Plot Size Effects on Disease Progress and Yield of Wheat Infected by *Mycosphaerella graminicola* and Barley Infected by *Pyrenophora teres*

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ABSTRACT

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Areas under disease progress curves (ADPC) for two cereal pathogens of different spore dispersal mechanisms (*Pyrenophora teres* on barley and *Mycosphaerella graminicola* on wheat) and grain weights obtained from field plots were subjected to pertinent orthogonal comparisons to determine if ADPC and crop loss estimates are functions of plot size. The study was made in Morocco. ADPC from plots 40 × 40 m and infected with *P. teres* were statistically greater than ADPC from plots 20 × 20 and 10 × 10 m, yet grain weights were not significantly different. Initial severities were similar in all plots, but final severities at hard dough to ripeness were 23–36% greater in plots 40 × 40 than in plots 20 × 20 and 10 × 10. ADPC from plots 40 × 40 and infected with *M. graminicola* also were statistically greater than ADPC from plots 20 × 20 and 10 × 10, but final severities were only 2–10% greater in plots 40 × 40 than in plots 20 × 20 and 10 × 10. As with *P. teres*, grain weights were not significantly different. ADPC from plots 20 × 20 and 10 × 10 were not significantly different for *P. teres* or *M. graminicola*. The proportion of *P. teres* conidia escaping from plots was inversely proportional to plot size at Ellouzia and Jamâa Shaim.

A major concern in crop loss studies is the capability of experimental methods to simulate farming practices so that differences between plot yields with disease and without disease match those from commercial fields. Prior to publication of studies on wheat stem rust epidemiology in 1959 (16,25), field trial methodology to assess yield loss due to plant disease was predictable by its similarity to plot techniques long employed by plant breeders to test yield differences among advanced lines. That is, sprayed and unsprayed plots like resistant and susceptible lines were arranged in a randomized block design with three to six blocks. Plots were approximately 1–10 m^2 and adjacent.

Changing the design of disease epidemiology and crop loss experiments gathered momentum after Vanderplank (27) signaled the danger of underestimating the impact of disease in field plots meant to simulate large fields (representational errors). Without experimental evidence but with sound logic (26), he estimated the proportion of airborne spores escaping from square plots 10^{-4}–10^{8} m^2 and inferred that unsprayed plots would lose a larger proportion of spores than unsprayed fields and, therefore, that plants in unsprayed plots would have less disease than plants in unsprayed fields.

Since 1963, those involved in studying crop loss methodology have become increasingly skeptical of disease measurements and crop loss estimates obtained from conventional agronomic designs that do not allow for treatment separation to limit interplot spore movement or that do not allow for adequate plot size to permit unrestricted disease development. It is now documented that representational errors can invalidate loss estimates and render questionable descriptive and predictive crop loss models built on data from unsound experiments (9,10).

More recent studies have employed plots of 10–2,000 m^2 with treatments separated by sprayed areas of the same crop or by zones of a related but nonsusceptible crop (2–7,11–13,15,17,19,22). None of those studies mentioned that plot size was adequate to permit unrestricted disease development and that plot separation was adequate to prevent significant interplot interference.

In perhaps the most definitive study made to measure the impact of interplot interference by a foliage pathogen, James et al (10) compared rates of disease development and areas under disease progress curves (ADPC) for epidemics of *Phytophthora infestans* in uninoculated plots adjacent to either uninoculated or inoculated plots. When adjacent to inoculated plots, uninoculated plots gave ADPC and yield loss estimates 50 and 10.8% greater, respectively, than when adjacent to other uninoculated plots. Similarly, development of barley mildew was greater in adjacent plots than in plots separated by 20 m of treated barley (1).

James and Shih (9) also examined the effect of plot size and shape on yield variability in wheat and oats uniformly infected with *Erysiphe graminis* f. sp. *tritici* and *Septoria avenae* f. sp. *avenae*, respectively. From plots 42 × 124 ft (≃12.8 × 37.9 m) they harvested 1,280 units each 3.5 ft^2 (≃0.33 m^2). They organized those units into various combinations to compare grain weights from plots of different shapes and sizes ranging from 3.5 to 140 ft^2 (≃13 m^2). The minimum plot size for detecting a 10% yield loss was found to be approximately 100 ft^2 (≃9.3 m^2), and coefficients of variability decreased as plots approached squareness. As in previous studies, the assumption implied that disease development was unrestricted. A plot 42 × 124 ft might permit unencumbered disease development for both *E. graminis* f. sp. *tritici* and *S. avenae* f. sp. *avenae*. Yet, studies on horizontal dissemination of spores (21,23) suggest that the minimum plot size necessary for unrestricted disease development and therefore for maximum impact of disease on crop productivity is not arbitrary but is a function of spore dispersal mechanisms. Roelfs (21) used regression analysis in the form $\log y = \log a + b \log x$ to predict numbers of urediospores of *Puccinia graminis* f. sp. *tritici* (disseminated primarily by wind) and annuli downwind from an area source, while Rowe and Powelson (23) used the same model to predict dispersal of conidia of *Pseudocercosporella herpotrichoides* (disseminated primarily by rain) from a point source. Regression coefficients (b) associated with dissemination of urediospores and conidia were −0.5 and −1.06, respectively. If we assume $\log a = 1$ (source strength is equal) and $\log x = 1$ (a point 10 m from source), then for *P. herpotrichoides* $\log y = -0.06$ (≅0) and $y = 0.87$ (≅1). But for *P. graminis* f. sp. *tritici*, $\log y = 0.5$ and $y = 3.16$. Therefore, approximately three times more urediospores than conidia are expected at 10 m from a source of equal strength. At 100 m from a source ($\log x = 2$), the equation predicts a 10-fold difference. A plot of sufficient size, therefore, to permit unrestricted development of fungi with splash-dispersed spores may not be adequate for fungi with wind-dispersed spores.

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TABLE 1. Pertinent information for orthogonal comparisons of area under disease progress curve (ADPC) and plot size for *Pyrenophora teres* at Ellouzia, Morocco

Treatments[a]	40_1	40_2	40_3	40_4	40_5	40_6	40_7	20_1	20_2	20_3	20_4	20_5	20_6	20_7	10_1	10_2	10_3	10_4	10_5	10_6	10_7			
Treatment totals (T_i)	0.31	0.36	1.83	6.35	34.05	20.92	63.66	0.20	0.22	1.12	3.59	19.48	12.51	35.79	0.25	0.27	1.23	3.89	17.77	11.33	34.64	Q[b]	K(r)[c]	SS[d]	F[e]
Comparison and no.																									
1. 40_1 vs. $20_1 + 10_1$	+2[f]	0	0	0	0	0	0	−1	0	0	0	0	0	0	−1	0	0	0	0	0	0	0.17	6(3)	0.0015	<1
2. 20_1 vs. 10_1	0	0	0	0	0	0	0	+1	0	0	0	0	0	0	−1	0	0	0	0	0	0	−0.06	2(3)	0.0005	<1
3. 40_2 vs. $20_2 + 10_2$	0	+2	0	0	0	0	0	0	−1	0	0	0	0	0	0	−1	0	0	0	0	0	0.24	6(3)	0.0031	<1
4. 20_2 vs. 10_2	0	0	0	0	0	0	0	0	+1	0	0	0	0	0	0	−1	0	0	0	0	0	−0.06	2(3)	0.0005	<1
5. 40_3 vs. $20_3 + 10_3$	0	0	+2	0	0	0	0	0	0	−1	0	0	0	0	0	0	−1	0	0	0	0	1.31	6(3)	0.0950	<1
6. 20_3 vs. 10_3	0	0	0	0	0	0	0	0	0	+1	0	0	0	0	0	0	−1	0	0	0	0	−0.11	2(3)	0.0020	<1
7. 40_4 vs. $20_4 + 10_4$	0	0	0	+2	0	0	0	0	0	0	−1	0	0	0	0	0	0	−1	0	0	0	5.22	6(3)	1.5140	12.4[g]
8. 20_4 vs. 10_4	0	0	0	0	0	0	0	0	0	0	+1	0	0	0	0	0	0	−1	0	0	0	−0.30	2(3)	0.0145	<1
9. 40_5 vs. $20_5 + 10_5$	0	0	0	0	+2	0	0	0	0	0	0	−1	0	0	0	0	0	0	−1	0	0	30.85	6(3)	52.8800	433[g]
10. 20_5 vs. 10_5	0	0	0	0	0	0	0	0	0	0	0	+1	0	0	0	0	0	0	−1	0	0	1.71	2(3)	0.4880	4.0
11. 40_6 vs. $20_6 + 10_6$	0	0	0	0	0	+2	0	0	0	0	0	0	−1	0	0	0	0	0	0	−1	0	18.00	6(3)	18.0040	147[g]
12. 20_6 vs. 10_6	0	0	0	0	0	0	0	0	0	0	0	0	+1	0	0	0	0	0	0	−1	0	1.18	2(3)	0.2320	1.9
13. 40_7 vs. $20_7 + 10_7$	0	0	0	0	0	0	+2	0	0	0	0	0	0	−1	0	0	0	0	0	0	−1	56.88	6(3)	179.7400	1,473[g]
14. 20_7 vs. 10_7	0	0	0	0	0	0	0	0	0	0	0	0	0	+1	0	0	0	0	0	0	−1	1.16	2(3)	0.2220	1.81

[a] Treatments are ADPC for intervals between consecutive disease assessments. Treatments 40_7, 20_7, and 10_7 are sums of six intervals for plots 40×40, 20×20, and 10×10 m, respectively.
[b] $Q = \Sigma_i C_i T_i$.
[c] $K(r) = \Sigma C_i^2$ (no. reps.).
[d] $SS = Q^2/K(r)$.
[e] $F = SS/MSE$, where MSE = 0.122.
[f] Orthogonal coefficient (C_i).
[g] Significant at 5%.

To test the hypothesis that disease development of fungi with different spore dispersal mechanisms is a function of plot size, we compared ADPC values for *Pyrenophora teres* Drechs. and *Mycosphaerella graminicola* (Fuckel) Schroeter from plots 10×10, 20×20, and 40×40 m. These fungi were chosen because they represent species with wind-dispersed (*P. teres*) and splash-dispersed (*M. graminicola*) conidia and because they are indigenous to cereal-growing regions of Morocco where this study was made. ADPC was used to compare epidemics because it expresses the interaction between disease severity and duration of an epidemic.

MATERIALS AND METHODS

Square plots of barley (*Hordeum vulgare* L.) and wheat (*Triticum aestivum* L. emend. Thell.) were planted at Ellouzia, Jamâa Shaim, Tadla, Douyet, and Sidi Kacem, Morocco. Plot sizes were 10×10, 20×20, and 40×40 m. Plots were seeded in a checkerboard pattern, with barley plots separated from wheat plots by 10 m of open ground. Plots of the same crop, however, were separated by 40 m (20 m of open ground plus 20 m of other crop) at Ellouzia and Jamâa Shaim and by 30 m (20 m of open ground plus 10 m of other crop) at Douyet, Sidi Kacem, and Tadla. The checkerboard pattern was used to limit spore dissemination between plots of the same crop while maximizing numbers of treatments on available land.

Barley and wheat cultivars used were chosen because of their susceptibility to *P. teres* and *M. graminicola*, respectively, and because they were grown commercially in the vicinity of the experimental sites. Both crops were seeded in rows spaced 20 cm apart at 110 kg/ha (barley) and 100 kg/ha (wheat). Only plots at Jamâa Shaim were fertilized (190 kg/ha of ammonium sulfate, 88 kg/ha of potassium sulfate, and 83 kg/ha of triple superphosphate); none was artificially inoculated.

Disease assessment. The percentage of leaf area affected by disease was assessed on individual leaves from 10 culms at several growth stages from tillering to ripeness using a key we developed for *P. teres* and one developed by James (8) for *M. graminicola*.

Grain was harvested from five areas in each plot except at Ellouzia, where heads were collected randomly and 1,000 grain weights were taken. Each area was 1 m^2 (two adjacent rows 2.5 m long). Grain weight was expressed in grams at Ellouzia and as kilograms per hectare at all other locations.

ADPC was calculated by the method of Shaner and Finney (24) for each interval between two consecutive disease assessments. ADPC and grain weights from Ellouzia and Jamâa Shaim were analyzed separately according to model I (fixed) analysis of variance (ANOVA), but data from Douyet, Sidi Kacem, and Tadla were combined and analyzed by model II (random) ANOVA, as location was considered a random effect. The method of orthogonal contrasts (18) was used to make pertinent comparisons between plot size and ADPC for each interval. We have presented one table (Table 1) of orthogonal comparisons to show the method of analysis. All other comparisons between ADPC and plot size were made in the same manner. Tables of all analyses are available on request from the first author.

Spore dispersal. To evaluate *P. teres* spore movement from plots as a function of plot size, Rotorod spore samplers were placed in the center and 1 m from the upwind and downwind edges of barley plots at Ellouzia, Jamâa Shaim, and Tadla. Samplers were operated in 10-min segments per sample, with eight samples taken from each plot size at Ellouzia, three at Jamâa Shaim, and four at Tadla. Rods were examined under a light microscope and spore numbers were counted visually from each sampling rod and expressed as numbers of spores per cubic meter of air. The percentage of spores escaping from plots (PSE) was calculated as $PSE = 100\times/((x + y) - z)$, where x = number of spores per cubic meter 1 m downwind from plot edge, y = number of spores per cubic meter in plot center, and z = number of spores per cubic meter 1 m upwind from plot edge. Orthogonal comparisons were made of PSE values at Ellouzia, but one-way ANOVA was used at Jamâa Shaim and Tadla because only two plot sizes were present.

Dispersal distance of *M. graminicola* pycnidiospores as a function of rainfall was studied by subjecting freshly excised wheat leaves containing pycnidia to simulated rainfall. Twenty leaves were placed on a paper support under a tripod 3 m high to which was fixed a nozzle. Rainfall of two intensities (63.5 and 82.5 $mm.hr^{-1}$) but similar quantity (13.75 mm) was created by selecting appropriate nozzle sizes and regulating water pressure (confirmed with an in-line tensiometer) and exposure time. Rotorod samplers were placed on annuli 20 (two samples), 50 (three samples), and 100 (three samples) cm from the leaves. The samplers were started 10 min after simulated rain began, then stopped for 13 and 10 min, the intervals necessary for 13.75 mm of rain at 63.5 and 82.5 $mm.hr^{-1}$, respectively. The experiment was repeated three times, each time with fresh leaves. Spores were counted as described above.

RESULTS

Pyrenophora teres. Indigenous inoculum provided for relatively uniform incidence and percent severity within each site at the time initial disease assessments were made (Table 2). ADPC in plots 40 × 40 m appears different from those in plots 20 × 20 and 10 × 10 at Ellouzia (Fig. 1A), and orthogonal comparisons confirm that those

TABLE 2. Summary of pertinent information regarding effect of plot size on development of *Pyrenophora teres*[a]

Location	Plot size (m)	Cultivar	Initial observation: Growth stage	Initial observation: Prevalence (%)	Initial observation: Severity (%)	Final observation: Growth stage	Final observation: Severity (%)	r[b]	ADPC[c]	PSE[d]	Weight 1,000 kernels (g)	Yield (kg/ha)
Ellouzia	40 × 40	071	Tillering	97	0.6	Ripening	87	0.088	21.22	39.5	53.0	···
	20 × 20	071	Tillering	87	0.5	Ripening	54	0.067	11.93	53.3	52.5	···
	10 × 10	071	Tillering	91	0.6	Ripening	51	0.065	11.55	70.0	50.7	···
Jamâa Shaim	40 × 40	43/75	Tillering	83	0.05	Ripening	86	0.135	15.94	24.0	···	1,574
	20 × 20	43/75	Tillering	75	0.04	Ripening	63	0.123	5.59	34.0	···	1,526
Composite	20 × 20	013	Boot	100	9.8	Hard dough	82	0.089	17.75	35.0	···	2,168
	10 × 10	013	Boot	100	10.5	Hard dough	80	0.084	16.79	29.0	···	2,178

[a] Percent prevalence, percent severity, r, ADPC, and grain weight are means of three plots at Ellouzia and Jamâa Shaim but means of one plot at each of three locations for the composite.
[b] Apparent infection rate per unit per day, from Vanderplank (27).
[c] Area under disease progress curve, from Shaner and Finney (24).
[d] Percentage of spores escaping from plots.

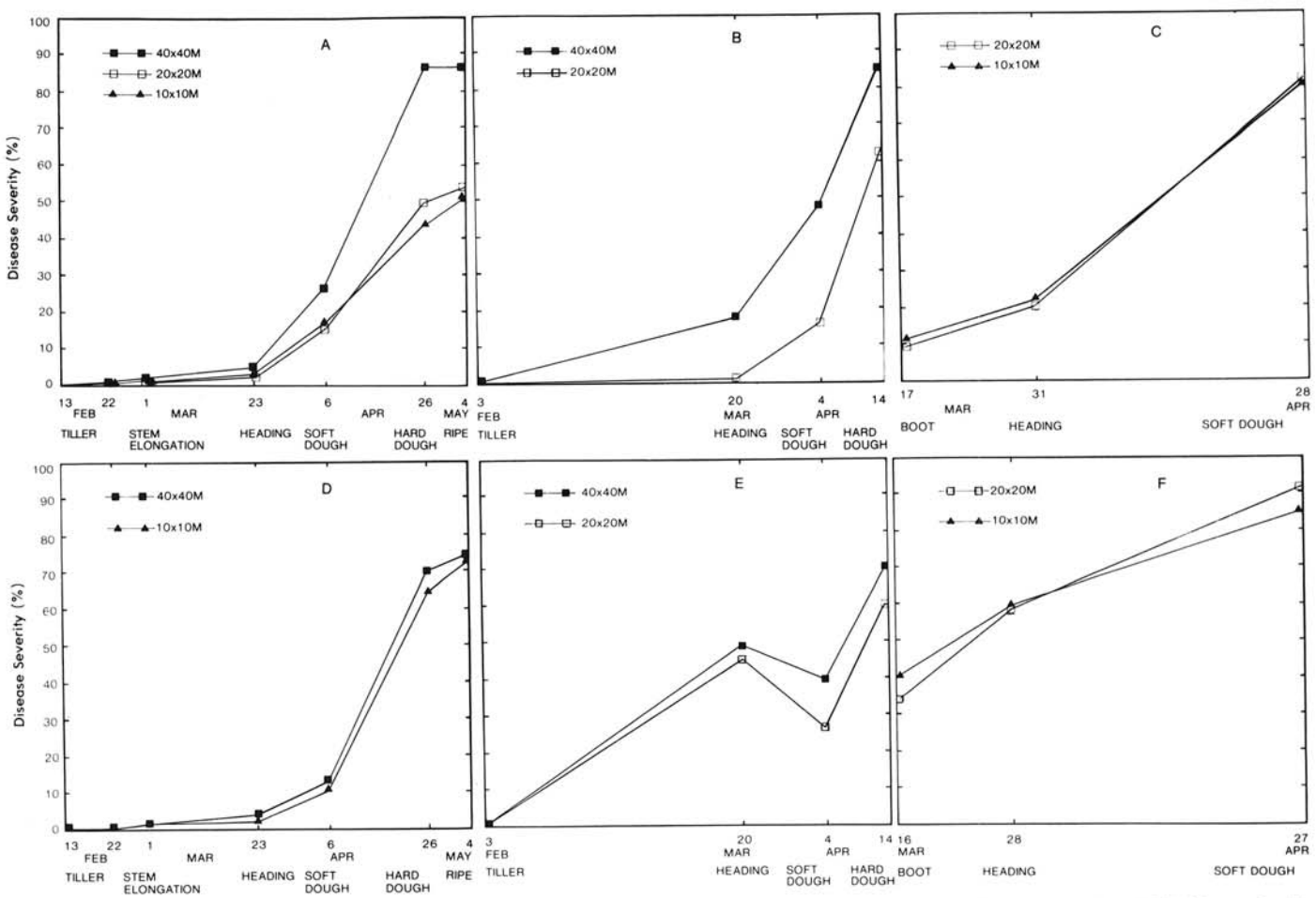

Fig. 1. A, Progress of *Pyrenophora teres* in plots 40 × 40, 20 × 20, and 10 × 10 m at Ellouzia. **B,** Progress of *P. teres* in plots 40 × 40 and 20 × 20 m at Jamâa Shaim. **C,** Progress of *P. teres* in plots 20 × 20 and 10 × 10 m expressed as a composite from Tadla, Douyet, and Sidi Kacem. **D,** Progress of *Mycosphaerella graminicola* in plots 40 × 40 and 10 × 10 m at Ellouzia. **E,** Progress of *M. graminicola* in plots 40 × 40 and 20 × 20 m at Jamâa Shaim. **F,** Progress of *M. graminicola* in plots 20 × 20 and 10 × 10 m expressed as a composite from Douyet and Sidi Kacem.

visual differences are significant (Table 1). ADPC values for seven intervals between tillering and ripeness show that plots 40 × 40 had greater values than plots 20 × 20 or 10 × 10 after heading. When ADPC values for all intervals between tillering and ripeness were summed (Table 1), values from plots 40 × 40 were significantly greater than those from plots 20 × 20 and 10 × 10 but values from plots 20 × 20 and 10 × 10 were not significantly different for any interval. Apparent infection rates and final disease severities from plots 40 × 40 were significantly greater than rates and severities from plots 20 × 20 and 10 × 10. Rates and severities from plots 20 × 20 and 10 × 10 were not significantly different (Table 2).

At Jamâa Shaim there was a clear difference in disease development between plots 40 × 40 and 20 × 20 (Fig. 1B). As at Ellouzia, initial disease severities in all plots were similar, but by hard dough, severities in plots 40 × 40 and 20 × 20 were significantly different even though apparent infection rates were not (Table 2). Orthogonal comparisons of ADPC showed significant differences at all intervals, including that between tillering and heading. A composite of disease development at Douyet, Sidi Kacem, and Tadla (Fig. 1C) shows similar disease severities between plot sizes at each assessment. ADPC values were not significantly different for any interval.

Regardless of location, ADPC values calculated from disease assessments made on the uppermost leaf (flag) and from assessments made on the penultimate leaf (flag-1) in plots 40 × 40 were significantly greater than values from plots 20 × 20 for the cumulative interval from heading to hard dough. No significant differences were noted between ADPC values from plots 40 × 40 and values from plots 20 × 20 for the intervals from heading to soft dough and from soft dough to hard dough. ADPC values from plots 20 × 20 and 10 × 10 were not significantly different.

The mean ADPC from plots 40 × 40 was two times greater than those from plots 20 × 20 and 10 × 10 at Ellouzia and almost three times greater than that from plots 20 × 20 at Jamâa Shaim, yet grain weights were not significantly different (Table 2). ADPC values from plots 20 × 20 and 10 × 10 were not significantly different, and neither were grain weights taken from three locations used in the composite.

Orthogonal comparisons showed significant differences between the percentage of conidia escaping from plots 40 × 40, 20 × 20, and 10 × 10 at Ellouzia (Table 3). But at Jamâa Shaim and Tadla, where similar tests were made, differences between the percentage of conidia escaping from plots 40 × 40 and 20 × 20 and between plots 20 × 20 and 10 × 10, respectively, were not significant.

Mycosphaerella graminicola. As in the companion study with *P. teres*, natural inoculum provided for relatively uniform incidence and percent severity within each site at the time initial disease assessments were made (Table 4). Disease progress, expressed as the apparent infection rate, and final disease severity were not significantly different in plots 40 × 40 and 10 × 10 at Ellouzia (Fig. 1D) and in plots 40 × 40 and 20 × 20 at Jamâa Shaim (Fig. 1E), yet orthogonal comparisons showed significant differences in ADPC at both locations. Differences in ADPC at Ellouzia, however, occurred only for the interval from soft dough to hard dough and when ADPC values were summed for all six intervals. Similarly, differences at Jamâa Shaim occurred only when ADPC values were summed for the three intervals between four disease assessments. Disease progress in plots 20 × 20 and 10 × 10 at Douyet and Sidi Kacem is presented as a composite (Fig. 1F). As suggested by the similarity between disease progress curves, there are no significant differences in ADPC, apparent infection rate, and final disease severity (Table 4). ADPC calculated from disease progress on flag leaves and from disease progress on flag-1 leaves did not show significant interplot differences. As with *P. teres*, there were no significant interplot differences in grain yield (Table 4).

TABLE 3. Pertinent information for orthogonal comparisons of plot size and percentage of spores escaping from plots infected with *Pyrenophora teres*

Treatments[a]	40 × 40 (m)	20 × 20 (m)	10 × 10 (m)				
Treatment totals (T_i)	334.03	395.94	580.93	Q[b]	K(r)[c]	SS[d]	F[e]
Comparison and no.							
1. 40 vs. 20 + 10	+2[f]	−1	−1	−308.81	6(8)	1,986.74	6.26[g]
2. 20 vs. 10	0	+1	−1	−184.99	2(8)	2,138.83	6.74[g]

[a] Treatments are percentage of spores escaping from plots 40 × 40, 20 × 20, and 10 × 10 m.
[b] $Q = \Sigma_i C_i T_i$.
[c] $K(r) = \Sigma C_i^2$ (no. reps.).
[d] $SS = Q^2/K(r)$.
[e] $F = SS/MSE$, where MSE = 317.36.
[f] Orthogonal coefficient (C_i).
[g] Significant at 5%.

DISCUSSION

P. teres and *M. graminicola* were chosen because of their known differences in spore dissemination characteristics (14,28) and because of their importance to Moroccan cereal culture. Our preliminary investigations showed that conidia of *M. graminicola* were dispersed less than 50 cm from a point source by rainfall intensities of 63.5 and 82.5 $mm.hr^{-1}$ but that 52, 26, 10.8, 2.8, 1.4, and 0.05% of the initial number of *P. teres* conidia released from a point source were in a horizontal plane 5, 10, 20, 30, 40, and 50 m, respectively, from the source. Those data suggested to us, therefore, that minimum plot size needed to permit unrestricted development of *M. graminicola* might restrict development of *P. teres*. Further experimentation indicated that ADPC was a function of plot size and that *P. teres* was more severely restricted than *M. graminicola* within the range of plot sizes tested. That is, if ADPC from plots 40 × 40 represents the maximum area attainable (100%), then ADPC values from plots 20 × 20 and 10 × 10 infected with *P. teres* (Ellouzia) were 56 and 54% of the maximum, respectively, whereas at Jamâa Shaim, ADPC from plots 20 × 20 was 35% of the maximum and those differences occurred primarily after heading. Differences in ADPC from tillering to heading in plots 40 × 40 and

TABLE 4. Summary of pertinent information regarding effect of plot size on development of *Mycosphaerella graminicola*[a]

Location	Plot size (m)	Cultivar	Initial observation: Growth stage	Initial observation: Prevalence (%)	Initial observation: Severity (%)	Final observation: Growth stage	Final observation: Severity (%)	r[b]	ADPC[c]	Yield (kg/ha)
Ellouzia	40 × 40	Siete cerros	Tillering	87	0.13	Ripening	75	0.096	15.91	···
	10 × 10	Siete cerros	Tillering	77	0.12	Ripening	73	0.096	14.75	···
Jamâa Shaim	40 × 40	Siete cerros	Tillering	9	0.004	Ripening	70	0.159	23.16	1,995
	20 × 20	Siete cerros	Tillering	21	0.006	Ripening	60	0.146	19.79	1,859
Composite	20 × 20	Siete cerros	Heading	100	34.0	Hard dough	92	0.074	28.32	2,968
	10 × 10	Siete cerros	Heading	100	27.0	Hard dough	86	0.067	25.08	2,643

[a] Percent prevalence, percent severity, r, and ADPC are means of three plots at Ellouzia and Jamâa Shaim but means of one plot at each of three locations for the composite.
[b] Apparent infection rate per unit per day, from Vanderplank (27).
[c] Area under disease progress curve, from Shaner and Finney (24).

20 × 20 at Jamâa Shaim perhaps are exaggerated, since we made only two observations rather than four, as at Ellouzia. Additional observations, therefore, might have revealed greater similarity in disease progress between tillering and heading than that presented. In contrast, ADPC values for *M. graminicola* in plots 10 × 10 (Ellouzia) and 20 × 20 (Jamâa Shaim) were 93 and 85% of the maximum, respectively, and those small differences, although statistically significant, were uniformly distributed throughout the entire assessment period and do not appear to be biologically significant. Even when ADPC for *P. teres* was calculated from disease on flag and flag-1 leaves only, values from plots 40 × 40 were significantly different from values obtained from plots 20 × 20 and 10 × 10. Similar comparisons for *M. graminicola*, however, gave no significant differences, again emphasizing the differential effect of area on development of these two diverse pathogens, particularly after heading.

Despite interplot differences in ADPC, apparent infection rate, and final disease severities for *P. teres*, there were no significant interplot differences in grain weight and grain yield. Because *P. teres* has been reported to reduce kernel numbers but not to affect grain weight (20), perhaps the similarity in grain weights from plots that differed markedly in ADPC, r values, and final disease severities (Ellouzia, Table 2) is not unusual. However, grain yields from plots that showed significant differences in ADPC and final disease severities (Jamâa Shaim, Table 2) also were similar. That is, disease progress, characterized by the severities 0.05, 19, 48, and 86% at tillering, heading, soft dough, and hard dough, respectively, had no greater impact on grain yield than the respective severities 0.04, 1, 17, and 63%. If *P. teres* affects primarily kernel numbers (determined prior to the completion of anthesis), then the results from Jamâa Shaim imply that disease severities at tillering and heading necessary to sustain crop loss must exceed 0.05 and 19%, respectively.

Vanderplank (27) was the first to signal that small research plots might lose a greater proportion of spores than commercial fields and therefore experience a reduced rate of development. Our data for *P. teres* from Ellouzia support that view, as the proportion of spores escaping from plots was inversely proportional to plot size (Table 2). The same trend occurred at Jamâa Shaim, but differences were not significant because experimental error was large. The trend was reversed with the composite data from Douyet, Sidi Kacem, and Tadla, but, again, the experimental error was large so differences were not significant. In direct contrast to the effect of plot size on development of *P. teres*, relatively small plots appeared to permit unencumbered development of *M. graminicola*.

These results reflect perhaps fundamental differences in the response of *P. teres* and *M. graminicola* to area available for development. And those differences are in part linked to or associated with spore dispersal mechanisms. It seems reasonable to assume, therefore, that the area required for unrestricted development of a pathogen with wind-dispersed spores will be greater than the area needed for a pathogen disseminated by rainfall. Although compensating factors such as differences in the efficiency of spore deposition and spore infectivity might negate apparent differences in spore dispersal patterns, our results suggest that plot size should be added to plot shape and plot separation as a key consideration in disease epidemiology and crop loss studies and that optimum experimental plot size will be a function of spore dispersal characteristics.

LITERATURE CITED

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