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INTEGRATING PAN-GENOMES WITH MULTIPARENT MAPPING POPULATIONS: PRELIMINARY RESULTS FROM A ZEA MAYS PAN-GENOME DEVELOPED FROM THE MAGIC MAIZE PARENTAL LINES

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Structural genome variations play a key role in determining the great phenotypic and genetic diversity between maize lines. The abundance of Structural Variants (SVs) in maize led to the realization that a single reference genome does not represent the whole genetic diversity of the species. Access to a single reference genome can introduce biases and affects mapping of Quantitative Trait Loci (QTL). A Multi-parent Advanced Generation Intercrosses (MAGIC) population was established in maize from eight genetically diverse inbred lines and largely been used to map QTL. To fully exploit the potential of this population we aim to construct a comprehensive multiple-sequence alignment of the founders' genome. The concept of pan-genomes in crops has shed light on the extensive content variation within a species allowing to identify the effect of Structural Variants (SVs) and genomic rearrangements explaining trait variations. The MAGIC pan-genome that we are developing will capture the whole diversity of the MAGIC population, improving our understanding of the genetic architecture of complex traits.

The first step in the reconstruction of the pan-genome involves the extraction of High Molecular Weight (HMW) genomic DNA that is free from impurities. To generate long reads we employ Oxford Nanopore Technology (ONT), using a PromethION device. These long-reads are then used to perform de novo assemblies of the MAGIC founders with a hybrid strategy, in which

we also improve the outcome with previously produced short-read data. At present, the available results pertain one of the 8 founders, B73. This de novo assembly is obtained by combining reads from five PromethION runs, with run read length N50 ranging from 10.9 kb to 24.1 kb. The big amount of reads produced and used for the assembly results in an N50 scaffold length of about 2.8 Mb. The preliminary findings from sequencing the other lines suggest that improved HMW DNA extraction protocol leads to substantial increase in the average length of reads. This, in turn, offers the opportunity to generate high-quality assemblies.

The effectiveness of the newly produced set of assemblies will be tested to study the genetic architecture of photosynthesis-related traits previously identified on the MAGIC. Photosynthesis-related traits are among those on which it is still possible to intervene for the improvement of crops. Targeting photosynthesis and improving it by exploiting natural variation could be crucial to increase crop yields, fostering the sustainable intensification of agriculture.

By combining high-throughput phenotyping and genotyping with pan-genomic data, we can attain deeper comprehension of maize genome variation and its influence on complex traits. This knowledge will propel genetic improvement to address the challenges posed by a changing climate.