

SUNRISE PHENOTYPING DATABASE : A TOOL FOR THE SUNFLOWER COMMUNITY TO SHARE AGRONOMIC, PHYSIOLOGICAL AND MOLECULAR DATA

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ABSTRACT

In the SUNRISE project, a combination of several approaches is developed including the establishment of appropriate and high-throughput phenotyping strategies to characterize the molecular, physiological and agronomical responses of sunflower to variation of the abiotic environment. For instance, large-scale experiments are conducted in multi-environment by the different partners resulting in the acquisition of millions of molecular, physiological, agronomical data points, all associated e.g. through genotypes, and environments. In this context, our community needs to develop a resource to integrate, maintain, store, manage, connect and visualize these valuable data. Our team constituted of agronomists, physiologist, molecular biologist and bioinformaticians developed an information system composed of a database, a query system and a user interface allowing comprehensive data integration and fast interpretation of results. As a first step, the SUNRISE archive was created for collection, storage and long-term accessibility of raw data. From this step on, the collection protocol, description of the environment and data description (metadata) are bound to phenotypic data. Data archiving is made through a secure web portal with user access to identify responsible persons and property. Then, a second step generates from this archive a database for data exploitation. The database schema was built in collaboration between bioinformatics and biologists to structure different type of data and their properties (genotypic information, statistical design, environmental factors, geographical informations, partners,...). A web interface accessible at sunrise.toulouse.inra.fr/phenoDB allows querying the data, viewing them and exporting them. Data access is restricted to authorized users on a file-based system and is therefore very flexible. Importantly, the generic architecture of the archive and the database allows its potential expansion to other types of phenotypic data on sunflower and other species and its use at a larger scale for other public or private projects.

Key Words : Database ; Transcriptomics ; metabolomics ; proteomics ; agronomics ; phenomics