Half sib selection for resistance to powdery mildew
(*Erysiphe graminis* DC. f.sp. *secalis* Marchal) in rye populations

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**Summary.** Three rye populations originating from different cultivars were subjected to half sib progeny selection for three cycles to improve their resistance to powdery mildew (*Erysiphe graminis* DC. f.sp. *secalis* Marchal). Selection was carried out in the greenhouse (measurement of spore production at the three-leaf stage), in the field (scoring of mildew infections at ear emergence) or at both locations. All selections resulted in significant responses, the level of which varied depending on the genetic base of mildew resistance in the populations. Greenhouse selection was most effective when the frequency of dominant genes could be increased, whereas field selection was less effective. Estimates for heritability in the narrow sense ranged from 0.42–0.94 indicating that mildew resistance can be increased effectively. Inbred lines should be selected in base populations with a high level of quantitative resistance and/or a high frequency of dominant genes. For an effective resistance strategy in hybrid breeding such dominant genes are most valuable, and can be selected in young growth stages. In 'Strain CG' the increase of dominant resistance genes by early selection resulted in a significant improvement of kernel yield.

**Key words:** *Secale cereale* L. – *Erysiphe graminis secalis* – Half sib selection – Heritability – Resistance breeding

**Introduction**

The study of rye (*Secale cereale* L.) populations revealed a great variability for resistance to powdery mildew (*Erysiphe graminis* DC. f.sp. *secalis* Marchal). Frequency distributions showed that the majority of plants have a quantitative level of resistance, but low reesistance occurs much more frequently than high resistance, which in many populations is completely absent (Lind and Wenzel 1984). Recurrent selection increased the proportion of resistant genotypes and thus the resistance level of populations (Lind and Züchner 1985). The selection experiments provided information about the genetic base of resistance and the method to be used for population improvement.

From population studies (Lind and Züchner 1985) it was concluded that mildew resistance is controlled by a few too many genes. Kast (1983) used inbred lines and identified monogenic as well as polygenic resistance. Information about the genetics of mildew resistance is of increasing importance in rye breeding, since hybrid cultivars are grown. The low genetic variability of these cultivar types, compared with the populations, demands preventive action against attack by different pathogens. Hybrids make it possible to establish planned breeding for disease resistance by using isolated genes.

In the present study, populations from different breeding programs selected for high kernel yield under German agricultural conditions are used to demonstrate the effect of different selection methods on mildew resistance and its influence on yield potential. Selection aims at the production of populations applicable as pools for dominant resistance genes that can be used for hybrid breeding.

**Materials and methods**

**Original populations**

The selection experiments were performed with rye populations from three genetic sources.

1) A population originating from 'Halo' × 'Danko' (provided by Dr. Wagner, Saatzucht Dr. h.c. R. Carsten oHG, FRG). The cross population was selected for high kernel yield...
without considering mildew resistance. Both parents are commercial cultivars. The first parent contributed a low level of quantitative resistance in the young growth stages but had a high level of adult plant resistance (Lind et al. 1986). The second parent was characterized by a high level of quantitative resistance in all growth stages and had dominant genes conditioning complete resistance.

(2) Population 'Strain CG' (provided by Saatzucht P. H. Petersen, FRG), a selection from the German cv 'Carogold'. It had a medium level of resistance in the very early growth stages but was less resistant than 'Halo' at the adult stage. It also carried a few dominant resistance genes.

(3) Population 'Strain CG' × 'Halo' combined the resistances of both parents described above.

Selection for resistance

Three different selection methods were applied.

(1) Selection in the greenhouse (early selection) after artificial inoculation with a mildew population propagated on the cv 'Halo'. For the inoculation of trays, each containing 100 plants, a spore settling tower was used in which 200 spores/cm² were applied on the leaves. Resistance was evaluated by spore production measurements of seedlings (Lind 1983) at the three-leaf stage which corresponds to stage 13 in the decimal code system for growth stages (Zadoks et al. 1974).

(2) Selection in the field at ear emergence (late selection) after natural inoculation, which was secured by the adjacent growth of highly susceptible genotypes. Resistance was determined on the two leaves below the flag leaf by the use of a scale from 1–9, in which 1 indicated complete resistance and 9 high susceptibility. The mean of both scores, which were taken at ear emergence (stage 55), was used for selection.

(3) Selection in two successive steps by the combination of early and late selection (combined selection) within the same population. Table 1 shows experiment surveys that were conducted with each population. Depending on the genetic base of mildew resistance, not all selection methods were used in each population. All populations that originated from a cross with 'Halo' were subjected to early or combined selection, as this cultivar lacked resistance at the young stages; whereas the 'Carogold' population was used in all selection methods.

Population improvement

Single plant and progeny selection were combined to produce populations with improved mildew resistance. As starting material, 3,000 kernels of the original populations, partitioned into two replications, were sown in the greenhouse for each of the five selection experiments (Table 1). They had to be sown once for 'Halo' × 'Danko' and 'Strain CG' × 'Halo' and three times for 'Strain CG'. At this first step, selection was based on single plants. In the case of early selection at the three-leaf stage, 12% of plants (360 genotypes) from these populations were transplanted to an isolated field plot. This portion included the majority of genotypes with the lowest spore production. If late selection was applied all the kernels were sown directly in the isolated field plot. As in separate early and late selection, low spore production and low mildew scores were used as selection criteria. In all five populations the plants were harvested individually.

### Table 1. Selection methods applied to different rye populations at the three-leaf stage and at ear emergence

<table>
<thead>
<tr>
<th>Populations</th>
<th>Selection experiment</th>
<th>Stage of selection</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>three leafs</td>
<td>ear emergence</td>
</tr>
<tr>
<td>Halo × Danko (original)</td>
<td>1</td>
<td>+</td>
</tr>
<tr>
<td>Halo × Danko</td>
<td>2</td>
<td>+</td>
</tr>
<tr>
<td>Strain CG (original)</td>
<td>3</td>
<td>+</td>
</tr>
<tr>
<td>Strain CG</td>
<td>4</td>
<td>+</td>
</tr>
<tr>
<td>Strain CG × Halo (original)</td>
<td>5</td>
<td>+</td>
</tr>
</tbody>
</table>

* *13, 55 = selection at the 3-leaf stage and at ear emergence, respectively*

In the two following selection steps the size of selected populations was kept constant (12% of 3,000 plants). Selection, however, was carried out on a family base, i.e. the most resistant plants from the families with the highest mean resistance were used to compose the next population. Finally, after the second step of family selection, the most resistant plants were bulked to form the final populations that were compared for their resistance and yield properties.

Comparison of populations

The yield comparisons between the original and final populations were performed in a randomized complete block design with four replications at four environments (Bad Schönborn, Niendorf, Grünbach 1986 and 1987). The trials were sown in 10 m² plots without fungicide treatment.

Comparison of resistance was performed with field and greenhouse data. The field data were obtained from the two Grünbach yield trials (two environments) and were used to determine adult plant resistance. For this purpose 100 plants per plot were scored for mildew attack. The greenhouse data were obtained from measurements of spore production at the three-leaf stage in two succeeding test sets, where the original and final populations were arranged in the same experimental design as in the yield comparison. Per greenhouse plot, 150 plants were measured. In all tests the cvs 'Halo' and 'Danko' were included. Comparisons of mildew resistance were performed by using: (a) the mean spore production and mean mildew score of whole populations; and (b) the 10% fraction of populations that include the most resistant genotypes. The observed selection response of populations was expressed as a percentage decrease of mildew scores and spore production in the final populations compared to the original populations. A t-test at the 0.05 level of significance was used to compare the population means.

The yield and the resistance data from populations were subjected to analyses of variance, where replications (R), environments or test sets respectively (S), families (F), interactions (SF) and error (E) were regarded as sources of variation. The error term was used for comparisons between population means based on least significant differences (Snedecor and Cochran 1973). In addition, the coefficients of variation (C.V.) averaged over replications and locations were calculated as $C.V. = \frac{\sigma}{x}$.