PHENOPSIS: from a phenotyping platform to a whole pipeline of analyses

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Interactive exhibit

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A major goal of the life sciences is to understand and model how molecular processes control phenotypes and their alteration in response to biotic or abiotic stresses. The study of *Arabidopsis thaliana* genomics is providing new insights into the understanding of these processes. The functional analysis of genes associated with these responses is made possible by the phenotypic analyses of mutants or natural genetic variants, high-throughput genetic mapping and large-scale analyses of gene expression. Ten years ago, an important bottleneck was the phenotypic analysis of the genetic variability, which requires simultaneous analysis of hundreds to thousands of plants. The PHENOPSIS platform provide since 2002 large quantities of micro-meteorological data, images and phenotypical data for the study of genotype x environment interaction effects on different plant processes in *A. thaliana*. Protocols have been standardised to allow reproducibility between experiments and facilitate meta-analyses. Phenopsis is part of the M3P facility (https://www6.montpellier.inra.fr/lepse/M3P). It is accessible to public or private scientists via the website of the national project Phenome-FPPN *(https://www.phenome-fppn.fr/)*. Database, ontologies, image analyses and statistical tools ensure that the data produced by specific groups can benefit other groups in analyses of which the purposes extend beyond the ones that have been published.