
# *ABSTRACT*

*"Innovation through gen(om)e duplication"*

**Dr Steven Maere**

**VIB, Dept. of Plant Systems Biology**

**Ghent University**

**Gent**

**BELGIUM**

Gene and genome duplications are believed to facilitate evolutionary innovation. However, the mechanisms shaping the fate of duplicated genes remain heavily debated because the molecular processes and evolutionary forces involved are difficult to reconstruct. The first part of the talk will focus on the MALS gene family, a large family of fungal glucosidase genes with members generally having activity on only one of two broad substrate classes. We reconstructed several key ancestral enzymes and show that the very first preduplication enzyme was primarily active on maltose-like substrates, but had trace activity for isomaltose-like sugars. Structural analysis and activity measurements on resurrected and present-day enzymes suggest that both activities cannot be fully optimized in a single enzyme. However, gene duplications repeatedly spawned daughter genes in which mutations optimized either isomaltase or maltase activity. Interestingly, similar shifts in enzyme activity were reached multiple times via different evolutionary routes. Together, our results provide a detailed picture of the molecular mechanisms that drove divergence and innovation in the MALS gene family. In the second part of the talk, I will discuss a framework we developed for simulating the evolution of small biological systems in silico. The genotype-phenotype map (GPM) of any molecular system results from a highly multilayered information processing cascade, in which gene regulatory networks (GRNs) play a crucial role. Several simplifying mathematical representations of GPMs have been developed in the past. However, these representations generally lack biological realism in the genotypic encoding of the structure and parameters of GRNs. To study GPMs in mechanistic detail, we have developed a sequence-based dynamical modeling framework built upon biochemical first principles. As a proof of concept, we focus on genomes coding for small GRNs displaying oscillatory expression phenotypes. We show that genome duplication drastically impacts the navigability of the fitness landscape and the accessibility of novel phenotypes.