

## **Models of expansive growth as a function of temperature and water deficit with explicit genetic variability**

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Most crop models use a single set of parameters per species. In the context of ModExtreme, we aim at simulating virtual genotypes (genotypes in the future) in virtual scenarios (future climatic scenarios). Model formalisms need therefore to integrate explicit genetic variability for model parameters which can be phenotyped in platforms. By coupling such crop models with Ecophysiological models (used for phenotyping) and Genetic models, we will be able to simulate which combination of trait / alleles is likely to improve crop performances in any targeted climatic scenario. In this project, the LEPSE-INRA laboratory worked on ecophysiological models with easily phenotyped genetic variability, as new bricks of crop models. We focused on the responses of development/expansive growth to temperature, and the responses of water transfer / expansive growth to soil water deficit and evaporative demand.

-We first tried to reconcile the traditional approaches of temperature response in crop models and the non-linear approach proposed for this project (PT12). We tested if the differences between temperature responses found in some crop models, such as between development and expansive growth, or between development stages, or between day and night could be due to external effects such as the evaporative demand, the effect of the temperature ranges, and the time step used for development calculation. Because we concluded that the previously observed differences were due to such external effects, we propose that these different approaches were actually similar, except the equation of temperature response. We provide a process to calculate parameter values from linear or bilinear models to parameters of PT12. All R scripts are available.

-We updated the model of hydraulics and stomatal conductance of Tardieu and Davies (1993) by (i) including possible changes in tissues hydraulic conductances in the model (tissue conductances are now controlled by the circadian clock, transpiration and ABA), (ii) leaf has now a capacitance and (iii) leaf expansion rate is calculated from xylem water potential and ABA. The model has been validated in controlled or fluctuating conditions, and with natural or transgenic genotypes. It has been published recently, and all R scripts are available.

-We developed a new module of development and growth in maize, taking into account the evaporative demand and soil water deficit. This model is valid for genotypes with a large range of leaf number and contains only few parameters with genetic variation which are easily measurable in phenotyping platforms. This module will be inserted in APSIM for testing.