Model-assisted estimation of the genetic variability of tomato growth physiological parameters under contrasted water conditions

Dario Constantinescu, Mohamed Memmah, Gilles Vercambre, Michel Génard, Valentina Baldazzi, Nadia Bertin

Model-based analysis of the genetic variability in tomato fruit growth under contrasted water conditions

Dario Constantinescu, Gilles Vercambre, Michel Génard, Mohamed-Mahmoud Memmah, Valentina Baldazzi, Nadia Bertin

INRA - Centre d'Avignon, UR1115 Plantes et Systèmes de culture Horticoles, Domaine Saint Paul - Site Agroparc, 228 route de l'aérodrome, CS 40509, 84 914 Avignon Cedex 9, France

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Drought stress seriously limits plant and crop productivity and is one of the major abiotic stress factors, which represents the primary cause of crop loss worldwide. Understanding mechanisms governing plant adaptation to water deficit and identifying genes, QTLs and phenotypes that will enable a plant to maintain yield under water deficit (WD) conditions is a crucial challenge for breeder and growers, in the light of current issues concerning climate change. In the present work, 119 recombinant inbred lines of a population of *Solanum lycopersicum* were phenotyped under control and WD condition. Data of plant water status, fruit growth and composition were used to calibrate a process-based model describing water and carbon fluxes in growing fruit as a function of plant and environmental factors, in order to analyse the principal mechanisms involved in the plant adaptation to WD. The model calibration was performed assuming the same value for each parameter in controlled and WD conditions. Six parameters selected through a sensitivity analysis, were estimated using the NSGA2 evolutionary algorithm in order to minimize model prediction error of fruit dry and fresh masses. The variability in model parameters allowed us to explore diverse genetic strategies in response to water deficit.