

ADAMs family values: Gene family evolution of ADAM peptidases

Haerty group

The extracellular matrix (ECM) is a three-dimensional network of large molecules that surrounds cells. It has important roles in the way cells behave, communicate with each other, and divide during development. Due to these fundamental functions, the genes involved in making the ECM work have a fascinating and ancient evolutionary history. Understanding the evolution of these genes could yield unique insight into human physiology.

The ADAM peptidases are a large and variable gene family with fundamental roles in human development. They control the way signalling proteins interact with the ECM and are major players in the process of tissue remodelling during development. ADAM stands for **A** Disintegrin **A**nd **M**etallopeptidase, due to the characteristic structure of the secreted and transmembrane proteins that make up this family. Variation in the DNA that codes for these proteins is associated with many serious disease states such as coronary heart disease and stroke, as well as a range of cancers.

We are interested in understanding the evolution of this important group of genes in vertebrate organisms. This project will utilise an existing dataset developed from the whole genomes of 24 species spanning 500 million years of evolution. The student will use computational methods to identify gene duplications and losses in the ADAMs family and contribute to ongoing research on the formation of ADAM pseudogenes. The student will work within a group with strong interests in evolutionary biology, population genetics and genomics. This project presents the opportunity to learn many skills essential to computational biology, including working in the Linux command line, scripting, and using a range of bioinformatics software.

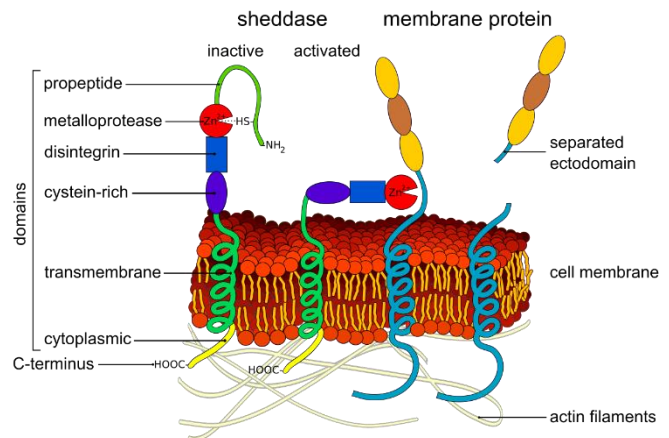


Figure 1) An ectodomain shedding ADAM metallopeptidase. Diagram by Kuebi, Wikimedia Commons