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Pukhalskiy VA, Bilinskaya EN, Martynov SP, Dobrotvorskaya TV, and Obolenkova GA. 2008. New data on the distribution of hybrid necrosis genes in winter bread wheat (*Triticum aestivum* L.) cultivars. *Rus J Genet* 44:171-179.

ITEMS FROM SPAIN

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Ascorbate peroxidase induction in wheat lines infected by Heterodera avenae.

The cereal cyst nematode (CCN) (*Heterodera avenae* Woll.) is the most widely distributed and damaging species on cereals cultivated in less temperate regions. This nematode species has been detected in many countries and it is responsible for yield losses in wheat of up to 30%. The CCN induces syncytial feeding sites in the roots of its hosts. Infective, second-stage juveniles (J2) enter the plant roots at the level of the differentiation zone and penetrate intracellularly towards the vascular cylinder. Here, they select and pierce with their stylet a single cell where they release oesophageal secretions. In the following hours, the affected plant cells start to develop the feeding structures (Das et al. 2008). Plants defend themselves from nematodes using a variety of mechanisms, including rapid induction of localized necrosis at the site of infection (the hypersensitive response: HR), increased expression of defense-related proteins, production of antimicrobial compounds, lignin formation, and oxidative burst. Among the altered biochemical pathways are those involving peroxidases, which comprise a large group of enzymes that use different peroxides (ROOH) as electron acceptors. According to Welinder (1992) these enzymes in plants are classified into three classes (I, II, and III). Class-I enzymes are intracellular and are known as ascorbate peroxidase (APX, EC 1.11.1.11). Reactions catalyzed by APX and the cycle-coupled of AsA-GSH prevent the accumulation of toxic levels of H₂O₂ in photosynthetic organisms. APX activities are located in chloroplasts (chAPX), cytosol (cAPX), peroxisomes, or microbodies (pAPX) and mitochondria, each cellular compartment possessing one or several APX isoforms. In *Arabidopsis*, the same protein is dually targeted to mitochondria and chloroplast stroma (Chew et al. 2003).

Changes in APX enzyme activity in response to nematode *H. avenae* attack were studied in roots of three hexaploid wheat lines carrying *Cre2*, *Cre5*, and *Cre7* resistance genes and the susceptible *T. aestivum* cultivar Anza. Spectrophotometric analysis to study these changes was carried out with root extracts of infected and uninfected plants 4, 7, 11, and 14 days after nematode infection. APX induction in all infected resistant genotypes was higher than in the susceptible control. We analyzed whether this increase of activity was related to an increase of APX gene expression. This study was performed with the introgression wheat-*Ae. ventricosa* H-93-8 line, carrying *Cre2* gene, using its parental H-10-15 as susceptible control. APX genes of cytosolic location were induced in roots of plants attacked by the nematode. This induction took place earlier and with more intensity in the resistant line than in the susceptible one, and it was bigger in the root area where the nematode was settled down. Our results suggest that APX present in wheat roots could play a role in *Cre*-mediated resistance to *H. avenae*, either directly or indirectly. They also demonstrated that the biochemi-

cal basis of defence in hexaploid wheat against the Ha71 pathotype of *H. avenae* could be the same in all the genotypes tested.

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CONSEJERÍA DE INFRAESTRUCTURAS Y DESARROLLO TECNOLÓGICO SIDT (SERVICIO DE INVESTIGACIÓN Y DESARROLLO TECNOLÓGICO)

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New Hessian fly resistant lines releases.

Hessian fly (Hf) is a significant insect pest of wheat in many of the wheat-producing areas around the world. Since its detection in Spain in 1896, it has become a major economic pest of common wheat. At this moment, deployment of resistant cultivars is providing the most efficient and economical means of crop protection against this damaging insect (Berzonsky et al. 2003). The continuous evolution of virulent biotypes makes necessary the identification of new resistance genes from wheat or relative species. The will grass genus *Aegilops* has been recognized as an important potential donor of genes that govern characteristics of agronomic interest, such as resistance genes (Schneider et al. 2008, review). Previous work from our group has demonstrated the transference of *H30* gene, conferring resistance to *Mayetiola destructor*, from *Ae. triuncialis* to hexaploid wheat *T. aestivum* (Martín-Sánchez et al. 2003). Breeding lines (2n=42) were obtained by backcrossing introgression line TR-3531 (with 42 chromosomes) as donor parent of Hf resistance, and hexaploid wheat cultivars carrying good agronomic characteristic as alternative recurrent parent. The *AcpH-U1* marker linked to gene *H30* on this line was used for MAS. Advanced wheat lines were evaluated for Hessian fly resistance (described in Delibes et al 1997) in field and growth chamber tests, and for other agronomic traits during several crop seasons at different localities of Spain. Hessian fly resistance level of lines was high but, in all cases, it was lower than its progenitor *Ae. triuncialis*. In collaboration with Agros Semillas Selectas SA, we have obtained several wheat lines with good performance for resistance and/or agronomic characteristics. Two of them were recently submitted to the Spanish Plant Variety Office for their evaluation. T-2004 (TR-3531/Betrés//Alcotán/3/Recital/4/3*Betrés) and ID-2105 (TR-3531/Be-

trés//Alcotán/3/Recital/4/5*Betrés) are two-awned and facultative wheat lines, which present tolerance to the population of Hessian fly present in southwestern Spain. These lines are medium-maturing, medium tall, with thin stems, and have dark green foliage at anthesis, with medium-strong glaucosity of sheath and spike.

Cooperation with other institutions. We are cooperating with 'Agrosa Semillas Selectas SA'.

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ITEMS FROM UNITED KINGDOM

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Genetic biodiversity for stripe and stem rust resistance in African wheat genotypes.

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Over 500 African wheat genotypes have now been screened for resistance to the new virulent stem rust, *Puccinia graminis* Ug99-derived strains, and to stripe rust, *P. striiformis*, at Njoro, Kenya. Some 300 genotypes have been selected for genetic diversity and association analyses using SSR and DArT markers. This program is a collaboration between Dr. Lesley A. Boyd at the JIC, Norwich, UK; Prof. Zakkie Pretorius and Dr. Renée Prins of the University of the Free State, Bloemfontein, RSA; Dr. Ruth Wanyera and Davinder Singh, KARI, Njoro, Kenya; and Dr. Susanna Dreisigacker, CIMMYT, Mexico. This work is supported by UK, BBSRC/DfID funding under the Sustainable Agriculture Research for International Development (SARID) initiative.