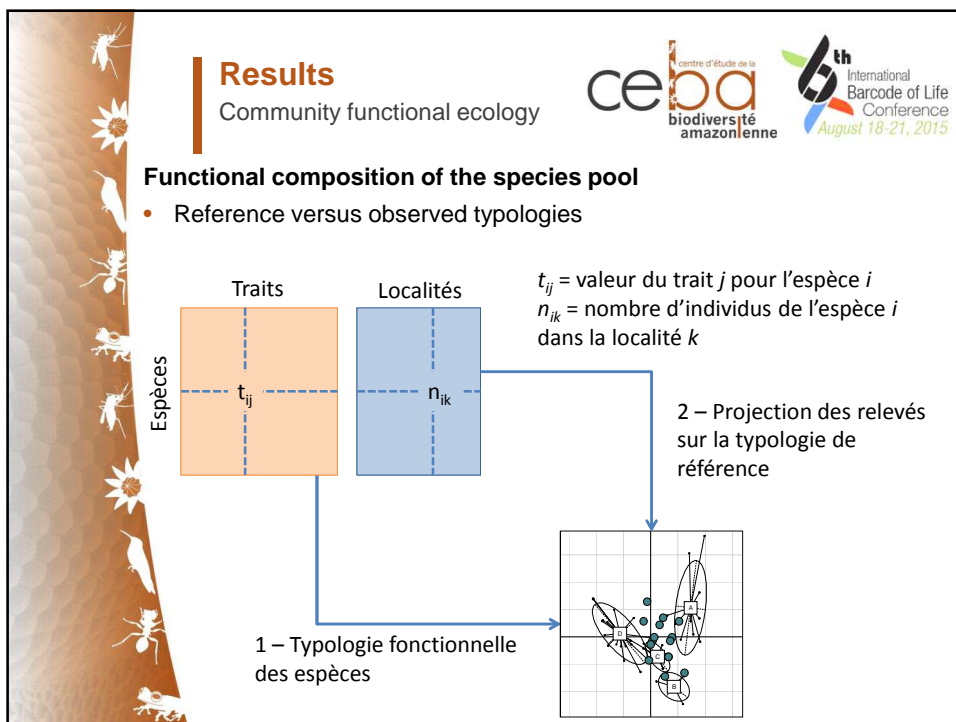
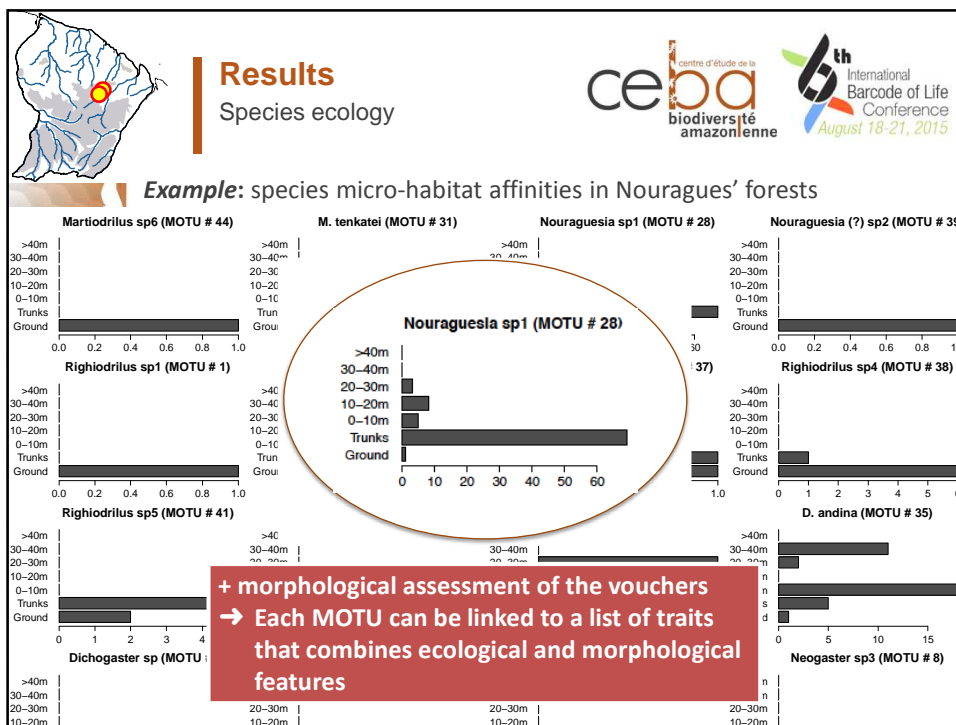
→ Coexistence of clusters of closely related species (cradle hypothesis)

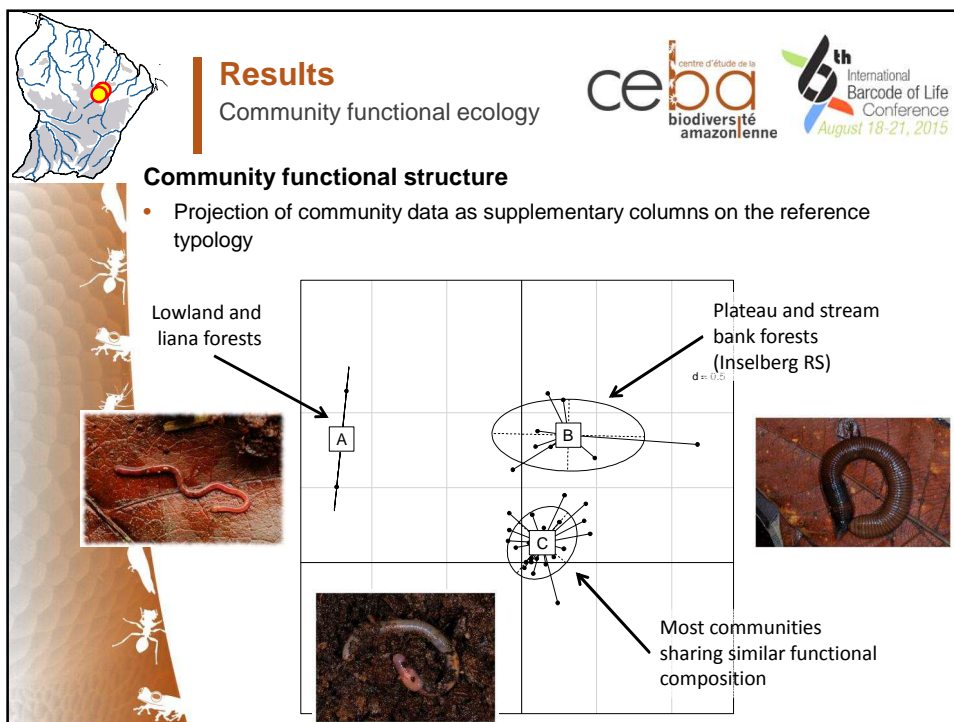
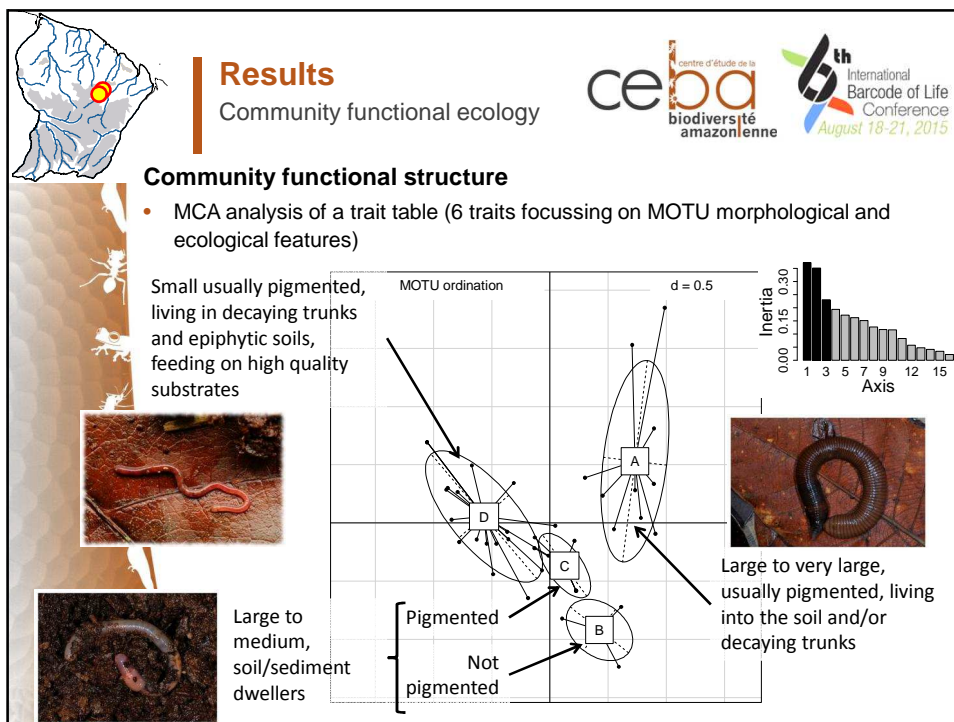
Family / genus	# of MOTUs
<i>Rhinodrilidae</i>	
<i>Rhinodrilus</i>	2
<i>Pontoscolex</i>	3
<i>Urobenus</i>	1
<i>Glossoscolecidae</i>	
<i>Atatina</i>	1
<i>Glossodrilus</i>	4
<i>Martiodrilus</i>	8
<i>Nouraguesia</i>	1
<i>Righiodrilus</i>	6
<i>Acanthodrilidae (Benhaminae)</i>	
<i>Dichogaster</i>	3
<i>Neogaster</i>	7
<i>Wegeneriana</i>	6
<i>Haplotaxidae</i>	
<i>Haplotaxis</i>	1
<i>Ocnerodrilidae</i>	
<i>Ocnerodrilidae</i>	3
<i>Not identified</i>	
<i>Not identified</i>	2
Total	48

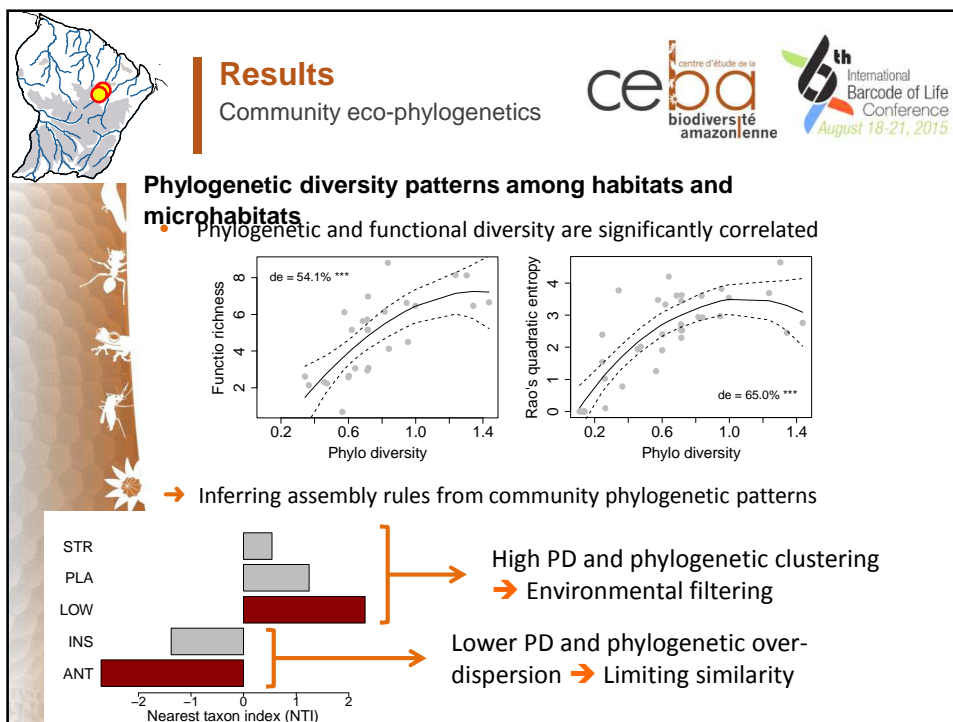
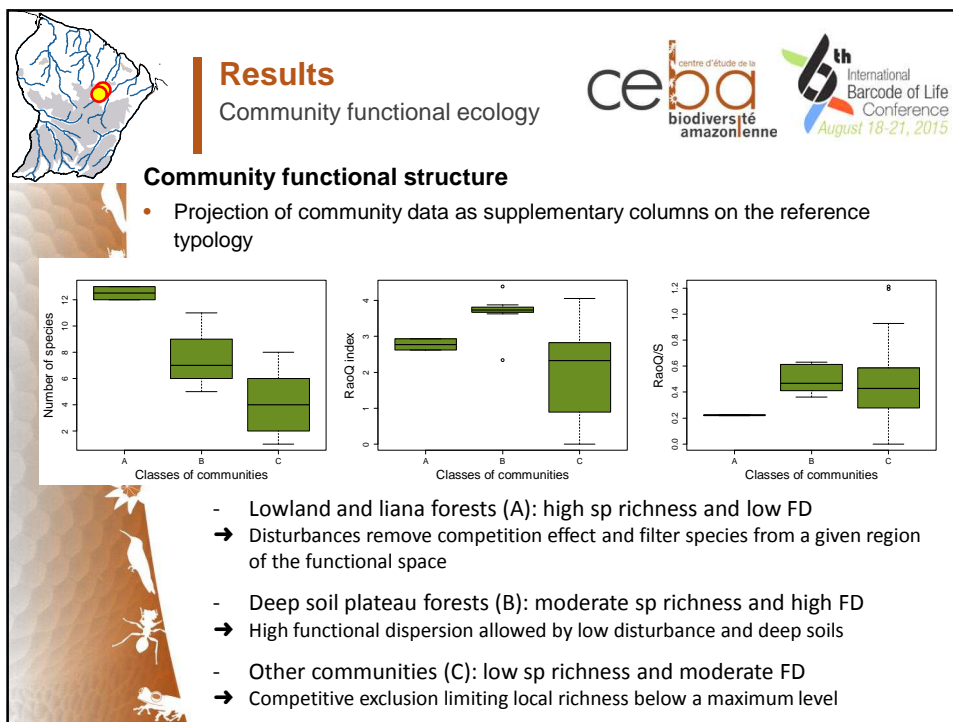
















Conclusions


Highlights


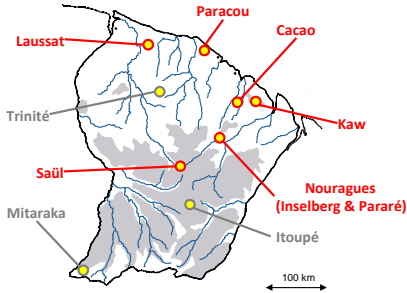
- High levels of local diversity
- High levels of spatial turnover
- Consistent functional structure among communities

Perspectives

- Extend the sampling coverage
- Develop a comprehensive functional trait database
- Beta diversity patterns for TD, FD, PH
- Historical biogeography and diversification processes
- DNA barcode libraries for other studies using environmental DNA









Merci de votre attention