Disease Resistance in Wild *Pennisetum* Species

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ABSTRACT

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Ninety-eight accessions of wild *Pennisetum glaucum* from the primary gene pool (1° *Pennisetums*) and 27 species from the tertiary gene pool (3° *Pennisetums*) of *P. glaucum* were evaluated for disease resistance. The 1° *Pennisetums* were also evaluated for morphologic traits to further differentiate the accessions. The 1° *Pennisetums* were evaluated for resistance to *Pyricularia grisea, Puccinia substriata* var. *indica*, and *Moesziomyces penicillariae* and also for height, diameter of the fifth internode, number of nodes, heading date, and panicle length and morphology. Species in the 3° gene pool were evaluated for resistance to *P. s. indica, Pyricularia grisea, Bipolaris setariae, Drechslera dematioidea, Phyllosticta penicillariae*, and *Exserohilum rostratum*. Within the 1° *Pennisetums*, frequencies of plants resistant to *Pyricularia grisea* and *P. s. indica* averaged 90.5 and 29.8%, respectively. Smut severities averaged 3.8%. Twenty-two accessions with characteristics of the subspecies *stenostachyum* tended to have greater frequencies of rust-resistant plants. Forty-six accessions with characteristics of the subspecies *monodii* were more smut-resistant. The 3° *Pennisetums* were immune to *P. s. indica*. On the basis of reactions to the leaf blighting fungi, the 3° species were clustered into two groups, one with relatively high levels of resistance to the five pathogens and the other with less effective resistance.

Pennisetum is a diverse genus with over 100 species (16). The wild gene pool available for improvement of pearl millet (*P. glaucum* (L.) R. Br.) consists of *Pennisetum* species with chromosome numbers in multiples of x = 5, 7, 8, or 9 (13). Use of these germ plasm resources in pearl millet breeding has been limited.

The primary gene pool (1° *Pennisetums*) of pearl millet consists of *P. glaucum* and its wild subspecies, which all have x = 7 chromosomes homologous to those of pearl millet. *P. glaucum* land races, the weedy subspecies *stenostachyum* (Klotzch) Brunken, and the wild subspecies *monodii* (Maire) Brunken all cross easily with pearl millet and can be useful for increasing growth rate and grain yield of pearl millet (1). Genes for resistance to *Pyricularia grisea* (Cooke) Sacc. and *Puccinia substriata* Ellis & Barth. var. *indica* Ramachar & Cummins have been transferred from the subspecies *monodii* and are present in the hybrid Tifleaf 2 (12).

The secondary gene pool, comprising napiergrass (*P. purpureum* Schumach) (n=14), can be a source of useful traits. Hybrids with forage potential were produced by crossing diploid and tetraploid pearl millets with napiergrass (11). Genes for fertility restoration, stiff stalk, and other traits have been transferred to pearl millet from napiergrass (10).

Use of the tertiary gene pool (3° *Pennisetums*) has been limited because of difficulties with interspecific hybridization. Chromosomes of these species are generally nonhomologous to those of pearl millet. *Pennisetum* species with x = 9 can hybridize with pearl millet more easily than can species with x = 5 or 8 (6). Some species in the 3° gene pool are potential sources of genes for apomixis (7).

Disease resistance in the wild subspecies of *P. glaucum* and the 3° *Pennisetum* species has not been evaluated in any detail in spite of the diversity present in noncultivated *Pennisetum* species. The objectives of this study were to evaluate disease resistance and morphologic traits within a sample of wild 1° *Pennisetum* accessions, to determine disease resistance within *Pennisetum* species from the 3° gene pool of pearl millet, and to classify the accessions in an attempt to identify potentially different sources of disease resistance.

MATERIALS AND METHODS

The 1° *Pennisetums*. Ninety-eight wild *P. glaucum* accessions were evaluated: 44 from Niger, 37 from Mali, 15 from Senegal, and 1 each from Sudan and Cameroon. These accessions have been maintained by sibbing and are heterogeneous and heterozygous.

For field evaluations, seed were sown in Styrofoam flats with 5 × 5 cm compartments containing a previously described potting mix (26) in the greenhouse in May 1990. Greenhouse temperatures were maintained at approximately 30 C. Plants were grown under natural lighting and were watered daily. Groups of about five plants at the four-leaf stage were transplanted into two blocks in the field in June. Hills were spaced 0.6 m within rows, and row widths were alternated between 0.6 and 1.2 m.

An average of 2.9 panicles per accession were inoculated with *Moesziomyces penicillariae* (Bref.) Vánky to evaluate smut resistance. When panicles were half-emerged from the boot, flag leaf sheaths were removed and panicles were misted to dripping with a sporidial suspension (2×10^7 sporidia per milliliter) of *M. penicillariae* isolates 1, 6, and 39. Isolates 1 and 6 are highly pathogenic in combination, and isolate 39 has a high level of solo pathogenicity (23). Isolates were grown separately on V8 agar (20% V8 juice + 1.5% NaOH) for 6-10 days at 25 C under continuous fluorescent lighting, and equal quantities of the isolates were mixed for the inoculum. After inoculation, panicles were covered overnight (17 hr) with prewetted plastic

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bags, which were replaced by glassine bags in the morning.

Approximately 6 wk after inoculation, the percentage of florets with sori was estimated for each panicle. In addition, panicles were classified on a 1–4 scale for their degree of resemblance to the subspecies *stenostachyum* (classified as 1) or to the subspecies *monodii* (classified as 4) (2,3). Classification was based on the degree of shattering, density of florets along the panicle, and exposure of grain apices from the floral bracts. Classifications of 2 or 3 were assigned to intermediate panicle types.

Seed of the 1° *Pennisetums* were planted in the greenhouse 30 April 1991 as in 1990, then transplanted into single plant hills in May. Hills were spaced 0.7 m within rows and 1.3 m between rows. Plantings were arranged in a randomized complete block design with eight replications.

Inoculations with *M. penicillariae* and evaluations of panicle type were performed as in 1990, with the exception that up to two panicles of each plant were inoculated. An average of 9.1 panicles per accession were inoculated.

Inoculation date was considered the heading date. Diameters of the fifth internode, number of nodes, height, and panicle length were measured from two of the main culms of each plant.

In greenhouse evaluations, seed of the 1° *Pennisetums* were planted into 16-cm plastic pots under conditions described above. One replicate (one pot) was randomized within each of four blocks. Blocks were grown and inoculated at different times. Greenhouse temperatures were maintained at approximately 30 C. Plants were grown under natural lighting.

An average of 21.6 plants per replicate of each accession were inoculated at the three-leaf stage with *Pyricularia grisea* (1×10^4 conidia per milliliter). Inoculum culture, inoculation procedures, and reaction evaluations were performed as previously described (26). During evaluation of reactions to *Pyricularia grisea* infection, small and uncompetitive plants were thinned from pots. Two days later, remaining plants (an average of 16 plants per replicate) were inoculated with urediniospores of *P. s. indica* collected from a susceptible cultivar from the field as previously described (26). Plants were evaluated 11 days after inoculation. Infection types 0, 1, 2, and X (the mesothetic reaction) were considered resistant (19). The X type suggested the presence of resistance in an accession because races of *P. s. indica* exist in the United States (22).

Two replicates were inoculated with *M. penicillariae*. An average of 3.7 panicles per accession were inoculated with a sporidial suspension as described above, except that emerging panicles were immersed into test tubes containing inoculum. About 1 mo after inoculation, panicles were evaluated for smut severity and panicle type.

The 3° *Pennisetums*. The following 3° *Pennisetum* species were evaluated: one accession of *P. flaccidum* Griseb., one of *P. macrourum* Trin., two of *P. orientale* Rich, one of *P. pedicellatum* Trin., two of *P. polystachyon* (L.) Schult., two of *P. setaceum* (Forssk.) Chiov., four of *P. squamulatum* Fresen, one of *P. subangustum* Schumach, two of *P. villosum* R. Brown ex Fresen, two of *Cenchrus ciliaris* L. (syn *P. ciliare* (L.) Link), three of *P. alopecuroides* (L.) Spreng., one of *P. hohenackeri* Hochst. ex Steud., two of *P. nervosum* (Nees) Trin., two of *P. ramosum* (Hochst.) Schweinf., and one of *P. sweinfurthii* Pilger. The first 10 species are apomictic and true-breeding, and the latter five are sexual and have been maintained by selfing.

Plants of the 3° *Pennisetum* species were transplanted into the field in two replications in June 1990 to examine general characteristics. Moderate to severe leaf blight developed on some accessions. Blighted leaves were surface-disinfected for 1 min in 0.05% NaOCl and plated on water agar, then incubated at 25 C under continuous fluorescent lighting. Fungi growing from leaves were transferred to V8 agar for purification and identification. The predominant pathogens isolated were used in the greenhouse inoculations.

In each of two replications in the greenhouse, seed of the 3° *Pennisetum* species were sown in Promix potting mix (Premier Brands, Stamford, CT) in Styrofoam flats with 5×5 cm compartments. Plants were grown under conditions described above. Approximately five plants of each 3° species were inoculated with each pathogen by replication combination. Plants at the three- to five-leaf stage were placed in an inoculation chamber and inoculated either with *Pyricularia grisea* or *P. s. indica*, as described above, or with fungi isolated from plants grown in the field. Conidia of 10- to 16-day-old cultures from 10 petri plates were suspended in 500 ml of deionized water for the following inoculum suspensions: *Phyllosticta penicillariae* Speg. (2.8×10^6 conidia per milliliter), *Bipolaris setariae* (Sawada) Shoemaker (1.8×10^3 conidia per milliliter), *Exserohilum rostratum* (Drechs.) K.J. Leonard & E.G. Suggs (5.5×10^4 conidia per milliliter), and *Drechslera dematioidea* (Bubak & Wroblewski) Subram. & Jain (7.3×10^5 conidia per milliliter). Plants were misted to dripping with inoculum and kept in the inoculation chamber for approximately 20 hr, where they were automatically misted with deionized water for 1 min every 30 min.

Plants were evaluated 6 and 11 days after inoculation for reaction to *Pyricularia grisea* and *P. s. indica*, respectively, as described above. Eleven days after inoculation, plants were evaluated on a 0–4 scale for their reactions to fungi isolated from plants in the field. In evaluations of reaction to *Phyllosticta penicillariae*, 0 = no visible sign of infection, 1 = limited chlorosis, 2 = chlorosis with limited tip and margin necrosis of lower leaves, 3 = chlorosis with water-soaked lesions, and 4 = 1- to 5-mm necrotic lesions with extensive chlorosis and tip and margin necrosis. In evaluation of reactions to *B. setariae* and *E. rostratum*, 0 = no visible sign of infection, 1 = brown flecks up to 1 mm in diameter, 2 = brown or necrotic flecks up to 2 mm in diameter, 3 = 2- to 5-mm necrotic lesions with chlorosis, and 4 = 2- to 7-mm coalescing lesions with extensive chlorosis and necrosis. In evaluating reactions to *D. dematioidea*, 0 = no visible sign of infection, 1 = diffuse chlorosis, 2 = diffuse chlorosis with 1- to 3-mm diffuse brown flecks sometimes with limited leaf tip necrosis, 3 = distinct chlorosis with tip and margin necrosis, and 4 = chlorosis with 1- to 3-mm coalescing lesions with extensive necrosis.

Reisolations from surface-disinfected leaves plated on V8 agar were made to confirm pathogenicity.

Data analysis. Means for percentages of plants resistant to rust and Pyricularia leaf spot, smut severities, panicle characteristics, days to heading in 1991, height, panicle length, internode diameter, and number of nodes were calculated for the 1° *Pennisetums*. Because a severe infestation of chinch bug (*Blissus leucopterus leucopterus* Say) limited data that could be recorded on the accessions in 1990, most of the data on morphologic traits were obtained from the 1991 field experiment.

Reaction means of the 3° *Pennisetums* inoculated with foliar pathogens in the greenhouse were calculated.

Data for the 1° and 3° *Pennisetums* were evaluated separately. In an attempt to group the accessions on the basis of their similarities and to identify potentially different sources of disease resistance, data were standardized and analyzed by principal component and Ward's cluster analysis (18). Misclassified accessions were identified by discriminant analysis, which was used to test homogeneity of within-cluster covariance matrices.

RESULTS

The 1° *Pennisetums*. Percentages of plants with resistance to *Pyricularia grisea* ranged from 50 to 100% ($\bar{x}$ = 90.5%) (Fig. 1), and resistance to *P. s. indica* ranged from 0 to 82.2% ($\bar{x}$ = 29.8%) (Fig. 2). Smut severities from inoculations in the field and greenhouse ranged from 0 to 21.2% ($\bar{x}$ = 3.8%) (Fig. 3).

Principal component analysis of dis-

ease resistance and morphologic traits revealed three components with a variance greater than one. These components accounted for 70.4% of the standardized variance in the data. The most significant component accounted for 34.3% of the variation.

Several of the morphologic traits were correlated (Table 1), often with respect to robustness. The generalization could be made that tall accessions had more nodes, thicker internodes, and longer panicles that more closely resembled the subspecies *stenostachyum*. Short accessions had fewer nodes, more slender internodes, and shorter panicles that more closely resembled the subspecies *monodii*. These correlations agree with the generalizations of Brunken (2) and Brunken et al (3), since *stenostachyum* is intermediate in type to cultivated pearl millet and *monodii*.

Some associations between morphologic traits and disease resistance existed. Smut susceptibility was correlated with longer, *stenostachyum*-like panicles, thicker internodes, and greater numbers of nodes (Table 2). Smut susceptibility was also correlated with a greater frequency of rust resistance. Rust resistance was correlated with *stenostachyum*-like panicles and had low correlations with thicker internodes and frequency of Pyricularia leaf spot resistance. Pyricularia leaf spot resistance was correlated with a greater number of nodes and thicker internodes as well as with later maturity. These associations suggest that *monodii*-like accessions were more resistant to *M. penicillariae* and *stenostachyum*-like accessions were more resistant to *P. s. indica* and, to some extent, *Pyricularia grisea*.

Ward's cluster analysis grouped accessions into three hierarchical clusters. Discriminant analysis reclassified eight accessions from the cluster analysis. Four accessions from cluster 1 were reclassified into cluster 2, two accessions from cluster 2 were reclassified into cluster 1, and two accessions from cluster 3 were reclassified into clusters 1 and 2.

Seventeen pairs of accessions and two accessions clustered with pairs had squared multiple correlations greater than 0.99, indicating that data were insufficient to differentiate them. There were some associations of country of origin among these similar accessions. An accession from Senegal was clustered with a pair from Mali, four pairs were collected in Mali, eight pairs had an accession each from Mali and Niger, three pairs were collected in Niger, and the Cameroon accession was clustered with an accession from Niger.

Cluster means for the descriptors indicated that cluster 1 included accessions that were *monodii*-like and cluster 3 included *stenostachyum*-like accessions (Table 3). Cluster 2 means either were intermediate to means of clusters 1 and 3 or had means similar to those of cluster 1 or 3.

Accessions from Niger were distributed among all the clusters (Fig. 4). The majority of accessions from Mali (97%)

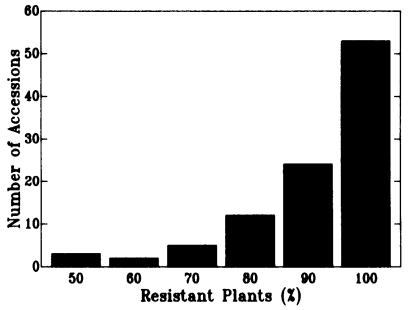

Fig. 1. Resistance to *Pyricularia grisea* in wild *Pennisetum* species of the primary gene pool. Seedlings were inoculated in the greenhouse and examined for percentage of resistant plants. Values are the means of four replicates.

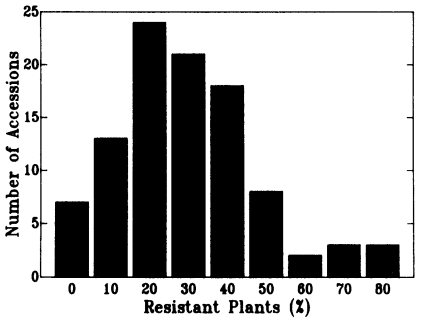

Fig. 2. Resistance to *Puccinia substriata* var. *indica* in wild *Pennisetum* species of the primary gene pool. Seedlings were inoculated in the greenhouse and examined for percentage of resistant plants. Values are the means of four replicates.

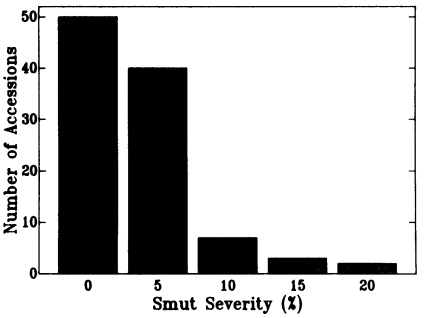

Fig. 3. Resistance to *Moesziomyces penicillariae* in wild *Pennisetum* species of the primary gene pool. Plants in the greenhouse and field were inoculated as the panicles emerged from the boot. Values are the means of three experiments.

Table 1. Correlations between morphologic traits of wild 1° *Pennisetum* germ plasm

Correlated traits	*r*	*P*
Height : number of nodes	0.74	0.0001
Panicle length : panicle type[a]	−0.59	0.0001
Internode diameter[b] : number of nodes	0.59	0.0001
Internode diameter : panicle type	−0.59	0.0001
Panicle length : internode diameter	0.48	0.0001
Panicle length : number of nodes	0.40	0.0001
Panicle length : heading date	−0.37	0.0002
Height : panicle length	0.35	0.0004
Number of nodes : heading date[c]	0.31	0.0019
Heading date : panicle type	0.29	0.0033
Height : internode diameter	0.28	0.0051
Number of nodes : panicle type	−0.28	0.0046

[a] 1 = Weedy subspecies *stenostachyum*, 4 = wild subspecies *monodii*, and 2 and 3 = intermediate types.
[b] Diameter of fifth internode.
[c] Days after planting.

Table 2. Correlations between disease resistance and morphologic traits in wild 1° *Pennisetum* germ plasm

Correlated traits	*r*	*P*
Smut severity : panicle type[a]	−0.46	0.0001
Smut severity : internode diameter[b]	0.28	0.0052
Smut severity : panicle length	0.26	0.0088
Smut severity : number of nodes	0.21	0.0338
Rust resistance[c] : smut severity	0.38	0.0001
Rust resistance : panicle type	−0.31	0.0020
Rust resistance : internode diameter	0.17	0.0791
Rust resistance : *Pyricularia* resistance[d]	0.18	0.0741
Pyricularia resistance : heading date	0.32	0.0011
Pyricularia resistance : number of nodes	0.28	0.0060
Pyricularia resistance : internode diameter	0.23	0.0206

[a] 1 = Weedy subspecies *stenostachyum*, 4 = wild subspecies *monodii*, and 2 and 3 = intermediate types.
[b] Diameter of fifth internode.
[c] Percentage of plants resistant to *Puccinia substriata* var. *indica*.
[d] Percentage of plants resistant to *Pyricularia grisea*.

were grouped into clusters 1 and 2, and 67% of the accessions from Senegal were included in cluster 3.

The 3° *Pennisetums*. Fungi isolated from the 3° *Pennisetums* in the field in 1990 included *Curvularia* and *Alternaria* spp., *Phyllosticta penicillariae, E. rostratum, B. setariae*, and *D. dematioidea*.

The 3° *Pennisetums* showed no signs of infection by *P. s. indica*, classified as infection type 0, while the Tift 23DB control plants were susceptible. Most of the 3° *Pennisetums* were highly resistant to *Pyricularia grisea* and had infection type 0. All of the *P. squamulatum* accessions were moderately susceptible, with infection type 3.

Reactions to the other fungi ranged from highly resistant to highly susceptible. *E. rostratum* and *B. setariae* were generally more pathogenic than *D. dematioidea* and *Phyllosticta penicillariae* (Table 4). The pathogens were reisolated from most leaves with infection types 1–4 but never from leaves with infection type 0.

Principal component analysis of the data of the 3° *Pennisetums* identified two components with a variance greater than one; these components accounted for 78.6% of the standardized variance. Ward's cluster analysis grouped accessions into two clusters, one of which had higher levels of resistance to all the pathogens (Table 4).

Among the nine species with more than one accession evaluated, all accessions of seven species were clustered together. One accession each of *P. orientale* and *P. ramosum* was included in separate clusters. Species from the section Eu-pennisetum (*P. setaceum* and *P. villosum*) were included in cluster 1 and were separated from those species belonging to sections Brevivalvula and Heterostachya (*P. pedicellatum, P. polystachyon, P. subangustum, P. squamulatum*, and *P. sweinfurthii*), which were included in cluster 2. Although several of the species have not been assigned to sectional taxa, our data suggest that *P. alopecuroides, P. hohenackeri*, and *P. macrourum* express some similarities to the species in the section Eu-pennisetum and were included in cluster 1 on the basis of their higher levels of resistance. *C. ciliaris, P. flaccidum*, and *P. nervosum* share similarities with the species in sections Brevivalvula and Heterostachya and were included in cluster 2 on the basis of their lower levels of disease resistance.

Table 3. Disease resistance and morphologic traits of wild 1° *Pennisetum* germ plasm and groups defined by cluster and discriminant analyses

Trait	Collection Mean ± SD	Cluster mean 1	2	3
Pyricularia resistance[a]	90.5 ± 12.2	86.3	96.4	91.2
Rust resistance[b]	29.8 ± 17.9	24.6	23.4	49.4
Smut severity	3.8 ± 4.0	2.4	2.9	8.0
Height (m)	2.5 ± 0.4	2.2	2.9	2.4
Number of nodes	12.7 ± 1.5	11.6	14.2	13.0
Internode diameter (cm)[c]	2.4 ± 0.5	2.1	2.6	2.9
Heading date[d]	135.5 ± 11.2	135.7	139.1	130.3
Panicle length (cm)	11.0 ± 2.6	9.4	12.0	13.0
Panicle type[e]	2.7 ± 0.7	3.1	2.7	1.9
Number of accessions	98	46	30	22

[a] Percentage of plants resistant to *Pyricularia grisea*.
[b] Percentage of plants resistant to *Puccinia substriata* var. *indica*.
[c] Diameter of fifth internode.
[d] Days after planting.
[e] 1 = Weedy subspecies *stenostachyum*, 4 = wild subspecies *monodii*, and 2 and 3 = intermediate types.

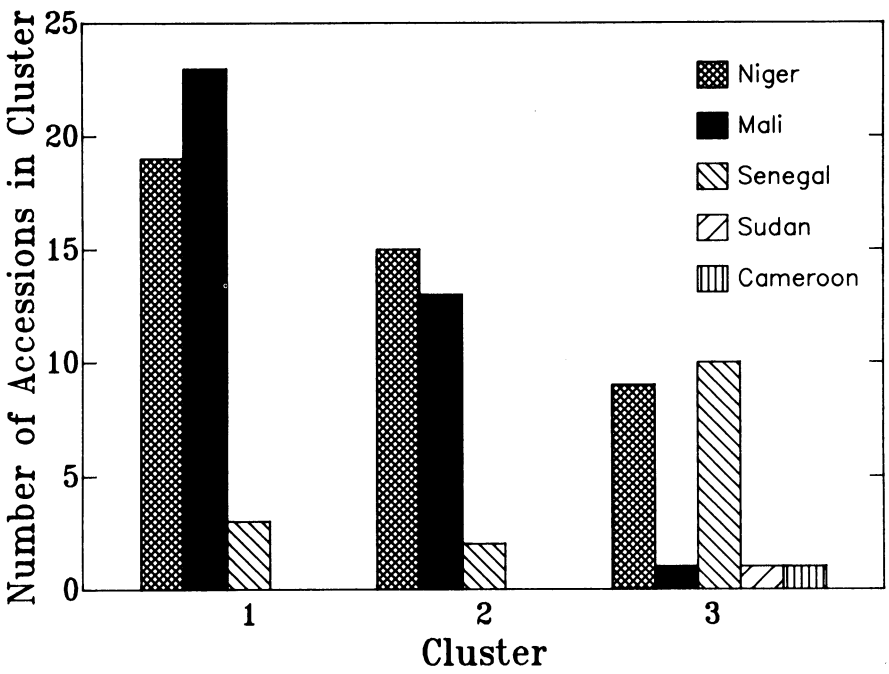

Fig. 4. Distribution of wild *Pennisetum* species of the primary gene pool by country of origin into clusters defined by cluster and discriminant analyses of disease resistance and morphologic traits.

Table 4. Disease ratings[a] of 3° *Pennisetum* species and groups defined by cluster analysis to inoculations with leaf-blighting fungi

Pathogen	Collection Mean ± SD	Cluster mean 1	2
Pyricularia grisea	0.6 ± 1.2	0.3	0.8
Phyllosticta penicillariae	1.3 ± 0.9	0.4	1.9
Bipolaris setariae	2.0 ± 0.9	1.6	2.2
Exserohilum rostratum	2.3 ± 1.3	1.1	2.9
Drechslera dematioidea	1.4 ± 1.1	0.4	2.0
Number of accessions	27	11	16

[a] 0 = Highly resistant, 4 = highly susceptible.

DISCUSSION

Our data support the hypothesis that wild species of *Pennisetum* may be useful sources of genes for disease resistance (9). Disease resistance, particularly to *P. s. indica*, was more commonly found and more effective in the wild *Pennisetum* species examined in this study than in the pearl millet land races collected in Burkina Faso (25,26).

Cluster analysis of the 1° *Pennisetum* accessions did not reveal a great deal of phenotypic diversity. Three clusters were identified in accessions from five countries, as compared with nine and five clusters within land races from central and south Burkina Faso, respectively (24,25). The limited number of clusters in the present experiments could in part be the result of fewer discontinuities in the range of phenotypes found in the wild

Pennisetums. Tostain (20) studied 188 accessions of wild pearl millet and identified five groups based on polymorphisms in eight enzymes. Tostain's analysis of specific, qualitative characteristics had an advantage over the analysis of quantitative traits in defining clusters in the wild *Pennisetums*. Although a small number of clusters were identified in the present experiments, these clusters differ in several characteristics, indicating that the gene pools are somewhat divergent. Phenotypic divergence suggests genotypic divergence, and it is possible that genes for disease resistance differ between clusters.

Resistance genes in the wild 1° *Pennisetums* may differ from those in cultivated pearl millet, since the gene pools have diverged to some extent. Wild pearl millets differ in frequencies of alleles at the *Est-1* locus (14), and nuclear rRNA genes of wild pearl millets are more diverse than those in cultivated millets (8). Prolamin polymorphism levels are more diverse in *monodii* accessions than in cultivated pearl millet (15). On the basis of polymorphisms in genes coding for eight enzymes, wild pearl millets are enzymatically distinct from cultivated millets (21). Divergence of the wild and cultivated millet gene pools is not complete, however. Several of the studies mentioned above identified similarities in addition to differences.

It is more likely that resistance genes in the 3° *Pennisetum* species differ from genes in cultivated pearl millet. Natural hybridization between these gene pools is restricted (6). Most of the 3° species differ from pearl millet in various enzymes (14), seed storage proteins (15), and restriction endonuclease fragment patterns of mtDNA (4). Because of the considerable genetic and cytoplasmic divergence between cultivated and 3° *Pennisetums* and because of barriers to interspecific hybridization, the gene pools and genes for disease resistance in the 3° species and cultivated pearl millet probably differ.

Several similarities between *P. glaucum* and *P. squamulatum* have been identified through partial chromosome homology (5), enzymes (14), seed proteins (15), and mtDNA fragments (4). In our studies, all accessions of *P. squamulatum* were moderately susceptible to *Pyricularia grisea*. The only other susceptible accession was *P. macrourum*. *P. pedicellatum* has been reported to be susceptible to *Pyricularia grisea* (17), but the single accession we evaluated was resistant.

Resistances in the gene pool of wild 1° *Pennisetums* can be utilized more readily because of the homology between their chromosomes and those of pearl millet. Although resistance from 3° *Pennisetum* species could be transferred through interspecific crosses, use of this resistance in improved cultivars will require greater allocation of resources than use of resistance from the 1° gene pool. Germ plasm resources of the wild 1° and 3° *Pennisetums* offer valuable genetic diversity for disease resistance.

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