Poster 15. Molecular breeding in wheat: findings from an international survey.

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Molecular breeding for crop improvement has the target to create gene-to-phenotype knowledge for breeding objectives and to use this knowledge in product development and deployment. Molecular techniques can impact every stage of the breeding process from parental characterization and selection for cross prediction to introgression of known genes and population enhancement via allele enrichment or gene stacking. It is often reported that molecular breeding through gene transfer and marker-assisted selection has been successfully applied especially in the private sector and that its wider use especially in the public sector institutions in the developing world is still limited due to various bottlenecks. Tangible information on the application of molecular breeding tools in public sector wheat programs is however fragmented. During the preparation of the 21st ITMI in Mexico City in 2011, we distributed a survey to the participants and CIMMYT collaborators addressing this subject. The survey included questions regarding the magnitude of application of molecular markers in the respective breeding programs, the form of deployment and trait target, bottlenecks in the case molecular markers are not used, and questions regards logistic and molecular marker systems. A total of 220 responses form 58 countries were received. The outcome of the survey will be presented.

Poster 16. Imprints of selection in CIMMYT wheat lines targeted to irrigated and rain-fed environments.

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CIMMYT international yield trials sent to national collaborators globally and targeted to diverse growing environments have been analyzed, but genotypic characterization of this elite material has not been extensively carried out. Twenty-three Elite Spring Wheat Yield Trials (ESWYT) and 17 Semi-Arid Wheat Yield Trials (SAWYT) together with recent CIMMYT elite lines were therefore genotyped with DArT and partly GBS markers. The high-throughput genotyping platforms were able to assign the lines in both yield trials into various but mainly two germplasm groups according to their targeted environment reflecting the establishment of diverse germplasm pools due to breeding for improved adaptation. Constant genetic diversity was observed across the years of trial distribution. The average genetic distance was slightly higher in the ESWYT than in the SAWYT and significantly increased in both trials with a growing difference in distribution years, suggesting a systematic change in allele frequencies during the breeding process. Observed frequencies for each marker allele, and haplotypes with a four-marker, sliding window, were determined for each of the ESWYT and SAWYT to further identify regions in the genome under selection. Markers and haplotypes displaying a significant change in allele frequency across years were identified and interpreted as an indicator for constant selection. Markers identified were partly linked to traits under CIMMYT breeder's selection and point to key genomic regions for further investigation.

Poster 17. Deriving a hard red winter wheat prebreeding population suitable for marker-facilitated recurrent mass selection.

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A new hard red winter wheat pedigree breeding program is being established at NDSU. As a result, there is an urgent need to develop improved breeding stock that can be used for making elite crosses. The most important demand is to develop breeding parents with high levels of cold-hardiness coupled with effective resistance against the major diseases, which include Fusarium head blight, leaf and stem rust, tan spot, and the *Septoria* complex. Backcrosses of resistance sources to a winter-hardy variety, such as Jerry, can only partially solve the problem as it restricts overall genetic variability. Recurrent selection is a population improvement strategy that is ideally suited to the development of improved germplasm as it maximizes opportunities for genetic recombination and gene pyramiding and allows for shorter genera-

tion cycles and more rapid progress while not imposing yield or genetic diversity ceilings typical of backcrossing. The effectiveness of a recurrent selection program can furthermore be greatly enhanced by using genetic male sterility and by supplementing phenotypic selection with marker-aided selection strategies.

A highly diverse, prebreeding base population is being produced. It incorporates a wide range of native and exotic resistance and adaptation genes, most of which derive from either spring wheat or less cold-hardy winter wheats from the southern United States. These will be involved in a complex cross that will eventually combine genes from approximately 150 diverse genotypes contained within five parental populations. While making the cross, the *Ms3* (dominant male sterility) gene is simultaneously being established within the hybrid population such that the final F_1 will segregate 1:1 for male sterility/ fertility. This final F_1 will be randomly intercrossed for two further cycles to fully disperse the target genes before the onset of selection. The intermediate and final hybrid populations will furthermore be evaluated to confirm the genetic diversity that it contains by employing phenotypic and/or marker-based evaluations of disease resistance, adaptation and performance. Concurrent with the development of the program, a procedure for random, large-scale intercrossing of individual plants through the use of *Ms3* will be optimized.

Poster 18. Creation of a new resource for fine mapping in wheat: a nested association mapping population.

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Linkage mapping using recombinant inbred lines usually achieves high power of QTL detection, but suffers from relatively poor accuracy of QTL location. Association or linkage disequilibrium (LD) mapping using panels of unrelated lines enables high mapping accuracy, depending on the range of LD, but is prone to several sources of false positive results if the panel is genetically structured. Nested association mapping (NAM) has been recently proposed as a method that combines the advantages of both linkage and LD mapping. It consists of developing a set of recombinant populations which are 'connected' by at least one common parent. The parental lines (founders) must be genotyped with a high marker density; the accuracy of QTL detection will rely on the short range LD among the founders. Then the recombinant progeny will be genotyped at low density. The small number of recombination events from founders to progeny enables large LD blocks to be conserved. The high density markers can therefore be imputed in the progeny from the information of low density markers thus keeping the high detection accuracy. On the other hand, recombination is sufficient to reshuffle the genetic background, thus limiting the source of spurious association with unlinked markers. Roughly, a NAM population achieves nearly the same accuracy as an unrelated association panel of similar size, while high-density genotyping or resequencing is only needed on a few dozen of founders. Simulations results suggest an optimal number of founders of 80-100 for a total sample size of 2,500–5,000.

In a cooperative program between Biogemma and INRA (ARN-08-GENM-005), we have developed a NAM population of RILs, and DHs, by producing recombinant progeny from a 'star' mating design. The pivot parental line was Altigo, a high-yielding, modern French cultivar. The other founders were taken either in the elite European cultivars or in a worldwide core collection built up at INRA GDEC Clermont-Ferrand France (http://www4.clermont.inra.fr/umr1095_eng/Teams/Technical-and-Experimental-Platforms/Genetic-Resources-Centre). Seed increase of the 5,000 progenies is now in progress. This new resource will be available soon for collaborative programs.