Poster Communication Abstract – 6.20

HIGH-DEFINITION MAPPING OF MAIZE SEED TRAITS COMBINING GENOMICS AND AUTOMATED PHENOTYPING IN A MULTIPARENT MAPPING POPULATION

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maize, MAGIC population, QTL mapping, seed traits, SPET genotyping

Maize is the most produced cereal worldwide, yielding more than one billion metric tons per year. Further improving maize yield is a challenging task, and even slight changes in yield components may result in great impacts in terms of achieved yield. The weight and size of maize seeds are important factors that may contribute increasing final yield. In this work, we characterized seed traits of an eight-way maize Multi-parent Advanced Generation Inter-Cross (MAGIC) population using high throughput imaging technology. Within the H2020 project CAPITALISE, we selected and characterized 554 MAGIC RILs along with the eight population's founders. After DNA extraction and quality control, we genotyped the MAGIC using Single Primer Enrichment Technology (SPET) with a custom set of probes designed in silico starting from the founders and their hybrids as to target highly polymorphic loci.

A total of 502 RILs, including the founder lines, were subsequently phenotyped with imaging technology and hundred seed weight. All seeds were sourced from the same field multiplication, and traits describing size and shape of the seeds were extracted with the *SeedExtractor* software from orthogonal photos of seed samples. The imaging-based phenotyping allowed to derive length, width, area, perimeter, and circularity as well as seed colour; trait distribution and pairwise correlations correlation were tested in R. The derived dataset was then used to map QTL. The genotyping produced about 76K SNPs after strict quality control while the final phenotyping dataset accounted over 14K data points. We reconstructed the mosaic genomes of the 554 RIL in terms of the founder haplotypes using Hidden Markov Model implemented in *R/qtl2*. We then mapped QTL with the same software using a linear mixed model accounting possible relatedness among

individuals using the leave-one-chromosome-out (LOCO) method. Significant peaks were defined using a trait-specific threshold based on 100 permutations. QTL confidence intervals defined by a 2-LOD drop from the maximum LOD score, resulting in 26 QTL. Here we describe the diversity of the MAGIC population and the relevance of the mapped QTL in a pre-breeding perspective.