

CAPITALISE

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BREEDING FOR BETTER PHOTOSYNTHESIS

EXPLOITING NATURAL VARIATION



An enormous variation for photosynthetic traits exists in natural populations. Genomics and phenotyping tools now allow efficient exploitation of this variation for crop improvement

WHY USE NATURAL VARIATION? GENETIC DIVERSITY

Cultivated crop plants carry only a small portion of the variation present in the gene pool. Early landrace varieties and crop wild relatives, on the other hand, represent a rich source of biodiversity that can be utilised for crop improvement. Growing scientific evidence indicates that large natural variation exists in core photosynthetic elements.



HOW WE USE NATURAL VARIATION

i) Phenotyping

ii) Genotyping

iii) Crop breeding



The central focus of the CAPITALISE project is to identify naturally occurring genetic variation for target photosynthetic traits in diverse plant populations (germplasms).

The CAPITALISE project workflow: (i) identification of naturally occurring genetic variation for the target photosynthetic subtraits in diverse plant populations, (ii) localisation of regions of the genome that are associated with this variation and (iii) increasing photosynthetic efficiency in the target crops.

GERMPLASMS

A wide range of germplasm collections have been developed in different crops to conserve their genetic diversity. These collections include crop varieties, landraces, and crop wild relatives. These represent essential resources for plant breeding.

CAPITALISE partners have developed innovative germplasms in three major crops barley, maize and tomato.



BARLEY-1K 350 accessions of wild barely (Hordeum spontaneum) from Israel [1].

BARLEY-CMPP

Cytonuclear Multi Parental Population (CMPP), 900 lines deriving from BARLEY1K accessions.

BARLEY-MPP

an interconnected multiparent advanced intercross (iMAGIC) population of 2,500 recombinant inbred lines (RILs).



MAIZE-PHOTO a set of 10 maize lines with contrasting photosynthetic traits.

MAIZE-MU 6,000 mutants with insertions identified by Mu-Illumina sequencing from the Barkan Lab [2].

MAIZE-MPP

a multi-parental population (MPP) built by the intercross of eight diverging parental lines resulting in RILs.



TOMATO-LR a collection of ~10,000 tomato varieties and breeding lines.

TOMATO-MUT

saturated mutation libraries in the processing variety M82, an indeterminate background with thousands of mutants.

TOMATO-BIL

450 backcross inbred lines (BILs) derived from the wild species Solanum pennellii and the reference lines M82 and E6203.

References: [1] DOI: 10.1111/j.1365-294X.2009.04106.x; [2] http://pml.uoregon.edu/photosyntheticml.html.

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