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Oral Communication Abstract - 3.04

COMBINING PHENOMICS APPROACHES FROM POT TO PLOT TO IDENTIFY CANDIDATE GENES FOR PHOTOSYNTHESIS IMPROVEMENT IN THE MULTI PARENT MAGIC MAIZE POPULATION

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Enhancing photosynthesis is widely acknowledged as an underutilized strategy for increasing crop productivity. For crops like maize, even small improvements in yield can have significant implications for global food security. As part of the H2020 project CAPITALISE, we emplov а comprehensive approach to measure photosynthetic efficiency in maize using an eight-way maize Multi-parent Advanced Generation Inter-Cross (MAGIC) population.

We selected and genotyped a sample consisting of 347 MAGIC RILs and their founders using Single Primer Enrichment Technology (SPET). Plants were grown at the IPK automated non-invasive phenotyping system for large plants, capable to measure kinetic chlorophyll fluorescence on dark-adapted plants once a week and to collect daily imaging data over the course of the three five-weeks experiments. The same sample was also grown in two field experiments, at NIAB (UK), over the summers of 2021 and 2022, where highresolution photosynthetic parameters such as light-saturated photosynthetic gas exchange, leaf reflectance, and NPQ induction and relaxation were measured at silking. Best linear unbiased predictors (BLUPs) from both approaches were used for QTL mapping, allowing to identify three common

regions underling large variation on photosynthetic efficiency: a total of signals were identified in the high-throughput platform with the 103 kinetic chlorophyll fluorescence system, whereas 53 were detected through the use of joint model BLUPs from the field experiments. These signals exhibited varying intensity at different time points in the platform, as well as at different stages of spectra measurement from field data. Daily imaging data, yielded over 18 million raw images, that mapped over 2600 signals at different time points. To further investigate, we utilized parental coefficients at QTL loci and examined the differential expression using transcript levels of the founders at the fourth leaf stage. Through this analysis, we identified a group of candidate genes, including proteins involved in the functional organization of photosystem II antenna complexes, carotenoids catabolism as well as in the regulation of the photosynthetic electron flow. Our results demonstrate that integrating multiple phenomics approaches is a successful strategy to disentangle the genetic control of complex traits.