ria at Holetta. The lower number of materials maintained at Holetta is mainly due to Septoria. Most leaves were killed by the time the plants flowered causing shriveled grain with poor germination.

ITEMS FROM GERMANY

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Association mapping in hexaploid wheat – The project GABI-Wheat.

GABI-Wheat is designed as an association mapping study in hexaploid wheat. The aim of the project is the identification of associations of molecular marker data with traits that are important for breeding new cultivars. Populations employed in association studies consist of (mostly) unrelated individuals from a broad population. In this project, the population comprises 358 elite, Western-European hexaploid winter wheat cultivars and 14 spring wheat cultivars. The wheats were cultivated on one location in 2009 and three locations in 2010 in France, and on two locations in 2009 and 2010 in Germany, utilizing an alpha-design. Field trials and phenotyping for yield, yield components, and baking quality traits were performed by industrial project partners. Genotyping was performed for a total of 800 microsatellite markers. Inoculation trials for *Fusarium culmorum*/*Fusarium graminearum*, *Septoria tritici*, and *Drechslera tritici-repentis* were performed by the Julius-Kühn-Institut (B. Rodemann) in 2009 and 2010 for each disease at two locations in Germany.

After correction for rare alleles (less than 3% frequency in the population), data from 781 loci, corresponding to 732 microsatellite marker and from 17 candidate genes chosen from the literature, are available for the 372 cultivars. From those microsatellites, 650 are mapped in the ITMI mapping population with an average distance of 7.6 cM. No apparent population structure was detected employing the STRUCTURE program and principal component analysis. Hence, a marker-based kinship matrix was used to reduce the number of false positive associations caused by spurious relationships between the cultivars. Linkage disequilibrium analysis showed small values for R^2 between unlinked markers as well as physically linked markers. The correlation between R^2 and physical marker distance also is weak. Mixed linear models are employed for the analysis of marker–trait associations. The Genstat and Tassel programs are currently used to evaluate the data. Preliminary results revealed significant associations for the first traits investigated so far.

Sustainable grain yield loci in bread wheat detected via an association mapping approach.

A core collection of 96 winter wheat genotypes from 21 different countries and five continents was considered for a genome-wide association mapping analysis. These genotypes were selected from a larger collection created at the Institute of Field and Vegetable Crops, Novi Sad, Serbia. The collection was phenotyped for grain yield in field plots in Novi Sad during six growing seasons between 1994 and 1999. Genotyping using DArT markers was performed by Triticarte Pty. Ltd. (Canberra, Australia). The calculation of testing for an association between markers and traits was done with the software programs TASSEL 2.01. and TASSEL 2.1 exploiting the general linear model and mixed linear model, respectively.

Only stable marker–trait associations (MTAs) significant in both models in three out of five years were considered. In total, 10 MTAs were identified on chromosomes 1AL, 3AL (two), 3BL, 4AL, 4BL, 5BL, 6BS, 7AS, and 7BL. Interestingly, there was coincidence with MTAs described in a study performed by CIMMYT using different sets of germ plasm. Identical MTAs were detected on chromosomes 1AL, 3AL, and 7BL. In addition, we found grain yield MTAs in highly comparable regions on chromosomes 3BL and 7AS.

Mapping of QTL for resistance to stem rust (Ug99) in durum wheat.

Ninety-seven recombinant inbred lines (RILs) that were developed from the cross 'Kristall / Sebatel', both durum wheat cultivars, has been characterized for stem rust response in Ethiopia. Seven consecutive field trials at two locations were carried out in main- and off-season under natural and artificial inoculation with stem rust race Ug99 and a mixture of highly virulent races of Ethiopia. Based on the means of the seven environments, the phenotypic distribution showed that resistance to Ug99 in this population is controlled by major gene/QTL, accounting for most of the phenotypic variation. The parents were screened for polymorphism with 502 SSR markers. We have found 258 polymorphic and, accordingly, we used these markers to genotype the whole population. Using composite interval mapping, eight consistent and major QTL for stem rust (Ug99) were identified on chromosomes 1AS, 2AL, 2BS, 3AS, 4BS, 6AL, 7AS, and 7AL. An additional, minor consistent QTL also was identified on the long arm of chromosome 5B. From these QTL regions, 1AS, 2AL, 3AS, 4BS, and 7AS are not harboring any of the characterized stem rust resistance genes of durum wheat. These results suggest that durum wheat resistance to the Ethiopian races of stem rust (Ug99) is likely oligogenic and that there is potential to identify previously uncharacterized resistance genes of minor effect. If successfully validated, the markers associated with these QTL will be useful for breeding new durum wheat cultivars that are resistant to Ug99 and related races.

The relationship among seed characters based on QTL analysis in bread wheat.

QTL mapping was applied on a new mapping population (HTRI 11712/HTRI 105), which was developed at IPK, Gatersleben, and contained 133 $F_{2:3}$ families (see Annual Wheat Newsletter Vol. 55:56). Mapping analysis revealed four QTL for 1,000-kernel weight on chromosomes 7A, 4B (two QTLs), and 1B of which three were detected repeatedly in two experiments. The explained phenotypic variation (R^2) by a single QTL ranged from 8.7 to 26.5% and both parents contributed increasing alleles. For seed length, 13 QTL were detected of which three were identified repeatedly in at least two experiments. The R^2 for a single QTL ranged from 8.3 to 26.9%, and the increasing alleles originated from both parents. QTL analysis for seed width showed five QTL of which two were identified repeatedly in at least two experiments. The R^2 of a single QTL ranged from 7.9 to 15.7%.

Thousand-kernel weight showed a higher correlation with seed width compared to seed length. With regard to the co-localization of the QTL for seed-related traits, and considering only the repeated QTL in the present study, there was only one QTL on chromosome 4BL common among all the traits. However, seed width showed another QTL on chromosomes 4BS in common with 1,000-kernel weight. This is in agreement with the coefficient of correlation observed in the present study between these traits, which show higher correlation of 1,000-kernel weight with seed width compared to seed length. This might suggest that 1,000-kernel weight is determined more by seed width than seed length. Therefore, in order to increase 1,000-kernel weight, seed width should be enhanced, in accordance with practical wheat breeding.

Studies on seed longevity in bread wheat.

An association mapping approach was utilized to visualize the genomic regions responsible for the maintenance of viability of bread wheat seeds. Seeds of 96 accessions selected from a large panel based on contrasting agronomic and phenotypic traits were available from the regeneration cycle of 2009. The genetic map for these lines consisted of 525 mapped and 315 unmapped DArT (Diversity Arrays Technology) markers.

The lines showed high initial germinations after standard germination tests, which ranged from 68% to 98.5% with the mean germination of 93.72±5.05%. Accelerated ageing tests were performed to assess the seed longevity. Germination percentages after artificial ageing (AA) and controlled deterioration tests (CD) ranged from 0% to 60.5% and 5.5% to 95% with the mean of 10.97±12.80% and 61.05±25.33%, respectively. In total, association mapping revealed 73 significant marker trait associations (MTAs) for seed longevity, 38 of which were with mapped markers, 20 with unmapped markers with known chromosomal location only, and 25 with completely unknown location. The MTAs were located on 14 out of 20 marked chromosomes. When the two methods were compared, AA gave 40 and CD gave 33 significant MTAs. Based on bin information, 15 markers with significant MTAs were genetically characterized.

The bins carrying these markers contain many genes important in various aspects of seed vigor and viability such as encoders of seed maturation protein, cold- and heat-shock proteins, plasma membrane proteins, biostress-related proteins, senescence-related proteins, and membrane proteins along with various enzymes associate with seed longevity. When compared with the similar studies performed in barley, we found that the chromosomal segments of 7B MTAs in wheat matches with the location of a 7H QTL for longevity in barley giving the indication of shared mechanisms of seed viability in both cereals.

Variability of Rc (red coleoptile) alleles in wheat and wheat–alien genetic stock collections.

Anthocyanin accumulation in vegetative organs has a relationship to stress resistance in plants. In wheat, the ability to accumulate anthocyanins in the coleoptile is inherited and controlled by the *Rc* (red coleoptile) genes. Our goal was to find potential sources of 'strong' *Rc* alleles conferring very high levels of anthocyanin production and to study the effect of genetic background on *Rc* expression. We measured the relative anthocyanin content (OD530) in the coleoptile of different wheat and wheat–alien genetic stocks and accessions to find potential sources of strong *Rc* alleles conferring very high levels of anthocyanin production. The OD530 values varied from 0.514 to 3.311 in genotypes having red coleoptiles. The highest anthocyanin content was detected in coleoptiles of four *T. turgidum* subsp. *dicoccoides* accessions originating from Israel and the Russian *T. aestivum* cultivar Novosibirskaya 67, suggesting that their *Rc* alleles can be used to increase anthocyanin content in the coleoptile of wheat cultivars. Rye *Rc* alleles, such as that of Russian cultivar Selenga, can possibly be used to increase anthocyanin content in triticale seedlings.

Embryo lethality in wheat x rye hybrids: mode of inheritance and identification of a complementary gene in wheat.

Crosses between hexaploid wheat and rye can only succeed when pre- and post-zygotic barriers are overcome. A rye gene determining embryo lethality (*Eml-R1*), which is involved in post-zygotic isolation, has been mapped to chromosome 6R. The mode of inheritance of *Eml-R1* was studied using a wheat-rye chromosome 6R addition line. *Eml-R1* exists in at least two alternative forms, with the mutant allele *Eml-R1b* dominant with respect to wild-type allele *Eml-R1a*. The attempt to test whether the Dobzhansky-Müller model can explain the embryo lethality seen in wheat–rye hybrids was performed by examining hybrid caryopses formed by a cross between the set of nullisomic-tetrasomic (NT) lines of Chinese Spring and rye lines carrying *Eml-R1b*, since differentiated embryos should only be formed in hybrids lacking the wheat chromosome carrying a complementary wheat gene. In parallel the NTs were crossed with rye inbred lines carrying *Eml-R1a* to prove the capacity of each of the lines to produce differentiated viable hybrid seeds. The crosses of NT lines with rye lines carrying *Eml-R1b* detect a complementary wheat gene present on chromosome 6A. This gene has been designated *Eml-A1*. Crosses of NT lines with rye lines carrying wild-type allele *Eml-R1a* revealed that wheat chromosomes 1B, 1D, and 6B carry genes indispensable for normal development of wheat-rye caryopses.

Publications.

Achtar S, Moualla MY, Kalhout A, Röder MS, and MirAli N. 2010. Assessment of genetic diversity among Syrian durum (*Triticum turgidum* ssp. *durum*) and bread wheat (*Triticum aestivum* L.) using SSR markers. Genetika 46:1500-1506.

Börner A, Neumann K, Kobiljski B, and Lohwasser U. 2011. Association mapping for flowering time in wheat using an ex situ core collection. Agriculturae Conspectus Scientificus (in press).

Börner A, Landjeva S, Salem KFM, Kobiljski B, and Lohwasser U. 2010. Plant genetic resources - a prerequisite for drouhgt tolerance breeding in wheat. *In:* Proc 60th Tagung der Vereinigung Pflanzenzüchter und Saatgutkaufleute Österreichs. pp. 11-13.

Castillo A, Budak H, Martín AC, Dorado G, Börner A, Röder M, and Hernandez P. 2010. Interspecies and intergenus transferability of barley and wheat D-genome microsatellite markers. Ann Appl Biol 156:347-356.

Diaz de Leon JL, Escoppinichi R, Zavala-Fonseca R, Castellanos T, Röder MS, and Mujeeb-Kazi A. 2010. Phenotypic and genotypic characterization of salt-tolerant wheat genotypes. Cereal Res Commun 38:15-22.

Garcia-Suarez JV, de Leon JLD, and Röder MS. 2010. Identification of QTLs and associated molecular markers related to starch degradation in wheat seedlings (*Triticum aestivum* L.) under saline stress. Cereal Res Commun 38:163-174.

Kerfal S, Giraldo P, Rodriguez-Quijano M, Vazquez JF, Adams K, Lukow OM, Röder MS, Somers DJ, and Carrillo JM. 2010. Mapping quantitative trait loci (QTLs) associated with dough quality in a soft x hard bread wheat progeny. J Cereal Sc i 52:46-42.

Khlestkina EK. 2010. Regulatory-target gene relationships in allopolyploid and hybrid genomes. *In:* Adv Genet Res Vol. 3 (Urbano KV, Ed). NOVA Science Publishers. pp. 311-328.

Khlestkina EK, Kumar U, and Röder MS. 2010. Ent-kaurenoic acid oxidase genes in wheat. Mol Breed 25:251-258.

Khlestkina EK, Röder MS, and Börner A. 2010. Mapping genes controlling anthocyanin pigmentation on the glume and pericarp in tetraploid wheat (*Triticum durum* L.). Euphytica 171:65-69.

Khlestkina EK, Röder MS, Pshenichnikova TA, and Börner A. 2010. Functional diversity at *Rc* (red coleoptile) locus in wheat (*Triticum aestivum* L.). Mol Breed 25:125-132.

Khlestkina EK, Salina EA, Matthies I, Leonova IN, Börner A, and Röder MS. 2011. Comparative molecular marker-based genetic mapping of flavanone 3-hydroxylase genes in wheat, rye and barley. Euphytica DOI: 10.1007/s10681-010-0337-2 (Online First).

Khlestkina EK, Antonova EV, Pershina LA, Soloviev AA, Badaeva ED, Börner A, and Salina EA. 2011. Variability of Rc (red coleoptile) alleles in wheat and wheat-alien genetic stock collections. Cereal Res Commun (in press).

Kumar U, Joshi AK, Kumar S, Chand R, and Röder MS. 2010. Mapping of quantitative trait loci for resistance to spot blotch caused by *Bipolaris sorokiniana* in wheat (*T. aestivum* L.) lines 'Ning 8201' and Chirya 3'. Mol Breed 26:477-491.

Kumar U, Joshi AK, Kumari M, Paliwal R, Kumar S, and Röder MS. 2010. Identifikation of QTLs for stay green trait in wheat (*Triticum aestivum* L.) in the 'Chirya 3' × 'Sonalika' population. Euphytica 174:437-445.

Landjeva S, Lohwasser U, and Börner A. 2010. Mapping QTL for germination, seed vigour and longevity on wheat D genome. Berichte der Gesellschaft für Pflanzenbauwissenschaften 5:104-107.

Landjeva S, Lohwasser U, and Börner A. 2010. Genetic mapping within the wheat D genome reveals QTL for germination, seed vigour and longevity, and early seedling growth. Euphytica 171:129-143.

Leonova IN, Budashkina EB, Flath K, Weidner A, Börner A, and Röder MS. 2010. Microsatellite mapping of a leaf rust resistance gene transferred to common wheat from *Triticum timopheevii*. Cereal Res Commun 38: 211-219.

Nagel M and Börner A. 2010. The longevity of crop seeds stored under ambient conditions. Seed Sci Res 20:1-20.

Nagel M, Rehman Arif MA, Rosenhauer M, and Börner A. 2010. Longevity of seeds and the intraspecific differences in the Gatersleben genebank collections. *In:* Proc 60th Tagung der Vereinigung Pflanzenzüchter und Saatgutkaufleute Österreichs, Gumpenstein, Austria, 24-26 November, 2009. pp. 179-181.

Navakode S, Weidner A, Varshney RK, Lohwasser U, Scholz U, Röder MS, and Börner A. 2011. A genetic analysis of aluminium tolerance in cereals. Agriculturae Conspectus Scientificus (in press).

Neumann K, Kobiljski B, Denčić S, Varshney RK, and Börner A. 2011. Genome-wide association mapping – a case study in bread wheat (*Triticum aestivum* L.). Mol Breed 27:37-58.

Osipova SV, Permyakov AV, Permyakova MD, Davydov VA, Pshenichnikova TA, and Börner A. 2011. Tolerance of prolonged drought among a set of bread wheat chromosome substitution lines. Cereal Res Commun (in press).

Rehman Arif MA, Nagel M, Lohwasser U, and Börner A. 2010. Seed longevity in wheat (*Triticum aestivum* L.) – genetics and beyond. Berichte der Gesellschaft für Pflanzenbauwissenschaften 5:11-15.

Simon MR, Khlestkina EK, Castillo NS, and Börner A. 2010. Mapping quantitative resistance to *Septoria tritici* blotch in spelt wheat. European J Plant Pathol 128:317-324.

Szira F, Börner A, Neumann K, Zaynali Nezhad K, Galiba G, and Bálint AF. 2011. Could EST-based markers be used for marker-assisted selection of drought tolerant barley (*Hordeum vulgare*). Euphytica DOI 10.1007/s10681-010-0317-6 (Online First).

Tikhenko N, Tsvetkova N, Priyatkina S, Voylokov A, and Börner A. 2011. Gene mutations in rye causing embryo lethality in hybrids with wheat – allelism test and chromosomal localisation. Biol Plant (in press).

Tikhenko N, Tsvetkova N, Voylokov A, Dobrovolskaya O, Zaynali Nezhad K, Röder M, and Börner A. 2010. Embryo lethality in wheat x rye hybrids – mode of inheritance and the identification of a complementary gene in wheat. Euphytica 176:191-198.

Zaynali Nezhad K. 2010. Genetic linkage map construction and identification of quantitative trait loci (QTLs) determining post-anthesis drought tolerance and other agronomic traits in bread wheat. Ph.D. thesis, Martin-Luther-University, Halle-Wittenberg, 162 pp.