Poster 21. A genomewide SNP scan of the diversity, population structure, and Linkage disequilibrium in East African wheat (Triticum aestivum L.).

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For over a century, wheat has been a valued food crop in the East Africa region, but production is threatened by drought, insect pests, and a recurrence of rust disease epidemics as characterized by the recent highly virulent race Ug99 of stem rust. Recent effort is dedicated to genomewide association mapping (GWAM) for resistance loci and their deployment into the commercial cultivars. The objectives of this study were to dissect the diversity of the East African wheats and explore the nature of population structure and extent of linkage disequilibrium (LD), both of which have implications on the power and resolution of GWAM. A panel of 300 lines was assembeled, 90% of which are past and present East African cultivars as well as a few landraces and breeder lines. The material was genotyped using the 9000 SNP chip and a genome-wide set of 6,488 informative SNPS successfully called. An implementation of the model-based cluster analysis revealed a relatively strong population structure identifying five genetically distinct subpopulations (denoted as CIMMYT1, CIMMYT2, North America, Landraces, and Mixed). These were enriched with lines known to have initially originated from the international center for wheat and maize improvement (CIMMYT) and North America, consistent with known pedigree history, plus recognized landraces and a mixed group. The number of polymorphic loci was relatively high, ranging between 87% and 97%. Differences among the subpopulations were observed in the number of alleles, expected heterozygosity, and polymorphic information content (PIC). Estimates of relative kinship revealed a complete spectrum of values, with about 40% of the lines scoring above 0.5. The Level of LD (r^2) was higher and LD extend persisted longer in the CIMMYT1 subpopulation both in the A (13cM) and D (11cM) genomes. In the B genome, the LD extended longest (18 cM) in the North America subpopulation. This work hints at the suitability of the assembled panel for GWAM, if supported by a sufficient control of population structure and kinship.

Poster 22. Sequence-based, SNP genotyping in durum wheat.

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The availability of Single Nucleotide Polymorphism (SNP)-based platforms is highly desirable for the mapping and selection of loci (genes and QTL) of breeding value. As compared to other crops, SNP discovery and validation in durum wheat is lagging behind and only recently a number of SNPs were described and validated (Trebbi et al. 2011 Theor Appl Genet 123:555-569). A novel SNP discovery and genotyping technology, developed by KeyGene and called random Sequence Based Genotyping (rSBG), was tested and validated in both durum and bread wheat. This technology enables sequence-based SNP discovery and genotyping in a single assay, which is cost-effective (no separate costs for SNP discovery and genotyping) and robust (no marker conversion required). Within the EU FP7 BioExploit project, the rSBG technology was adjusted to highly repetitive, polyploid genomes and optimized on the durum wheat parental lines Colosseo (CLS) and Lloyd (LLD). This protocol was subsequently used to genotype 91 'CLS x LLD' recombinant inbred lines (RILs) in a single GAII run. A total of 10,761 putative SNPs in 10,729 loci were identified between the parents, using stringent SNP mining rules. Out of these, 1,038 were mapped with high confidence (two-point LOD > 6) to a pre-existing framework map containing 709 markers (SSRs, DArT® markers, SNPs from CRoPS® technology). The relatively low percentage of SNPs available for mapping was mainly due to lack of sequencing depth. Nevertheless, this rSBG experiment allowed for the genotyping of the RILs at a density of approximately one SNP marker every 2.8 cM. It is expected that an increased sequencing output will generate a higher number of genetically informative SNPs. Because the SNPs are associated with unique sequences, we will explore the possibility of linking them to the reference conserved orthologous sets from the grass genomes, which could add additional value to the rSBG SNP set. The rSBG and CRoPS® technologies are covered by patents and patents owned by Keygene N.V. CRoPS is a registered trademark of Keygene N.V. Other (registered) trademarks are the property of their respective owners.