

GENETIC STUDIES ON POWDERY MILDEW RESISTANCE OF FLAX, YIELD AND SOME YIELD COMPONENTS

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Abstract

A study was conducted at Giza Agricultural Research Station in 1999/2000 and 2000/2001 growing seasons with the following objectives: (1) screen some flax genotypes for powdery mildew resistance, (2) determine the potential productivity of such genotypes, (3) define the genetic basis for powdery mildew resistance, yield and some yield-related traits, and (4) assess the type and the degree of association between powdery mildew intensity rating and each of yield and yield-related traits. All possible crosses without reciprocals were made among the four parental genotypes Dakota, Wilden, Cortland, and Linore. Dakota and Wilden were highly resistant to powdery mildew, while Cortland and Linore were highly susceptible. The parental genotypes and their F₁ six populations were subjected to diallel crossing program analysis for the following traits: total plant length, technical stem length, fruiting zone length, number of basal branches/plant, seed yield per plant, straw yield per plant, disease intensity variables (disease incidence and disease severity) at two dates. Significant differences in all the traits were observed among the parental genotypes. Highly significant mean squares of general combining ability (GCA) were observed for all the traits. Significant differences for specific combining ability (SCA) were observed for most of the traits. GCA was greater than SCA for most of traits indicating the predominance of additive gene effects in the inheritance of most of the traits. Powdery mildew resistance in flax was not a simple inherited trait; therefore, parental contribution should be carefully investigated before incorporation into a breeding program for powdery mildew resistance. Correlation analysis showed that total plant length was negatively correlated ($P \leq 0.10$) with each of the early and the late disease incidence, while straw yield/plant was negatively correlated ($P \leq 0.10$) only with the late disease incidence. Seed yield/plant showed highly significant ($P \leq 0.01$) positive correlation with the early disease incidence and significant ($P \leq 0.05$) positive correlation with each of the early and the late disease severity. These results suggest that selection for fiber type flax would result in an increase in powdery mildew resistance, while selection for seed type flax would result in a decrease in such a resistance.

INTRODUCTION

Flax (*Linum usitatissimum* L.) is considered as the most important bast fiber crop, and it ranks second after cotton (seedy fiber) in relation to economic importance and production. Powdery mildew (PM) caused by *Oidium lini* Skoric is currently the most common, conspicuous, widespread and easily recognized foliar disease of flax in Egypt.

Over the last decade, the importance of this disease has increased probably due to the appearance and rapid distribution of new races capable of attacking the previously resistant cultivars (Aly *et al.*, 1994). Accurate assessment of losses due to the disease in Egypt has not been reported. However, Aly *et al.* (1994) found significant negative correlation between disease intensity ratings and agronomic traits (yield and yield components).

In India, Pandey and Misra (1993) reported that as the disease increased, yield losses increased ranging from 11.8 to 38.9%, and yield losses were greater when the disease appears earlier in the season. Currently, all the commercially grown flax cultivars in Egypt are susceptible to PM, although field observations indicate that some experimental lines are more susceptible than others (A.A. Aly, Personal observations).

Fungicides are currently the only commercially available management practice for controlling the disease and minimizing associated losses in seed and straw yield (Aly *et al.*, 1994). Complete dependence on fungicides for the disease control carries risks for the producers, in that accurate coverage and distribution of fungicides may not be achieved and there are potential problems with correct timing of application. Furthermore, increasing concern for the environment will likely lead to greater regulation of pesticide usage (Pearce *et al.*, 1996).

Use of cultivars with PM resistance can resolve all these problems. Therefore, there is a need to improve PM resistance in flax cultivars through the introgression of resistance genes. Successful breeding for PM resistance in flax requires the knowledge of genetic basis of such a resistance. Few references were found in the literature on the genetic basis of PM resistance in flax. For example, Goray *et al.* (1989) studied the genes conditioning resistance of linseed to PM in a population derived from 15 crosses, 45 F_1 's and their F_2 . Their segregation analysis indicated that inheritance of resistance was dominant and monogenic. Islam (1992) also found that resistance to PM in flax was governed by a single dominant gene.

The objectives of the present study were to (1) screen some flax genotypes for PM resistance, (2) study the potential productivity of such genotypes since they are not commercially grown, (3) study the genetic basis for PM resistance and some yield-related traits, and (4) assess the type and the degree of association between PM intensity ratings and each of yield and yield-related traits.

MATERIALS AND METHODS

Field performance of flax cultivars Dakota (P_1), Wilden (P_2), Cortland (P_3) and Linore (P_4) over three successive growing seasons, indicated that Dakota and Wilden were highly resistance to PM, while Cortland and Linore were highly susceptible (A.A. Aly, Personal observation). Seeds of the four flax cultivars were planted on No-

vember 15, 1999 at Giza Agricultural Research Station. All the possible crosses without reciprocals were made. Seeds of the resulting ten populations (four parental populations and six hybrid lines) were planted on November 11, 2000 in autoclaved soil dispensed in 25-cm diameter clay pots (20 seeds/pot). The pots were distributed outdoors in a randomized complete block design with three replicates. Powdery mildew was allowed to develop naturally. Disease incidence and disease severity (Aly *et al.*, 1994) were rated visually on April 4 and 19, 2001. Disease incidence (DI) was measured as the percentage of infected plants/pot. Disease severity (DS) was measured as the percentage of infected leaves/plant. At harvest, observations were recorded on ten randomly selected individual plants for each of the following agronomic traits:

Total plant length (TPL): plant height (cm) from the cotyledonary node to the apical bud of each plant.

Technical stem length (TSL): the length (cm) of the main stem from the cotyledonary node to the first or lowest branching point.

Apical branching (fruiting) zone length (FZL): the length (cm) from the first or lowest branching point to the top of the plant.

Number of basal branches (BB): number of bottom branches without main stem which arise from cotyledonary node.

Seed yield/plant (SY): weight (g) of harvested seeds per plant.

Straw yield/plant (St/Y): weight (g) of the mature air-dried stems per plant after removing the capsules.

Statistical analysis of the data:

General and specific combining abilities were estimated according to Griffing (1961). The relative magnitude of variance components were estimated according to Mather and Jinks (1982) in order to study the genetic architecture of each trait. Heterotic effects over the best parent were obtained according to Griffing (1961). Pearson's correlation coefficient was calculated to evaluate the degree of association between disease intensity variables and agronomic traits. Statistical analysis was carried out by computerized programs (M stat-c).

RESULTS AND DISCUSSION

Studying the genetic basis of certain traits using diallel crossing program gives a clear idea of the types of inheritance in this specific groups of genotypes, identifies certain parents to transmit their traits to the subsequent generations, and shows the type of correlation between the different studied traits. This information help breeders

select the superior parents for certain traits, which have the ability to transmit them to their progeny. Data obtained from diallel crossing programs also help in selecting the methods of improving a given trait according to certain estimates such as heritability, types of gene expression and number of genes controlling the trait.

The present study was designed to study the inheritance of PM resistance and its relation to some yield traits in flax. The mean performance of the ten studied traits of the parental genotypes and their six F_1 hybrids are shown in Table 1. Significant differences were observed between parents for almost all the studied traits. P_2 showed the highest mean values for TPL, FZL, and StY. It also showed the lowest mean value for DI on both dates and DS on the first date. Considering the hybrids which contained P_2 as one of their parents, one can conclude that P_2 could be considered as a good combiner for TPL and SY. P_2 could also be considered as a good combiner for PM resistance, which was measured as DI or DS on both dates. The critical test in F_1 hybrids is the expression of heterosis, which indicates the superiority of F_1 hybrids over the best parent.

General combining ability (GCA):

Mean squares for the diallel crosses of the four parental lines and their F_1 s, according to Griffing's (1961) is presented in Table 2. Almost all the studied traits showed highly significant differences ($P \leq 0.01$) among parents, except for BB, which was non significant. The significant differences among parents indicate the presence of sufficient variability for each of the studied traits.

Variances for GCA (Table 2) were significant ($P \leq 0.01$) for all the studied traits. Estimates of GCA for the four parental lines are presented in Table 3. From the data, it can be concluded that P_2 possessed favorable additive genes for all yield traits except TSL, StY and BB. Moreover, P_2 also seems to possess favorable additive genes for disease resistance as measured by DI1, DI2, DS1 and DS2. The negative values for GCA estimates for the two resistant genotypes Dakota and Wilden (P_1 and P_2) indicate the presence of additive genes contributing to resistance. This is because the estimated values showed the presence of the disease. Data indicate that P_2 (Wilden) could be considered a good combiner for disease resistance. The same behavior was observed for P_1 (Dokata), while the reverse was true for P_3 (Cortiand) and P_4 (Linore). It is worthy to mention that, according to the preliminary investigations, P_1 and P_2 were characterized by high resistance to PM, while P_3 and P_4 were characterized by high susceptibility. Our results are in accordance with Singh *et al.* (1987) who stated that, data from F_1 and F_2 linseed indicated the predominance of additive gene actions together with partial dominance in the inheritance of TPL. Ashry (1998) also reported that additive type of gene actions were important in the inheritance of TPL, TSL, SY and StY. Singh *et al.* (1987) and Ashry (1998) found that non-additive gene effects were more

Table 1. Mean performance of the four parental cultivars and their six straight F₁'S for the ten studied characters.

Genotype	Traits									
	Total plant length	Technical stem length	Fruiting zone length	No. of basal branches	Seed yield/ plant	Straw yield/ plant	Disease incidence		Disease severity	
	(cm)	(cm)	(cm)	(BB)	(g)	(g)	First (%)	Second (%)	First (%)	Second (%)
	(TPL)	(TSL)	(FZL)	(BB)	(SY)	(ST Y)	(DI1) ^a	(DI2) ^b	(DS1)	(DS2)
Parents										
Dakota P ₁	78.78	66.78	13.67	1.33	0.87	1.34	35.00	45.00	4.44	6.06
Wilden P ₂	83.33	66.20	18.40	1.33	0.62	1.43	0.00	17.0	4.33	12.23
Cortland P ₃	81.17	68.45	16.98	2.07	1.07	1.41	100.00	100.00	80.83	100.00
Linore P ₄	68.40	55.91	12.70	1.82	1.30	0.90	100.00	100.00	75.90	98.95
F₁'s										
P ₁ x P ₂	83.58	65.42	12.29	2.89	0.93	1.33	9.00	17.00	2.10	3.03
P ₁ x P ₃	75.62	61.58	17.31	2.91	0.95	0.97	73.33	100.00	68.31	100.00
P ₁ x P ₄	84.17	61.38	22.21	2.25	0.93	1.36	33.33	100.00	40.75	99.45
P ₂ x P ₃	86.44	65.51	19.68	2.80	1.10	1.56	67.67	100.00	24.07	75.05
P ₂ x P ₄	78.83	63.50	14.67	2.92	1.00	1.16	39.67	66.00	23.82	43.23
P ₃ x P ₄	73.58	62.58	13.50	1.75	1.04	1.00	100.00	100.00	72.22	100.00
C.V.	5.24	4.35	5.55	28.65	7.51	8.54	34.99	8.02	18.69	9.47
LSD at										
P<5%	5.13	4.75	1.59	1.08	0.13	0.18	33.42	10.25	12.72	10.20
P<1%	9.77	6.51	2.17	1.49	0.17	0.25	45.77	14.04	17.42	13.97

important in the inheritance of the BB trait in a set of F₁ flax hybrids. However, these results disagreed with Singh *et al.* (1995) who reported the predominance of additive gene effects for BB.

Specific combining ability (SCA):

Analysis of variance for SCA showed highly significant differences ($P \leq 0.01$) for all the studied traits except TPL, TSL, StY and DI1 (Table 2).

Estimates for SCA of the six hybrids are shown in Table 4. The two crosses P₁ x P₄ and P₂ x P₃ showed significant SCA effects for most of the studied traits. P₁ x P₄ exhibited highly significant differences ($P \leq 0.01$) for TPL, FZL, StY, DI2 and DS2, while the differences were significant ($P \leq 0.05$) for SY. The hybrid P₂ x P₃ showed highly significant differences ($P \leq 0.01$) for SY, DI2 and DS2, while differences were significant ($P \leq 0.5$) for FZL, StY and DS1.

In general, it is clear that both additive and non-additive types of gene actions are involved in determining the performance of the crosses in the studied traits.

Table 2. Mean squares of the ten studied characters in the 4x4 diallel cross (straight set).

Source of variation	Traits									
	TPL	TSL	FZL	BB	SY	ST Y	DI1	DI2	DS1	DS2
Parents	131.15**	97.39**	21.81	0.40	0.254	0.189**	7418.75**	5153.00**	5484.71**	9096.02**
F ₁ 's	79.50**	9.97	30.61**	0.70	0.014**	0.141**	3200.37**	3450.10**	2267.54**	4736.85**
Error	17.29	7.67	0.85**	0.40	0.005	0.011	379.44	35.70	54.96	35.38
GCA ^a	50.92	28.65**	4.73**	0.39**	0.060	0.067**	3902.87**	2970.50**	2786.10**	4848.58**
SCA ^b	20.88	5.08	11.38**	0.60**	0.027**	0.037	183.69	424.17**	154.15**	541.74**
Error	5.77	2.56	0.29	0.13	0.002	0.004	126.479	11.90	18.32	11.79
GCA/SCA	2.44	5.64	0.45	0.65	2.2	1.8	21.23	7.00	18.07	8.95

^a GCA: General combining ability.

^b SCA: Specific combining ability.

** Significant at $P \leq 0.001$

* Significant at $P \leq 0.05$.

Table 3. Estimates of general combining ability for ten studied characters in the 4x4 diallel crossing program (straight set).

Parents	Traits									
	TPL	TSL	FZL	BB	SY	ST Y	DI1	DI2	DS1	DS2
P ₁	0.663	0.546	0.157	-0.052	-0.059	0.011	-15.556*	-0.675**	-13.057**	-16.567**
P ₂	3.094**	1.363	0.872*	0.039	-0.106**	0.107	-27.111**	-1.816**	-23.289**	-31.372**
P ₃	0.170	1.320	0.209	0.093	0.055*	0.027	27.00**	1.401**	21.312**	26.842**
P ₄	-3.927**	-3.229**	-1.239**	-0.081	0.111**	-0.146	15.667*	1.089**	15.034**	21.097**
SE (g _i) ^a	0.85	0.57	0.19	0.13	1.50	2.18	3.98	9.13	1.51	1.21
LSD (g _i -g _j) ^b 5%	2.91	1.94	0.65	0.44	0.05	7.49	13.64	0.31	5.19	4.17
(g _i -g _j) ^c 1%	3.99	2.66	0.89	0.61	0.07	0.10	18.69	0.43	7.11	5.71

^a Standard error for general combining ability.

^b LSD value for general combining ability ($P < 0.05$).

^c LSD value for general combining ability ($P < 0.01$).

Significant at $P \leq 0.05$ (*) or $P \leq 0.01$ (**).

Table 4. Estimates of specific combining ability effects for the ten studied traits.

Cross	Traits									
	TPL	TSL	FZL	BB	SY	ST Y	DI1	DI2	DS1	DS2
P ₁ x P ₂	0.43	-0.22	-0.38	0.70	-0.12*	-0.04	-0.52	-1.64**	-1.23	-11.83**
P ₁ x P ₃	-4.60	-4.02*	0.30	0.67	-0.02	-0.33**	0.32	0.96**	20.37**	26.93**
P ₁ x P ₄	8.04**	0.33	6.65**	0.18	-0.10*	0.24**	-1.99	1.27**	-0.90	32.12**
P ₂ x P ₃	3.78	-0.90	-1.61*	0.46	0.17**	0.18*	1.70	2.10**	-13.63*	16.78**
P ₂ x P ₄	0.28	1.64	-2.11**	0.75	0.01	-0.06	0.70	0.56	-7.61	-9.29*
P ₃ x P ₄	-2.05	0.76	0.19	-0.47	-0.11*	-0.06	-0.12	-0.81*	-3.81	-10.74*
SE	2.77	1.85	0.62	0.42	4.91	7.13	1.12	0.30	4.94	3.97
LSD at										
P < 5%	5.82	3.88	1.29	0.89	0.10	0.15	2.35	0.63	10.38	8.33
P < 1%	7.98	5.31	1.77	1.21	0.14	0.21	3.22	0.86	14.22	11.41

Significant at $P \leq 0.05$ (*) or $P \leq 0.01$ (**).

The ratio between GCA and SCA for the studied characters could be used to determine whether one genetic effect is predominant over the other. GCA was greater than SCA for TPL, TSL, SY, StY, O11, O12, OS1 and OS2 (Table 2), thus revealing that the major part of the total genetic variability in these traits was mainly due to additive and additive x additive types of gene actions. Since additive gene action plays the major part in the inheritance of these traits, it is suggested that such traits could be improved through selection. Results reported herein agree with those of Singh *et al.* (1987), Ashry (1998) for TPL and TSL.

The ratio GCA/SCA mean squares for FZL and BB indicate that non-additive genetic effects played major role in the inheritance of these traits and that improving such traits may successfully be achieved through hybridization. These results agree with those of Ashry (1998), while they disagree with the findings of Singh *et al.* (1995), who reported the predominance of additive gene action in the inheritance of BB.

Genetic architecture:

The genetic components of variation D, F, H₁, H₂, h² and E as described by Math-er and Jinks (1982) are presented in Table(5). D and H₁ represented the components of variation due to additive and dominant effects of the genes, respectively. D and H₁ were statistically significant ($P \leq 0.01$) for all the studied traits except the estimate of H₁ for BB and D for both FZL and BB, confirming that additive and dominant types of gene action were involved. The components of variation due to dominant effects correlated to gene distribution (H₂) were highly significant ($P \leq 0.01$) for all studied traits except TSL and FZL, which were only significant ($P \leq 0.05$) and BB, which was nonsignificant, confirming the presence of asymmetrical distribution of dominant genes in the genetic background of the parents. The overall dominant effects of heterozygous loci (h²) were found to be highly significant ($P \leq 0.01$) for SY, DI1 and DS2, while h² estimate was significant ($P \leq 0.05$) for DI1. Negative values for both StY and DI1 were observed. H₂ is the algebraic sum of the dominant effects of genes and negative values reveal that most of dominant effects are the results of genes with negative effects. F value, which indicates the covariance of additive and dominant effects, was found to be statistically highly significant ($P \leq 0.01$) for TSL, SY, StY and DI1, while it was significant ($P \leq 0.05$) for DS1 indicating that dominant and recessive alleles are not equally distributed among parents. F had positive values for the above mentioned traits except DS1, which lead to the conclusion that there is an excess of dominant alleles. As for DS1, negative value indicates an excess of recessive alleles.

Table 5. Genetic components of variation for the ten studied traits derived from the diallel crosses program.

Genetic components of variation	Traits									
	TPL	TSL	FZL	BB	SY	StY	DI1	DI2	DS1	DS2
D	38.00**	29.74**	6.89	0.01	0.08**	0.06**	17.45**	7.92**	1608.16**	3020.40**
H1	68.64**	15.05**	44.18**	1.64	0.07**	0.14**	5.75**	7.59**	547.72**	2034.17**
H2	62.50**	9.95*	38.94*	1.43	1.05**	0.13**	3.66**	7.33**	455.78**	1749.52**
h^2	9.20	0.24	8.84	1.93	1.14**	-0.001	-0.62**	2.22*	62.71	746.82**
F	14.97	21.62**	9.47	0.21	0.08**	0.03**	2.63**	-1.70	-222.09*	-118.53
E^a	5.72*	2.72*	0.29	0.13	1.70**	0.004	1.02**	6.08**	18.53	11.29
$(H_1/D)^{1/2}$	1.34	0.71	2.52	16.60	0.91	1.57	0.57	0.98	0.58	0.82
$H_2/4H_1$	0.23	0.17	0.22	0.22	0.17	0.23	0.16	0.24	0.21	0.22
$[(4DH_1)^{1/2} + F / (4DH_1)^{1/2} - F]$	1.18	0.024	1.37	1.37	1.89	1.23	1.16	0.88	0.87	0.97
h^2/H_2	0.15	2.42	0.205	1.35	1.086	-0.008	-0.169	0.765	0.137	0.427

Significant at $P \leq 0.05$ (*) or $P \leq 0.01$ (**).

A Environmental component of variation.

For more information about each trait, several ratios were calculated. These ratios included $(H_1/D)^{1/2}$, which measures the average degree of dominance at each locus. This ratio indicates an almost complete dominance for TSL, SY, DI2 and DS2, while it indicates over dominance for TPL, FZL, BB and StY and partial dominance for both DI1 and DS1.

The ratio $H_2/4H_1$, which measures the proportion of genes with positive and negative effects proved that negative and positive alleles were not equally distributed among parents for all studied traits. The ratio $(4DH_1)^{1/2} + F / [(4DH_1)^{1/2} - F]$, which measures the proportion of dominant and recessive genes in the parents, was found to be greater than 1 for the studied traits except TSL, DI2, DS1 and DS2, suggesting that dominant genes are in excess for controlling such traits, while the reverse was true for DI1, DS1 and DS2.

Number of groups of dominant genes controlling each of the studied traits were estimated using the ratio h^2/H_2 . The estimated values revealed that only one dominant group of genes was involved in controlling each of the traits except SY, which was found to be controlled by two dominant group of genes.

Heterosis:

The heterotic effects over the best parent for the ten studied traits are presented in Table 6. Data show that most of the heterotic values were negative. In case of TPL, only cross $P_2 \times P_4$ exhibited positive and significant heterotic effects, while in case of TSL no positive heterotic effects were observed. Crosses $P_1 \times p_3$, $P_1 \times P_4$, and $P_2 \times$

P₃ exhibited positive and highly significant effects ($P \leq 0.01$), while the other crosses exhibited high but negative heterotic effects. As for FZL and BB, heterotic effects were positive and highly significant for all crosses except the cross P₃ x P₄, which showed negative and significant heterotic effects. Both of the crosses P₁ x P₂ and P₂ x P₃ showed positive and high heterotic effects for SY, while the others showed negative effects. As for StY, both crosses P₁ x P₄ and P₂ x P₁ showed highly significant positive heterotic effects, while the other crosses showed negative effects. DI1 showed significant and negative values for all crosses except the cross P₃ x P₄. As for DI2, only P₁ x P₂ and P₂ x P₄ exhibited highly significant ($P \leq 0.01$) and negative heterotic effects. DS1 showed negative and highly significant ($P \leq 0.01$) heterotic effects for all the crosses except the cross P₃ x P₄. DS2 showed negative highly significant ($P \leq 0.01$) heterotic effects over the best parent for P₁ x P₂, P₂ x P₃ and P₂ x P₄. It should be mentioned that negative values of DI and DS indicate an improvement in the disease resistance over the best parent. Heterotic effects for yield-related traits were reported by Singh (1982) for TPL, Galkin and Shorchirskava (1984) for TPL and StY, Naqvi *et al.* (1987) for straw yield, Tyson (1989) for seed weight, Saraswat and Kumar (1993) for SY, and Singh *et al.* (1995) for BB and SY.

Table 6. Heterotic effects over the best parent value for the ten studied traits.

Cross	Trait									
	TPL	TSL	FZL	BB	SY	ST Y	DI1	DI2	DS1	DS2
P ₁ x P ₂	0.30	-2.04	-6.01	11.75**	7.69**	-6.99**	-51.75**	-37.02**	-52.74**	-50.03**
P ₁ x P ₃	-6.68*	-10.04**	1.92**	40.97**	-11.21**	-31.44	-18.13**	0.00	-15.49**	0.00
P ₁ x P ₄	6.48*	-8.09**	62.51**	23.85**	-28.71**	1.75**	-49.40**	0.00	-46.31**	0.51
P ₂ x P ₃	3.72	-4.29*	6.94**	23.85**	2.80**	9.32**	-18.73**	0.00	-70.22**	-24.95**
P ₂ x P ₄	-5.40	-4.08	-20.29**	60.55**	-23.33**	-19.11**	-36.89**	-18.66**	-68.62**	-56.31**
P ₃ x P ₄	-9.34**	-8.57**	-20.51**	-15.32**	-20.00**	-23.40**	0.00	0.00	-10.65	0.00
LSD at										
P < 5%	6.18	4.11	1.37	0.94	0.11	0.16	2.50	0.66	11.01	8.84
P < 1%	8.46	5.64	1.88	1.29	0.15	0.22	3.42	0.91	15.09	12.11

Significant at $P \leq 0.05$ (*) or $P \leq 0.01$ (**).

Correlation analysis:

It is well known that the type and degree of correlation between characters may facilitate or complicate selection process in breeding programs. Selection for a character may result in an improvement or deterioration in other characters according to the type and degree of correlation. Hence, it was desirable to assess the type and degree of association between disease intensity variables (DI and DS) and agronomic traits. Pearson's correlation coefficient was calculated between the pairs of characters (Table 7).

TPL was negatively correlated ($P \leq 0.10$) with each of DI1 and DI2, while StY was negatively correlated ($P \leq 0.10$) only with DI2. SY showed highly significant ($P \leq 0.01$) positive correlation with DI, and significant ($P \leq 0.05$) positive correlation with each of DS1 and DS2. All the other correlation coefficients were nonsignificant. Increasing seed yield is always accompanied with increasing growth habit (Singh *et al.* 1995). Increasing growth habit would reduce penetration of light and circulation of air within and beneath plant canopy, ultimately increasing relative humidity and creating more favorable ecosystem for spore germination and germ tube elongation (A.A. Aly, personal observations), consequently the significant positive correlation between disease intensity variables and SY. On the other hand, it seems reasonable to conclude that selection for fiber type flax, characterized by limited growth habit, narrow leaves and less branches would result in an increase in PM resistance by providing less favorable environmental conditions for, *Oidium lini* growth.

Table 7. Correlation coefficient (r) between yield components and disease intensity variables.

Disease intensity	Yield components					
	TPL	TSL	FZL	BB	SY	STY
DI 1	-0.61 ^x	-0.35	-0.40	-0.01	0.79 ^{**}	-0.46
DI 2	-0.62 ^x	0.46	-0.23	0.01	0.64 [*]	-0.57 ^x
DS 1	-0.35	-0.44	0.03	0.19	0.70 [*]	-0.32
DS 2	-0.39	-0.50	0.07	0.18	0.66 [*]	-0.40

Pearson's correlation coefficient (r) is significant at $P < 0.01$ (**), $P < 0.05$ (*), or $P < 0.10$ (x).

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دراسات وراثية على مقاومة مرض البياض الدقيقى و المحصول و بعض مكوناته فى الكتان

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أجريت هذه الدراسة خلال موسمى ١٩٩٩/٢٠٠٠ و ٢٠٠٠/٢٠٠١ وكانت اهداف الدراسة على النحو التالى :

(١) تقييم مقاومة بعض التراكيب الوراثية لمرضى البياض الدقيقى. (٢) دراسة القدرة الانتاجية لهذه التراكيب الوراثية. (٣) دراسة الأساس الوراثى لصفة مقاومة مرض البياض الدقيقى و المحصول و بعض مكوناته. (٤) تقييم درجة و نوع الارتباط بين المتغيرات الدالة على كثافة المرض و كل من المحصول و مكوناته. أجريت جميع التهجينات الممكنة فى اتجاه واحد بين أربعة آباء تتباين فيما بينها من حيث درجة المقاومة لمرض البياض الدقيقى. طبقت طريقة التحليل الدائرى على الآباء الأربعة و نباتات الجيل الأول و ذلك للصفات التالية:

الطول الكلى للنباتات و الطول الفعال للنباتات و طول المنطقة الثمرية و عدد الأفرع القاعدية للنبات و محصول القش للنبات و المتغيرات الدالة على كثافة المرض (حدوث و شدة المرض) فى ميعادين. كان التباين الراجع للآباء معنويا بالنسبة لجميع الصفات موضع الدراسة. كانت متوسطات المربعات الراجعة للقدرة العامة على التآلف عالية المعنوية لجميع الصفات موضع الدراسة ، كما كانت متوسطات المربعات الراجعة للقدرة الخاصة على التآلف معنوية بالنسبة لأغلب الصفات.

أظهرت الدراسة أن التباين الراجع الى القدرة العامة على التآلف أكبر من ذلك الراجع إلى القدرة الخاصة على التآلف و ذلك لأغلب الصفات، مما يدل على أهمية التباين المضيف فى توريث أغلب الصفات. تشير الدراسة الى ان صفة المقاومة لمرض البياض الدقيقى ليست بسيطة التوريث. و على ذلك فمن الضرورى دراسة توريث التوافق الأبوية المختلفة لصفة مقاومة مرض البياض الدقيقى قبل إدخال هذه الآباء فى برامج التربية لمقاومة المرض. وجد ارتباط معنوى سالب بين الطول الكلى للنباتات و حدوث المرض فى الميعادين المبكر و المتأخر ، كما وجد ارتباط معنوى بين محصول القش للنباتات و حدوث المرض فى الميعاد المتأخر. إرتبط محصول البذرة للنبات ارتباطا موجبا عالى المعنوية مع حدوث المرض فى الميعاد المبكر، كما ارتبط محصول البذرة للنبات ارتباطا موجبا معنويا مع شدة المرض فى الميعادين المبكر و المتأخر. تدل هذه النتائج على أن انتخاب طرز الكتان الليفية يؤدى إلى زيادة فى مستوى المقاومة لمرض البياض الدقيقى، أما الانتخاب لطرز الكتان الزيتية فإنه يؤدى إلى انخفاض فى مستوى المقاومة لمرض البياض الدقيقى.