

# Comparative and Integrative Genomics of Organ Development, Lyon



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Co PI

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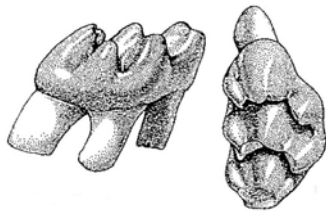
# Interplay between evolution, development and genome

Biological systems (Genome + Development) are the product of evolution

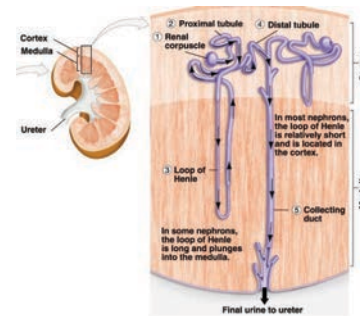
In turn, how do

- Development properties
- Genome properties

shape phenotypic evolution?



Rodent molar shape

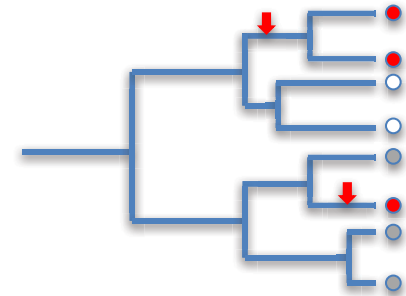


Kidney of rodents adapted to aridity

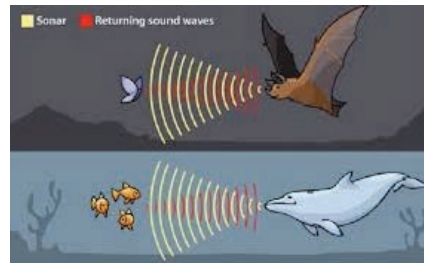
Tooth Development >> Tooth evo-devo >> Comparative transcriptomics >> Molecular evolution >> Methodology

# Studying repeated evolution

= Independent acquisition (≠heritage)  
of the same trait during species evolution



Placentals /mammals  
adapted to the same niche



Bat/dolphin  
echolocation

## Why?

Is there a strong ecological  
trigger?

Is it especially easy to do?

## How?

Is it done the same way?

Reveal hidden:

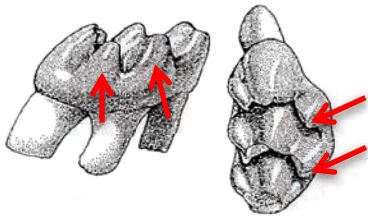
Developmental properties

Genomic properties

# Overview

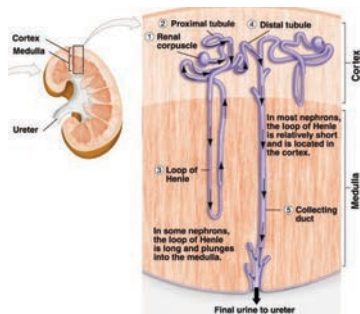


1: Repeated elongation of first upper molar in mice by developmental facilitation



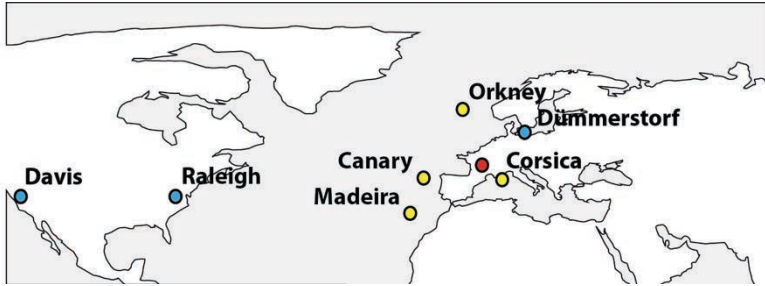
2: Repeated evolution of the murine dental plan: same mechanisms?

3: Tools to study the molecular basis of convergent evolution

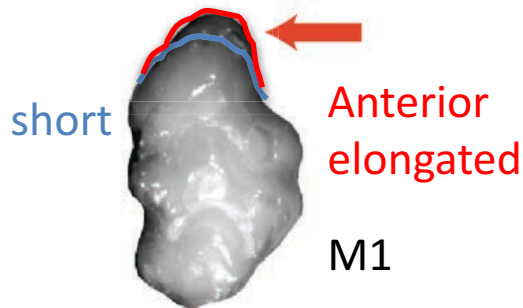


4: Repeated adaptation of rodents to arid environments

# 1: Repeated elongation of first upper molar in mice by developmental facilitation

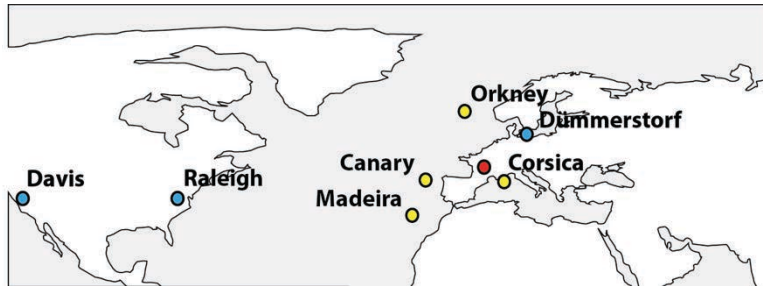


Adult



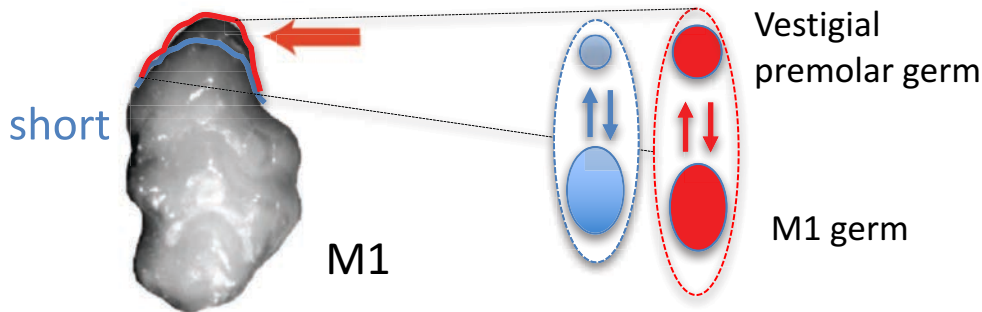
- Repeated evolution (lab and wild)
- First upper molar only
- Collab. Sabrina Renaud, Pascale Chevret
- ANR Bigtooth (inc. Julien Claude)

# 1: Repeated elongation of first upper molar in mice by developmental facilitation



Adult

Embryo



- Heritage of evolutionary history: in embryos, abortive premolar germ found anterior to M1. Traced=> anterior part

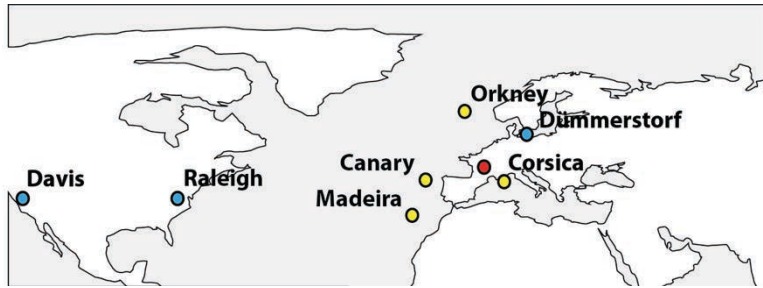
*Hayden et al. submitted*



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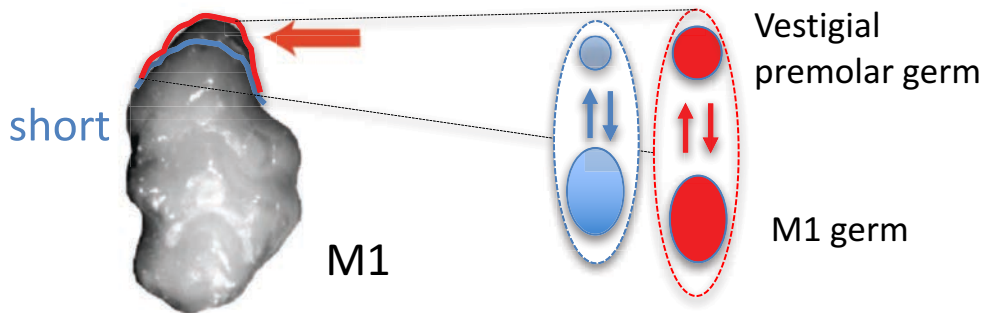
Explains why repeated evolution occurs,  
and why it occurs only in upper molar

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Adult

Embryo



- Heritage of evolutionary history: in embryos, abortive premolar germ found anterior to M1. Traced=> anterior part
- Short/elongated strain differences in:
  - Size, persistence and positioning,
  - expression of premolar rescuing genes

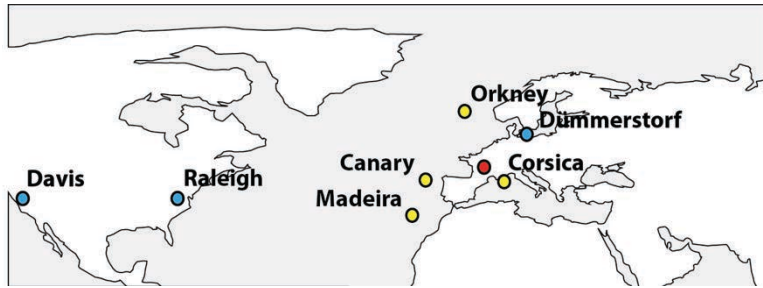
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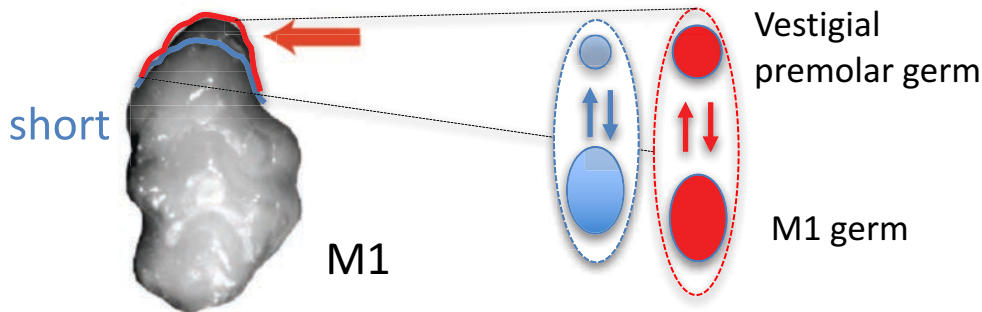
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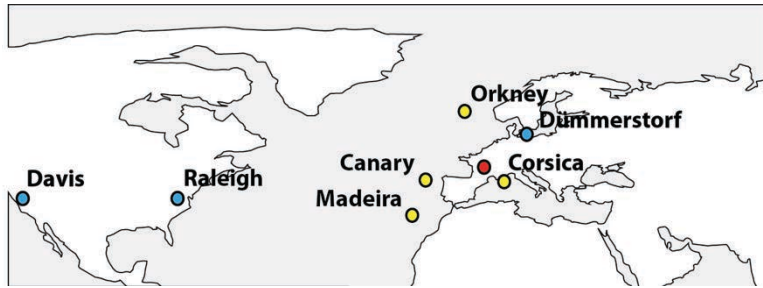


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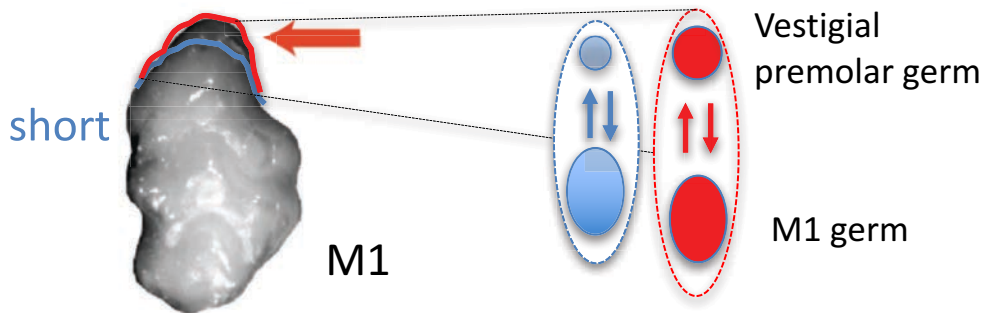


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- intra-strain variation (inbred mice)

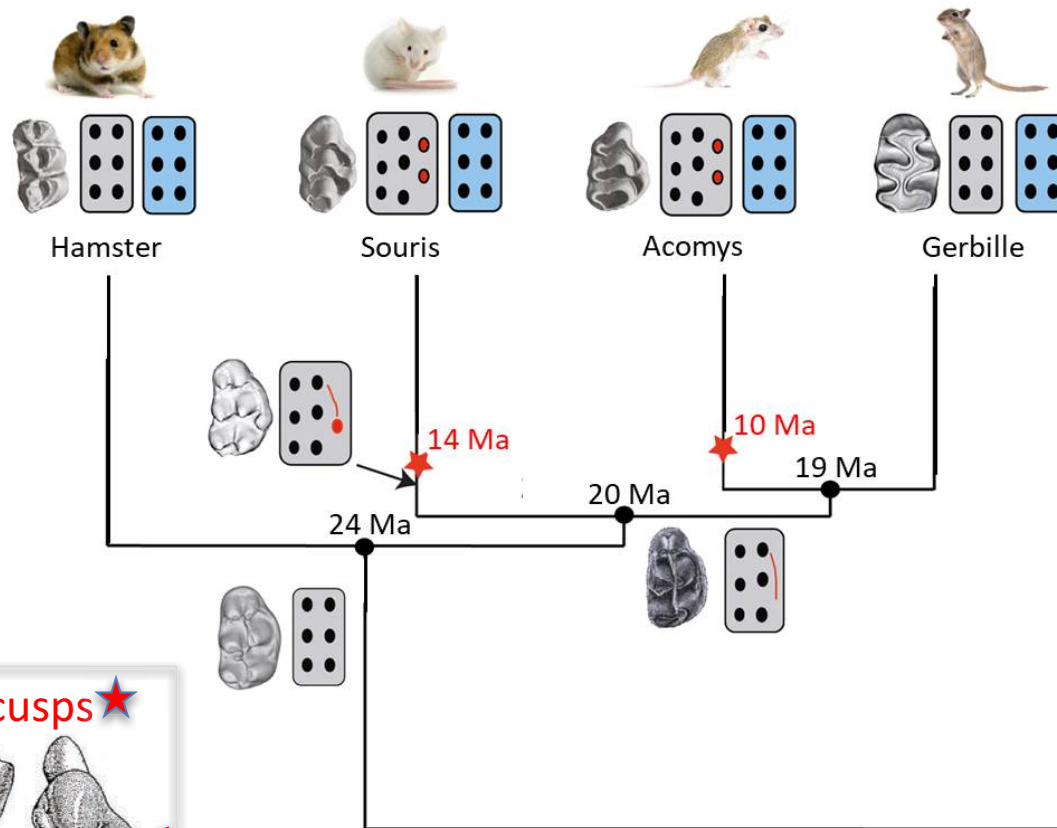
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“easy” variation (achille’s heal)  
=> Repeated evolution

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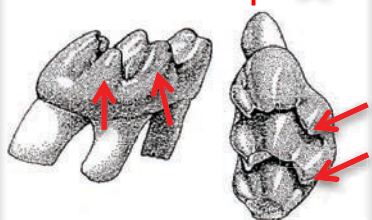
## 2: Repeated evolution of the murine dental plan: same mechanisms?



Is development also similar??

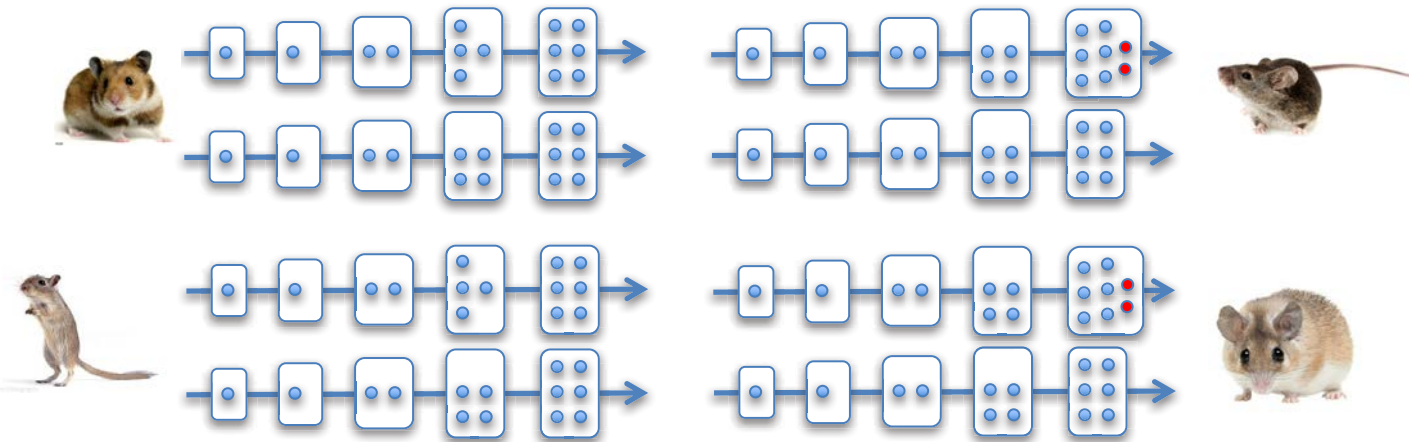
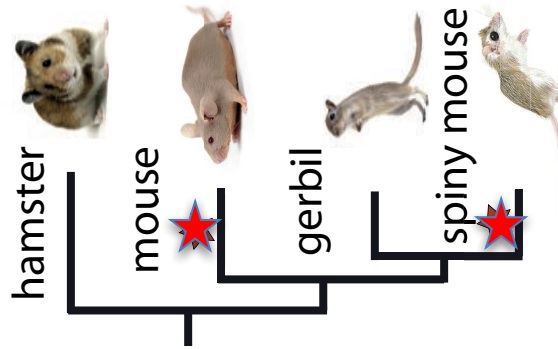
- Same genes?
- Same pathways?
- Same developmental processes?

Extra cusps ★



Side view Top view

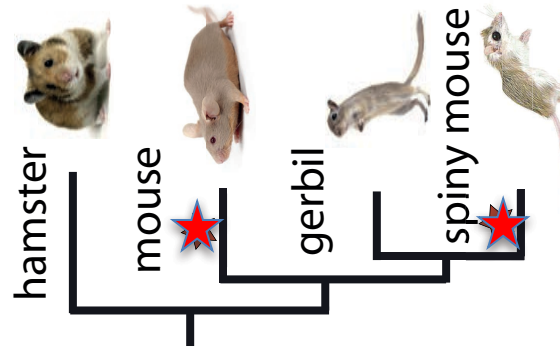
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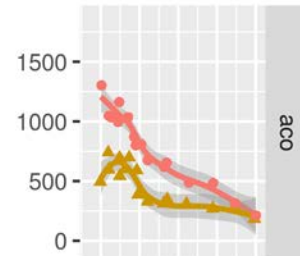
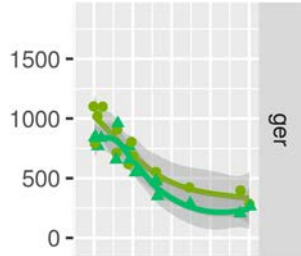
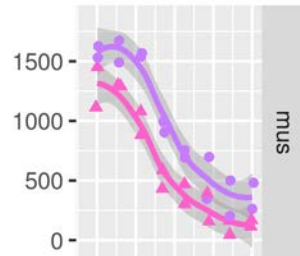
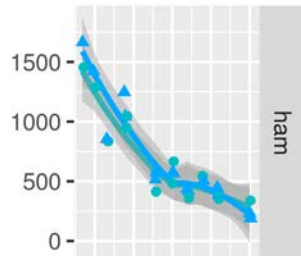
**Spiny mouse colony**

+ Advanced comparative transcriptomics  
(RNAseq timeseries)

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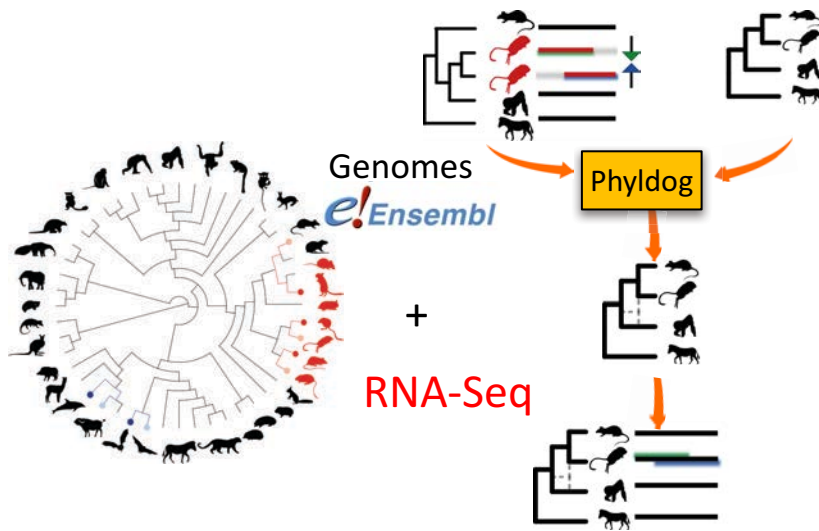


**Spiny mouse colony**



+ Advanced comparative transcriptomics (RNAseq timeseries)

# 3: Tools to study the molecular basis of convergent evolution



- Tools to assemble transcriptomes *de novo* in a phylogenetic context (*Caars*, Rey et al. in review)
- Tools to detect and model convergent evolution in coding sequence (*Pcoc*, Rey et al. MBE 2018) + expression levels + timeseries

=> **QUANTIFY: Extent of convergent evolution at the molecular level?** more than the false positives expected by chance? (Rey et al. , submitted)

=> Take into account confounding factors (pop size, bias in sequence composition...)



# 4: Repeated adaptation of rodents to arid environments

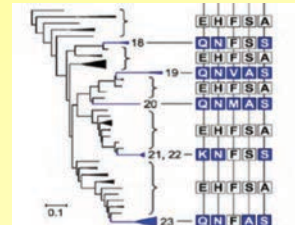
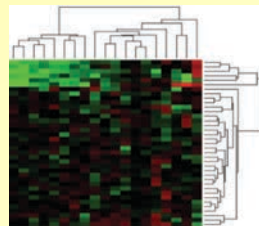


# Questions and interests

- Are some genes repeatedly involved in adaptation to xeric life ?
  - Do plasticity and adaptation involve the same genes ?
    - Can we predict « markers of adaptation » ?

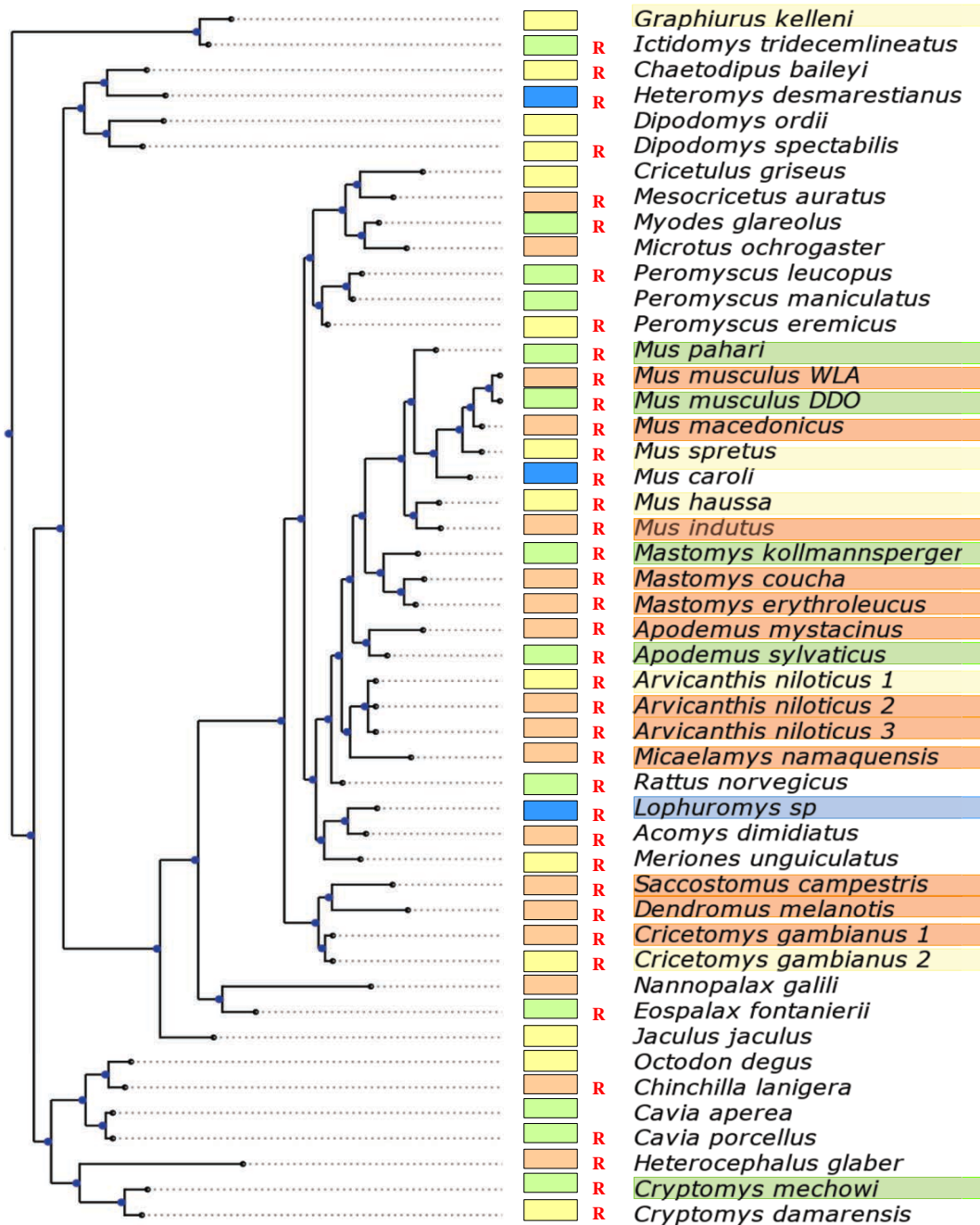


Changes in gene expression in kidney?



Changes in gene coding sequences?

# Strategy



## Living condition

- Xeric <300 mm (16/9)
- Semi-Xeric 300<SM<600 mm (17/14)
- Mesic 600<M<1000 mm (17/13)
- Super-Mesic >1000 mm (3/2)
- R Available RNA-Seq data

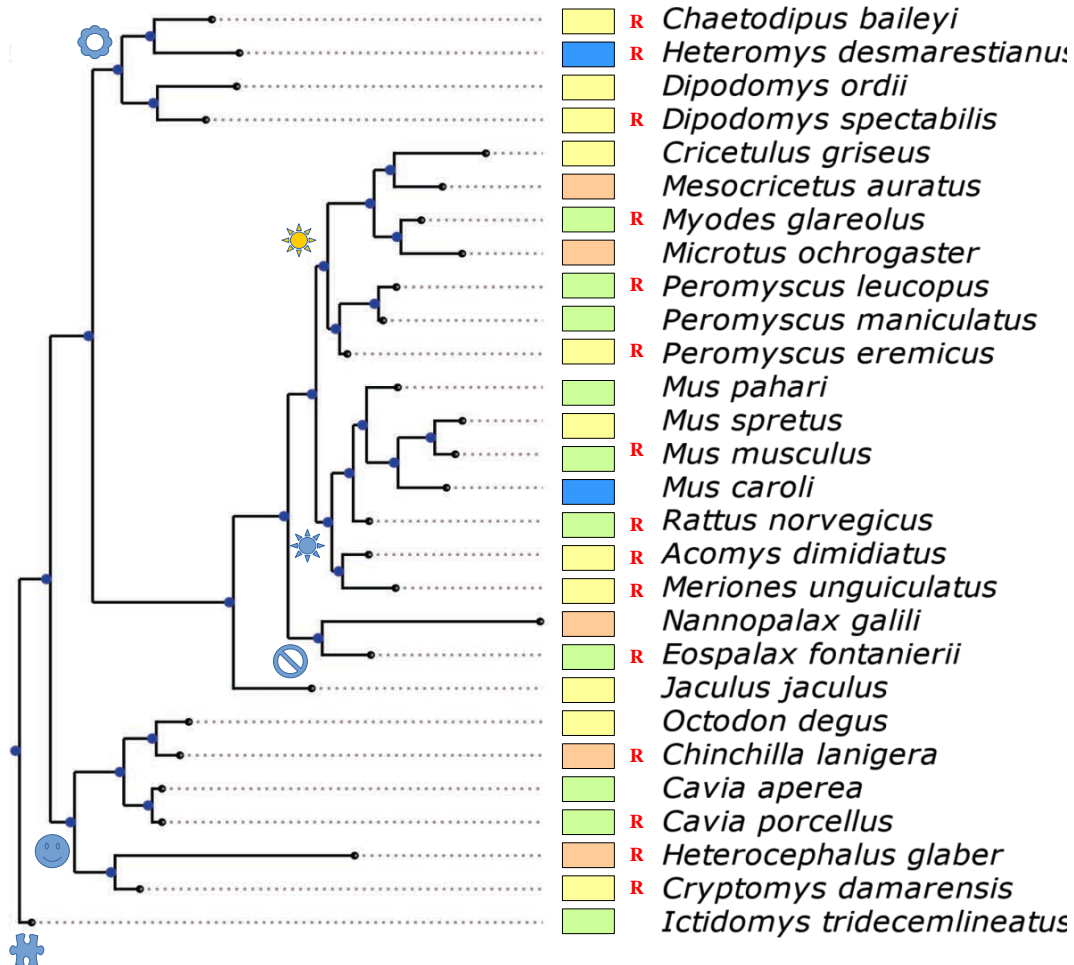
## Phylogenetic families

- ✳ Muroidea - Muridae
- ✳ Muroidea - Cricetidae
- ⚙ Heteromyidae
- 😊 Bathyergidae
- ⊘ Spalacidae
- ⚙ Sciuridae

Total : 48 species



# Pre-Strategy (online dataset)



## Living condition

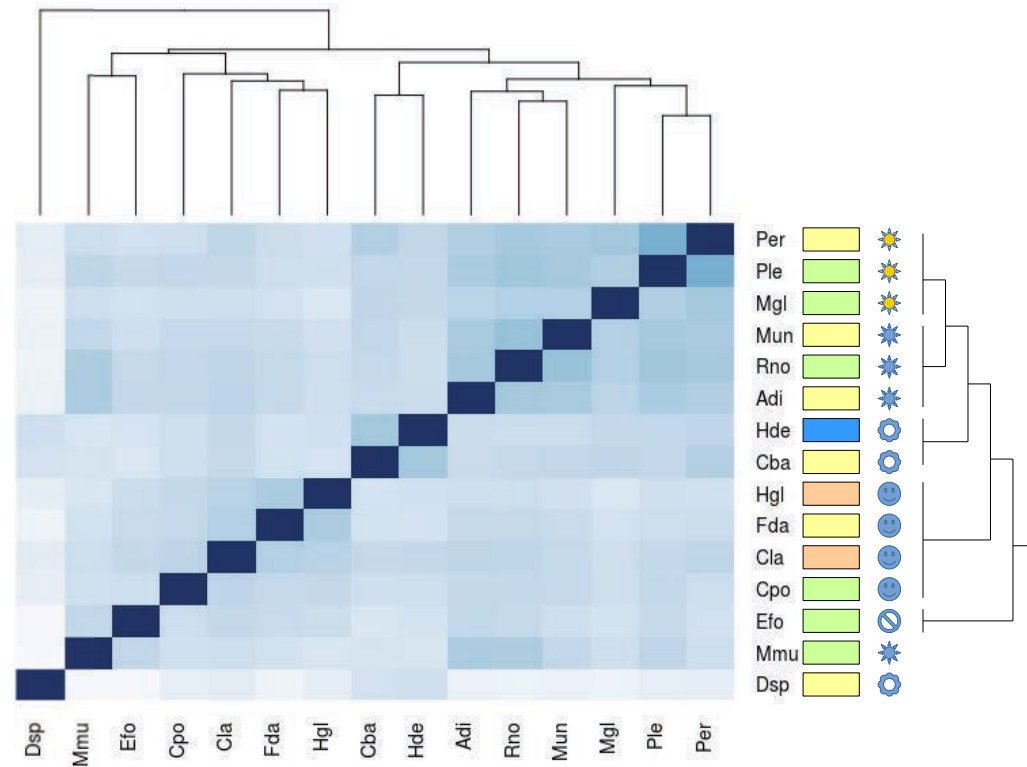
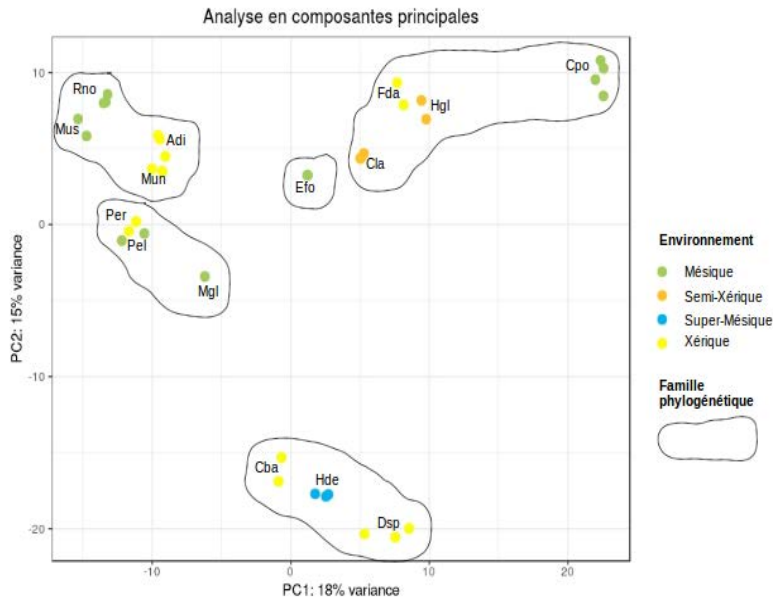
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Total : 28 species

# Transcriptome data



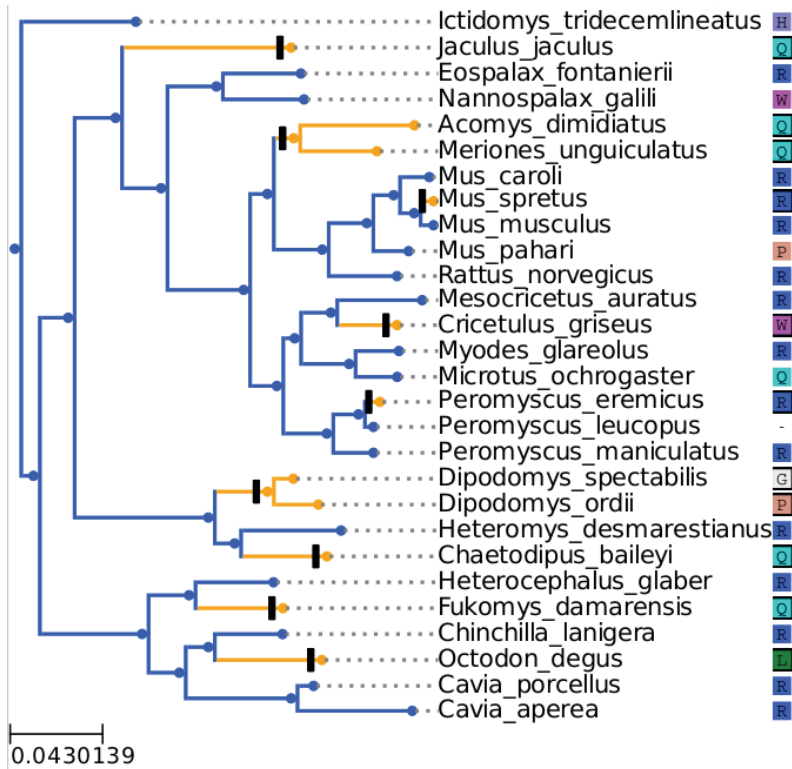
Strong phylogenetic effect



# Changes in gene sequences

Preliminary analysis

Sdc1



105 detected genes with  
Xeric versus all species  
design  
3 common genes with the DE  
list

PCOC – Rey et al. MBE 2018

# Acknowledgments

## •Team Comparative and Integrative Genomics of Organ Development

- Marie Sémon
- Sophie Pantalacci
- Carine Rey
- Marion Mouginot
- Jeremy Ganofsky

## •Convergenomix collaborators

- Bastien Boussau
- Pascale Chevret
- Abderrahman Khila
- Tristan Lefébure



“You can’t be thirsty again. You had a drink three weeks ago!”

Jerboa pic © 2015 - 2018 2 New Things

## •Sampling

- Gauthier Dobigny
- Laurent Granjon
- Caroline, Madougou,
- Karmadine, Aurélien
- Frédéric Delsuc
- Nadine N’Dilimabaka
- Radim Sumbera
- François Bonhomme
- Petros Lymberakis
- Pierre-Henri Fabre
- Frederic Veyrunes,
- David Thybert

## •Kidney morphology

- Pr Laurent Juillard
- Dr Sandrine Lemoine
- Pr Fitsum Guebre

Genomic analysis of convergent evolution  
**CONVERGENOMIX**

