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Phylogenetic Functional Module Characterization of the ADAMTS / ADAMTS-like Protein Family

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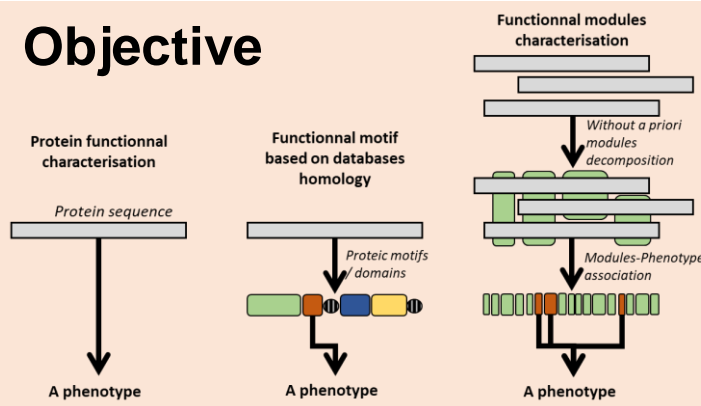
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Introduction

- ❖ Multi-genes (*e.g.*, *paralogs*, *orthologs*)
 - ❖ Multi-domains
 - ❖ Partial knowledge / experimental data [1]
- => A new method to identify functional protein regions

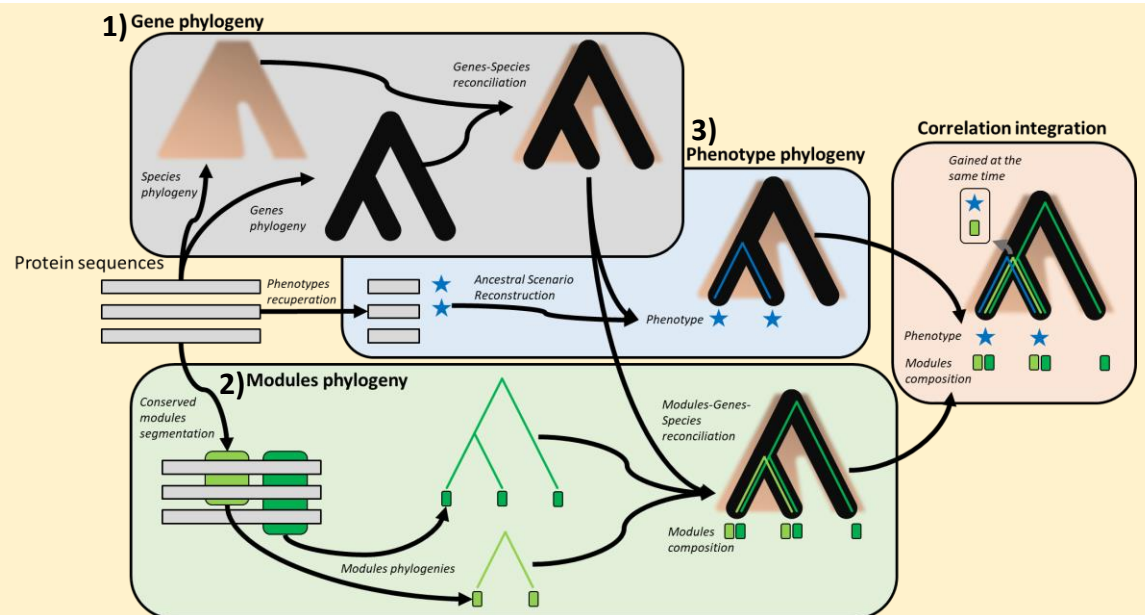
Objective



- ❖ **Module:** Ungapped conserved sequence regions, shared by at least 2 sequences
- ❖ **Hypothesis:** During evolution, modules gained at the same time than a phenotype, are involved in this phenotype

Methodology

- ❖ Sequence conservation and phylogenomic inference
- ❖ Segment *without a priori* protein sequences in modules
- ❖ Protein-protein interactions (PPI) [3] and modules evolution [2] on a common gene phylogeny
- ❖ Changes in module composition occurring at the same time than protein-protein interactions

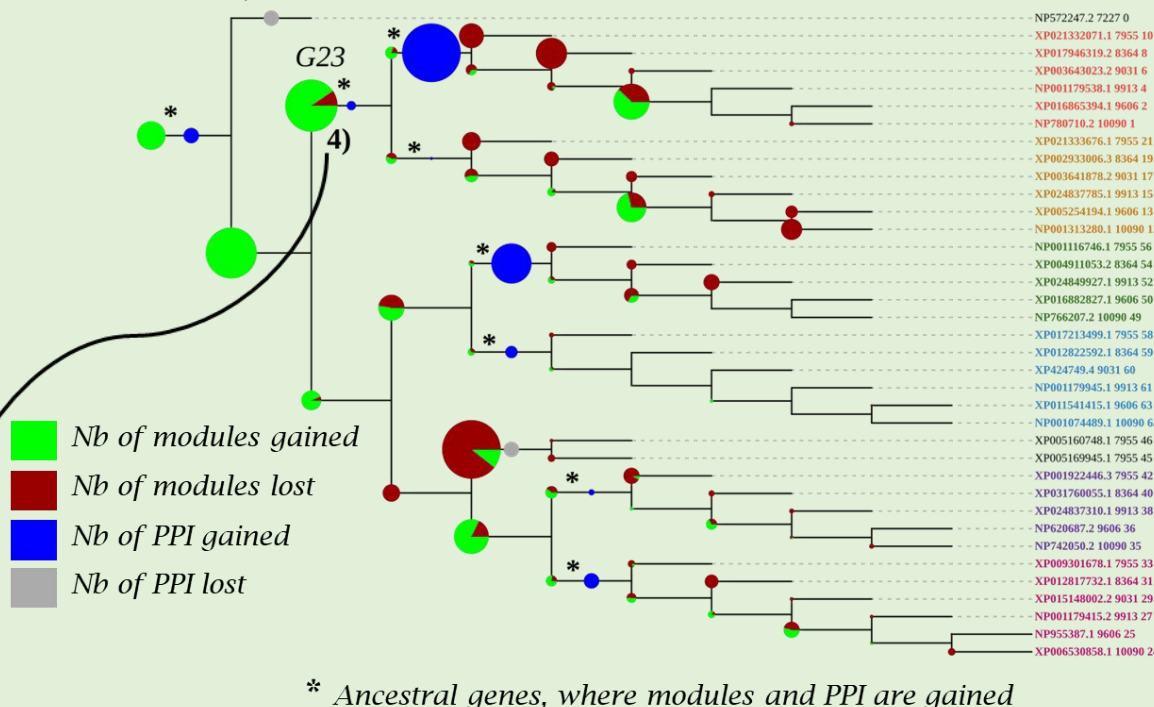


Results

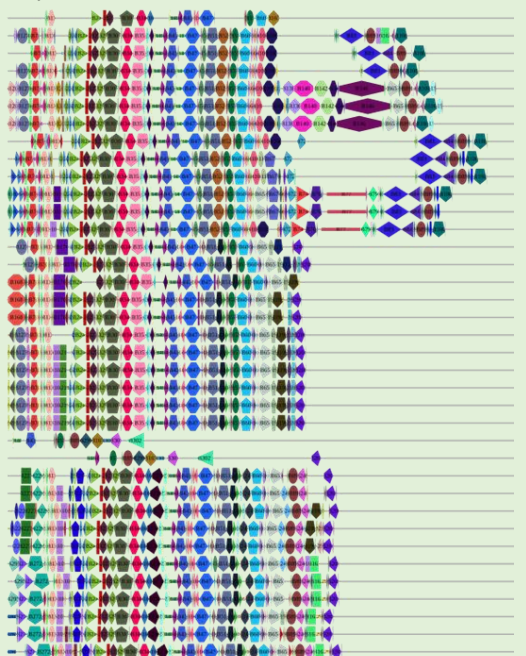
ADAMTS-12, -7, -16, -18, -6, -10 and their associated 1) orthologs, distributed in 7 species (1, 2)

2)

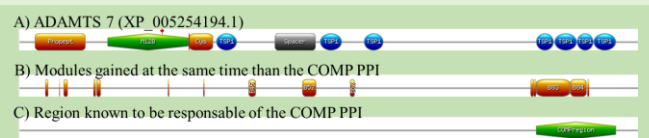
Segmentations *without a priori* in 3) 249 conserved modules (3)



ADAMTS 12
ADAMTS 7
ADAMTS 10
ADAMTS 6
ADAMTS 16
ADAMTS 18



G23 : Apparition of COMP-ADAMTS PPI and 32 Modules gained (4)



Conclusion

- ❖ Pipeline
- ❖ Correlate conserved sequence modules and phenotypes evolution
- ❖ Identify the co-appearance of conserved modules and phenotypes.

References

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