

# THE APPLE GENE EXPRESSION ATLAS

*Building, characterizing, and analyzing the apple transcriptome*

## BACKGROUND

'Gene expression atlases' bring together genome-wide expression measurements of as many diverse biological conditions (tissues, developmental phases, treatments, ...) as possible for a given organism of interest. Such atlases provide a tremendous resource for systems biology studies, elucidating gene expression coordination at a global level and the environmental conditions that drive these global expression responses.

This PhD project proposal is part of larger collaboration between the Integrative Genomics (CBC IG) and the Functional Genomics (DGBPF FG) research groups of FEM-IASMA, and the Bioinformatics and Systems Biology division of the VIB UGhent (Belgium). The goal of this overarching initiative is to build gene expression atlases for Rosaceae species to extract novel biological and physiological insights. *Malus domestica* (apple) will serve as the initial proof-of-concept case.

## PROJECT DESCRIPTION AND WORK PLAN

This PhD proposal represents the computational aspects of the initial phase (the Apple Gene Expression Atlas), integrating and analyzing the generated data described above, along with any publicly available data sets. It will have three main objectives:

1. Establishing a cross-platform, annotated gene expression compendium for apple.
2. Characterization and analysis of the different states of the apple transcriptome.
3. Transfer of the methodology for use on other Rosaceae species.

The Integrative Genomics group of Kristof Engelen (CBC) has created a methodology to build, update, and manage expression atlases (COLOMBOS tools). This will serve as the computational framework that the PhD scholar will rely on, and will further develop, to build the apple expression compendium from available RNAseq and microarray data. The second part of the PhD project will be executed during a visit to the Bioinformatics and Evolutionary Genomics lab (Ghent, Belgium) of the external tutor, Prof. Yves Van de Peer, relying on its long standing expertise in regulatory network inference. The apple expression compendium will be employed as a resource for (top-down) systems biology studies with a strong focus towards incorporating standardized sample descriptions in the modeling frameworks, as these provide an unprecedented level of power for explaining expression changes at a grand scale.

Detailed deliverables (D) and timing, expressed in units of 'years after project start' (YAPS):

- **D1.1** (1 YAPS) - apple gene expression compendium: preliminary version.
- **D1.2** (1.5 YAPS) - apple gene expression compendium: final version, explorative characterization, and submission of publication to international journal.
- **D2.1** (2-2.5 YAPS) - top-down systems biology study of the apple transcriptome: report of visit to external tutor (started after 1.5 YAPS).
- **D2.2** (2.5 YAPS) - top-down systems biology study of the apple transcriptome: submission of publication to international journal.
- **D3** (2.7 YAPS) - generalize developed methodologies for transfer to other Rosaceae.
- **D4** (3 YAPS) - submission of PhD manuscript and PhD defense.

### **HOSTING LABORATORIES**

- Fondazione Edmund Mach, Research and Innovation Centre, via E. Mach 1, 38010, San Michele all'Adige (Trento), Italy
- Bioinformatics & Systems Biology, VIB / Ghent University, Technologiepark 927, B-9052 Gent, Belgium

### **TUTORS**

- Kristof Engelen, group leader Integrative Genomics (Dept. Computational Biology), Fondazione Edmund Mach, Research and Innovation Centre, via E. Mach 1, 38010, San Michele all'Adige (Trento), Italy
- Yves Van de Peer, head of Bioinformatics and Systems Biology division (Dept. Plant Systems Biology), VIB / Ghent University, Technologiepark 927, B-9052 Gent, Belgium. CV: <http://bioinformatics.psb.ugent.be/people/profile/yvesvandepeer>

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