FEEDBACK CIRCUIT ANALYSIS OF THE GENETIC NETWORK CONTROLLING FLOWER MORPHOGENESIS IN *Arabidopsis thaliana*

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We present a qualitative analysis of the genetic network controlling flower morphogenesis in *Arabidopsis thaliana*. Eleven genes have been taken into account, namely *EMF1*, *STM*, *TFL1*, *LFY*, *AP1*, *AG*, *LUG*, *UFO*, *AP3*, *PI*, and *SUP*. Regulatory interactions among these genes have been inferred from published data, dealing with either morphological features or mRNA expression patterns under wild type and mutant backgrounds.

Using a logical formalism, our analysis emphasizes the dynamical and biological roles of the 'feedback circuits' present in the network. More precisely, we show that three circuits (involving the genes AP1 and AG, AP3 and PI, and UFO, respectively) play a crucial role in the generation of a series of attractors accounting for the patterns of gene expression associated with the four different floral organs of Arabidopsis (sepals, petals, stamens and carpels), as well as a non-floral state.

Despite its simplicity, our model provides a consistent picture of the dynamics of the genetic system controlling flower development in *Arabidopsis*. In addition, our analysis leads to at least three clear predictions: (1) the existence of sixth stable pattern of gene expression, still to be observed experimentally; (3) the existence of at least one additional regulatory factor for *LFY* activation, likely to play a crucial role in the transition between the vegetative state to the flowering pathways; (3) though STM is needed to initiate UFO expression, UFO should be able to sustain its own expression, even after the disappearance of UFO.