



HAL
open science

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

Olivier Dennler, Samuel Blanquart, François Coste, Catherine Belleannée,
Nathalie Theret

► **To cite this version:**

Olivier Dennler, Samuel Blanquart, François Coste, Catherine Belleannée, Nathalie Theret. Phylogenetic Functional Module Characterization of the ADAMTS / ADAMTS like Protein Family. WABI 2021 - Workshop on Algorithms in Bioinformatics, Aug 2021, Chicago (Online), United States. hal-03543214

HAL Id: hal-03543214

<https://hal.science/hal-03543214>

Submitted on 25 Jan 2022

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

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

Olivier Dennler^{1,2}, Samuel Blanquart², François Coste², Catherine Belleannée² and Nathalie Theret^{1,2}

¹ Univ Rennes, Inserm, EHESP, Irset - UMR S1085, F-35043 Rennes

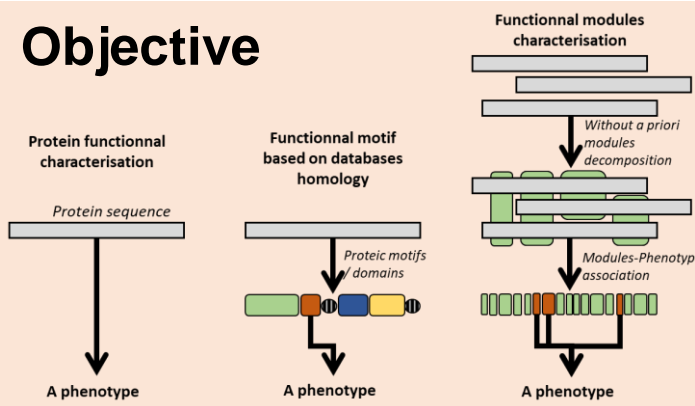
² Univ Rennes, Inria, CNRS, IRISA, UMR 6074, Rennes, France

olivier.dennler@inria.fr

Introduction

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

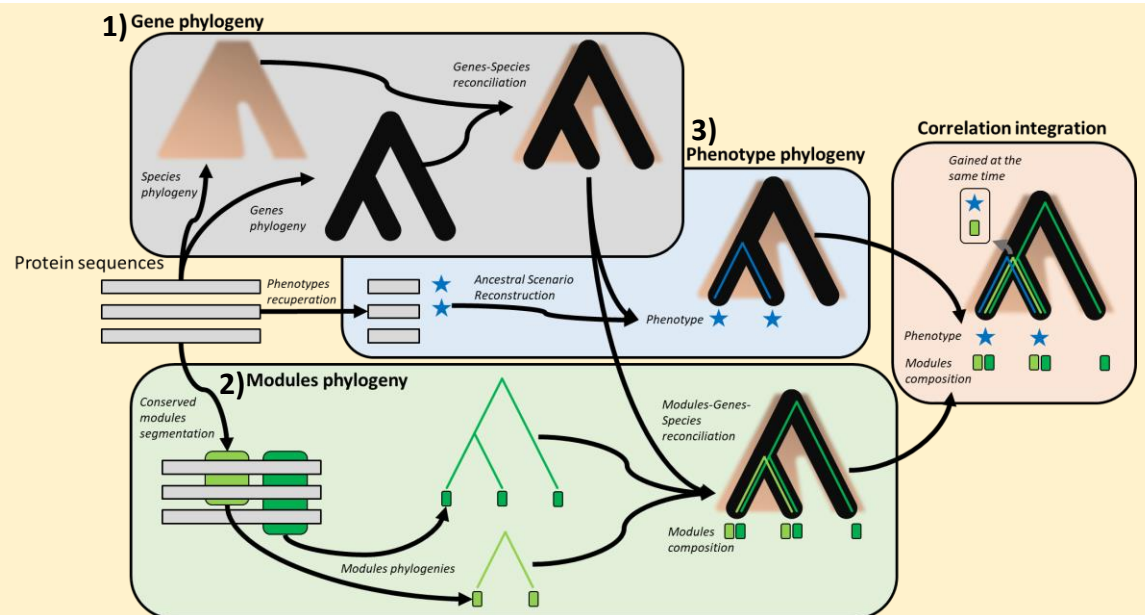
Objective



- ❖ **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

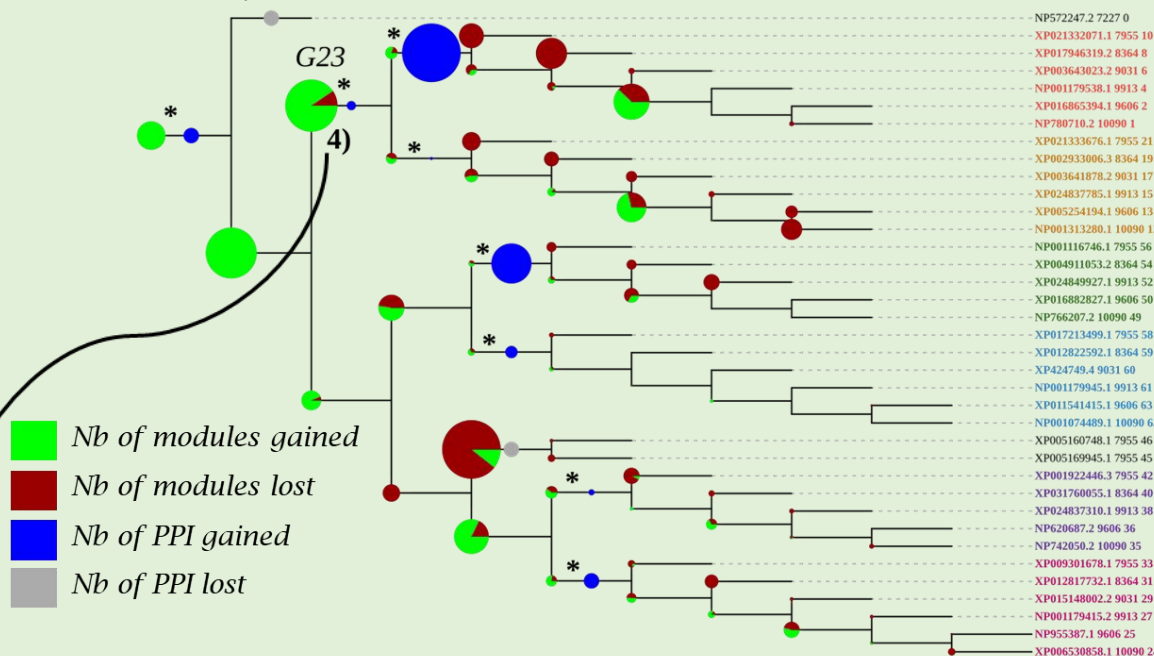


Results

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

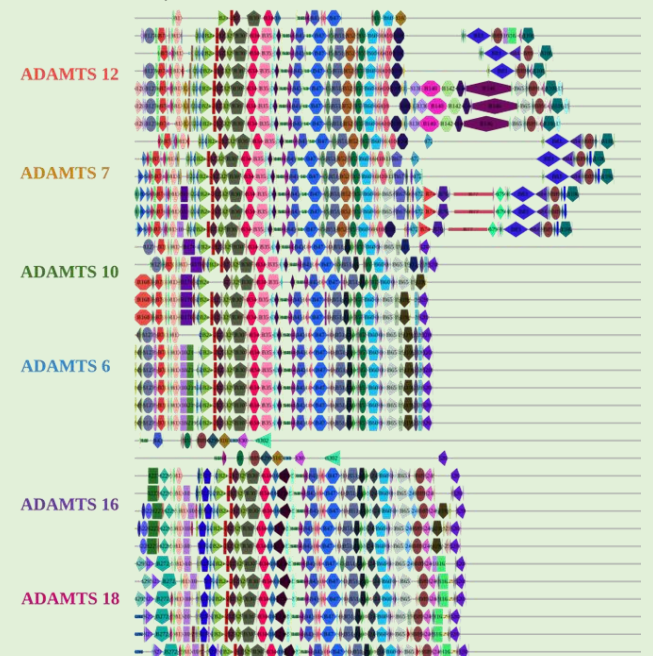
2)

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

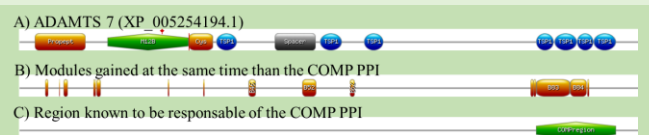


- Nb of modules gained
- Nb of modules lost
- Nb of PPI gained
- Nb of PPI lost

* Ancestral genes, where modules and PPI are gained



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

[1] Suneel S. Apte. ADAMTS Proteins: Concepts, Challenges, and Prospects. *Methods in Molecular Biology* (Clifton, N.J.), 2043:1-12, 2020. [2] Lei Li and Mukul Bansal. Simultaneous Multi-Domain-Multi-Gene Reconciliation Under the Domain-Gene-Species Reconciliation Model. pages 73-86. January 2019. [3] Sohta A Ishikawa, Wataru Iwasaki, and Olivier Gascuel. A Fast Likelihood Method to Reconstruct and Visualize Ancestral Scenarios. *Molecular Biology and Evolution*, 36(9):2069-2085, September 2019. [4] Chuan-Ju Liu, Wei Kong, Kiril Ilalov, Shuang Yu, Ke Xu, Lisa Prazak, Marc Fajardo, Bantoo Sehgal and Paul E. Di Cesare. ADAMTS-7: a metalloproteinase that directly binds to and degrades cartilage oligomeric matrix protein. *FASEB journal: official publication of the Federation of American Societies for Experimental Biology*, 20(7):988-990, May 2006.