Inoculant promotes wheat yield increase.

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Azospirillum brasiliense is a facultative, endophytic bacteria capable of fixing nitrogen from the atmosphere, providing part of the N required to the associated plant. The bacteria also may induce plant hormones, which stimulate the growth of plant roots, improves water and nutrient absorption, and increases chlorophyll content of the leaves and tolerance to stress, especially that caused by drought. Field experiments at Fepagro Nordeste, Vacaria, with five wheat cultivars from the state of Rio Grande do Sul, Brazil, evaluated the effect of *A. brasiliense* inoculant on wheat yield. Wheat seed inoculated with *A. brasiliense* increased grain yield from 165 to 555 kg/ha (3–15%). Considering the statistical analysis, in 67% of the experiments, the grain yield average from the inoculated treatments were higher than that from the non-inoculated treatments (Tukey Test, $p \leq 0.05$). This technology may reduce the economic and environmental costs related to the production, transport, and use of nitrogen fertilizers for the wheat crop. As a follow-up step ro these studies, a core collection of genotypes from the active germ plasm bank of Embrapa Trigo are under testing to observe the response to inoculation with *A. brasiliense*.

ITEMS FROM GERMANY

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Haplotype analysis of molecular markers linked to stem rust resistance genes in Ethiopian durum wheat cultivars and landraces.

Wheat is one of the most important cereals cultivated in Ethiopia. In the country, more than 70 bread and 30 durum wheat cultivars have been released for production since the 1940s. However, the national average yield of wheat is still about 1.4 tons/ha. Even though over 30 fungal diseases of wheat have been identified in Ethiopia, stem rust, caused by *Puccinia graminis* Pers. f. sp. *tritici* (Pgt), is a major production constraint in most wheat-growing areas and causes up to 100% yield losses in epidemic outbreaks. The recent emergence of wheat stem rust race Ug99 (TTKSK) and related strains threaten Ethiopian as well as world wheat production because they overcome widely used resistance genes that had been effective for many years. The major cause that aggrivates the ineffectiveness of Ethiopian wheat cultivars against stem rust is the narrow genetic base on which breeding for resistance has been founded, however, little is known about the resistance genotypes of Ethiopian tetraploid wheat cultivars and landraces.

Our objective was to identify the stem rust resistance genes that are present in the Ethiopian tetraploid wheat cultivars and landraces using molecular markers and assess which genes are effective for current Ethiopian stem rust races of Pgt including Ug99. A total of 58 tetraploid wheat accessions consisting of 22 Ethiopian cultivars released during from 1966–2009, four ICARDA cultivars, and 27 landraces were genotyped using 17 molecular markers (SSR, EST, and InDel) linked or diagnostic for stem rust resistance genes *Sr2*, *Sr13*, *Sr22*, and *Sr35*. Haplotype analysis indicated that many of the Ethiopian durum wheat cultivars carried *Sr13*. The resistant cultivar Sebatel showed a haplotype for *Sr2* and *Sr22* and cultivar Boohai for *Sr22*. However, further evaluation for the diagnostic value of these haplotypes is needed. This study is the first report on the presence of stem rust resistance genes in Ethiopian durum wheat cultivars and tetraploid landraces based on linked or associated molecular markers and may help to identify cultivars carrying resistant

alleles, which will provide valuable genetic material for the development of new, improved cultivars in further breeding programs.

Rht genes – agronomic comparison under the climate of Southeastern Europe.

Sets of *Rht* NILs in four genetic backgrounds (April Bearded, Bersée, Maris Huntsman, and Maris Widgeon) were grown in a 4-year field experiment in Sofia, Bulgaria (42o41′N, 23o19′E). Plant height and yield components were genetically variable due to both cultivar background and *Rht* genic effects and were significantly influenced by the growing season, accounting for the climatic fluctuations. Averaged over all cultivars and years, plant height reductions relative to the tall control (*Rht-B1a*+-*D1a*) were in the order *Rht-B1b* ≈ *Rht-D1b* < *Rht-B1b*+-*D1b* < *Rht-B1c* < *Rht-B1c*+-*D1b* and amounted to 22, 53, 58, and 68%, respectively. Tillering was consistently greater in the *Rht-B1c* isolines, and the two double dwarfs. Although the spike was longer only in *Rht-D1b* and *Rht-B1b*+-*D1b* isolines, all alleles increased the spikelet number/spike up to 5%. *Rht-B1b* and *Rht-D1b* increased grain number/spike by 16% and 20%, respectively, and significantly reduced the grain mass per plant by 10% and 20%, respectively. *Rht-B1c*, *Rht-B1b*+-*D1b*, and *Rht-B1c*+-*D1b* reduced considerably both the grain number and grain mass per spike and per plant. All *Rht* alleles reduced the 50-grain mass within the range from 12% (*Rht-B1b*) to 20% (*Rht-B1c*).

Linkage between the red coleoptile (Rc-1) and purple pericarp (Pp-1) color genes.

We scored coleoptile color in durum wheat of F_3 families of the cross 'TRI 15744/TRI 2719' used previously for mapping *Pp-B1*. Among 113 F_3 families from this cross, 26 were homozygous red, 59 heterozygous, and 28 homozygous white, consistent with a monogenic 1:2:1 segregation ($\chi^2 = 0.292$, $P > 0.80$). The genetic distance between *Rc-B1* and *Pp-B1* was 7.6 cM (*Rc* proximal to *Pp*).

In bread wheat, an allelism test showed that the *Rc* genes determining dark-red coleoptile color in the Purple Feed and Purple lines are allelic to the *Rc-D1* gene of Novosibirskaya 67. In a 'Saratovskaya 29/Purple' cross, we distinguished F_3 families having plants with dark-red coleoptiles (97 F_3 families) from those having light red (from Saratovskaya 29) or noncolored coleoptiles (30 F_3 families), consistent with a monogenic 3:1 segregation ($\chi^2 = 0.129$; $P > 0.70$). The genetic distance between *Rc-D1* and *Pp-D1* was 2.5 cM (Rc proximal to Pp).

Thus, bread wheat did not inherit purple glumes from durum wheat as was thought earlier, but obtained only one of the two complementary *Pp* genes from durum wheat. The other gene came to bread wheat with the D genome of *Ae. tauschii*. Close linkage between *Rc-1* and *Pp-1* and similar function (regulation of anthocyanin biosynthesis) suggest that they are likely duplicated from a single locus.

Susceptibility to wheat midge infestation.

A panel of 96 winter wheat accessions originating from 21 countries were investigated in 2011 with the aim of finding genotypes resistant to the orange (*Sitodiplosis mosellana* (Géhin)) and yellow (*Contarinia tritici* (Kirby)) wheat midges. The accessions were highly variable in their phenotype with respect to growth pattern and coloration. In addition, there was variation for ear morphology and hairiness of different organs. We evaluated three flowering times, early, intermediate, and late.

Wheat midges were surveyed using pheromone traps, white water traps, and evaluation of insects in the spike samples. The pheromone traps were activated at BBCH 45 at a distance of 15 m in the experimental plots and took off at BBCH 75. The flight activity of the orange wheat midge was investigated weekly (nine times) by counting the orange midge males on the adhesive surfaces. To evaluate the larval infestation of wheat ears, six samples/plot were collected at three periods (flowering, milky, and late milky stages).

The results from the pheromone traps at the Gatersleben site showed a good activity of males of orange wheat midge; the maximum record was 59/trap/week. There was a weak coincidence between the main flight period of wheat midge and the optimum wheat stage of winter wheat for laying eggs (BBCH 47-60), because the weather conditions in 2011 were not suitable for wheat midge development. The results from the white traps were subjected to a genetic as-

sociation mapping study and analyzed with the STRUCTURE and TASSEL programs. Highly significant marker–trait associations for both wheat midge species were detected on different chromosomes.

Seed longevity and dormancy.

A total of 183 wheat accessions maintained in the cold store of the germ plasm repository at IPK–Gatersleben since 1974 were tested for viability in 2008. The mean germination in 1978 for this collection was 87%, which dropped to 56% after 34 years of storage. Seeds investigated in 2010 after regeneration exhibited a mean germination of 86%. Longevity of the 2010 seed was studied using artificial ageing (AA) and controlled deterioration (CD) tests. AA reduced the mean germination of the seed to 66%. Relative germination after AA was 77%. The mean germination after controlled deterioration was 59%, whereas relative germination after CD was 68%. The 2010 seed also were investigated for dormancy and preharvest sprouting (PHS). Mean percentages of dormant seed at 10°C and 20°C were 12% and 76%, respectively. Dormancy index reached a mean value of 33. Preharvest sprouting showed the opposite trend in relation to dormancy. The mean score for PHS was 4.0.

Association mapping analyses revealed 14 marker trait associations (MTA) for germination after long-term cold storage on chromosomes 1DC, 2AS, 2BL, 3AL, 4AL, 5BL, 6BS, and 7D. There were 14 MTAs recorded after AA of 2010 seed on chromosomes 1AS, 1BL, 2BS, 4BS, 5BS, 5BL, 6AC, 6BS, 7AS, 7BS, and 7D. Similarly, CD revealed 18 MTA for longevity on chromosomes 2AL, 2BS, 3BS, 4AL, 4B, 5B, 6BL, and 7BL. For dormancy and PHS, 23 and 30 MTA, respectively, were recorded. The MTA for dormancy were located on chromosomes 1DS, 2AS, 2BL, 2D, 3AL, 3BC, 3BL, 4AL, 4BL, 5AS, 5BS, 5BL, 6BL, and 7BL, whereas for PHS, they were located on chromosomes 1AS, 1BL, 1DL, 2BL, 3AL, 3BS, 3BC, 3BL, 4AL, 5AS, 5BL, 6AS, 6BS, 6BL, 7BC, and 7BL.

Genetic analysis of hybrid dwarfness aroused in crosses of common wheat with rye.

A set of 101 rye inbred lines originating from the Peterhof rye genetic stock collection of the Laboratory of Plant Genetics (St. Petersburg State University, Russian Federation) and selected from the rye cultivars Vyatka, Steel, Heine, Petkus, and Volkhova, was used to pollinate bread wheat cultivar Chinese Spring. Two unrelated self-fertile lines, V1 and V10, gave rise wheat–rye hybrids with a dwarf phenotype. The development of the dwarf, wheat–rye plants stopped at the stage of three leaves and the plantlets died at 6 weeks. For genetic analysis of the hybrid dwarfness, interline F_1 rye hybrids between lines L4 and L7 and V1 and V10 were produced. Interline hybrids F_1 (V1/L4), F_1 (L4/V1), and F_1 (L7/V1) were used as pollinators for crosses with Chinese Spring and Priekulskaya 421 wheat. For all cross combinations under investigation, a 1:1 segregation for the presence of normal vs. dwarf plants in the wheat–rye hybrids was obtained, as expected, with a total ratio of 212:196. Therefore, we concluded that hybrid dwarfness in wheat–rye crosses is determined in rye by one gene having two alleles. Rye lines V1 and V10 carry the allele preventing the development of hybrid plants in the seedling stage. This gene was named *Hdw* (Hybrid dwarfism). Because we cannot yet determine whether the allele for hybrid dwarfism is dominant or recessive, we designate the allele determining the production of wheat–rye hybrids with normal development (normal or wild-type) *Hdw-R1a* and allele determining dwarfism as *Hdw-R1b*.

Overcoming embryo lethality in wheat–rye hybrids.

Embryo lethality in crosses of common wheat with rye could be the result of complement interaction between the incompatible *Eml-R1b* rye allele and the *Eml-A1* gene in wheat. This kind of postzygotic barrier cannot be overcome by *in vitro* embryo rescue. Analysis of hybrid embryos revealed morphological differences at the age of 16 days after pollination (DAP). We found that the interaction of wheat and rye incompatible alleles arrests the formation of the shoot meristem but had no influence on root meristem formation. A method for overcoming such a hybrid embryo lethality was developed. The percent of embryos that produce embryogenic callus compose 73.3–100.0% for 14 DAP embryos and 92.3–100.0% for 16 DAP embryos. The numbers of green adventive buds with leaf primordial at one embryogenic callus were 5.2–8.0/callus and 3.2–5.9/callus for embryos at ages 16 DAP and 14 DAP, respectively. The number of regenerative plants per embryogenic callus were 2.8–5.4 and 2.3–4.9 for 16 DAP and 14 DAP embryos, respectively. A more complex parameter is the total number regenerative events per embryogenic callus, which was 9.7–12.0/callus for 16 DAP and 6.3–10.6/callus for 14 DAP embryos. Thus, our experiments showed that embryo lethality caused by complement interaction of incompatible wheat and rye alleles could be successfully overcome via somatic embryogenesis.

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