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Virtual plants in simulating resistance to stress

Modelling the architecture of sunflower and *Arabidopsis thaliana* subjected to environmental constraints

Computer modelling is essential in simulating the long-term effects on plant behaviour of stress and/or an allelic variation. A programme is under way to represent in real time the adaptive responses of sunflower and *Arabidopsis* genotypes to transient variations in environmental conditions. In *Arabidopsis*, several ecotypes have been systematically compared for the architecture model parameters.

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*Three-dimensional computer
representations of
*Arabidopsis thaliana**



▪ **Analysis of the expression of genes associated with adaptations in plants subject to known environmental conditions** (maize, *Arabidopsis*, *Dactylis*)

Gene expression analysis can now be done in the field or laboratory, thanks to advances in micrometeorological measurements. In collaboration with the B&BMP research group (see page 18), we assess mRNA (cDNA microarrays) and proteins (Western blots, analysis of activity) to establish correspondences between gene expression and a quantitative variable in different environmental scenarios (for example, expression of a cell cycle gene and the rate of cell division).

▪ **Systematic assessment of the effects of a gene manipulation on the genotype's responses to environmental conditions**

Because the plant is a regulated system, several variables characterizing the phenotype are functionally related. Modelling reduces the apparent complexity of the responses to the essential characteristics of each genotype. The main test consisted in the manipulation of a gene involved in the synthesis of one hormone that controls transpiration and growth in plants subject to water shortage.

▪ **Modelling of the behaviour of a given genotype in a large number of pedoclimatic scenarios** (*Arabidopsis*, sunflower)

The microclimatic characteristics and genotypic traits are fed into a computer in order to calculate water uptake, biomass production, etc. This operation has a low marginal cost, therefore it is possible to simulate a large number of scenarios and calculate the risks associated with a genotype. This work is in its early stages, and as yet we cannot establish a correspondence between one gene and a simulation of yield. However, it is already possible to establish this correspondence for the simplest functions, such as transpiration or the rate of foliage growth (in collaboration with the Cirad-INRA-AMAP unit). ■