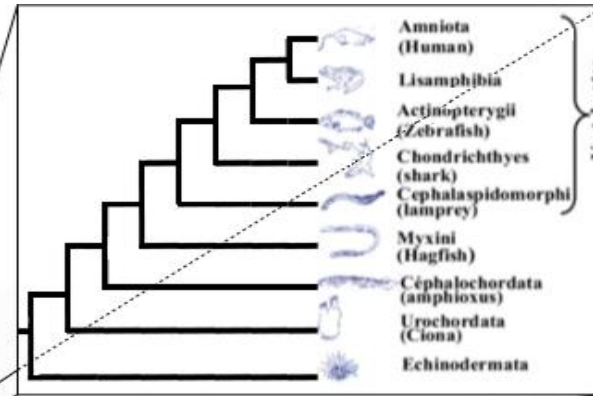
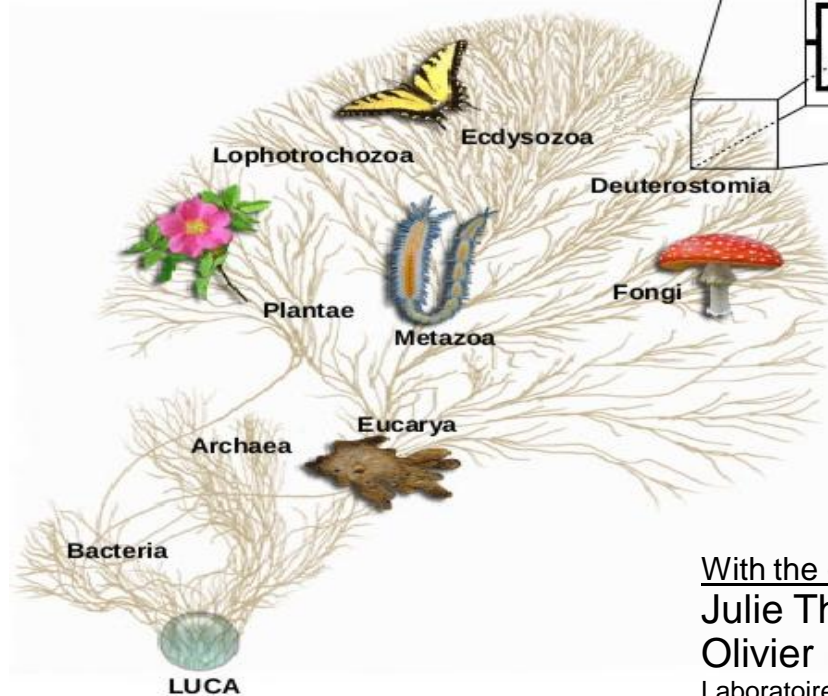


GeneLoss: Automation of the study of lineage-specific gene loss and pseudogenisation



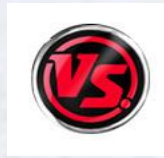
Dainat Jacques
PhD student in Bioinformatic

With the participation of
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With the cooperation of
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Well-established genes



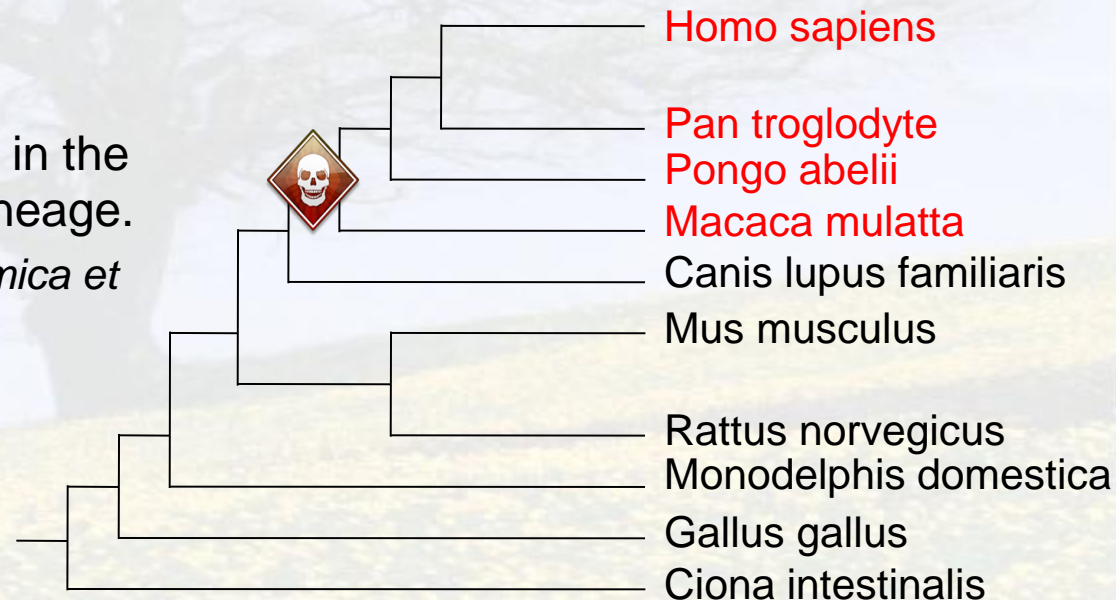
Fast evolution genes

The more ortholog genes result from a remote ancestor, the more the gene is well-established and probably plays an important role,

and the more these orthologs loss can reflect a loss of function
=> significant evolutionary changes

=> Example of the GULO gene involved in the vitamin C synthesis, lost in the primate lineage.
(Yuriko Ohta and Morimitsu Nishikimi; *Biochimica et Biophysica Acta*; 1999)

Establishment of this gene: since Chordata (800 million years)



Development of the GeneLoss module to study automatically the loss of gene and the pseudogenisation to **Metazoans**



Choose a reference **protein**
and a species **dataset**



expert system supervision

Re-annotation,
interpretation
based on the
collection of
evidences

Recording
in Ontology

Pipeline platform:

- phylogenies
 - predictions
 - blasts
 - ancestral reconstructions
etc....
-



Result

Quality of the results with GeneLoss:

The efficiency was proved with more than 20 cases of gene loss and pseudogenisation described in literature:

We discovered the same results, and for most of them we identified new interesting information and further details

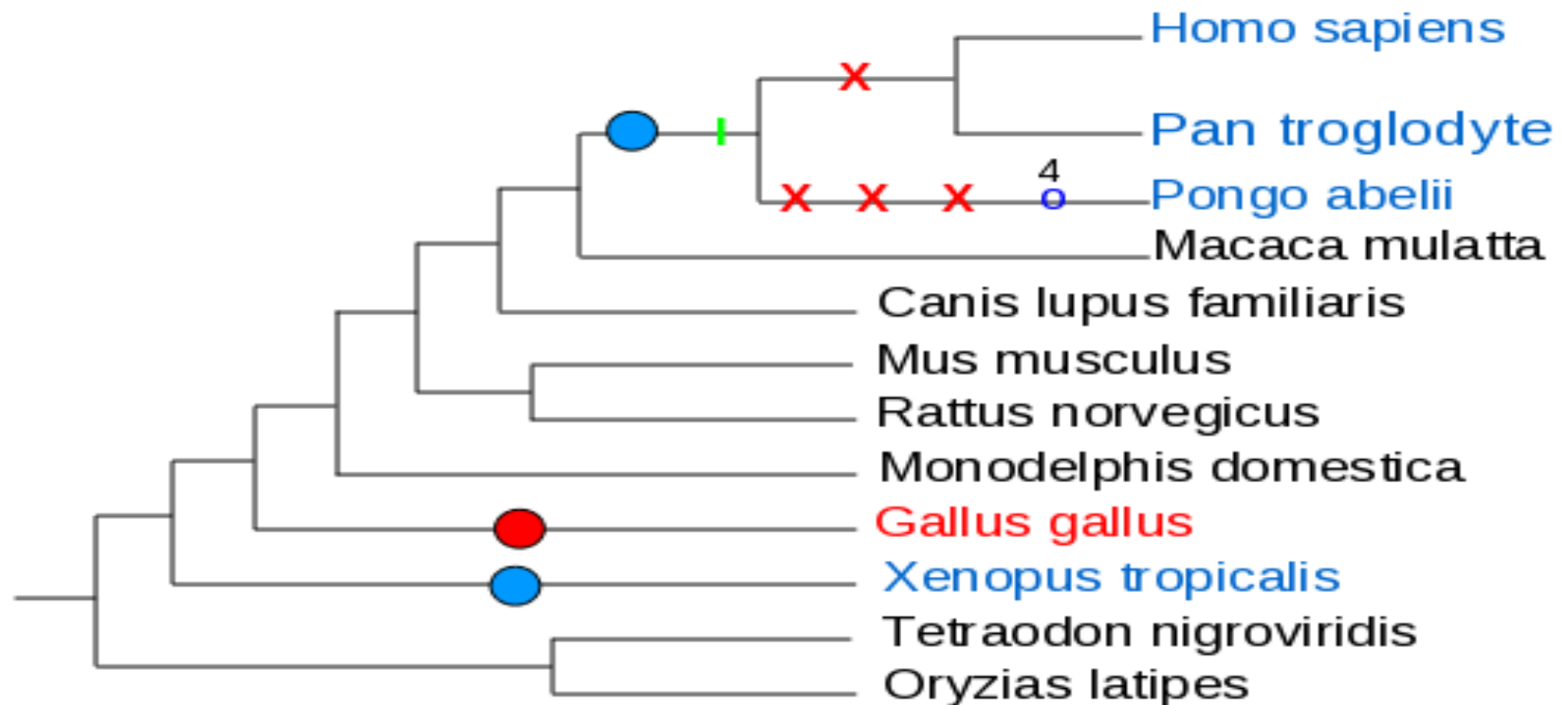


More information
More precision
Better interpretation

Result example: Acyl3 protein study

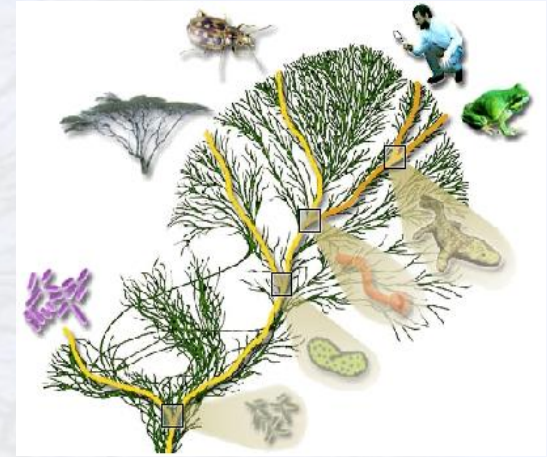
Legend

- | | | | | |
|---|---|---|---|-------------------------|
| ● = Perte | █ = Gene absent | X = stop codon appears | } | List of transformations |
| ● = Pseudogénéisation | █ = Pseudogene | = splice site mutation | | |
| ● = Apogénéisation | █ = Gene Present | ○ = deletion | | |
| | █ = Apogène | ○ = insertion | | |
| | | 4 = length | | |



Features of the studies performed with GeneLoss:

- New genes discovery
- Pseudogenes discovery
- Lost genes discovery
- Confirmation of already described pseudogenes
- Discovery of genomic transformations leading to the pseudogenisation
- Discovery of genomic transformations leading to derived gene
- Discovery of new orthology relationships



For more information, I am available near the poster N ° 6