Reference.

IBGE. 2014. Sistema IBGE de Recuperação Automática - SIDRA. Available at < http://www.sidra.ibge.gov.br/bda/tabela/listabl.asp?z=t&o=11&i=P&c=1612 >, 28 March 2014. Note: Bank of aggregate data studies and research conducted by IBGE.

ITEMS FROM GERMANY

LEIBNIZ–INSTITUT FÜR PFLANZENGENETIK UND KULTURPFLANZENFORSCHUNG — IPK GATERSLEBEN

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Grain size QTL region QTgw.ipk-7D in wheat: sequence analysis and synteny to related grass species.

The previously described QTL for 1,000-kernel weight *QTgw.ipk-7D* associated with microsatellite marker *Xgwm1002-7D* was originally detected in a BC_2F_3 advanced backcross population of the winter wheat cultivar Prinz and the synthetic wheat line W-7984 (lab designation: M6). We developed near-isogenic lines (NILs) carrying introgressions of M6 in the genetic background of Prinz with varying size on chromosome 7DS. The BC_4F_3 NILs had a 10% increase in 1,000-kernel weight compared to the control group and the recurrent parent Prinz. The same QTL was detected in another population of the winter wheat Flair and a synthetic wheat XX86. By using homozygous recombinant lines developed from both populations, it was possible to fine-map *QTgw.ipk-7D* to an interval of approximately 1 cM flanked by markers barc126, wmc405, and gwm44 on wheat chromosome arm 7DS. From a chromosome arm 7DS-specific BAC library (provided by J. Dolezel and H. Simkova), BACs covering the region of *QTgw.ipk-7D* were isolated, and their sequences were obtained by 454 sequencing. Of the sequenced BACs, new microsatellite markers were developed and used for anchoring the BACs to the genetic map. Finally, the region of *QTgw.ipk-7D* was delimited to 10 BACs carrying at least 12 predicted genes. Good synteny to the genomic sequences of rice, *Brachypodium*, and *Sorghum* was observed. A BAC contig covering the respective genomic region in barley was identified and also completely sequenced. A detailed comparison of the barley sequence to the wheat sequence with respect to genome evolution is currently conducted.

Genetic architecture of heading date in European winter wheat.

A genome-wide association study (GWAS) for heading date (HD) was performed with a panel of 358 European winter wheat and 14 spring wheat cultivars through the phenotypic evaluation of HD in field tests in eight environments in collaboration with breeding companies (2009 and 2010 in Andelu (FR), Seligenstadt (DE) and Wohlde (DE); 2010 in Janville (FR) and Saultain (FR)). Genotyping data consisted of 770 mapped microsatellite (SSR) loci and 7,934 mapped SNP markers derived from the Infinium 90K iSelect wheat chip. Best linear unbiased estimations (BLUEs) were calculated across all eight environments and ranged from 142.5 to 159.6 days after 1 January with an average value of 151.4 days. For association mapping, a mixed linear model corrected with a kinship matrix for population stratification was employed. Considering only associations with a –log10 (P-value) ≥ 3.0, a total of 358 SSR and 2,983 SNP marker-trait associations (MTAs) were detected. After Bonferroni correction for multiple testing, a total of 90 SSR and 438 SNP

MTAs remained significant. As candidate genes, the photoperiodism gene *Ppd-D1* and vernalization genes *Vrn-B1* and *Vrn-D1* were genotyped in all cultivars. Highly significant MTAs were detected for the *Ppd-D1* gene on chromosome 2D. Consistent associations were found on all chromosomes with the highest number of MTAs on chromosome 5B. Linear regression showed a clear dependence of the HD score BLUEs on the number of favorable alleles (decreasing HD) and unfavourable alleles (increasing HD) per cultivar, meaning that genotypes with a higher number of favorable or a low number of unfavorable alleles showed lower HD and, therefore, flowered earlier. Co-locating MTAs were detected for the *Vrn-A2* on chromosome 5A and for *Ppd-A1* on chromosome 2A and *Ppd-B1* on chromosome 2B. After the construction of an integrated genetic map of the SSR and SNP markers, and exploiting the synteny to sequenced species such as rice and *Brachypodium distachyon*, we were able to demonstrate that a marker locus on wheat chromosome 5BL with homology to the rice photoperiodism gene *Hd6* played a significant role in the determination of the heading date in wheat.

A novel flowering time QTL on chromosomes 4D and 7A.

Fine tuning of the initiation of reproductive period is important for optimizing grain yield in wheat. Precise genetic stocks were used to determine the chromosomal location and map the loci responsible for a few days difference in flowering time between two spring cultivars carrying dominant alleles at the *Vrn-1* locus. The plant material, consisting of inter-cultivar chromosome substitution lines in which individual chromosomes of the Russian variety Saratovskaya 29 (S29) were substituted by the homologous chromosomes of the late-heading, German cultivar Yanetzkis Probat (YP). A set of single-chromosome, recombinant lines was studied in contrasting environments in Novosibirsk (western Siberia), Sofia (southeastern Europe), and Gatersleben (western Europe). The substitution line S29 (YP 4D*7A), carrying the entire donor chromosome 4D and an additional fragment of chromosome 7A, showed the largest delay in flowering at all sites. Two QTL associated with flowering time were identified using a set of 110 recombinant, double-haploid lines obtained after crossing line S29 (YP 4D*7A) with the recipient S29. One QTL was mapped to chromosome 4D and was regarded as a photoperiod-response locus. The second QTL was associated with a polymorphism on the chromosome 7A fragment and represented an intrinsic earliness gene. This information could aid the subtle regulation of flowering in wheats tailored for growing in specific environments.

Genome-wide association mapping of tan spot resistance (Pyrenophora tritici-repentis) in European winter wheat.

Genome-wide association mapping revealed the genetic architecture of resistance to tan spot in a population of 358 European winter wheat and 14 spring wheat cultivars. All cultivars were genotyped with 732 microsatellite markers resulting in 770 mapped loci spread across all 21 chromosomes. Based on field data in two environments (2010 in Ahlum and Lafferde, carried out by B. Rodemann, Julius Kühn Institute, Braunschweig, Germany) and the resulting best linear estimations, a total of 90 MTAs were significant with –log10 (P value) ≥ 3.0 using a mixed linear model corrected with a kinship matrix. Although the inheritance pattern of resistance to tan spot appeared to be quantitative, a number of already known resistance or susceptibility loci were confirmed, such as *Tsn1* on chromosome 5B, *tsn2* or *tsn5* on chromosome 3B, and *Tsc2* or *Tsr6* on chromosome 2B. Additionally, evidence for novel loci was gathered. Additive effects of favourable or unfavorable alleles were observed and suggest the application of genomic selection as a possible strategy for further cultivar development.

Fusarium head blight inducible resistance.

The ITMI mapping population was tested for Fusarium head blight (FHB) tolerance during five years of trials under Argentinean conditions, including inoculums prepared with 67 of the more frequent isolates. Types I, II, and V resistance were tested. Tolerant RILs were identified by their low incidence, severity, and higher 1,000-kernel weight. In the subsequent three years, these tolerant lines were subjected to treatments with biotic and hormonal defence inductors, prior to *Fusarium* inoculation in order to assess the presence of inducible mechanisms of resistance. One line resulted with highly inducible type-II resistance after pretreatment with Jasmonic acid, because this type of tolerance can be switched on before FHB infections, providing a high level of protection. The detection of inducible defences could be useful because these types of mechanisms could be included in commercial wheat production priming the plants and bringing on a more sustainable FHB control.

Location of resistance to Mycosphaerella graminicola, plant height, and heading date through genome-wide association mapping in wheat.

Septoria leaf blotch, caused by *Mycosphaerella graminicola* (Fuckel) Schrot. (anamorph, *Septoria tritici* Rob. ex Desm), constitutes a major disease problem of wheat. This disease is widespread in wheat-growing regions all over the world and yield losses are often severe. Host resistance is the most effective and economic means to reduce yield losses from this disease, although so far, only a few genes have been identified mainly due to the high genetic variability of the pathogen. An important fact in the search for resistance to this disease is its possible association with plant height and heading date. Phenotypic studies have reported genetic association between these characters, whereas others argue that this association is due to epidemiological or environmental factors. On the other hand, only a few molecular works have determined the existence of linkage between those traits.

The test material consisted of two Argentinean spring wheat cultivars, susceptible to leaf blotch and used as controls, and 96 winter wheat accessions from 21 countries. Three field experiments were conducted at the Experimental Station J. Hirschhorn, Faculty of Agricultural and Forestry Sciences, National University of La Plata, Argentina, during 2012 and 2013 in a split-plot design. The entire collection was inoculated with two isolates from two locations in Argentina (Pla and Nueve de Julio), the conidial suspension was adjusted to 5×10^6 spores/ml and sprayed at the 2-leaf stage in both years. For two of the experiments, severity (expressed as necrosis) in seedlings was scored, and for the three experiments, heading date and plant height were evaluated. The percentage of necrosis, plant height, and heading date scores indicated a wide phenotypic variation of the cultivars ranging from 32.44% (most resistant) to 67.56% (most susceptible), 22.97 to 127.7 cm plant height, and 94 to 138 days-to-heading. A phenotype–genotype association analysis, employing the general linear model and the mixed linear model, was performed with software Tassel 2.1. Only loci significant with both models were considered.

QTL for *M. graminicola* resistance were detected on chromosome 1A (two) and 6B in both experiments, and 46 MTAs were significant in one of both experiments analyzed with the isolate from Pla. In addition, four significant MTAs on chromosome 1B (two), 2A, and 2D in the two experiments analyzed were effective against the isolate from Nueve de Julio, whereas 53 MTAs were significant in only one. For heading date, five significant MTAs were detected on chromosomes 1B, 2B, 4B, 5D, and 6A in the three experiments analyzed. Additionally, 13 other MTAs located on chromosomes 1A, 1B, 2B (two), 3B (three), 5D, 6A, and 6B (four) were significant in two of three experiments evaluated. For plant height, four significant MTAs were identified on chromosomes 2B, 3A, 4A, and 7A for the three experiments analyzed, whereas another eight MTAs located on chromosomes 1B, 3A, 6A, 6B (two), 7A, and 7B (two) were significant in two of the three experiments.

Additionally, a correlation analysis was performed, in which necrosis was negatively associated ($P < 0.01$) with both plant height ($r = -0.254$) and heading date ($r = -0.419$) for the Nueve de Julio isolate and with both plant height ($r = -0.094$) and heading date ($r = -0.188$) for Pla isolate, although this was only significant in the last case ($P < 0.05$).

Preliminary screening of wheat lines against stripe rust.

A set of 117, spring wheat genotypes assembled from the wheat collection at the Federal Genebank in Gatersleben, Germany, was planted at the PMAS-Arid Agriculture University research farms located at Koonth, Rawalpindi, Pakistan, in rain-fed conditions to test for their adaptability to grow in arid conditions and to disease resistance. The lines were grown in a randomized complete-block design with Chinese Spring planted between every 20 lines as a positive control. The only source of water was rain that occurred three times during the whole growing season, and all the lines showed 100% germination. These lines were evaluated for stripe rust resistance on a rating scale of 1–100% (% infected leaf area) in field where they showed mixed reactions. The mean infection of these lines ranged from 0 to 43%. Eight lines showed complete immunity to the stripe rust attack and did not show any sign of infection, whereas three lines had the highest reaction (43%) towards stripe rust. Thirthy-eight lines had infection between 0 and 5% and 22 lines showed an infection severity between 5 and 10%. The data will be used to map loci for stripe rust resistance. Furthermore, they will be compared with the historical data to locate stable loci for resistance against stripe rust. Overall, the panel proved effective to study abiotic stresses such as drought tolerance and biotic stresses such as stripe rust resistance.

Observations on Oscinella frit and various aphids in spring and winter wheat collections.

The Frit fly is an oligophagous fly assigned to the family Chloropidae and an important pest in wheat and maize. *Oscinella frit* has two generations, larvae penetrate into the stem core and crawl toward the tillering node. Only one larva lives in one stem. The female flies lay their eggs on stems of underdeveloped plants and on ears of spring crops. In wheat, various aphids cause damage by sucking the phloem on spikes and leaves. Major species are *Sitobion avenae*, *Metopolophium dirhodum*, and *Rhopalosiphum padi*.

The observed spring wheat collection, consisting of 111 different genotypes from 27 countries, was sown at Gatersleben in 2013. Using white dish traps in every plot, we caught adult flies and various stages of aphids to determine the activity of both pests. The white dish traps were controlled weekly, and an additional visual rating was used to identify aphid infestations on spikes and flag leaves. Sweep nets were used to catch aphids and flies for a complete determination of species. After sampling all traits, we calculated an association study to find out characteristic MTAs for resistance. For a potential resistance to *O. frit*, we detected 41 MTAs; for the aphids, we detected 44 MTAs on the different wheat chromosomes.

Secondary, observations were made in 2013 about potential resistance against aphids in a winter wheat collection consisting of 96 genotypes at Gatersleben and on a second experimental area provided by Limagrain GmbH in the proximity of Peine (Lower Saxony). We collected characteristic traits for an association study calculation to determine characteristic MTAs for the infestation with aphids on spikes and flag leaves. Major species found in winter wheat were *S. avenae* (67.5%), *R. padi* (18.8%), and *M. dirhodum* (13.7%).

Studies on frost tolerance in bread wheat using a genome-wide association mapping approach.

Frost tolerance in plants is decisive to increase yield security, but the molecular and genetic background for this trait is still poorly understood. Phenotyping a panel of up to 360 accessions was performed at several locations in Germany and Russia. Highly significant differences between locations, but also between tested genotypes, were observed. The genotyping employed an ILLUMINA infinium iSelect 90k wheat chip. The chip carries a total of 81,587 valid and functional SNPs. After a round of selections, 38,052 polymorphic markers were available for the analysis. For the population-tructure analysis, the software Structure was used. The Q-matrix for three groups was the best option. Results were validated using an evolutionary tree calculated by the PAUP software, which also showed three clusters. The detailed analysis shows three subgroups of North American, Russian, and North and Middle European samples. Furthermore, the kinship matrix was inferred in Tassel 2.1. First results of model comparison yield highly significant associations (LOD > 3).

Genotypic-phenotypic associations of traits contributing towards post-anthesis drought tolerance in spring wheat.

A spring wheat panel comprising 111 genebank accessions was sown at experimental fields of IPK during 2013. All genotypes were allocated randomly to experimental units replicated four times. After two weeks of anthesis, a foliar application of potassium iodide solution (KI 0.5%) was made to a single row of each double-row plot. Morphological, yield, and yield-component trait data of each genotype were recorded in parallel for desiccation and control. Highly significant differences were obtained for all traits (days-to-flowering, days-to-maturity, plant height, number of seeds and seed weight/spike, 1,000-kernel weight, seed area, spike length, and number of spikelets/spike) compared under chemical desiccation treatment and the control. The most tolerant accession did show tolerance indices of 94% and 95% for 1,000-kernel weight and seed area, respectively, although the accession most sensitive to desiccation stress exhibited a tolerance index of only 25% for 1,000-kernel weight. The number of spikelets/spike was positively correlated with number of seeds/spike, both under the control and desiccation treatments, although this trait was negatively correlated with 1,000-kernel weight under both control and stress. A strongly positive correlation was determined between 1,000-kernel weight and seed area, hence both parameters are the best indicator for post anthesis desiccation/drought tolerance. The identified tolerant and susceptible genotypes can be used for further population development and post anthesis drought-tolerance studies. Phenotypic and genotypic data will be analyzed to establish marker-trait associations and identify favorable alleles for further marker-assisted breeding.

Identification of QTLs associated with the lipoxygenase activity on the chromosomes 5D and 7D in hexaploid wheat.

Lipoxygenase (LOX; EC 1.13.11.12) catalyzes the addition of molecular oxygen to polyunsaturated fatty acids for the formation of fatty acid hydroperoxides. Lipoxygenase isozymes are involved in the processes of plant growth, development and defense against biotic and abiotic stresses. Using *Triticum aestivum–Aegilops taushii* introgression lines, we mapped minor QTL (LOD from 2.04 to 2.69) associated with the LOX activity in common wheat under stress.

Two QTL associated with the phenotypic expression of LOX activity were found on chromosome 5D. The first is related with the soluble enzyme activity in wheat seedlings germinated on 12% polyethylene glycol solution, which imitates the oxidative stress. This QTL is located on the long arm of chromosome 5D. The LOX biosynthesis gene, the vernalization responce gene *Vrn-D1*, and QTL of many wheat-development parameters are well know to be in a similar position. The second QTL associated with activity of membrane-bonded LOX in wheat seedlings germinated on 12% polyethylene glycol solution; it was located on the short arm of chromosome 5D. This locus may be responsible for the regulation of lipoxygenase isoenzyme activity, which besides plant defense may play a role in the formation of endosperm texture (softness or hardness). This assumption is based on the physiological and functional relationships between the puroindolines, being that lipid-transfer proteins are considered to be molecular markers of grain hardness, the lipid-degrading enzyme lipoxygenase, and the polar lipids of starch grains that serve as a preferable substrate for LOX. One of the known loci responsible for polar lipid levels, *Fpl-1*, was found on the short arm, but *Fpl-2* is on the long arm of chromosome 5D, and both may coincide with the LOX loci that were detected in this study. Now, grain hardness is considered to be mainly associated with allelic variation of puroindolins in locus *Ha* at the distal end of chromosome 5DS. However, other genes located on the short arm of chromosome 5D of hexaploid wheat possibly also are important in regulating grain texture.

On chromosome 7D, the phenotypic variation of LOX activity in leaves of wheat grown under drought were linked with a marker in the centromeric region. This QTL may be relevant for tolerance to both abiotic and biotic stresses, because the known locus is associated with resistance to Septoria tritici blotch in a similar position. Moreover, QTL associated with LOX activity on chromosome 7D probably also effect the endosperm texture, because it coincides with known loci of the variant form of puroindolin b, which were detected on all homoeologous group-7 chromosomes.

The antioxidant enzymes activity in leaves of inter-cultivar substitution lines of bread wheat with different tolerance to water deficit.

A set of bread wheat, inter-cultivar, single-chromosome substitution lines (ISCSLs) of wheat cultivar Janetzkis Probat (JP) in to the genetic background of Saratovskaya 29 (S29) were used to dissect drought tolerance as a polygenic trait. The drought tolerance associated with antioxidant protection mechanisms was studied. The recipient cultivar S29 is highly drought tolerant, whereas the donor JP is sensitive. Plants were grown under controlled conditions of either adequate or inadequate soil moisture. The activity of leaf catalase (CAT) and three enzymes involved in the ascorbate/glutathione cycle, ascorbate peroxidase (APX), glutathione reductase (GR), and dehydroascorbate reductase (DHAR), were measured. The yield components and indices of drought tolerance/susceptibility were studied in the same material. We found that substitutions of JP chromosomes 2A and 4D in the S29 genetic background were critical for drought tolerance of yield components and indices of drought tolerance/susceptibility. At the same time, the cumulative activity (CA) of CAT, DHAR, APX, and GR in leaves under drought consisted of 26% from the recipient in the line S29 (JP 2A) and 43% in the line S29 (JP 4D). All ISCSL from the homoeologous group-2 chromosomes manifested low leaf GR and CAT activities. The lowest leaf CAT activity, in line S29 (JP 4D), proves the presence of genes responsible for activity level of the enzyme on 4D chromosome, whereas the homoeologous group-2 chromosomes may carry the structural and (or) regulatory genes responsible for GR activity. If so, such genes should be amenable to standard mapping strategies. Under drought conditions, CA correlated positively with the retention of leaf moisture content and several indices of drought tolerance/susceptibility and may be considered as a reliable physiological indicator of drought tolerance in wheat.

The genetic control of root length and weight in bread wheat intercultivar substitutions and introgression lines in Chinese Spring (Synthetic 6x).

Root length and weight were studied in a set of intercultivar, single-chromosome, substitution lines of Chinese Spring (Synthetic 6x) (CS/Syn), where the donor of separate chromosome pairs was a synthetic hexaploid AABBDD (*Triticum dicoccoides*/*Aegilops tauschii*). These parameters were studied under normal and restricted water supply. We found that 1A substitution resulted in a substantial reduction of root size in plant. Substitution of chromosome 5D, on the contrary, led to a significant increase compared to the recipient and donor. For the next stage, a set of genotyped introgression recombinant lines CS (Syn 5D) was studied under the same conditions. The lines were studied after 30-days of vernalization, because the donor of chromosome 5D, synthetic 6x, has a winter growth habit. The greatest root weight and length as well as a number of days-to-flowering comparable to the 5D substitution line was detected in the introgression lines 5D-5, 5D-6, and 5D-10. These lines have a common introgression fragment in the long arm of chromosome 5D containing the gene *Vrn-D1*. The lines were additionally studied after 45- and 60-days of vernalization in order to associate vernalization requirements with root size. We found that, in both cases, these three lines had the most developed root system. Generally, drought depressed root development in all lines, but the greatest root weight and length were detected in the 5D chromosome substitution line and introgression lines 5D-5, 5D-6, and 5D-10. The data obtained may prove the existence of the locus responsible for root traits in this region of 5D chromosome.

Genome-wide association mapping reveals new aluminium-tolerance loci in bread wheat.

Aluminium (Al) stress in acid soils presents a major impediment for plant growth that eventually results in substantial yield loss. By and large, hexaploid wheats are moderately tolerant, and breeding new Al-tolerant cultivars depends explicitly on the discovery of novel loci or genes. Genome-wide association mapping was carried out utilizing a panel of 96 winter wheat accessions. Marker alleles occurring at low frequencies ($f < 0.05$) and markers with 20% missing data were excluded from the analysis. Aluminum tolerance was assessed using hematoxylin staining with root regrowth as the tolerance parameter. Marker-trait associations were identified by both mixed linear and general linear models based on the average phenotypic value over four experiments.

This study identified five MTAs that are highly significant ($p < 0.001$) or significant ($p < 0.01$) by both models on chromosomes 1AL, 1DL, 3BL, and 6AS. All five loci represent independent loci and are not in LD with each other. Except for the MTA on 1AL, all other mixed linear MTAs were confirmed by tje general linear model. Allelic effects ranged from ±0.22 to ±0.31. The MTA on chromosome 3B showed the highest allelic effect of all the MTAs. The MTA on chromosome 1D was allocated to the bin 1DL2-0.41-1.00 where pertinent Al-tolerance gene candidate, *wali5*, was previously identified. The novel loci identified on chromosomes 1D and 3B are strong candidates for future research, with the potential for developing tolerant wheat genotypes.

Seed longevity in Russian spring wheat.

An artificial-ageing method (AA) was applied in studies on seed longevity testing. This method implies processing plant seed with high temperature at 100% relative humidity for 72 hours. For bread wheat, the temperature is usually 42°C. Seed of some cultivars are not sensitive to the 42°C-AA test and require higher temperatures to achieve ageing, including Russian, spring wheat cultivars Saratovskaya 29 (S29) and Novosibirskaya 67 (N67). As shown earlier, seed of S29 and N67 require a 48°C-AA test to get at least one-fifth of the seed to lose their viability. However, the stable response to the adjusted AA-test conditions is observed on seeds harvested more than one year ago. Recently harvested seed can be much more sensitive to the AA test. For S29, one-fifth of the seed looses viability at 48°C (12- and 18-month-old seed), 46°C (3-month-old seed), or 44°C (2-month-old seed). Thus, the AA test on young wheat seed is not recommended. Furthermore, comparison studies using the AA test can be recommended only for seed of plants grown simultaneously under the same conditions. In our studies, seed of S29 were two-times more sensitive to the 48°C test if the experiment was performed on material grown in the field (in conditions of an extremely rainy summer), compared to those grown in the greenhouse. Following these recommendations, we applied a 48°C-AA test to 18-month-old seed of NILs of S29 harvested from plants grown simultaneously in the greenhouse. A significant difference was observed between S29 and the NILs differing from S29 by the *Pp* genes (purple pericarp), suggesting a relationship between the accumulation of anthocyanin pigments in pericarp and seed longevity.

The ecology and genetic mapping of QTL controlling economically valuable traits in hexaploid spring wheat grown in environmentally different regions of the Russian Federation.

For the first time, a set of 110 RILs of the spring wheat ITMI mapping population was evaluated in different eco-geographical regions of the Russian Federation. Thirty-nine economically important traits that manifest themselves at different stages of growth were examined in each eco-geographical locality under study for five years. A total of 186 QTL with LOD scores above 2.5 were identified out of which 97 reached LOD scores > 3.0. The QTL for traits studied mapped onall 21 chromosomes and manifested themselves under contrasting environmental conditions with varying degrees of reliability. The manifestation of the identified QTL has been shown to depend on the environment, but they interact and correlate with each other. The main loci controlled by the same QTL change depending on particular ecological-geographic environment. The complexity of environmental factors is assumed to determine the characters of co-adapted gene blocks formed during the evolution of each plant species, as well as the specific ones of the wheat genetic co-adaptation system. The identified QTL may be of interest for further experiments on the genetic control of the corresponding agriculturally valuable traits and for marker-assisted selection in wheat breeding.

Additionaly, QTL were revealed by growing the ITMI mapping population in the arid steppes of the Middle Volga region during three years. These QTL mainly determined the duration of the growing season, plant height, spike length, number of spikelets/spike, number of seeds/spike, and 1,000-kernel weight. A QTL with pleiotropic effects, which is localized on the distal end of the long arm of chromosome 2D, determines the wax bloom on the stem, spike, and flag leaf. A QTL for resistance to leaf rust was located at the distal end of the short arm of chromosome 3D, and probably is allelic to *Lr27*. On the short arm of chromosome 7D, a QTL associated with resistance to powdery mildew was detected, presumably *Pm38*.

Evaluation of bread wheat accessions for agronomic traits under Iranian conditions.

We evaluated a large number of bread wheat accessions, mainly from southwestern Asia, including Iran, Afghanistan, India, Turkey, Pakistan, and Iraq. About 60 accessions belong to bread wheat cultivars from the European countries. Our aim was to generate pure-line plant material suitable for eco-TILLING and association mapping. The seed for these genotypes mainly were received from the IPK–Gatersleben Genebank, Germany. The experiment was based on an augmented design in which three Iranian bread wheat cultivars were used as controls with replication in order to check the homogeneity of the experimental conditions. Traits such as days-to-flowering, plant height, peduncle length, spike length, awn length, glum color, seed length, seed weight, flag leaf length, and 1,000-kernel weight were recorded. In the first year, one single plant from each genotype was selected to develop a pure line form each genotype. Currently, the data recorded at the field experiments are being analyzed, which will help to classify the genotypes based on morphological traits. This experiment also continues this year as the third replication. These genotypes can be evaluated under different biotic and abiotic stress condition in Iran. The next step is the generation of genotyping data.

Publications.

Chesnokov YV, Pochepnya NV, Kozlenko LV, Sitnikov MN, Mitrofanova OP, Syukov VV, Kochetkov DV, Lohwasser U, and Börner A. 2013. Mapping of QTLs determining the expression of agronomically and economically valuable features in spring wheat (*Triticum aestivum* L.) grown in environmentally different Russian regions. Rus J Genet Appl Res 3:209-221.

Chesnokov YV, Sitnikov MN, Schumlyanskaya NV, Kocherina NV, Goncharova EA, Kozlenko LV, Syukov VV, Kochetkov DV, Lohwasser U, and Börner A. 2013. Recombinant inbred lines of ITMI mapping population of soft spring wheat *Triticum aestivum* L. (ecology-geographic trials and QTL mapping). Catalogue of VIR World Collection: Issue 813, Vavilov Inst Res, St. Petersburg, Russia. 68 pp (in Russian).

Haile J, Hammer K, Badebo A, Nachit MM, and Röder MS. 2013. Genetic diversity assessment of Ethiopian tetraploid wheat landraces and improved durum wheat varieties using microsatellites and markers linked with stem rust resistance. Gen Res Crop Evol 60:513-527.

Haile JK, Hammer K, Badebo A, Singh RP, and Röder MS. 2013. Haplotype analysis of molecular markers linked to stem rust resistance genes in Ethiopian improved durum wheat varieties and tetraploid wheat landraces. Gen Res Crop Evol 60:853-864.

Haile JK, and Röder MS. 2013. Status of genetic research for resistance to Ug99 race of *Puccinia graminis* f. sp. *tritici*: A review of current research and implications. Afr J Agric Res 8:6670-6680.

Keilwagen J, Kilian B, Özkan H, Babben S, Perovic D, Mayer KFX, Walther A, Poskar CH, Ordon F, Eversole K, Börner A, Ganal M, Knüpffer H, Graner A, and Friedel S. 2014. Separating the wheat from the chaff – a strategy to utilize plant genetic resources from *ex situ* genebanks. Sci Rep (in press).

Kocheva K, Nenova V, Karceva T, Petrov P, Georgiev GI, Börner A, and Landjeva S. 2014. Changes in water status, membrane stability and antioxidant capacity of wheat seedlings carrying different *Rht-B1* dwarfing alleles under drought stress. J Agron Crop Sci 200:83-91.

Kollers S, Rodemann B, Ling J, Korzun V, Ebmeyer E, Argillier O, Hinze M, Plieske J, Kulosa D, Ganal MW, and Röder MS. 2013. Whole genome association mapping of Fusarium head blight resistance in European winter wheat (*Triticum aestivum* L.). Plos One 8:e57500.

Kollers S, Rodemann B, Ling J, Korzun V, Ebmeyer E, Argillier O, Hinze M, Plieske J, Kulosa D, Ganal MW, and Röder MS. 2013. Genetic Architecture of resistance to Septoria tritici blotch (*Mycosphaerella graminicola*) in European winter wheat. Mol Breed 32:411-423.

Kollers S, Rodemann B, Ling J, Korzun V, Ebmeyer E, Argillier O, Hinze M, Plieske J, Kulosa D, Ganal MW, and Röder MS. 2014. Genome wide association mapping of tan spot resistance (*Pyrenophora tritici-repentis*) in European winter wheat. Mol Breed 34 (2):363-371.

Kruppa K, Sepsi A, Szakács E, Röder MS, and Molnár-Láng M. 2013. Characterization of a 5HS-7DS·7DL wheat-barley translocation line and physical mapping of the 7D chromosome using SSR markers. J Appl Genetics 54:251-258.

Leonova IN, Badaeva ED, Orlovskaya OA, Röder MS, Khotyleva LV, Salina EA, and Shumny VK. 2013. Comparative characteristics of *Triticum aestivum*/*Triticum durum* and *Triticum aestivum*/*Triticum dicoccum* hybrid lines by genomic composition and resistance to fungal diseases under different environmental conditions. Rus J Genet 49:1112-1118.

Lohwasser U, Rehman Arif MA, and Börner A. 2013. Discovery of loci determining pre-harvest sprouting and dormancy in wheat and barley applying segregation and association mapping approaches. Biol Plant 57:663-674.

Nagel M, Behrens AK, and Börner A. 2013. Effects of *Rht* dwarfing alleles on wheat seed vigour after controlled deterioration. Crop Pasture Sci 64:857-864.

Nagel M, Navakode S, Nachit MM, Baum M, Röder MS, and Börner A. 2013. Durum in a changing climate – drought stress during growing seasons in Syria. Tagungsband der 63. Jahrestagung der Vereinigung der Pflanzenzüchter und Saatgutkaufleute Österreichs, Raumberg-Gumpenstein, Austria. Pp. 83-85.

Nagel M, Navakode S, Scheibal V, Baum M, Nachit M, Röder MS, and Börner A. 2014. The genetic basis in durum wheat of germination and seedling growth under osmotic stress. Biol Plant (in press).

Navakode S, Neumann K, Kobiljski B, Lohwasser U, and Börner A. 2014. Genome wide association mapping to identify aluminium tolerance loci in bread wheat. Euphytica (in press).

Osipova SV, Permyakov AV, Permyakova MD, Pshenichnikova TA, Genaev MA, and Börner A. 2013. The antioxidant enzymes activity in leaves of inter-varietal substitution lines of wheat (*Triticum aestivum* L.) with different tolerance to soil water deficit. Acta Physiol Plant 35:2455-2465.

Timonova EM, Leonova IN, Röder MS, and Salina EA. 2013. Marker-assisted development and characterization of a set of *Triticum aestivum* lines carrying different introgressions from the *T. timopheevii* genome. Mol Breed 31:123-136.

Tocho E, Börner A, Lohwasser U, and Castro A. 2013. Mapping and candidate gene identification of loci determining tolerance to greenbug (*Schizaphis graminum* Rondani) in barley. Euphytica 191:173-182.

Tocho E, Lohwasser U, Börner A, and Castro A. 2014. Mapping and candidate gene identification of loci induced by phytohormones in barley (*Hordeum vulgare* L.). Euphytica 195:397-407.