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R.S. Zwart, H. Muylle, E. Van Bockstaele, J. Van Huylenbroeck, I. Roldán-Ruiz
Institute for Agricultural and Fisheries Research (ILVO), Unit Plant
Applied Genetics and Breeding, Caritasstraat 21, 9090 Melle, Belgium

Introduction

Fusarium head blight (FHB) is a devastating disease of wheat in wheat-growing regions throughout the world. FHB causes significant quality losses, yield losses and accumulation of hazardous mycotoxins in the grain. The most effective strategy to control FHB is to breed wheat lines with resistance. Resistance to FHB is quantitative and major and minor QTLs for FHB resistance have been reported in nearly every chromosome of wheat in different genetic backgrounds (Bai and Shaner, 2004). Currently in breeding programs there is a heavy reliance on the well-characterised resistance of a Chinese spring wheat, Sumai 3. Although Sumai 3 offers stable type II resistance (resistance to spread), this wheat line is of exotic origin and has poor agronomic traits. New sources of resistance are necessary to improve the level of resistance to FHB in wheat and to achieve durable and stable resistance through gene pyramiding, as well as to diversify the genetic basis of FHB resistance in elite wheat (McCartney *et al.,* 2004). The genetic diversity of genes controlling FHB resistance in Asian wheat lines has recently been investigated to identify sources of resistance different to that of Sumai 3 (Yang *et al.,* 2006, Yu *et al.,* 2006). Combining wheat lines with moderate levels of FHB resistance can result in increased progeny performance (Somers *et al.,* 2003).

To aid the challenge of breeding FHB resistant wheat we are investigating the genetic diversity of resistance genes controlling FHB in European wheat germplasm. Estimates of the genetic relationships among European wheat lines will be useful for the selection of parents in European FHB breeding programs.

Materials and methods

FHB evaluations

Field trials were conducted to measure type I resistance (resistance to initial infection) and type II resistance (resistance to spread). Overall (combined type I and type II) resistance and type I resistance were assessed in artificial spray inoculation trials conducted over consecutive years (2004, 2005, 2006). All plots were inoculated with a mixed conidial suspension of *F. graminearum* and *F. culmorum*, three times at three day intervals commencing at the date of ear emergence for over 50% of the plots. Plots were rated 22 days from the date of ear emergence for % FHB severity (number of diseased spikelets) and % FHB incidence (number of heads showing symptoms). Grain was assessed post-harvest for % diseased kernels.

Type II resistance of the wheat lines were assessed in replicated point-inoculation trials. Field trials were conducted in 2006 at two locations with two replications at each location. Ten heads per plot were inoculated at anthesis by injecting 10µl of a 100,000 conidia/ml suspension into the fifth spikelet from the tip of the head. A split-plot design was used with main plots (wheat genotypes) consisting of two sub-plots (*Fusarium* isolate). Two highly aggressive *Fusarium* isolates were used: *F. graminearum* IFA 65 and *F. culmorum* IFA 104. Disease symptoms were evaluated on days 10, 14, 18, 22, and 26 after inoculation and an area under the disease progress curve (AUDPC) was calculated.

Molecular marker analysis

Three hundred and fifteen wheat lines were genotyped with SSR markers associated with putative QTLs for FHB resistance across the wheat genome and additional SSR markers to give an even distribution of at least 1 SSR marker/chromosome arm. SSR marker assays were performed using M13-tailing (Schuelke, 2000) and fluorescent capillary electrophoresis on an ABI3130 sequencer. Allele sizes were compared with the FHB resistant wheat lines for which the genomic location of FHB resistance are known to identify potential new sources of FHB resistance.

Results

FHB evaluations

Broad phenotypic variation for type I and type II FHB resistance was present among the germplasm analysed. Preliminary results show that there is a correlation ($r=0,55$, $P<0,01$) between the FHB rating (combined type I and II resistance) for wheat lines evaluated in 2004 and 2005 (Fig. 1). Results from the 2006 and point inoculation trials will be presented in the poster.

Cluster analysis

Cluster analysis will be used to evaluate the genetic differences in FHB resistant lines and identify wheat lines with potentially new sources of FHB resistance genes. Results of cluster analysis were not available to the time of submission of this paper, however, will be presented in the poster.

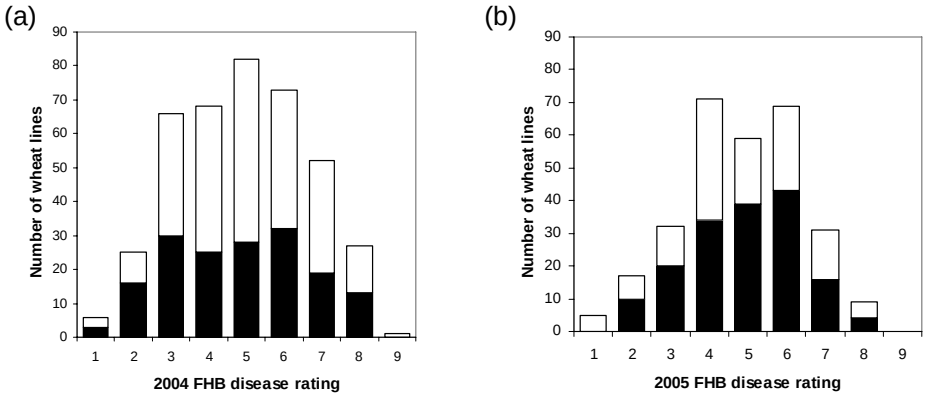

Fig. 1. Frequency histogram of FHB rating for (a) 400 wheat lines evaluated in 2004 and (b) 293 wheat lines evaluated in 2005. The 166 lines that were evaluated in both years are shown in black. FHB disease rating scale: 1 = resistant, 9 = susceptible.

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