岡大資生研報 (Bull. Res. Inst. Bioresour. Okayama Univ.) 3 : 43-53 (1995)

Selection Effectiveness for the Resistance to Net Blotch in Barley

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Selection effectiveness for the resistance to net blotch was estimated by using two sets of F_2 and F_3 populations derived from the crosses between resistant and susceptible parents. In every F_2 and F_3 population, disease ratings showed a continuous distribution. As many F_3 lines with intermediate resistance had a smaller variance and homozygous genotype, the resistance might be controlled by a few genes. The heritabilities of the disease rating were estimated by correlation coefficients and regression coefficients between each F_2 plant and the descended F_3 lines. Another estimate for heritability was calculated by the selection differential in the F_2 plants and genetic gain in the F_3 lines. Despite the different level of resistance in the resistant parents of the two crosses, the three kinds of heritabilities estimated were similar and ranged from 0.6 to 0.8. Because of the fewer number of genes controlling the disease resistance and the higher heritabilities, selection in a early generation may be effective for net blotch resistance in barley.

Key words: Net blotch, *Pyrenophora teres*, Selection, Barley, Disease resistance

INTRODUCTION

Net blotch, caused by a fungus *Pyrenophora teres* Drechs., is a serious disease of barley developing a net-like symptom on barley leaf blade and leaf sheath. Net blotch occurs mainly in warm and humid barley growing areas in the world (Shipton *et al.* 1973). The increased incidence of net blotch has been reported. Especially, continuous cropping of barley or the field irrigation promote the epidemic (Mathre 1982).

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Received November 1, 1994

As the severity of net blotch is also related to the susceptibility of cultivars (Mathre 1982), intensive effort for the breeding of resistance has been made (Metcalfe and Bendelow 1981, Metcalfe 1986), including the selection of resistant composite cross populations (Bockelman *et al.* 1983, Moseman and Smith 1985).

Four major genes for the resistance have been identified in net blotch (Davis *et al.* 1990). However, three of these genes did not show high resistance to the Japanese isolates (Sato and Takeda 1993a). Steffenson and Webster (1992) also reported that some genes showed different resistant reaction by the inoculation of isolates with different pathogenicities. Thus, the host-pathogen interaction or the race differentiation has been suggested to be responsible for the occurrence of net blotch.

On the other hand, contribution of minor genic resistance to net blotch have been also reported (Douglas and Gordon 1985, Arrabi *et al.* 1990). As the minor genic resistance generally does not show obvious race specificity, minor genic resistance is very useful for the breeding of resistant cultivars. In this report, selection effectiveness for the resistance to net blotch was estimated by using two sets of F_2 and F_3 populations crossed between resistant and susceptible parents which showed continuous variation.

MATERIALS AND METHODS

1. *Isolate preparation*

P. teres isolates were cultured on V-8 medium (V-8 juice 200ml, $CaCO_3$ 3g, agar 15g, distilled water 800ml) in 9cm styrene plastic petri dishes under an alternating irradiation period of 12 hours black light (Toshiba Co., range of wave length : 300～400nm) and 12 hours darkness at diurnal temperature variation of 25±6℃ for 14 days. In this condition most of the isolates produce conidia abundantly (Sato and Takeda 1991). After addition of water, the colonies were collected with a brush and filtered through double layers of gauze to remove mycelia and conidiophores from the conidia suspension. The concentration of the suspension was adjusted to $5～10\times10^3$/ml.

2. *Barley material*

Two sets of F_2 and F_3 populations, Hokuiku 17×OUK667 and Hokuiku 17×OUK751 were tested. About 200 plants in each F_2 population and ten plants of their parents were inoculated with *P. teres* isolate K105, collected from Hokkaido, Japan. After evaluating disease rating, the plants were transplanted into the field and grown to maturity. The seeds in each plant

were harvested to make F_3 lines. In the next season, ten plants of each F_3 line and the parents were inoculated with K105 for evaluating the disease rating.

3. *Inoculation test*

Barley materials were planted in seedling boxes (50×35×10cm) with two check varieties (susceptible and moderately susceptible). The seedlings were grown in a glasshouse at 20℃ for 14 days. At the time of inoculation, seedlings were at the second leaf stage. After addition of a drop of Tween-20, the suspension was sprayed onto seedlings with a glass atomizer driven by an electric air pump. Inoculated plants were maintained in a dew chamber at 20℃ for 48 hours and grown for ten days in a glasshouse at 20℃. The second leaf of each plant was used to score a numerical disease rating, one (resistant) to ten (highly susceptible), as proposed by Tekauz (1985).

4. *Estimating genetic parameters*

Heritabilities of disease rating were estimated by correlation and regression between the F_2 plants and the means of the F_3 line. Another estimate for heritability was calculated by selection differentials of F_2 plant groups and genetic gains of F_3 line groups (Falconer 1960). As selection criteria, the numbers of disease ratings under five (Hokuiku17×OUK667) and two (Hokuiku17×OUK751) were used toward resistance, and those above nine in both crosses were used toward susceptible (Figs. 5 and 6).

RESULTS AND DISCUSSION

As shown in Fig. 1, the disease rating of each F_2 population showed a continuous distribution. In the Hokuiku 17×OUK667 cross, the distribution was shifted to the susceptible range. The mean disease ratings was 7.29 with a mode of 9.0. On the other hand, the population of Hokuiku 17×OUK751 showed a flat distribution and the mean was 5.35. Disease ratings of resistant parent were moderately low in OUK667 (3.7) and very low in OUK751 (1.3). The susceptible parent Hokuiku 17 showed a very high rating (10.0).

Fig. 2 shows the distribution of the disease ratings in the two sets of the F_3 lines, which were descended from each F_2 plant. The disease ratings of the parents (OUK667 : 3.3, OUK751 : 1.2 and Hokuiuku 17 : 8.5) were almost the same as those in the previous year. In the Hokuiku 17×OUK667 cross, the means of F_3 line showed a continuous distribution similar to that in the F_2 population, and the mean of F_3 lines (7.14) was almost the same as that

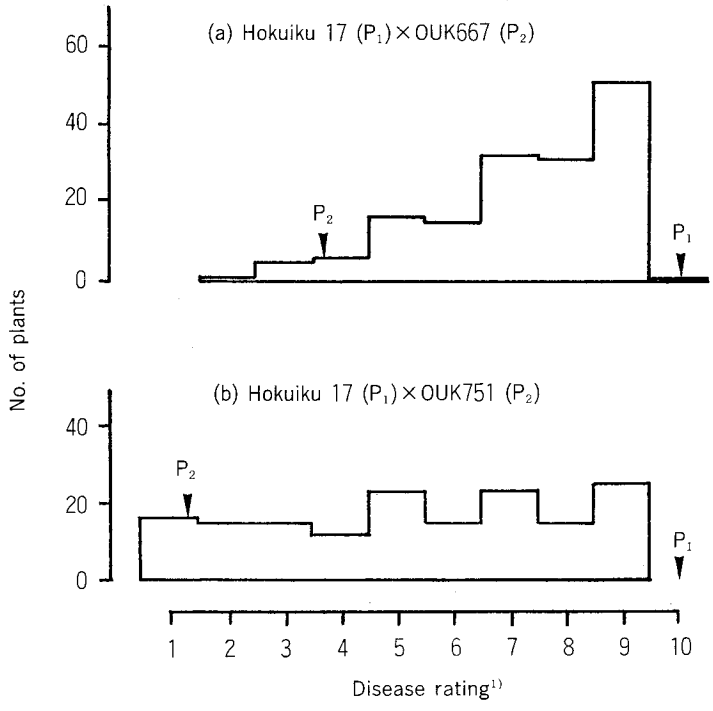

Fig. 1. Frequency distribution of disease ratings in two F_2 populations. The arrows indicate parental values.
1): From 1 (resistant) to 10 (highly susceptible) after Tekauz (1985).

in the F_2 population (7.29). In the Hokuiku 17×OUK751 cross, the mean of the F_3 line (3.66) showed a continuous distribution with a mode in the resistant range, and was obviously smaller (more resistant) than that in the F_2 population (5.35). The reason is not clear why the mean of the F_3 lines in the Hokuiku 17×OUK751 cross was lower than that in the F_2 population. One possibility is that the virulence of the isolate used to inoculate the F_3 lines in the Hokuiku 17×OUK751 cross was lower than that used in the other populations.

Fig. 3 shows the relationship between the mean and variance of disease ratings in the two sets of the F_3 lines. In both crosses, the lines with extremely high or low disease ratings showed a smaller variance within the line. These lines were considered to be homozygous for the resistant or susceptible gene(s). The lines in the middle range of ratings with larger variance might be segregating for the resistant genes. As the error variance within the variety (among plants) was from 0.5 to 1.0 (Sato and Takeda

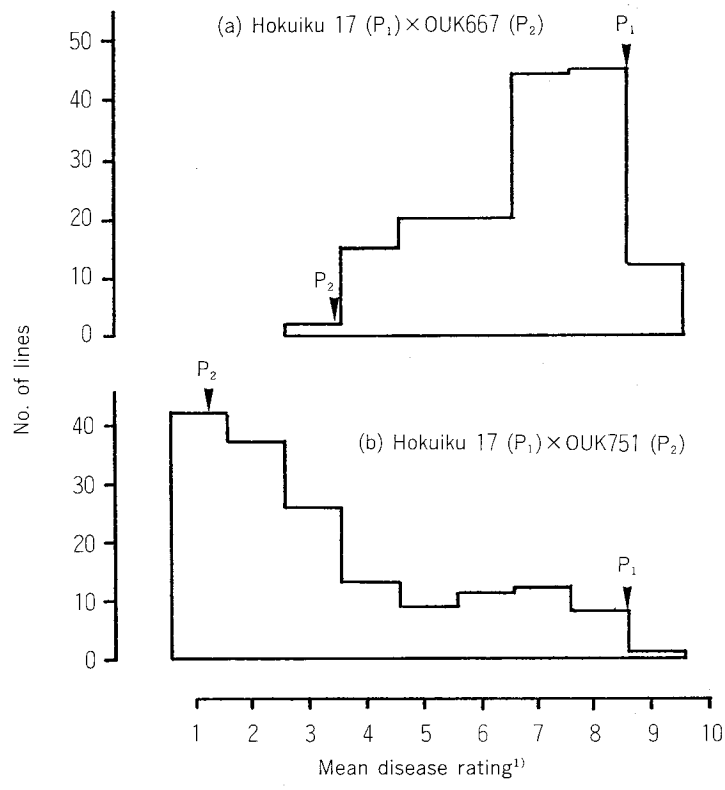

Fig. 2. Frequency distribution of mean disease ratings in two sets of F_3 lines. The arrows indicate parental values.
1): From 1 (resistant) to 10 (highly susceptible) after Tekauz (1985).

1992), the F_3 lines in the middle range of ratings with a lower variance (below 1.0) were considered to be homozygous. If many F_3 lines were already homozygous for the genes controlling disease resistance, the resistance might be controlled by a few genes.

The range of variance within the F_3 lines in the Hokuiku 17×OUK751 cross (0~9.3) was wider than that in the Hokuiku 17×OUK667 cross (0~3.0). This indicates that the resistance genes included in OUK751 were higher in number and/or had stronger effects than those in OUK667.

The heritabilities of disease rating, estimated by the correlation and regression between the F_2 plants and the means of the F_3 lines, were 0.767 and 0.645 in the Hokuiku 17×OUK667 cross, 0.783 and 0.674 in the Hokuiku 17×OUK751 cross, respectively (Fig. 4). Both coefficients were quite similar between the two sets of crosses. A few samples in Fig. 4 showed different disease ratings between the F_2 plants and the means of the F_3 line. As the

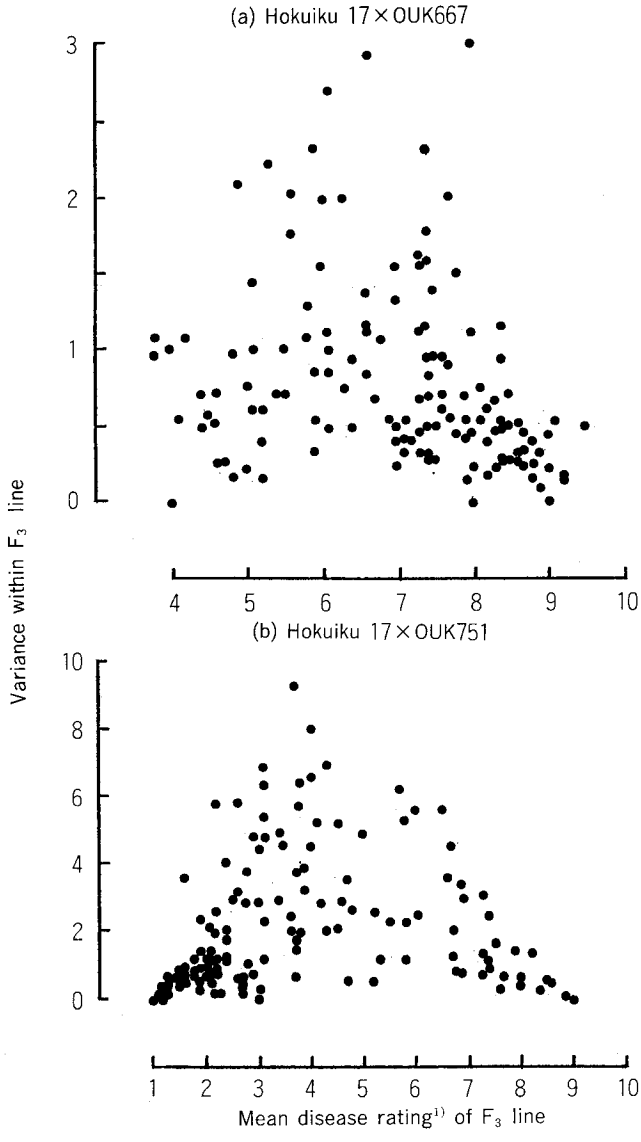

Fig. 3. Scatter diagram of mean and variance of disease ratings to isolate K105 in two sets of F_3 lines.
[1]: From 1 (resistant) to 10 (highly susceptible) after Tekauz (1985).

disease rating of the F_2 plants was based on single plants and that of each F_3 line was the mean of ten plants, the error in the F_2 plants should be larger than that in the means of the F_3 lines. Therefore, the difference in the disease ratings between the generations could be caused by the larger error in the F_2 plants.

Other estimates for the heritability were calculated by selection differ-

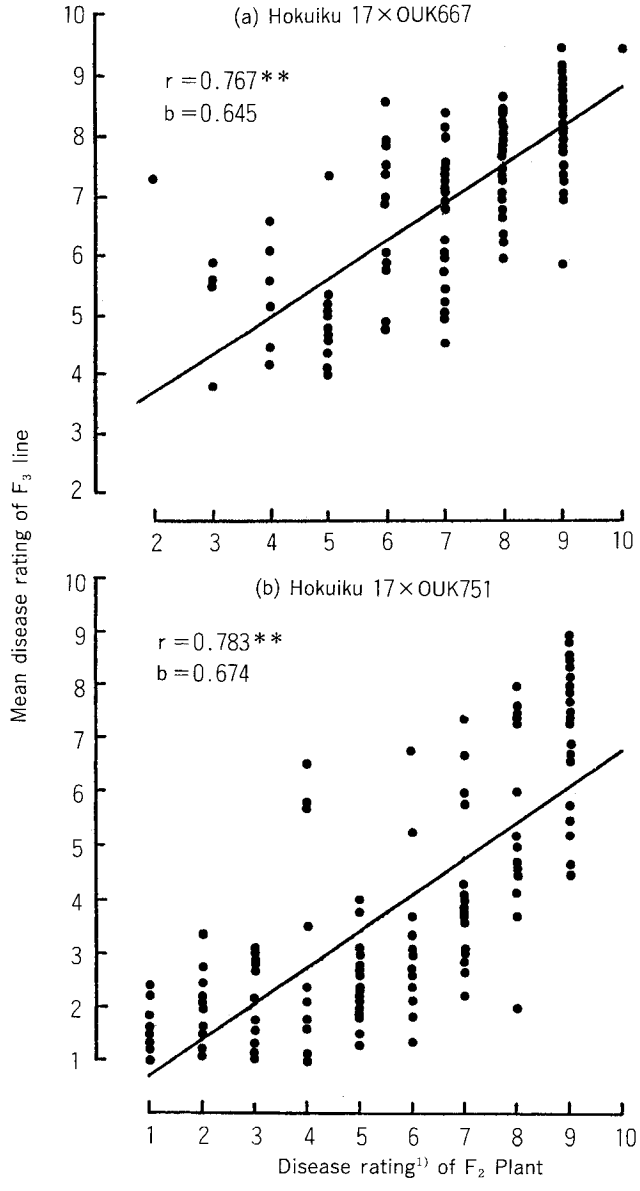

Fig. 4. Correlation of disease ratings to isolate K105 between F_2 population and F_3 lines.
**: Significant at the 1% level.
1): From 1 (resistant) to 10 (highly susceptible) after Tekauz (1985).

entials of the F_2 plant groups and genetic gains of the F_3 line groups (Figs. 5 and 6). Selection differentials, genetic gains and heritabilities were 4.70, 3.37 and 0.72 in the Hokuiku 17×OUK667 cross, and 7.52, 5.52 and 0.73 in the Hokuiku 17×OUK751 cross, respectively (Table 1).

Despite of the different level of resistance in the resistant parents of the

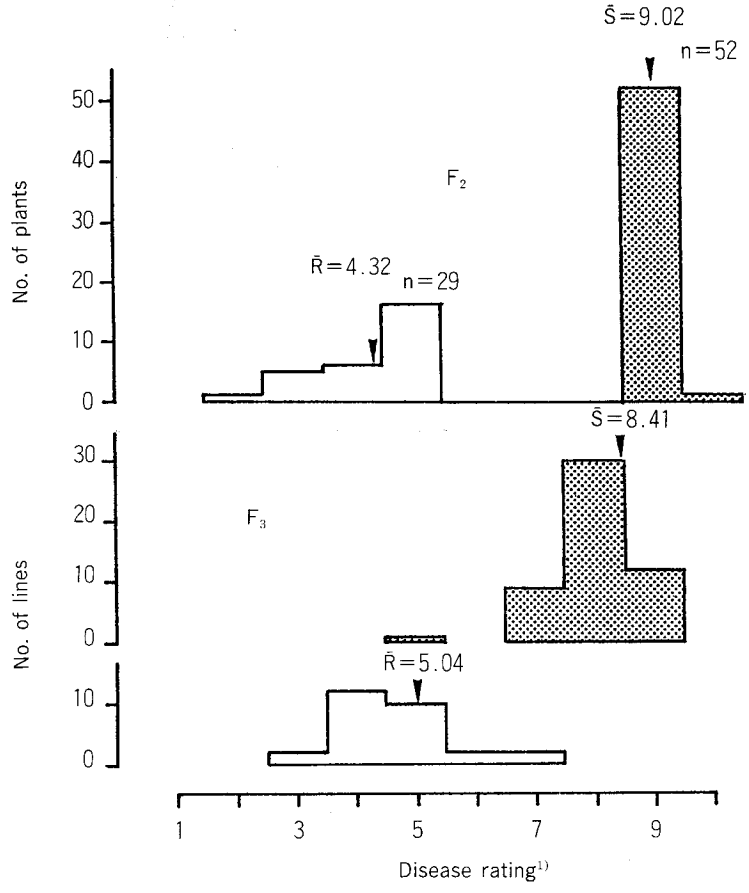

Fig. 5. Selection experiment for the disease ratings to isolate K105 in the cross Hokuiku17×OUK667.
1): From 1 (resistant) to 10 (highly susceptible) after Tekauz (1985).

two crosses (OUK667: 3.7~3.9, OUK751: 1.2~1.3), three kinds of heritabilities estimated were similar and ranged from 0.6 to 0.8. As the heritabilities of net blotch resistance using diallel analysis were from 0.72 to 0.87 (Sato and Takeda 1993b), these values may be reasonable as the heritability for net blotch resistance.

Because of the high heritability and the small number of genes concerned, selection of resistance with continuous distribution in net blotch may be effective even from the F_2 generation. Figs. 5 and 6 show examples explaining the selection effectiveness in which the most of the F_3 lines derived from the resistant F_2 plants were resistant.

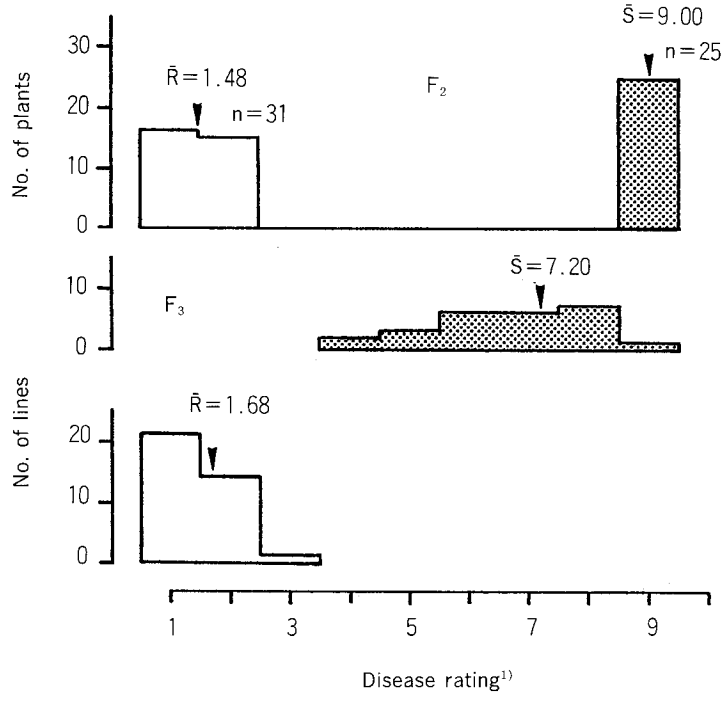

Fig. 6. Selection experiment for the disease ratings to isolate K105 in the cross Hokuiku 17×OUK751.
1): From 1 (resistant) to 10 (highly susceptible) after Tekauz (1985).

Table 1. Selection differential, genetic gain and heritability for the disease ratings[1] of F_2 and F_3 generations

Cross	F_2			F_3			
	S[2]	R[3]	d[4]	S[5]	R[6]	G[7]	H[8]
Hokuiku 17×OUK667	9.02	4.32	4.70	8.41	5.04	3.37	0.72
Hokuiku 17×OUK751	9.00	1.48	7.52	7.20	1.68	5.52	0.73

1): From 1 (resistant) to 10 (highly susceptible) after Tekauz (1985)
2): Mean disease rating of susceptible plants
3): Mean disease rating of resistant plants
4): Selection differential
5): Mean disease rating of susceptible lines
6): Mean disease rating of resistant lines
7): Genetic gain
8): Heritability

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大麦網斑病抵抗性の選抜効果

佐藤和広・武田和義

抵抗性と罹病性の両親間の交雑に由来する2組のF_2集団とその後代のF_3系統を用いて，大麦網斑病における抵抗性の選抜効果を推定した．F_3系統の平均値と分散から，病斑指数の分散が小さく，すでに固定した系統が多数存在したので，抵抗性は少数の遺伝子に支配されているとみられた．F_2個体とF_3系統間の親子相関，親子回帰およびF_2の選抜差とF_3系統の遺伝獲得量から遺伝率を推定したところ，2組の交雑組合せで抵抗性親の病斑指数は異なっていたにもかかわらず，3種類の遺伝率の推定値はいずれも0.6～0.8の値を示した．遺伝率が高く，しかも関与する遺伝子数が少数であるため，雑種集団で連続変異を示す場合の大麦網斑病抵抗性の選抜はF_2からでも効果的とみられた．

キーワード：網斑病，*Pyrenophora teres*，選抜，オオムギ，病害抵抗性