DNA Metabarcoding to quantify the ecological impact of climate-induced forest diebacks in the Pyrenees

Paul Schmidt Yanez, Rodolphe Rougerie, Annie Bézier, Béatrice Courtial, Christophe Bouget, Laurent Larrieu, Douglas W. Yu, Michael T. Monaghan, Elisabeth A. Herniou, Carlos Lopez-Vaamonde

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SIRE Lucas

Lucas.sire@univ-tours.fr

SCHMIDT YÁÑEZ Paul, ROUGERIE Rodolphe, BEZIER Annie, COURTIAL Béatrice, BOUGET Christophe, LARRIEU Laurent, YU Douglas W., MONAGHAN Michael T., HERNIOU Elisabeth A., LOPEZ-VAAMONDE Carlos

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Insect Biology Research Institute

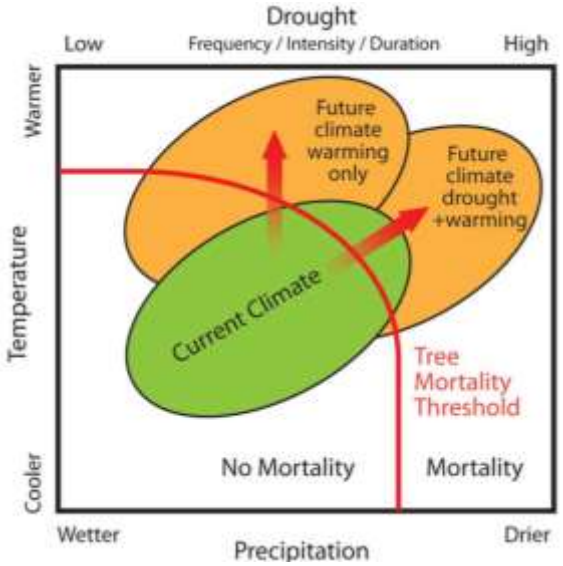
IRBI - UMR 7261 - CNRS/University of Tours - Faculty of Science and Technology
Parc de Grandmont - Avenue Monge - 37200 TOURS - FRANCE

contact.irbi@univ-tours.fr
+33 (0) 2 47 36 69 11

Global changes and forestry management

Global changes

"Climate change, insect infestations, drought…"

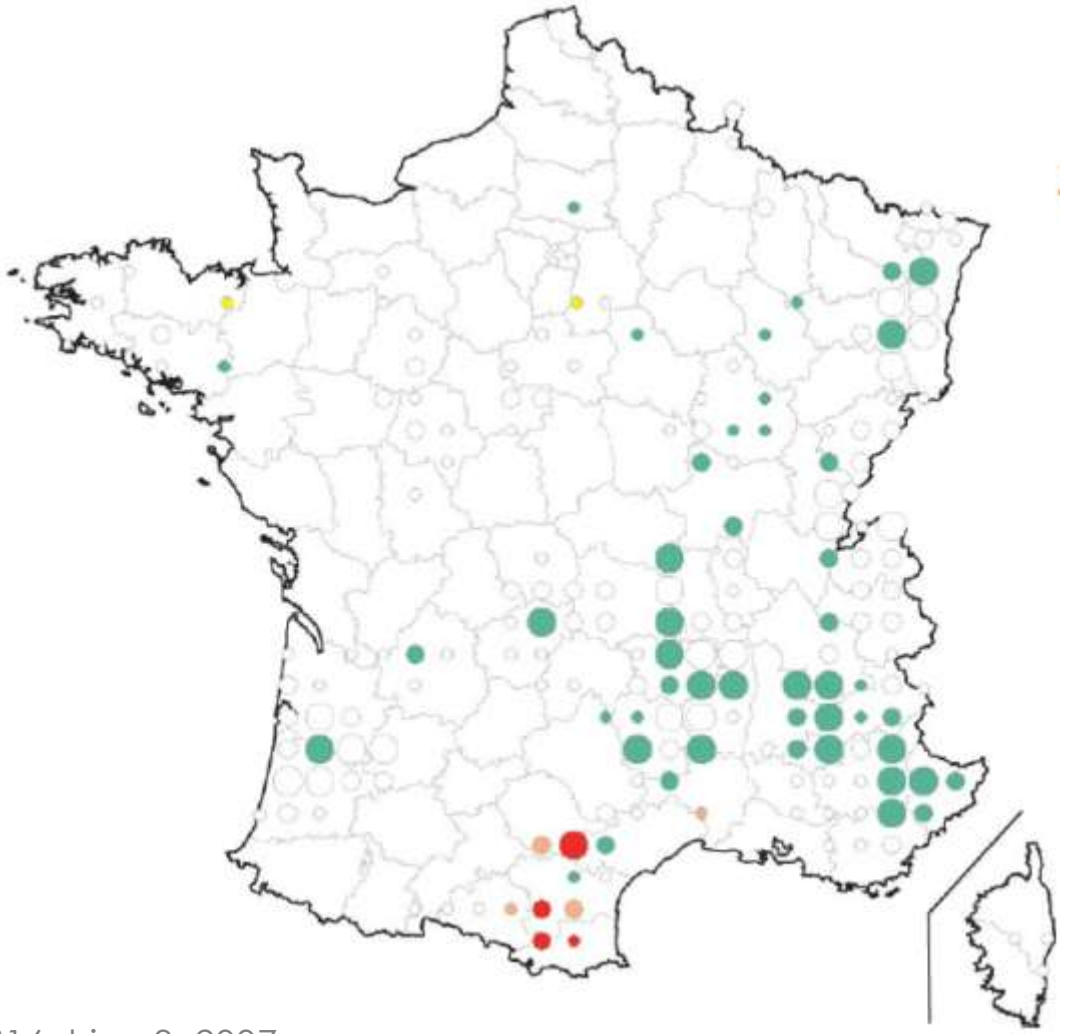


Allen *et al.*, 2015

Salvage logging

"To harvest damaged trees in order to recover economic value otherwise lost. "

Droughts induce silver fir (*Abies alba*) die-off in Pyrenees



Proportion of dominant trees with more than 25% of dead branches

- More than **35%**
- From **20** to **35%**
- From **10** to **20%**
- Less than **10%**
- No tree in that case

Number of living and dominant trees

- More than **100**
- From **50** to **100**
- From **25** to **50**

Flot *et al*. IF n°16, trim. 3, 2007

Studied areas

N_{total} = **56 plots**

2 valleys

Vallée d'Aure
Pays de Sault

~190km distance

3 dieback level conditions

- **Healthy** *(20 plots)*
- **Low dieback level** *(12 plots)*
- **High dieback level** *(24 plots)*

2 salvage logging conditions within high dieback level

- **Not harvested** *(12 plots)*
- **Harvested** *(12 plots)*

Characteristics of each plot

1 Malaise trap in the center of **each plot**

Sampled **4 times** (each month) from **May** to **September**

Micro Dendro-habitats

Larrieu et al., 2018

Canopy openness

N_{total} = **224 samples**

$n_{ecological\ variables}$ = **84+**

Sample preparation for metabarcoding

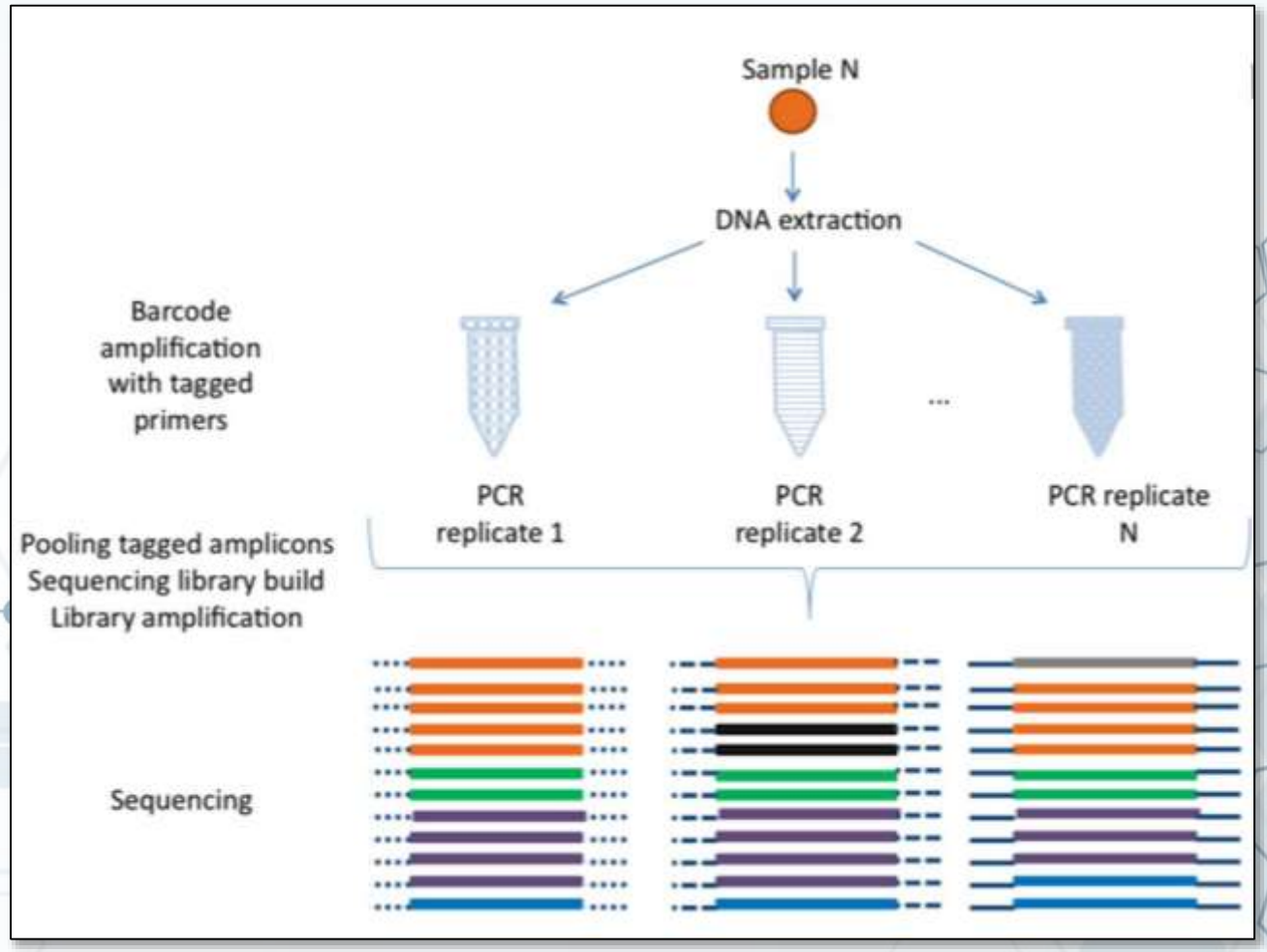
- Processed sample randomization
  Bálint et al., 2018
- Filtration & Rincing
- Drying overnight
- Homogeneization
  Elbrecht et al., 2017
- Grinding

Metabarcoding pipeline

- **COI** marker (313bp)

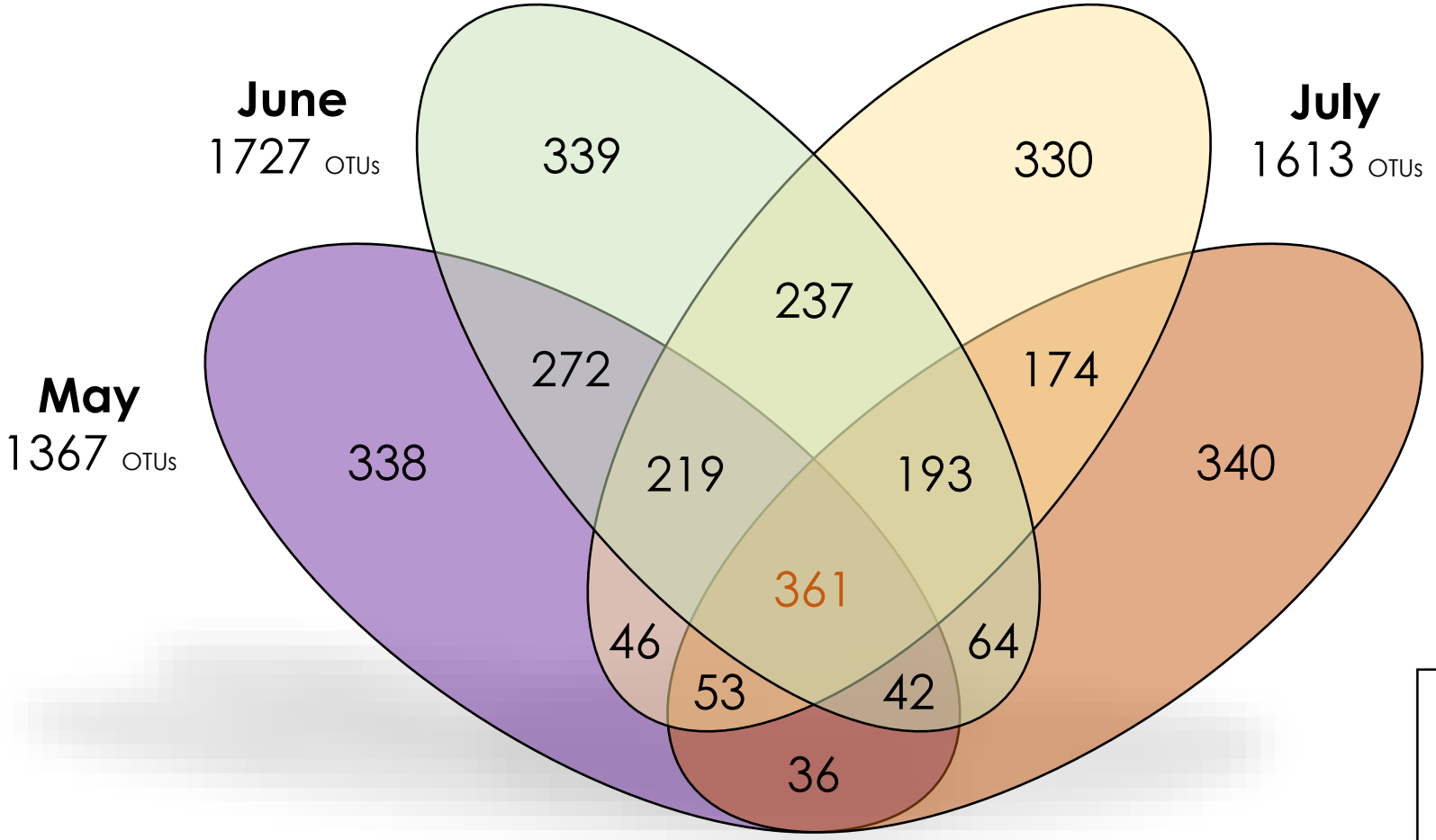
  Leray *et al.*, 2013

  Geller *et al.*, 2013
- PCR triplicates
- Illumina MiSeq V3 paired-end
- OTU clustering **97%** (sumaclust)
- **3 PCRs** & **3 reads** minimum
- Taxonomic assignement using **BOLD**



Zepeda-Mendoza et al., 2016

High general temporal turnover



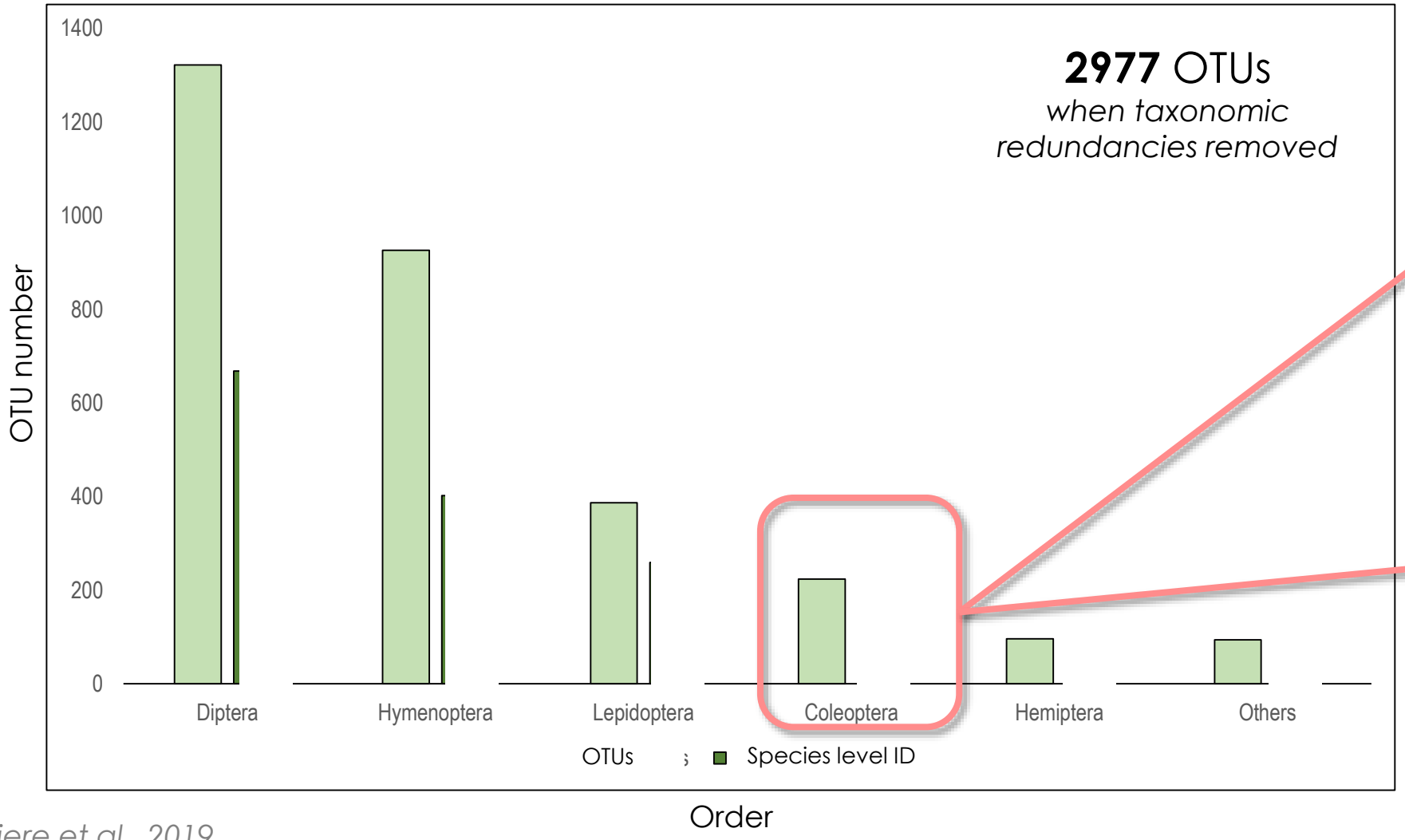
3041 OTUs

11.9% shared by all

Jaccard Index : $J_{May / August} = 0.23$

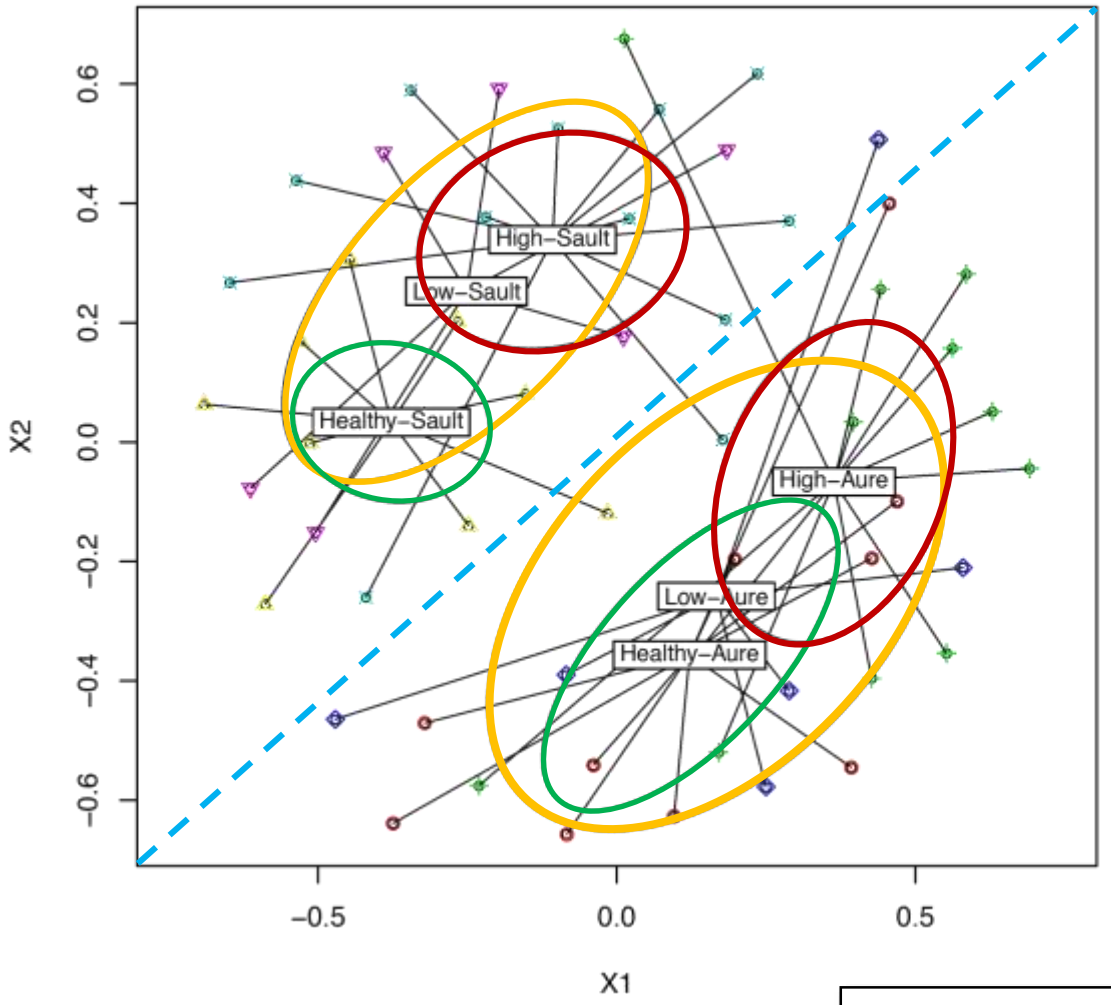
Jaccard Index : $J_{June / July} = 0.43$

Incomplete reference libraries & taxonomic assignment



Moriniere et al., 2019

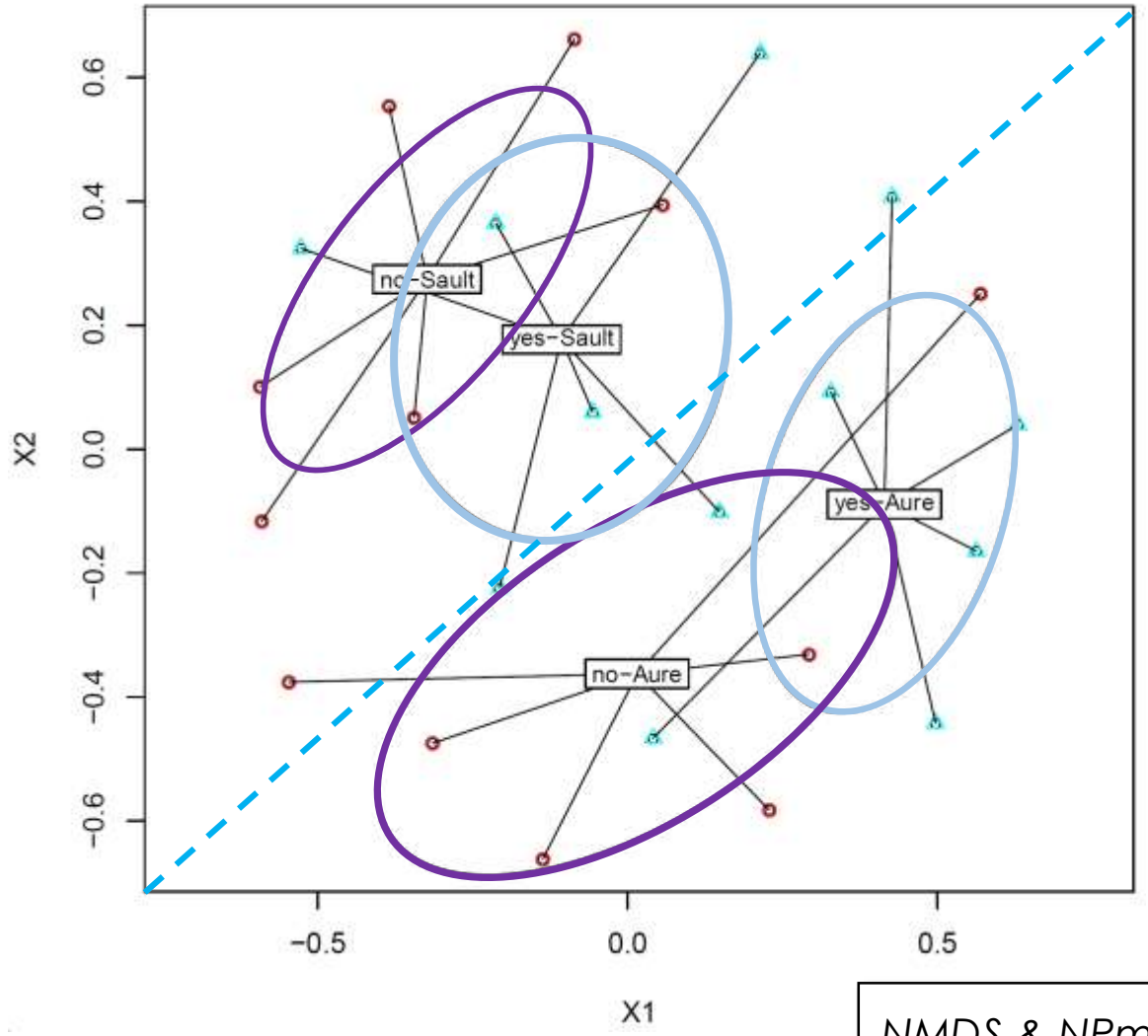
Insect composition varies with dieback level



- Strong **difference** in insect composition **between both valleys**
- **Highly significant difference** (***) between **healthy** & **high level of dieback**
- **Low level of dieback** shows **no difference** in insect composition

NMDS & NPmanova

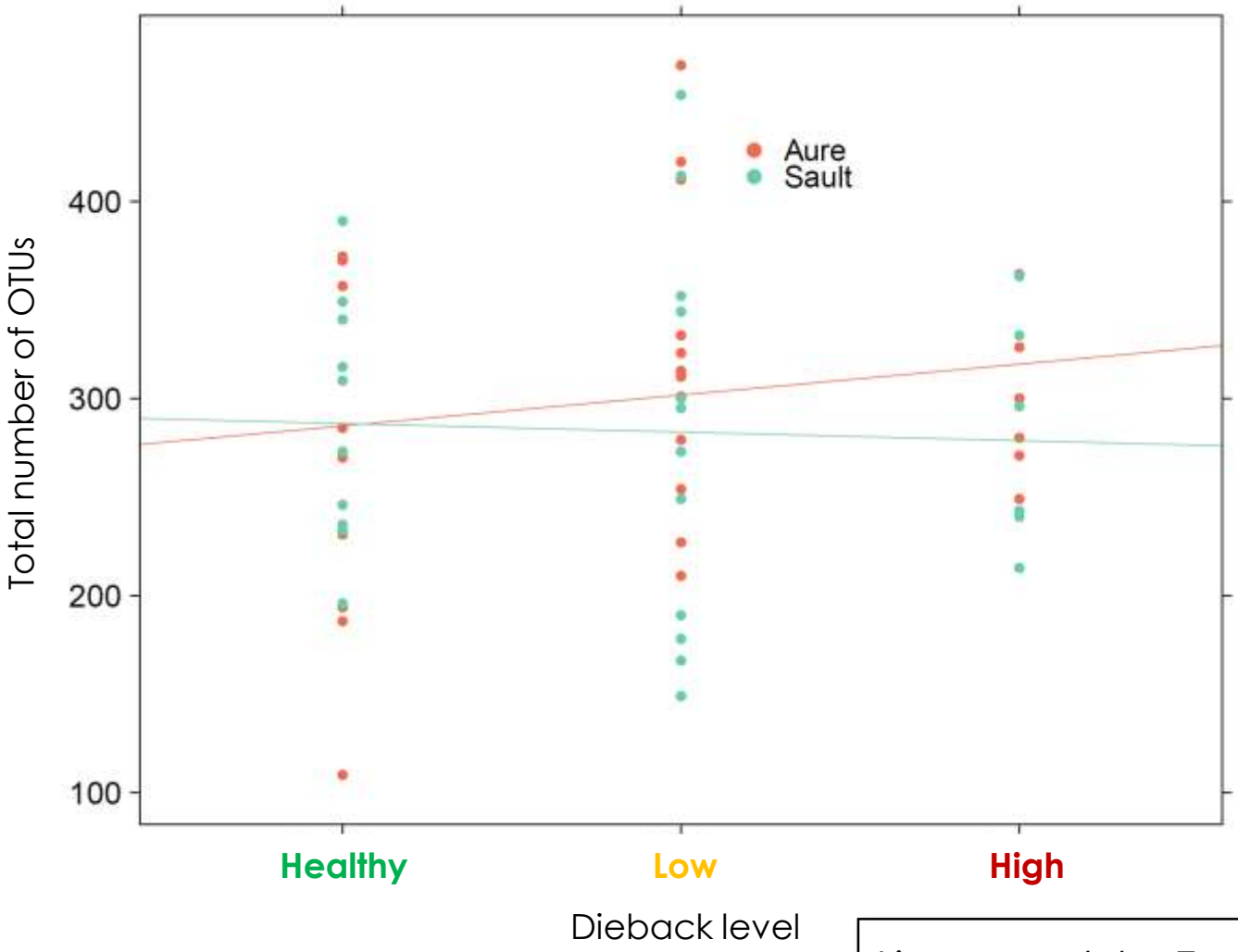
Insect composition does not change with salvage logging



NMDS & NPmanova

- Strong **regional effect**
- **No significant difference** between **not harvested** and **salvage logged**
- **No direct impact** of **salvage logging** on total insect composition **detected**

Species richness does not vary with dieback level



- **No valley difference**
- **No significant difference** between **Healthy**, **Low** and **High** **dieback levels** in terms of species richness **detected**

Linear model & Type II Anova

Species associated with dieback levels

Potential candidates for bio-indication

Healthy

12 specific OTUs

CBG Photography Group - CC

Fannia abrupta

Native from Nearctic
Apparently introduced in China (2016)
No information about France

Low dieback level

21 specific OTUs

Pungeleria capreolaria

Feed on *Picea abies* and *Abies alba*
Fly from mid June to September

High dieback level

10 specific OTUs

Marko Mutanen - CC

Botanophila brunneilinea

Larval stage on *Centaurea sp.* plants

Leuchtmann et al., 2015

Package R Indicspecies

OTUs found at least in 10 plots

To sum up before flying away!

- Usefulness of **metabarcoding on Malaise** trap samples for **bio-monitoring**
- Strong **temporal** and **regional effects**
- **Need to complete reference libraries** for European **Diptera** and **Hymenoptera** in BOLD
- **Direct impact** of **high dieback level** on insect composition
- **No direct impact** of salvage logging
- Potential **bio-indicator candidates** for **dieback levels**

Thank you for your attention !

Thank you to:

- Kévin Speder
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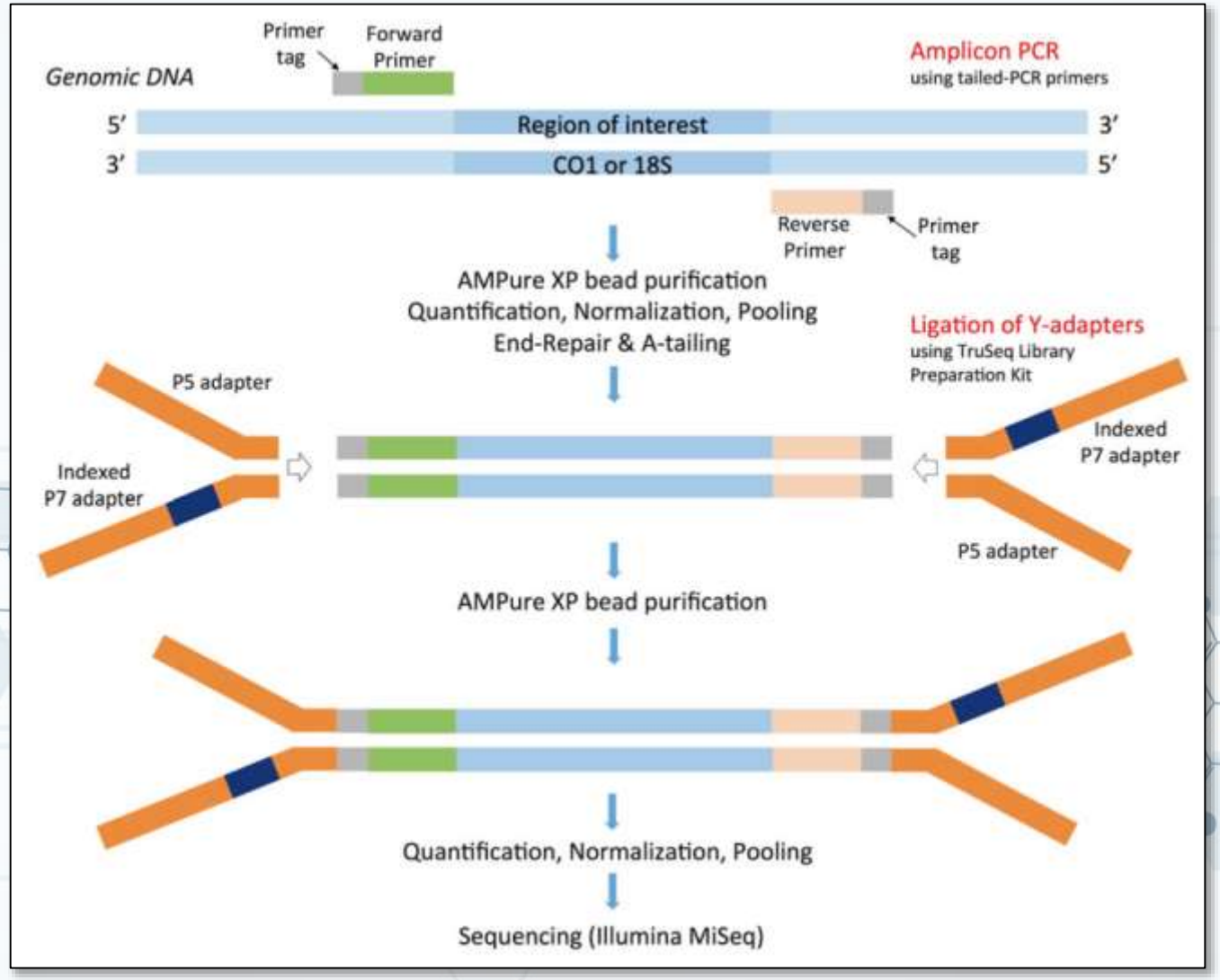
- Laurent Burnel
- Jérôme Molina
- Carl Moliard

Twin-tagging – Dual Indexing PCRs



Leray et al., 2016 (chap. 14)