

# Modelling the Organization of Flower Morphogenesis by Transcription Factor Networks Using Lindenmayer Systems

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## ABSTRACT

Regulatory gene networks, consisting of transcription factors and the genes encoding them, are an important mechanism for organizing developmental processes according to genetic information. As a generic formalism for specifying dynamic models of regulatory gene networks, **transsys** has been developed (see <http://www.inb.mu-luebeck.de/transsys/>). The **transsys** formalism has been designed to (1) allow compact and flexible representations of arbitrary regulatory networks, (2) to make the structure and dynamics within regulatory gene networks accessible to a variety of simulation and analysis tools, and (3) to provide interfaces that allow using **transsys** models of regulatory gene networks as modules within larger modelling frameworks. The scientific objective which motivates **transsys** is abstracting and understanding of fundamental principles underlying the organization of morphogenesis and other complex phenotypic processes by regulatory gene networks.

Recently, **transsys** has been integrated within an Lindenmayer system framework, called **L-transsys** [1]. **L-transsys** combines the power of Lindenmayer systems for modelling plant morphogenesis on a macroscopic, phenotypic level with the modelling potentials opened up by **transsys**. Thus, **L-transsys** provides a basis for systematically investigating the organization of morphogenetic processes in plants by regulatory gene networks.

Regulatory control by heterodimers (or higher order protein complexes) is an important aspect of such regulatory networks. Therefore, modelling of gene expression control by heterodimers with **transsys** is introduced and focused on in this contribution.

Genes belonging to the DEF subfamily and the GLO subfamily of MADS box genes [2] encode transcription factors which act as heterodimers [3]. In this contribution, an **L-transsys** model of flower morphogenesis which includes this mechanism is presented. DEF/GLO heterodimers function as master switches activating the morphogenesis of petals and stamens. The *def* and *glo* are autoregulated by the DEF/GLO heterodimer. All these aspects are accurately reflected by the **L-transsys** model of flower morphogenesis. As a result, simulating mutations by alterations of the **transsys** specification induce realistic homeotic trans-

formations on the level of simulated phenotypes.

## REFERENCES

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