COMPARISONS AMONG SELECTED UPLAND COTTON CULTIVARS AND STRAINS UTILIZING THE METHODS OF NUMERICAL TAXONOMY

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Comparisons Among Selected Upland Cotton Cultivars and Strains Utilizing the Methods of Numerical Taxonomy[1]

ABSTRACT

The objectives of this study were to describe 24 selected upland cotton (Gossypium hirsutum L.) cultivars and strains from eight countries for 52 characteristics, to determine the phenotypic relationships among those entries utilizing the methods of numerical taxonomy (and cluster analysis), and where possible to estimate within-country phenotypic variability (and indirectly genetic vulnerability) of its cottons.

Mean data are provided for the 24 entries for all 52 characters. These data should be of practical use to cotton breeders searching for specific characters to include in their programs.

The most dissimilar cultivars phenotypically were '4F' from Pakistan and 'Del Cerro' from Peru while the most similar were 'Deltapine Land 16' from the US and 'Minas Dona Beja' from Brazil. When all 24 entries were studied simultaneously, four groups of multiple cultivars were formed. Group I included three US, three Brazil, and two USSR entries; Group II, two from the USSR; Group IV, two from the USSR and two from Bulgaria; and Group VIII, two from the US. All other groups were single entries. Excluding the South American entries, the

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US cultivars clustered into a distinct group from the Old World cultivars. Within the latter group, the Bulgarian entries were the most similar, followed by those from the USSR, and then individually by the entries from Thailand, Uganda, and Pakistan. The US cultivars formed three groups--Group I, Plains-type cultivars; Group III, Delta-types; and Group II, a surprising grouping of a Coker with an Acala cultivar. In the South American group, a cluster of three Brazilian cultivars was then joined by Del Cerro from Peru before being joined by another Brazilian entry --SU 0450/8909. The clustering patterns within a dendrogram should also contain information of value to a cotton breeder.

Estimates of within-country variability were possible for those countries contributing two or more entries to this study. The differences in mean estimates among the US, the USSR, and Brazil were likely of no consequence; whereas, all three were considerably higher than the estimate for Bulgaria. Compared to the other three countries, Bulgaria appears to be in a genetically more vulnerable position.

Additional index words: Gossypium hirsutum L., Upland cotton, Phenetic analysis, Phenetic relationships, Numerical analysis, Infraspecific classification, Cultivar classification.

INTRODUCTION

Genetic variability is the basic resource utilized by plant breeders to improve crop yield, quality, pest resistance, and other traits of economic importance. Such variability can be found naturally in "land races", cultivars, or wild species; can be maintained in the form of germplasm collections; and can be artificially induced with mutagens. Classification systems can be used in plant species to characterize the existing variability within available gene pools as an aid in the selection of parents for use in breeding programs and to trace the origin and evolution of species (31).

A traditional, but simplistic, definition of classification is that it is the process of grouping together like individuals (32). The criteria for judging "likeness" in "conventional" taxonomy usually include only a few basic attributes considered by the taxonomist as being relevant to the classification process. Such procedures involve a great deal of arbitrariness and subjectivity on the part of the taxonomist. In an attempt to avoid these criticisms, numerical taxonomy was devised (40). This method utilizes a large number of characters expressed numerically and without intentional weighting. Each character contributes equally to the final classification allowing relatively more rapid, accurate, and repeatable results. Coefficients of affinity among the taxonomic units are generated through computer processing of all attributes measured, and clustering procedures are

applied to those coefficients for their further representation in the form of dendrograms.

The objectives of this study were to describe 24 selected upland cotton (Gossypium hirsutum L.) cultivars and strains from eight countries for 52 characteristics, to determine the phenotypic relationships among those entries utilizing the methods of numerical taxonomy (and cluster analysis), and where possible to estimate within-country phenotypic variability (and indirectly genetic vulnerability) of its cottons.

LITERATURE REVIEW

Over the past 20 years, numerical taxonomy and cluster analysis methods have been used extensively in systematics and related studies over a wide range of taxa in the plant kingdom. Such techniques have been applied particularly in attempts to clarify existing controversial classifications, in the improvement of classification for problematic organisms (such as those presenting extreme morphological variation), and even in composition description of complex populations.

A sampling will be discussed herein of the already vast literature in numerical taxonomy as applied to plants. For a more orderly presentation, this review will be divided into three sections, i.e., studies concerned with classifications of taxa higher than species (multispecies population composition and intergeneric classifications), studies concerned with interspecific (intrageneric) relationships, and those involved with infraspecific relations (to which class the present study belongs).

Higher Taxa Classification Studies

To illustrate a proposed method for the classification of photosynthetic aerobic nanoplankton, 10 species of two closely related groups of alga contained within a sample were classified by Van Valkenburg et al. (42). They applied numerical taxonomy and cluster analysis to 188 morphological, ultrastructural, physiological,

and biochemical characters and reported that the final grouping obtained of the species involved was in good agreement with the results of classical taxonomic approaches.

Birks (13) classified 144 species of European pteridophytes (vascular plants with roots, stems, and leaves but no flowers or seed) in 65 areas of the continent to determine floristic regions and elements. Jaccard similarity coefficients (transformed into dissimilarity coefficients) were computed for all pairs of regions based on floristic composition and for all pairs of species based on geographical distribution. Both a hierarchical clustering (a method of minimum variances) and an ordination procedure (principal coordinate analysis) were used to represent the relationships in the multidimensional matrices. The results were similar for both methods, but the latter was more difficult to visualize. The 15 regions and their 21 floristic elements were represented graphically. The floristic regions ranged from groups containing single areas to groups of eight, and five distinct groups were recognized at a high level of dissimilarity. Six floristic elements (each composed of several species) were recognized.

The family Portulacaceae, composed of annual and perennial succulent herbs, was unsatisfactorily classified by traditional methods, according to McNeill (33); it was unknown whether a single genus or up to 10 genera existed. The author numerically classified 37 species complexes as defined in recent taxonomic studies, on the basis of 65 traits which were standardized and submitted to eight methods of cluster analysis. All methods clearly separated the units into one group of 24 species and one of 13. The former group corresponded to the genus Claytonia in which four sections could be recognized. The latter

group corresponded to the proposed genus Montia with four subgenera and nine sections as suggested by the clusters obtained.

Clayton (18) applied numerical taxonomy and centroid clustering to 48 traits of 88 species within the tribe Arundinelleae of the Gramineae, a taxa notorious for its difficult classification. The dendrogram obtained allowed him to divide the tribe into nine genera. He stressed that the proper choice of characters of generic significance was important because it greatly influenced the results obtained, that several clustering methods should be used to check the results, and that numerical methods give a better overall understanding of the variation patterns of the material being classified than do orthodox taxonomic methods. One should note, however, that the "choice of characters" point he makes is directly opposed to the central idea of numerical taxonomy. Baum (4) defined 45 characters which were utilized in numerical taxonomic studies of another tribe within this family, the Triticeae. Difficulties in classification arose because of the likeness of the genera involved. The same author (5) applied several numerical analyses, using the previously defined traits (4), on 28 entries (27 genera plus a controversial species) and proposed a new system of classification and a synoptic key for genera within the tribe (6). In a subsequent study of the same tribe (7), based on the application of the Jardine-Sibson B_k clustering method to 28 entries, he found that several new relationships among the genera were revealed and many of the older ones (based on traditional classifications) were confirmed.

Interspecific Classification Studies

The genus Quercus is normally classified on the basis of variation in qualitative characters (28). Naturally occurring hybridization makes its subdivision into clear-cut species difficult, and many trees "challenge" a reliable identification. The author applied numerical and principal component analyses to quantitative characters in 40 specimens of red oak representing five species and a group of assumed hybrids. The final diagrams showed that the five species clustered in more-or-less discrete groups surrounding the hybrids which were located in an intermediate position near the center of the plots.

Species of the genus Pyrus were classified numerically by Challice and Westwood (17) using 51 botanical and chemical characters. Two hundred and forty-four specimens were characterized using botanical or chemical characters or both. Using both types of characters produced a classification which more closely agreed with the known geographical distribution of the species; whereas, classifications based on either one type of trait or the other resulted in serious misclassifications. The evidence indicated that pears should be grouped into four main groups.

Eleven herb species of the genus Alysicarpus were classified using numerical taxonomy (12). Nineteen qualitative and quantitative characters were used in a cluster analysis with grouping patterns suggesting the existence of two distinct groups of species.

According to Mannetje (30), the tropical legumes of the genus Stylosanthes have an unsatisfactory taxonomy for a number of species, primarily because of their extreme phenotypic variation. An attempt

was made to better understand the relationships among 21 accessions within the genus by employing numerical taxonomy and clustering methods on 34 morphological, floral, and cytological characters and also by measuring their affinities with the symbiont bacteria Rhizobium. Clustering was accomplished initially using only Rhizobium affinity, from which two main groups of the host species were defined. Six main groups were recognized when the other traits were considered alone, but several conflicting placements did appear. The author indicated that Rhizobium affinities should be used together with all other available traits in any attempt to classify species of the genus. The most variable and controversial species S. guyanensis could be divided, according to the affinity data, into four groups which supported the argument that more than one taxon is contained within that species complex.

Species of the genus Vaccinium, wild blueberries, are extremely variable due to genetic, environmental, and ecological factors which make difficult the assignment of species, varieties, and forms to particular groups. Smith (39) studied five taxonomic groups as well as natural hybrids by means of numerical and cluster analyses. Populations from three locations were sampled, and measurements were taken for 45 characters which were standardized for the computation of dissimilarity coefficients (taxonomic distances). The dendrograms obtained for each location separated the populations at two levels corresponding to the species and subspecies levels. The dendrograms were in general agreement with conventional taxonomic groupings, although some differences were detected. The author suggested that some inconsistencies may have occurred due to unintentional weighting

being given some plant parts because of the different number of traits studied for some plant organs. The hybrid complex, although unstable, was separated at the specific level. Extremes in expression make the separation of hybrids difficult when using conventional taxonomy, but not with numerical taxonomic methods.

The narrow-leaved taxa of the genus Chenopodium are another group of plants of controversial and difficult taxonomy. Crawford and Reynolds (21), utilizing numerical methods, studied five plants from each of 35 populations for 35 morphological and chemical traits (flavonoid compounds). The data matrix was standardized, and Euclidean distances were computed. Several methods of clustering were used, and principal component analysis was also employed. The dendrogram originated by the weighted pair-group method using arithmetic averages indicated the existence of seven groups. In general, all clustering methods suggested similar groupings and were consistent in disagreeing with the prevailing literature.

Hauptli and Jain (25) attributed the confusion concerning classification of the pseudo-cereal amaranth species to their wide range of phenotypic variation, the lack of discrete qualitative traits which could be used to define species, and the hybridization and introgression which occur between weedy and cultivated species. Numerical methods were employed, coupled with principal component analysis, on 20 populations of three weedy and three domesticated species and a naturally occurring hybrid between the two types. All 504 individual plants used in this study were grown in the greenhouse, and 25 traits (quantitative and qualitative) were recorded for each plant. The plots obtained showed that domesticated and weedy groups were distinct

from each other and that the hybrid population studied was at an intermediate position (although closer to the cultivated group). The authors stressed the importance of using both qualitative and quantitative characters to generate informative groupings and to better classify the species.

El-Gadi and Elkington (23) applied numerical methods to 15 species in the genus Allium (subgenus Rhizirideum) using 87 characters including morphological, cytological, and chemical traits. Separate hierarchical cluster analyses were applied to the first two types of traits, the last type, and to all three types together. The morphological and cytological data yielded a dendrogram which indicated three major divisions among the species. The analysis based on chemical data did not show similiarities to that based on morphological and cytological traits while using all types of data produced a dendrogram with six main clusters. This last dendrogram produced results consistent with classifications based on hybridization data (indicating that the phenetic classification was a "natural" one) although no published classification agreed exactly with the groupings delineated in this study. Also in the genus Allium (but in the subgenus Molium), 22 species, subspecies, and varieties were classified by Badr and Elkington (1) using numerical classification methods on 86 cytological, morphological, and chemical characters. After clustering, six major groups could be distinguished, and those groups were the basis for a reclassification within the subgenus. The proposed classification did agree well with groupings based on isolation barriers and biosystematic investigations.

The genus Cucurbita, although showing high intraspecific uniformity, exhibits large variation among its 27 component species. Rhodes et al.

(36) classified 21 species of this genus utilizing 93 primarily morphological traits, three measures of phenetic relationship (Q-correlation coefficient, Sokal's distance coefficient, and Clark's divergence coefficient), and several clustering techniques. Dendrograms based on Q-correlation coefficients appeared more similar to classifications based on cross-compatibility data, geographical distribution, and ecological adaptation than did the others. The dendrograms based on distance and divergence coefficients were similar to each other. Bemis et al. (11), utilizing the methodology and information gained in the previous study (36), classified 53 species, F_1 hybrids, and unclassified accessions within the same genus. The authors noted that, in practice, F_1 hybrids may cluster in several ways, i.e., they may remain independent of the parent species, they may cluster with one or both parents, or they may cluster with a third species (which would be a strong indication of the origin of that species). The 21 species studied were divided into 10 groups in the dendrogram obtained from the clustering of Q-correlation coefficients. In the dendrogram representing all 53 entries, 12 groups could be distinguished. The F_1 hybrids generally clustered with one of their parents, although two did not cluster with either (suggesting the lack of genetic homology between their parents).

Seventy-five members (17 species at several ploidy levels, artificial polyploids, and hybrids) of the section Morella of the genus Solanum were studied numerically by Heiser et al. (26). Fifty-eight characters were used for the computation of Q-correlation coefficients, and clustering was performed by Sokal and Michener's variable group method. Dendrograms revealed little about the origin of the hybrids

and alloploids. Autoploids clustered near their diploid parents, and alloploids generally placed near one of their parents. Some agreement was found between their results for species and the results of traditional taxonomy, but they also found several serious disagreements such as the splitting of species generally regarded as conspecific. The authors speculated whether or not weighting of characters would make their classification more realistic. A later examination of the above results by Schilling and Heiser (38) revealed that the distortion observed was caused mainly by inclusion of the hybrids. By excluding those entries, a more satisfactory classification resulted.

Sixteen cultivars of oats of known genealogy belonging to four species (Avena sativa L., A. byzantina C. Koch, A. orientalis Schreb., and A. nuda L.) were classified for 36 characters by Baum and Lefkovitch (10) in an attempt to study the relationships between phenetics and phylogeny. Gower's similarity coefficients were computed for all possible pairs of cultivars for agronomic, non-agronomic, and both types of traits; and several clustering procedures were used. The dendrograms based on either set of data were closely related to the real cladistic dendrogram. However, the authors cautioned that indiscriminate selection and non-weighting of characters might tend to obscure phylogenetic relationships among entries. Baum (3) classified 28 species of Avena using 29 traits, Gower's coefficient of resemblance (transformed into dissimilarities), and several clustering methods. The characters used were a sample of micromorphological, histological, embryological, and cytological features. Dendrograms presenting "chaining," great unevenness, or with too many clusters were rejected. Based on correlations between pairs of classifications, the author

regarded the flexible-sort clustering technique as giving the best classification. This procedure divided the cultivars into seven groups designated as "sections" to provide a new classification for oat species.

According to Broué et al. (15), members of the subgenus Glycine (genus Glycine) are rare in nature; and there is little phylogenetic and evolutionary information about them. Twenty populations representing the four recognized species [Glycine canescens F. J. Herm., G. tabacina (Labill.) Benth., G. tomentella Hayata, and G. clandestina Willd.] were compared based on isoenzymatic configuration from protein electrophoresis. Gower's maximal predictive classification, a non-hierarchical method, was used as a numerical procedure. The results indicated that G. canescens was polymorphic for the isoenzyme phenotypes. Some plants of G. canescens tended to group closer to G. clandestina and others to G. tomentella. It was speculated that G. canescens may be a diffuse ancestral type which evolved into other species, that it introgressed with other species at one or more times in its evolution, or both.

Optical density curves were obtained of electrophoretic protein banding patterns for crude seed extracts from 25 species in the genus Gossypium (29) and were compared on a pairwise basis by means of correlation coefficients. A correlation matrix was then assembled, and the weighted variable-group clustering method was applied. The classification generated was largely consistent with the conventional classification based on six genome groups (A through F). However, the Australian species (the C genome) showed close affinities with the African (B genome) and Arabian (E genome) species. The New World diploid species (D genome) were classified into two subgroups, β and

ε, according to their affinities with the African and Arabian genomes, respectively. Such evidence did not support the classical division of the D genome into three sections. The authors suggested that the β and ε subgroups indicated that the D genomic groups were probably derived from an African type and that they likely evolved in isolation from each other.

By using 25 characters to which a binary primitive/advanced state could be assigned and applying the Wagner Divergence Index to the data, Fryxell (24) constructed a branching sequence for the phylogeny of diploid species of Gossypium. Such phenetic analysis agreed in broad lines with the previously evaluated cladistic relationships based on chromosome pairing although some differences were noticed. The largest discrepancy was the positioning of the Australian species into three widely divergent lineages; whereas in previous studies they were generally grouped monophyletically.

Infraspecific Classification Studies

Numerical taxonomy was used by Martin and Rhodes (32) to group cultivars of eggplant (Solanum melongena L.) and to relate those cultivars to their geographical origins. Eighteen characters were studied in 475 entries, and after clustering, the dendrograms indicated the presence of 11 groups showing that the variation patterns studied were not random. In general, grouping eggplant cultivars by numerical methods reflected the geographical regions of the accessions; but grouping them by countries of origin was less consistent with the numerical groupings.

According to Martin and Rhodes (31), a classification of yam

(Dioscorea alata L.) cultivars would be useful for plant breeders because it should make easier the selection of superior germplasm. Using Mahanalobis distances, correlation coefficients, and cluster analysis, 235 cultivars were classified using 28 characters. No clear subspecies grouping was present for any of the classifications generated from the data, and the groups of cultivars presented an interconnected network instead of a dichotomously branched tree pattern.

Molina-Cano and Rossello (34) classified separately 20 two-row and 11 six-row cultivars of barley (Hordeum vulgare L.) using 35 and 27 characters respectively (both morphological and biochemical). The authors used Euclidean distances to compute similarity coefficients and both cluster and principal component analyses; and all proved to be satisfactory techniques for the classification of closely related barley genotypes.

Variation in 65 strains and hybrids of rice (Oryza perennis Moench) was studied by Morishima (35), who applied the methods of numerical taxonomy to 24 morphological and physiological characters. He employed cluster analysis to correlation coefficients and taxonomic distances to generate the matrices and the dendrograms. Pattern analysis was also employed, and both techniques produced consistent results. The cultivars clustered in seven groups primarily according to geographic areas. Cladograms showing evolutionary trends through time were elaborated in an attempt to derive phylogenetic relationships from the phenetic relations, using Camin and Sokal's method (16). The results indicated that several groups may have evolved separately and that components of the Asian group may have evolved faster than the others. Janoria et al. (27) classified 18 dwarf rice (O. sativa L.) cultivars based on 50

characters. After standardization, correlation coefficients were computed and clustering was performed; seven groups were defined by the clustering patterns. The authors indicated that numerical taxonomy worked fairly well for classifying closely related cultivars.

Cultivars of oats (Avena spp.), according to Baum (2), are difficult to describe taxonomically because cultivars vary in phenotypic expression when grown in different environments (year and location effects). He stated that any classification of oats must include as many characters as possible and must also account for environmental variation and that numerical taxonomy could help in the construction of such a classification. Previous classifications of oats were based primarily on agronomic characters selected "a priori" on material of restricted variability. Baum and Lefkovitch (8) took one individual from each sample of 5000 collections and measured 21 traits of short life span to establish a classification for cultivated oats. Before calculating similarity coefficients, individual entries were grouped successively based on a divisive chain algorithm; otherwise, 12.5×10^6 comparisons would have had to be made. The 107 "secondary reference individuals" obtained in this manner were joined by a single linkage cluster analysis. The dendrogram obtained showed 14 groups of polymorphic populations of individuals. When the same authors in a later work (9) classified the 14 groups using Mahanalobis distances and cluster analysis, five main agglomerates resulted. Based on computer simulation, the authors suggested that 50 plants in an oat field were sufficient for the assignment of a given cultivar to one of the 14 previously described groups.

Glycine wightii Verdc. is a polymorphic twining legume found in

the pastures of Australia, Africa, and South America. Edye et al. (22) applied numerical analysis to 51 Australian introductions of this species using 31 morphological and agronomic attributes. Six cultivar groups were described based on the dendrogram obtained. They stated that numerical techniques were useful tools for the classification of polymorphic pasture species cultivars.

Samayoa-Armienta (37) classified 39 cultivars of cotton (G. hirsutum L.) from 12 countries using 53 quantitative and qualitative traits. The raw data matrix was standardized for all characters, and generalized Euclidean distances were computed as measures of dissimilarity between all possible pairs of entries studied. The dendrogram generated therefrom grouped the cultivars into 12 clusters. Another analysis was performed utilizing only 16 economically important characters, and that dendrogram characterized seven groups of cultivars. The author stated that this last classification, as far as the US cultivars were concerned, was in fairly good agreement with known phylogenetic relationships. He also compared within-country variability and discussed its consequences in terms of genetic vulnerability.

MATERIALS AND METHODS

Germplasm, Characters, and Experimental Methods

The 24 cotton cultivars and strains included in this study are listed in Table 1 with their respective countries of origin, plant introduction numbers, and entry codes. These entries do not necessarily constitute a random sample of the cultivars grown in each of the eight countries represented herein nor do these countries represent a random sample of all those which grow cotton.

Fifty-two characters were employed for the classification of these entries. No particular criterion was used to choose characters, other than that they must differ among entries within this set and that as many traits as possible be included in the study. No intentional differential weighting was given to characters included herein; however, some parts of the plant were obviously measured for a greater number of traits than were others and, therefore, probably had greater influence on the classifications obtained.

Both qualitative (two-state and multistate) and quantitative (continuous) traits were utilized in the computation of distance coefficients. Qualitative two-state characters can be described as binary traits [i.e., those which can be recorded as + or -, 1 or 0, or some similar such coding (40)]. Qualitative multistate characters are those recorded in more than two categories. Some arbitrariness was unavoidably involved in coding such traits because a linear order for

the character-states must necessarily be assumed (which in reality may not be the case). Quantitative characters present continuous distributions and may receive any measurable value. For the analyses undertaken in this study, all characters were considered as continuous (quantitative) because, even in the discrete two-state traits studied, a difference in degree of expression could easily be assumed.

Several of the economically important traits (especially those likely to interact with the environment) were measured in replicated experiments. Those tests were conducted in 1978 and 1979 near Chickasha and Tipton, Okla., under both irrigated and dryland conditions. At Chickasha the tests were grown on the South Central Research Station in a Reinach silt loam soil (a coarse-silty, mixed, thermic Pachic Haplustolls) and at Tipton on the Southwest Agronomy Research Station in a Tipton silt loam (a fine-loamy, mixed thermic Pachic Argiustolls). These tests incorporated randomized complete-block experimental designs with three replications and with single-row plots 9.1 m long. The 1.0 m spacing between rows was common to all experiments in this study, and plant spacing was typical of a commercial planting. A 15-boll sample was taken from each plot in the replicated tests for the evaluation of several agronomically important traits and for the analysis of fiber properties. Most agronomic traits from both years and the fiber data from 1978 were included in this study.

The 10 agronomic and fiber characters studied in the replicated tests were defined as follows: Lint yield was the lint weight/plot obtained after ginning the seedcotton harvested from that plot, converted into kg/ha. Picked lint percent was the ratio of lint weight to seedcotton weight, expressed as a percentage. Pulled lint percent

was the ratio of lint weight to pulled cotton weight (i.e., seedcotton plus burs), expressed as a percentage. 2.5 and 50% span (fiber) lengths were measured on the digital fibrograph and are the lengths (converted into millimeters) at which 2.5 and 50% of the fibers, respectively, are of that length or longer (when caught at random along their lengths). Uniformity index was calculated as the ratio of 50 to 2.5% span length, expressed as a percentage. Micronaire is a measure of fiber coarseness and was measured on the micronaire instrument in standard micronaire units, i.e., micrograms/inch. T_0 and T_1 fiber strength were the strengths of a bundle of fibers as measured on the stelometer instrument with the jaws (which hold the lint) spaced 3.18 and 0.00 millimeters apart, respectively, and these traits were expressed in millinewtons/tex. Plant height was measured as the distance in centimeters from the soil surface to the plant apex after harvest. Ten representative plants/plot were measured in the 1979 experiments.

Responses among entries to three of the more important cotton diseases in the US were studied in several experiments. The replicated tests in 1979, grown under irrigation at Chickasha and Tipton (as previously described), were utilized to evaluate reactions to natural infestations of verticillium wilt (incited by Verticillium dahliae Kleb.). Ten plants/plot were scored for their disease reaction based on a scale from "2" to "10" [a slight modification of the grading system used by Verhalen et al. (43)]. A grade of 2 indicated none or very mild external symptoms. As disease expression became progressively more severe, the scores gradually increased to a grade of 10 which indicated a completely defoliated plant with stems dead down to ground

level. The grade of 1, used in the earlier work (43), was not used here because it would have required observation of the plant's vascular system which would have biased the yield data in these experiments.

To evaluate responses to bacterial blight [caused by Xanthomonas malvacearum (E. F. Sm.) Dows.], three two-replicate experiments were planted in 1979 in randomized complete-block experimental designs at Perkins, Okla., in a Teller loam soil (a fine-loamy, mixed, thermic Udic Argiustolls). Plants, spaced 30.5 cm apart, were inoculated at the four-to-six true leaf stage with pathogen races 1, 2, and a mixture of the races 1 and 2 in the three respective experiments. Inoculation was attained by using a high pressure (17.6 kg/cm^2) sprayer to water-soak leaves of the plants with the bacterial inoculum, and 15 days later observations were made of plant reactions. The single-row plots were 8.5 m long; and all plants in a plot were scored according to size and overall appearance of the lesions, using a modification of the grading system devised by Brinkerhoff (14). A value of "0" was given to the immune ('0.0') reaction, and increasingly higher numbers were assigned to more susceptible reactions up to a value of "6" for the fully susceptible ('4.0') reaction. The value for an entry was expressed as the mean over all plants in a row.

At Hollis, Okla., in 1979, a two-replicate randomized complete-block, irrigated experiment was planted in a Hardeman fine sandy loam (a coarse-loamy, mixed, thermic Typic Ustochrepts) located on a private farm to study the entries' reactions to naturally-occurring infestations of the fusarium wilt [incited by Fusarium oxysporum Schlecht. f. sp. vasinfectum (Atk.) Snyd. and Hans.] --root-knot nematode [Meloidogyne incognita acrita (Kofoid and White) Chitwood] complex.

Rows were 7.6 m long, and all plants were spaced approximately 20 cm apart. Plants were evaluated for vascular and foliar symptoms, and scored on a binary scale where a score of "1" was recorded if no symptoms were observed and a "2" was assigned to a plant invaded by the pathogen.

To evaluate morphological attributes, several fiber spinning properties, and seed composition traits, single irrigated progeny rows 15.2 m long were planted in 1978 and 1979 at Perkins, Okla. To classify the morphological traits, 15 plants/entry generally were scored at random in the 1979 planting, although for a few traits the overall appearance of the row as a whole was used. In 1979 at harvesttime, a 12-boll random sample was taken from the entries to determine their degree of storm resistance and other agronomically important traits. In both years, large samples of lint and undelinted seed were also taken from each entry. The lint sample was sent to the U. S. Cotton Quality Laboratory in Knoxville, Tenn., for spinning tests. The seed samples were sent to Porter Testing Laboratory (a USDA-cooperating test laboratory) in Oklahoma City, Okla., for routine cottonseed evaluations. A brief description of the characters measured on these progeny rows (as well as information on methods of measurement) is presented as follows:

Growth habit characters

16. Branching pattern: a class number ranging from "0" (i.e., few and short branches) to "4" (many and long branches) subjectively assigned to the row as a whole;
17. Plant erectness: a class number ranging from "1" (i.e., an erect plant) to "4" (decumbent) subjectively assigned to the row as a whole;

Boll characters

18. Storm resistance: the mean force in grams/lock required to remove two mature, fluffy locks of cotton from their bur, as determined on 12 bolls using a 500-g force gauge.
19. Locks/boll: The mean number of locks/boll in a 12-boll sample;
20. Seed/lock: the mean number of seed/lock in a 12-boll sample;
21. Pittedness: a class number ranging from "1" (i.e., smooth boll surface) to "3" (pitted surface) subjectively assigned to 15 bolls, expressed as a plot mean;
22. Boll shape: the mean value of a ratio between boll length vs. width (both measured in centimeters) in a 15-boll sample. A lower value indicates a rounder boll--as opposed to a higher value which indicates a longer, more pointed one;
23. Boll size: the mean weight in grams of seedcotton/boll as measured from a 12-boll sample;
24. Waxiness: a class number ranging from "1" (i.e., a dull boll surface) to "3" (a glossy surface) subjectively assigned to 15 bolls, expressed as a plot mean;
25. Lint/boll: the mean weight in grams of lint/boll from a 12-boll sample;

Bract characters:

26. Boll coverage: the mean length in centimeters from the deepest indentation of the longest bract tooth to the apex of the boll from a 15-boll sample. A lower value indicates greater coverage of the boll and vice versa;
27. Teeth/bract: the mean number of teeth/bract taken from one bract/flower from a 15-flower sample;

28. Teeth shape: the mean value of a ratio between the length vs. width at the base of the tooth (both measured in centimeters) of the longest bract tooth taken from one bract/flower from a 15-flower sample;

29. Bract shape: the mean value of a ratio between bract length (measured from the base of the bract to its apex) and width (measured at the point of maximum value) both taken in centimeters from one bract/flower in a 15-flower sample. A lower ratio indicates a more regular shape, and a higher ratio is typical of a more pointed, triangular form;

30. Bract size: the mean length of the bract in centimeters measured from the base of the bract to the tip of the longest tooth, taken from one bract/flower from a 15-flower sample;

Leaf characters:

31. Color: a class number ranging from "0" (i.e., light-green leaves) to "4" (dark-green) subjectively assigned to the row as a whole;

32. Lobation: the mean value of a ratio between the distance from the point of petiole insertion on the leaf to the apex of the main lobe and the distance from that same apex to the projection of the indentation of that lobe, both taken in centimeters from a 15-mature leaf sample. Lower values indicate deeper indentations and vice versa;

33. Leaf size: a class number ranging from "0" (i.e., small leaves) to "5" (large) subjectively assigned to the row as a whole;

Pubescence

34. Apex: a class number ranging from "0" (i.e., nearly hairless) to "6" (maximum trichome density and length) subjectively

assigned to the apical region of the stem, expressed as a mean of 15 plants;

35. Leaf: a class number ranging from "0" (i.e., nearly hairless) to "5" (maximum trichome density and length) subjectively assigned to a 15-mature leaf sample, expressed as a mean;

36. Stem: a class number ranging from "0" (i.e., nearly hairless) to "4" (maximum trichome density and length) subjectively assigned to the median region of the stem, expressed as a mean of 15 plants;

Seed characters

37. Seed index: the weight in grams of 100 seed;

38. Fuzziness: a class number ranging from "0" (i.e., nearly naked) to "4" (very fuzzy) subjectively assigned to a saw-ginned sample of cottonseed;

39 to 41. Ammonia, free fatty acids in oil, and oil content: estimated from chemical analyses of a 454 g undelinted cottonseed sample, expressed as percentages of total cottonseed weight;

42. Cake yield: estimated yield of cake (based on standard milling efficiency) as extracted from a 454 g seed sample, expressed as a percentage of total cottonseed weight;

Yarn characters

43. Yarn tenacity: the strength of yarn expressed in centinewtons/tex;

44. Yellowness (Hunter's b value): a measure of increasing yellowness of cotton as determined on the Nickerson-Hunter colorimeter;

45. Reflectance (R_d value): a measure of increasing reflectance of cotton as determined on the Nickerson-Hunter colorimeter, expressed as a percentage;

Miscellaneous characters

46. Bur size: the mean weight in grams of burs/boll from a 12-boll sample.
47. Corolla color: a class number subjectively assigned with a value of "1" given to yellow and a value of "2" assigned to cream petal color, expressed as a mean for a 15-flower sample;
48. Extra-floral nectaries: a class number of "1" or "2" assigned to absence vs. presence, respectively, of extra-floral nectaries, expressed as a mean for a 15-flower sample;
49. Staminal column glands: a class number ranging from "0" (i.e., absence of glands) to "2" (maximum expression) subjectively assigned on the basis of presence and conspicuity of gossypol glands in the staminal column, expressed as a mean for a 15-flower sample;
50. Lint index: the mean weight of lint in grams/100 seed from a 12-boll sample;
51. Pedicel length: the mean pedicel length in centimeters from a 15-flower sample; and
52. Pollen color: a class number subjectively assigned with a value of "1" indicating yellow pollen grains and a "2" denoting cream, expressed as a mean for a 15-flower sample.

Statistical Analyses

For statistical analyses of the characters measured in replicated

experiments over locations and years, the model described by Comstock and Moll (20) was followed. The "entries" mean squares were tested using the method advocated by Cochran (19). Analyses of variance for characters tested in only one location and year followed the basic procedures described by Steel and Torrie (41).

After the replicated data were shown to exhibit significant differences among entries, a basic data matrix was constructed in which rows were cultivars and columns were characters (Table 2). Because the characters were measured on different scales, this matrix was then standardized by columns so that different characters would all have the same weight in the classification. Such standardization should give more reliable results, according to Rohlf [as cited by Heiser et al. (26)], because the data in the adjusted matrix are based on standard deviations rather than on unadjusted means. This operation was accomplished by dividing the mean value of a character for each entry by the standard deviation for that character across all entries.

From the resulting matrix, an entry-by-entry dissimilarity matrix was then computed (Table 3). The measure of relationship utilized, for all possible pairs of entries over all standardized characters, was the generalized Euclidean distance (40) which is a measure of dissimilarity and is defined as:

$$\Delta_{ij} = \left[\sum_{i=1}^{n} (X_{ij} - X_{ik})^2 \right]^{1/2}$$

where

X_{ij} is the standardized value of the $\underline{i}$th attribute for the $\underline{j}$th entry and

X_{ik} is the standardized value of the ith attribute for the kth entry.

The clustering procedure utilized in this investigation was the unweighted pair-group method using arithmetic averages (a hierarchical method). Details of this procedure are described in Sneath and Sokal (40). Using a computer plotting program (Univ. of Kansas Computer Contrib. 48) hierarchical dendrograms (i.e., tree-like diagrams showing phenetic distances between entries) were generated from the distance values obtained by cluster analysis.

For each subset of entries compared, the numerical taxonomic procedures described above were repeated to avoid confounding.

RESULTS AND DISCUSSION

Analyses of variance were performed for all characters measured in one or more replicated experiments (i.e., lint yield, picked and pulled lint percents, 2.5 and 50% span lengths, uniformity index, micronaire, T_0 and T_1 fiber strengths, plant height, and the five tests for disease reactions). All traits exhibited significant differences among entries at the 0.05 or lower probability levels.

The raw data matrix by entry and character as shown in Table 2 displays the phenotypic mean values over all observations for the 24 entries and 52 characters. Also shown in the table are the mean character values and standard deviations over entries and the number of observations within each entry mean. These observations should be of practical value to cotton breeders searching for specific characters to include in their programs, e.g., 'CA(68)41' exhibits excellent resistance to bacterial blight. Many other such examples could be cited. The dissimilarity matrix for all possible combinations of entries taken two at a time was computed from the raw data matrix in Table 2 and is presented in Table 3. Each cell in this matrix represents the dissimilarity level over all 52 characters, for the particular pair of entries indicated. The values obtained ranged from 4.59 for the most similar entries ('Minas Dona Beja' from Brazil and 'Deltapine Land 16' from the United States) to 16.43 for the most dissimilar ('4F' from Pakistan and 'Del Cerro' from Peru).

The overall pattern of phenotypic relationships among entries can

be judged more easily when presented in the form of a dendrogram (Fig. 1), than in Table 3. In this plot, as well as in those which follow, the vertical axis represents the dissimilarity level (or value) and the horizontal axis lists the entries in the study, their codes, and their countries of origin. A line, drawn arbitrarily at the 7.2 dissimilarity level, separates the entries in Fig. 1 into 12 groups --numbered I through XII. Minas Dona Beja and Deltapine Land 16 were the first two entries to join the Group I cluster. Although results from numerical classifications are not expected to coincide necessarily with phylogeny, the similarity between the two cultivars, as indicated in this study, agrees well with the known phyletic relationship between them. Minas Dona Beja originated from selections in later generations of a cross involving the cultivars 'Deltapine Land 11' and 'Auburn 56'. The next entry to join this cluster was the US cultivar 'Stoneville 213' followed sequentially by two others from Brazil, 'IAC-13-1' and 'IAC-RM_4-SM_5'. The last two entries were also derived from American upland cultivars, which helps explain their clustering in this manner. 'Tashkent-2' from the USSR was the next entry to join the cluster, followed by a subgroup composed of 'C-4727' and 'Coker 5110' which exhibited the approximate dissimilarity level of 6.6 units.

The two USSR cultivars '149-F ' and 'Tashkent-1' constituted Group II. Four cultivars, '153-F' and '2421' from the USSR as well as '6396' and '4959' from Bulgaria, comprised Group IV. Within this group, the most similar cultivars were the two from Bulgaria joined successively by 2421 and by 153-F. Samayoa-Armienta (37) also found great similarity among the Bulgarian cultivars he investigated. Group VIII was the result of a grouping between the US cultivars 'Paymaster 303' and

'Westburn M' at an approximate dissimilarity level of 5.9. All remaining groups in this figure were composed of individual entries. SU 0450/8909 from Brazil (Group IX), Del Cerro from Peru (Group X), CA(68)41 from Uganda (Group XI), and 4F from Pakistan (Group XII) were progressively more and more different from the other entries joining the cluster at sequentially higher dissimilarity levels.

To examine the relationships among entries from specific countries or regions of the world (without confounding with those from other groups), the same clustering procedures described earlier were applied, including recalculation of dissimilarity matrices for only those specific entries. The dendrograms which appeared more informative (i.e., those which presented obvious clustering patterns and little or no "chaining" and particularly those which exhibited patterns not shown in Fig. 1) were selected and are shown in Figs. 2 through 5.

When the South American group of entries was excluded from the classification and the numerical and clustering methods used previously were applied to the 19 remaining entries, a clear-cut separation between the US and the Old World cultivars was obtained (Fig. 2). Below the dissimilarity value of 6.0 units, the entries were clustered into two distinct groups. Group I included cultivars from the USSR, Bulgaria, Pakistan, Uganda, and Thailand. Group II included only the US cultivars. This dendrogram clearly shows that the within-continent phenotypic variation among entries was considerably smaller than the between-continent variability. These results were somewhat unexpected because, in Samayoa-Armienta's (37) study, cultivars from the USSR, Bulgaria, and Greece displayed closer relationships with US cultivars than did those from eight other countries (including Pakistan, Uganda,

and Thailand).

For a better understanding of the relationships within the Old World group, those cultivars were studied separately (Fig. 3). Below a dissimilarity value of approximately 8.0 units, five groups could be discerned. Group I consisted of the initial joining of the two very similar Bulgarian cultivars 4959 and 6396 with sequential linking to the USSR cultivars 2421, 'Tashkent-3', and 153-F. Group II included only USSR cultivars, i.e., Tashkent-1, C-4727, Tashkent-2, and 149-F. Groups III, IV, and V were composed of the single cultivars 'SK 14' from Thailand, CA(68)41 from Uganda, and 4F from Pakistan, respectively. At a slightly higher dissimilarity level, this phenogram clearly indicated that the USSR and Bulgarian cultivars were phenotypically closer to one another than to the Asian and African cultivars studied.

The phenetic relationships among the US cultivars can be observed in Fig. 4. A line drawn at the dissimilarity value of 9.0 separated the entries into three main groups. Within Group I, the most similar cultivars were Westburn M and Paymaster 303 which joined at the approximate value of 6.8. 'Lankart LX 571' joined them at a somewhat higher dissimilarity value. Group II was composed of 'Acala SJ-5' and Coker 5110, while Group III comprised the Delta-type cultivars Deltapine Land 16 and Stoneville 213. Group I is composed of Plains-type cultivars while Group III includes Delta-types. Intuitively, one would probably have expected the Coker (a southeastern US company) cultivar to be more similar to those in Group III than to the Acala cultivar from California. Judging from the high dissimilarity values at which these entries grouped, this sample of US cultivars probably represents a

relatively large phenotypic variation.

The last dendrogram (Fig. 5) depicts the relationships among the South American entries. A line at the dissimilarity level of approximately 8.0 revealed three clusters. Group I included the phenotypically most similar cultivars Minas Dona Beja and IAC-13-1 as well as IAC-RM_4-SM_5. Groups II and III were composed of the single entries Del Cerro from Peru and SU 0450/8909 from Brazil, respectively. Because of their respective countries of origin, one would have expected SU 0450/8909 to have joined the cluster before Del Cerro. SU 0450/8909 is obviously very different phenotypically (and probably genetically) from the other Brazilian entries studied.

The clustering patterns within the above dendrograms may be of some value to cotton breeders. The members within a cluster are relatively similar and crossing between such entries is unlikely to result in material very different from that already available. The members within different clusters are relatively more dissimilar and crossing between them is likely to result in materials very different from those currently available due to the accumulation of very different genes for quantitative characters within the same line.

In the strict sense, the results obtained above apply only to the actual entries studied. However, if one assumes that these are a random, or at least representative, sample of the cultivars actually grown in their respective countries, estimates of within-country variability, and thus, indirectly, of genetic vulnerability, can be made. Such estimates could be calculated only for those countries contributing two or more entries to this study. Utilizing the dissimilarity values in Table 3, the mean estimates among entries within those countries were

8.50 for the US, 8.35 for the USSR, 8.27 for Brazil, and 4.81 for Bulgaria. The differences in mean values among the US, the USSR, and Brazil were likely of no importance; whereas all three were considerably higher than the value for Bulgaria. Compared to the other three countries, Bulgaria is probably in a distinctly genetically more vulnerable position because its cultivars display relatively little genetic variability. The US-USSR-Bulgaria relationship was the same as found previously by Samayoa-Armienta (37). Brazilian cultivars were not included in his study.

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LIST OF TABLES

LIST OF FIGURES

Table 1. Entries included in this study, their respective countries of origin, plant introduction numbers, and entry codes.

Entry code	Entry	Country of origin	P.I. no.
A†	IAC-13-1	Brazil	414136
B	IAC-RM_4-SM_5	Brazil	414137
C	Minas Dona Beja	Brazil	414138
D	SU 0450/8909	Brazil	414141
E	4959	Bulgaria	‡
F	6396	Bulgaria	374725
G	4F	Pakistan	365533
H	Del Cerro	Peru	414135
I	SK 14	Thailand	365544
J	CA(68)41	Uganda	365540
K	Acala SJ-5	USA	-
L	Coker 5110	USA	-
M	Deltapine Land 16	USA	-
N	Lankart LX 571	USA	-
O	Paymaster 303	USA	-
P	Stoneville 213	USA	-
Q	Westburn M	USA	-
R	149-F	USSR	‡
S	153-F	USSR	358449
T	2421	USSR	358900
U	C-4727	USSR	‡
V	Tashkent-1	USSR	379624
W	Tashkent-2	USSR	379625
X	Tashkent-3	USSR	379626

†These codes (together with abbreviations of entry names and countries of origin) are used in the figures and tables throughout this study.

‡Number unavailable.

Table 2. Raw mean data matrix by entry and character.

Identification		Lint yield	Lint percent		Fiber characters						Plant height	Disease responses					Growth habit characters	
			Picked	Pulled	Span length 2.5%	Span length 50%	Unif. index	Micronaire	Strength 0	Strength 1		Vert. wilt	Bacterial blight Race 1	Bacterial blight Race 2	Bacterial blight Mixture	Fus. complex	Branching pattern	Plant erectness
		kg/ha	%		mm		%	µg/in	mN/tex		cm							
A IAC-13-1	(BR)	318	33.2	23.4	27.3	12.0	44.0	4.4	420	192	93	6.9	5.2	4.1	5.6	1.20	1	3
B IAC-RM4/5	(BR)	346	32.5	22.6	27.1	12.6	46.6	4.5	417	199	87	6.7	5.6	4.1	5.7	1.04	2	2
C MINAS DB	(BR)	354	34.0	23.4	27.4	12.7	46.3	4.6	402	201	87	6.4	5.9	4.3	5.9	1.07	1	3
D SU 0450/8	(BR)	92	26.9	19.1	28.1	13.0	46.2	4.0	413	201	106	5.8	5.9	4.0	5.9	1.26	1	3
E 4959	(BU)	429	32.2	22.4	24.5	11.7	47.7	4.5	414	197	75	6.6	5.4	4.4	5.7	1.34	0	2
F 6396	(BU)	429	33.3	23.2	24.6	11.7	47.4	4.4	404	192	75	6.8	5.7	4.2	5.7	1.47	0	3
G 4F	(PA)	188	30.7	20.5	23.5	11.7	49.5	3.9	457	214	107	6.8	4.1	2.6	4.1	1.05	4	3
H DEL CERRO	(PE)	391	31.7	21.1	31.3	14.6	46.4	3.8	526	269	84	6.5	6.0	4.8	5.9	1.48	1	3
I SK 14	(TH)	219	31.1	21.6	24.2	11.4	47.0	4.6	401	178	95	5.9	4.9	3.5	4.7	1.32	3	3
J CA(68)41	(UG)	274	29.3	19.3	28.4	13.2	46.3	4.2	448	220	88	6.4	2.7	2.6	2.7	1.50	1	4
K ACALA SJ5	(US)	410	35.5	24.1	27.8	13.5	48.4	4.2	497	242	72	4.2	6.0	4.1	5.8	1.05	0	3
L COKR 5110	(US)	438	35.2	24.7	28.2	13.1	46.4	4.3	419	202	83	6.4	5.8	3.7	5.9	1.17	0	3
M DPL 16	(US)	502	34.0	24.2	27.6	12.7	45.8	4.6	405	203	83	6.2	6.0	4.2	6.0	1.07	1	3
N LK LX 571	(US)	446	34.5	24.4	26.1	12.2	46.7	4.6	406	195	69	5.4	6.0	4.1	5.8	1.18	0	1
O PAYM 303	(US)	526	35.6	25.6	25.8	11.7	45.4	4.3	426	194	67	5.3	3.2	3.3	3.6	1.10	0	3
P STONE 213	(US)	492	34.8	24.2	27.2	13.8	47.1	4.8	401	195	76	6.2	6.0	4.6	6.0	1.32	0	3
Q WESTBRN M	(US)	555	34.3	25.3	26.4	12.1	46.0	4.3	424	203	70	6.0	3.5	2.4	3.7	1.14	0	2
R 149-F	(UR)	473	35.3	25.1	27.0	12.6	46.6	4.1	400	200	80	6.5	6.0	4.6	6.0	1.46	0	4
S 153-F	(UR)	519	35.9	25.9	24.8	12.1	48.6	4.8	402	197	84	6.5	6.0	4.9	5.9	1.64	3	2
T 2421	(UR)	376	30.4	20.8	24.6	11.7	47.7	4.4	407	201	72	6.3	5.9	4.3	5.7	1.58	1	1
U C-4727	(UR)	443	34.0	23.7	25.7	12.3	47.7	4.2	429	215	84	6.9	6.0	4.7	6.0	1.26	0	4
V TASHKNT-1	(UR)	377	34.0	23.7	25.3	12.2	48.1	4.1	420	211	89	6.6	6.0	4.9	6.0	1.73	1	4
W TASHKNT-2	(UR)	417	35.6	24.9	26.1	12.6	48.4	4.4	415	205	89	6.4	5.7	4.4	5.7	1.55	0	4
X TASHKNT-3	(UR)	358	32.4	22.4	25.9	12.1	46.6	4.1	413	203	88	6.2	6.0	4.4	5.8	1.70	2	3
Mean		390	33.2	23.1	26.5	12.5	46.9	4.3	424	206	84	6.2	5.4	4.0	5.4	1.32	0.9	2.9
SD		112	2.3	1.9	1.7	0.8	1.2	0.3	31	18	11	0.6	1.0	0.7	0.9	0.20	1.1	0.8
No. observations		24	24	24	12	12	12	12	12	12	120	60	56‡	56‡	56‡	56‡	†	†

†Overall appearance used to evaluate character.

‡Mean number of observations per entry.

Table 2. (Continued)

Identification		Storm-resis-tance	Boll characters							Bract characters					Leaf characters			Pubescence		
			Locks/ boll	Seed/ lock	Pitted-ness	Boll shape	Boll size	Waxi-ness	Lint/ boll	Boll cover-age	Teeth/ bract	Teeth shape	Bract shape	Bract size	Color	Loba-tion	Leaf size	Apex	Leaf	Stem
		g	no.				g		g	cm	no.			cm						
A IAC-13-1	(BR)	115	4.1	7.7	1.7	1.2	6.0	1.1	1.9	2.7	13.5	5.3	1.5	5.0	2	3.1	4	2.0	1.5	1.9
B IAC-RM4/5	(BR	153	4.4	6.7	2.1	1.4	5.7	1.2	1.9	3.3	14.0	5.1	1.4	5.3	2	2.7	3	1.9	1.7	1.7
C MINAS DB	(BR)	145	4.2	7.4	1.7	1.3	5.3	1.7	1.9	2.6	13.2	4.6	1.6	5.3	3	3.4	3	2.3	0.9	1.9
D SU 0450/8	(BR)	101	4.2	7.3	1.2	1.3	4.5	2.5	1.2	2.3	12.1	4.7	1.6	4.8	1	3.9	3	2.7	2.1	2.5
E 4959	(BU)	105	4.3	7.1	2.1	1.3	5.0	1.0	1.6	2.6	10.7	4.7	1.5	4.6	1	3.3	0	2.4	2.1	2.9
F 6396	(BU)	138	4.2	6.5	2.2	1.3	4.7	1.0	1.4	2.9	12.5	4.3	1.4	4.8	1	3.5	2	2.1	2.0	2.7
G 4F	(PA)	108	4.9	6.2	1.2	1.3	4.4	1.0	1.4	2.9	10.9	5.7	1.7	4.3	0	2.7	3	3.4	2.8	3.0
H DEL CERRO	(PE)	170	4.2	8.0	2.1	1.4	6.9	1.5	2.0	3.3	13.7	4.5	1.3	5.2	2	2.5	3	2.5	0.7	1.7
I SK 14	(TN)	78	4.6	7.1	1.3	1.3	4.7	1.9	1.4	3.2	11.5	4.6	1.7	4.5	4	3.2	4	4.9	4.3	3.7
J CA(68)41	(UG)	70	4.3	6.4	2.0	1.5	4.8	1.1	1.3	2.5	13.8	3.5	1.5	4.6	4	3.1	3	4.1	3.7	3.7
K ACALA SJ5	(US)	140	4.6	8.2	2.1	1.3	6.8	1.0	2.5	3.3	14.5	4.5	1.5	4.9	3	2.6	2	1.9	1.9	2.0
L COKR 5110	(US)	144	4.3	7.8	2.7	1.4	6.7	1.1	2.3	3.2	12.7	4.2	1.6	5.3	3	3.2	3	1.6	2.0	1.2
M DPL 16	(US)	116	4.3	6.7	1.9	1.3	4.8	1.2	1.6	2.9	13.7	4.7	1.6	5.2	2	3.3	3	1.9	0.0	1.1
N LK LX 571	(US)	172	4.5	7.8	2.6	1.2	7.9	1.0	2.5	3.3	11.7	4.5	1.5	5.2	1	3.4	3	1.8	3.0	1.2
O PAYM 303	(US)	147	4.8	7.4	1.9	1.3	6.2	1.1	2.0	3.3	10.7	4.4	1.5	4.9	3	2.5	1	1.3	1.1	1.1
P STONE 213	(US)	110	4.4	7.1	2.1	1.2	5.6	1.4	1.8	2.8	10.7	4.4	1.5	4.7	1	3.1	2	2.4	2.0	2.0
Q WESTBRN M	(US)	163	4.7	7.0	1.9	1.2	6.2	1.1	2.0	2.9	11.2	4.4	1.4	4.5	1	3.6	2	1.0	1.0	0.3
R 149-F	(UR)	154	5.0	6.7	2.0	1.2	6.2	2.0	2.0	2.9	13.8	4.2	1.5	5.3	2	2.9	3	3.0	2.3	2.8
S 153-F	(UR)	163	4.3	6.7	2.2	1.3	5.8	1.5	2.1	3.1	13.5	4.2	1.3	4.8	1	2.9	4	2.3	2.1	2.1
T 2421	(UR)	181	4.3	6.6	1.5	1.3	4.2	1.0	1.3	2.9	10.0	4.3	1.6	4.4	1	3.8	0	2.9	2.1	2.8
U C-4727	(UR)	175	4.4	7.6	2.1	1.3	6.6	1.1	2.3	3.1	14.0	4.4	1.3	4.7	2	4.2	4	2.5	1.7	2.5
V TASHKNT-1	(UR)	195	4.6	8.2	1.9	1.3	6.2	1.7	2.0	2.9	14.8	4.8	1.4	5.4	2	3.4	4	1.3	0.1	1.0
W TASHKNT-2	(UR)	146	4.0	6.9	1.9	1.2	5.2	1.3	1.7	2.7	13.4	4.4	1.4	4.9	3	3.5	5	2.3	0.9	2.3
X TASHKNT-3	(UR)	181	4.3	7.0	2.0	1.3	6.1	1.3	1.6	3.0	15.2	5.0	1.3	4.9	2	3.0	4	2.2	1.7	2.4
Mean		140	4.4	7.2	1.9	1.3	5.6	1.3	1.8	2.9	12.7	4.6	1.5	4.9	2.0	3.2	3.0	2.4	1.8	2.1
SD		33	0.2	0.6	0.4	0.1	0.9	0.4	0.4	0.3	1.5	0.4	0.1	0.3	1.0	0.4	1.2	0.9	1.0	0.9
No. observations		12	12	12	15	15	12	15	12	15	15	15	15	15	†	15	†	15	15	15

Table 2. (Continued)

Identification		Seed characters						Yarn characters			Miscellaneous characters						
		Seed index	Fuzziness	Ammonia	Free fatty acid	Oil	Cake yield	Yarn tenacity	Yellowness	Reflectance	Bur size	Corolla color	Extrafloral nectaries	Staminal column glands	Lint index	Pedicel length	Pollen color
		g		%				cN/tex	b	R_d	g				g	cm	
A IAC-13-1	(BR)	12.8	3	4.3	0.6	19.4	50.5	11.5	10.5	68.4	2.0	2.0	2.0	1.5	7.0	1.8	1.9
B IAC-RM4/5	(BR)	13.0	4	4.5	1.5	18.1	52.4	11.5	10.0	68.2	2.0	2.0	2.0	1.1	6.6	2.2	2.0
C MINAS DB	(BR)	11.4	3	4.4	0.9	19.0	51.6	11.5	10.3	68.0	1.9	2.0	2.0	1.2	5.6	2.2	1.7
D SU 0450/8	(BR)	10.9	4	4.2	0.7	19.6	49.7	13.0	10.5	70.3	1.5	2.0	1.2	1.0	4.5	2.3	2.0
E 4959	(BU)	11.1	3	4.5	0.6	17.7	53.3	11.8	8.3	69.6	1.8	2.0	1.5	1.7	5.4	1.7	2.0
F 6396	(BU)	11.6	2	4.5	0.6	17.4	52.9	10.9	8.7	70.4	1.8	2.0	1.9	0.8	4.7	1.9	2.0
G 4F	(PA)	9.9	1	4.5	0.5	20.3	52.7	11.7	8.6	69.7	1.7	2.0	1.4	1.5	5.3	3.2	1.2
H DEL CERRO	(PE)	14.8	3	4.2	0.8	17.5	50.0	15.6	9.0	72.6	2.7	2.0	2.0	2.0	5.5	1.9	2.0
I SK 14	(TH)	10.0	3	4.2	0.8	18.3	48.9	11.7	9.8	69.9	1.7	2.0	1.8	1.7	5.6	2.8	2.0
J CA(68)41	(UG)	12.6	3	4.8	0.5	19.5	56.8	13.6	8.4	67.8	1.7	2.0	1.9	1.3	4.9	1.9	1.3
K ACALA SJ5	(US)	11.9	3	4.7	0.7	19.9	55.8	15.4	9.0	71.8	2.5	2.0	2.0	1.6	6.6	1.6	2.0
L COKR 5110	(US)	12.7	3	4.6	0.7	18.8	54.2	12.0	9.4	71.1	2.2	2.0	2.0	0.9	6.1	2.4	2.0
M DPL 16	(US)	11.1	3	4.4	0.5	19.2	51.3	11.6	9.4	68.2	1.9	2.0	2.0	0.4	5.2	1.7	2.0
N LK LX 571	(US)	14.9	1	4.6	1.6	18.2	54.0	11.2	9.4	72.0	2.6	2.0	2.0	0.3	6.1	2.2	1.9
O PAYM 303	(US)	11.8	3	4.5	0.7	18.6	52.9	11.5	9.3	71.0	2.2	2.0	2.0	0.2	6.2	1.5	2.0
P STONE 213	(US)	11.8	3	4.2	0.6	17.3	49.9	11.6	10.1	67.4	1.9	2.0	2.0	0.1	5.4	1.5	2.0
Q WESTBRN M	(US)	12.2	1	4.6	1.0	18.5	54.3	11.5	9.4	72.8	1.8	2.0	2.0	0.1	5.9	1.4	2.0
R 149-F	(UR)	12.6	4	4.2	0.6	17.5	49.3	11.8	8.7	71.6	2.1	2.0	2.0	1.0	5.8	1.8	2.0
S 153-F	(UR)	12.7	0	4.7	0.6	18.8	55.0	11.5	9.0	71.9	1.8	2.0	2.0	1.1	5.5	1.2	2.0
T 2421	(UR)	10.8	3	4.7	0.6	18.4	54.8	10.8	8.3	69.6	1.8	2.0	1.9	1.0	4.6	1.5	2.0
U C-4727	(UR)	12.8	3	4.7	0.6	18.1	55.3	12.0	9.3	68.7	2.1	2.0	1.9	1.0	5.9	1.9	2.0
V TASHKNT-1	(UR)	12.0	3	4.2	0.7	17.6	49.2	12.0	9.4	68.0	2.2	2.0	1.9	1.0	6.0	2.1	2.0
W TASHKNT-2	(UR)	12.4	3	4.4	1.3	17.5	52.0	12.3	9.9	68.4	1.9	1.9	2.0	1.5	4.7	1.5	2.0
X TASHKNT-3	(UR)	11.0	3	4.5	0.7	18.3	52.4	12.1	8.9	70.2	2.0	1.6	2.0	1.0	5.3	2.3	2.0
Mean		12.0	2.7	4.5	0.8	18.5	52.5	12.1	9.3	69.9	2.0	2.0	1.9	1.0	5.6	1.9	1.9
SD		1.3	1.0	0.2	0.3	0.8	2.3	1.2	0.7	1.7	0.3	0.1	0.2	0.5	0.7	0.5	0.2
No. observations		12	+	2	2	2	2	2	2	2	12	15	15	15	12	15	15

Table 3. Dissimilarity matrix generated by pairwise computation of generalized Euclidean distances among the 24 entries over 52 characters.

Identification		A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X
A IAC-13-1	(BR)	0.00†																							
B IAC-RM4/5	(BR)	6.95	0.00																						
C MINAS DB	(BR)	5.60	6.11	0.00																					
D SU 0450/8	(BR)	10.30	11.55	9.09	0.00																				
E 4959	(BU)	8.98	8.78	8.01	10.49	0.00																			
F 6396	(BU)	8.73	11.16	7.37	11.02	4.81	0.00																		
G 4F	(PA)	12.69	12.78	12.35	11.90	11.26	12.05	0.00																	
H DEL CERRO	(PE)	11.70	10.66	11.45	13.82	12.77	12.47	16.43	0.00																
I SK 14	(TH)	9.94	10.28	9.02	9.64	9.76	9.94	10.25	15.12	0.00															
J CA(68)41	(UG)	12.60	12.41	11.45	12.55	11.30	11.17	12.22	14.01	11.70	0.00														
K ACALA SJ5	(US)	10.94	10.11	10.14	14.38	11.02	11.52	14.97	9.40	13.30	13.24	0.00													
L COKR 5110	(US)	7.86	6.73	6.57	12.45	8.90	7.97	14.09	9.92	11.53	11.84	7.73	0.00												
M DPL 16	(US)	6.70	6.93	4.59	10.34	7.76	6.49	12.70	11.80	10.45	12.00	10.19	6.74	0.00											
N LK LX 571	(US)	10.23	8.53	9.50	14.98	10.63	9.70	15.86	12.23	13.98	15.74	10.01	7.36	9.61	0.00										
O PAYM 303	(US)	9.25	8.82	8.95	13.91	9.15	8.79	13.81	12.80	11.76	12.71	9.28	7.47	7.89	8.75	0.00									
P STONE 213	(US)	7.75	8.06	6.31	11.02	7.02	6.26	13.79	12.44	10.24	12.93	11.10	8.00	5.67	9.38	8.22	0.00								
Q WESTBRN M	(US)	9.88	9.78	9.67	13.69	9.46	8.46	13.74	13.58	13.24	13.42	10.90	8.69	8.59	8.22	5.89	8.83	0.00							
R 149-F	(UR)	8.70	8.51	7.67	11.58	8.78	7.56	13.87	10.70	10.28	12.92	10.43	7.80	7.58	10.10	8.74	7.05	10.14	0.00						
S 153-F	(UR)	9.89	8.96	8.88	13.72	8.62	6.85	13.49	12.61	11.71	13.22	10.75	8.64	8.46	9.14	9.91	8.39	9.19	8.92	0.00					
T 2421	(UR)	10.84	10.10	9.18	11.06	5.44	5.84	11.69	14.01	10.36	11.72	12.45	10.50	8.71	11.48	10.28	8.58	9.97	10.29	9.19	0.00				
U C-4727	(UR)	8.00	7.74	7.25	11.98	8.00	6.62	13.41	10.66	11.44	11.79	9.07	6.49	7.61	8.92	9.32	7.85	9.24	7.67	7.64	9.16	0.00			
V TASHKNT-1	(UR)	7.93	7.87	6.93	11.37	9.55	8.27	13.95	10.14	11.55	14.06	10.66	8.00	7.54	9.90	9.89	8.20	10.60	6.91	9.11	10.91	6.78	0.00		
W TASHKNT-2	(UR)	7.94	7.91	6.19	11.03	8.39	6.55	13.87	11.29	10.50	12.00	10.78	8.33	7.04	10.08	10.11	6.96	9.97	7.67	8.09	9.60	6.52	6.96	0.00	
X TASHKNT-3	(UR)	8.80	8.18	8.25	11.25	9.04	7.48	12.58	11.36	10.60	12.28	11.15	9.07	8.20	11.12	10.51	9.32	10.85	8.48	8.71	9.48	8.00	7.65	7.54	0.00

†Only the lower half of the original matrix is presented here.

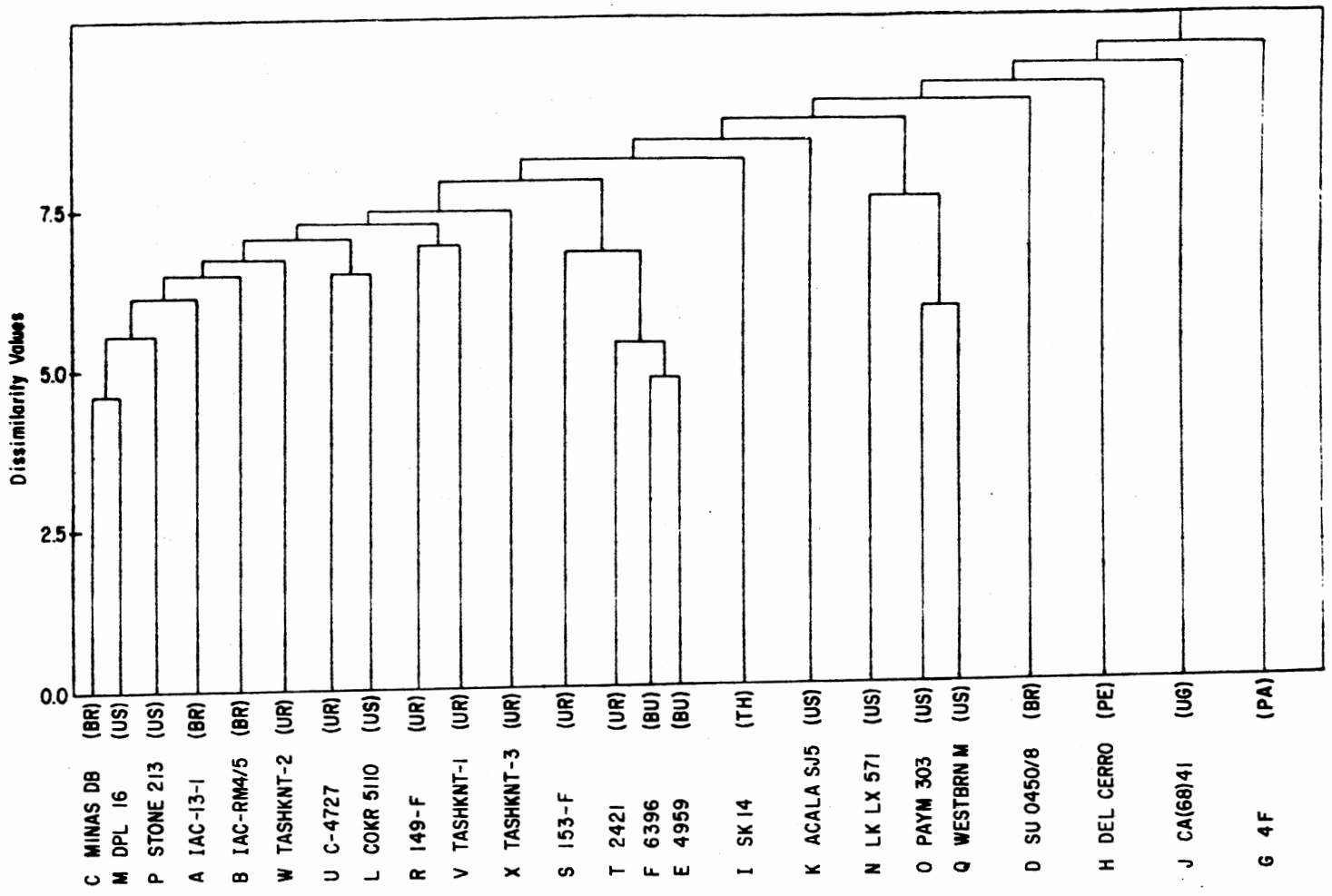

Fig. 1. Dendrogram representing relationships among 24 cultivars and strains from eight countries.

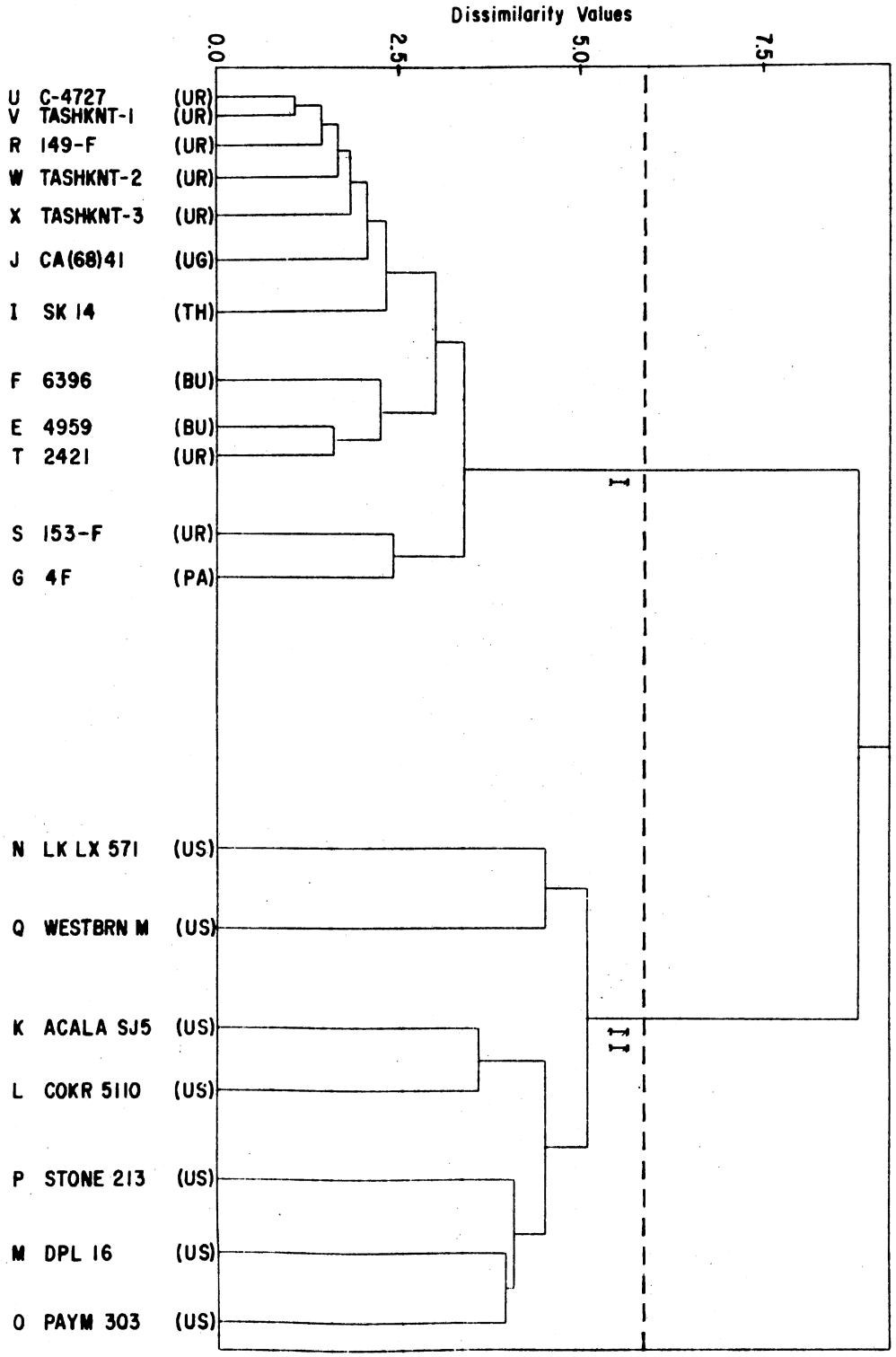

Fig. 2. Dendrogram representing relationships among 19 cultivars from the United States and the Old World.

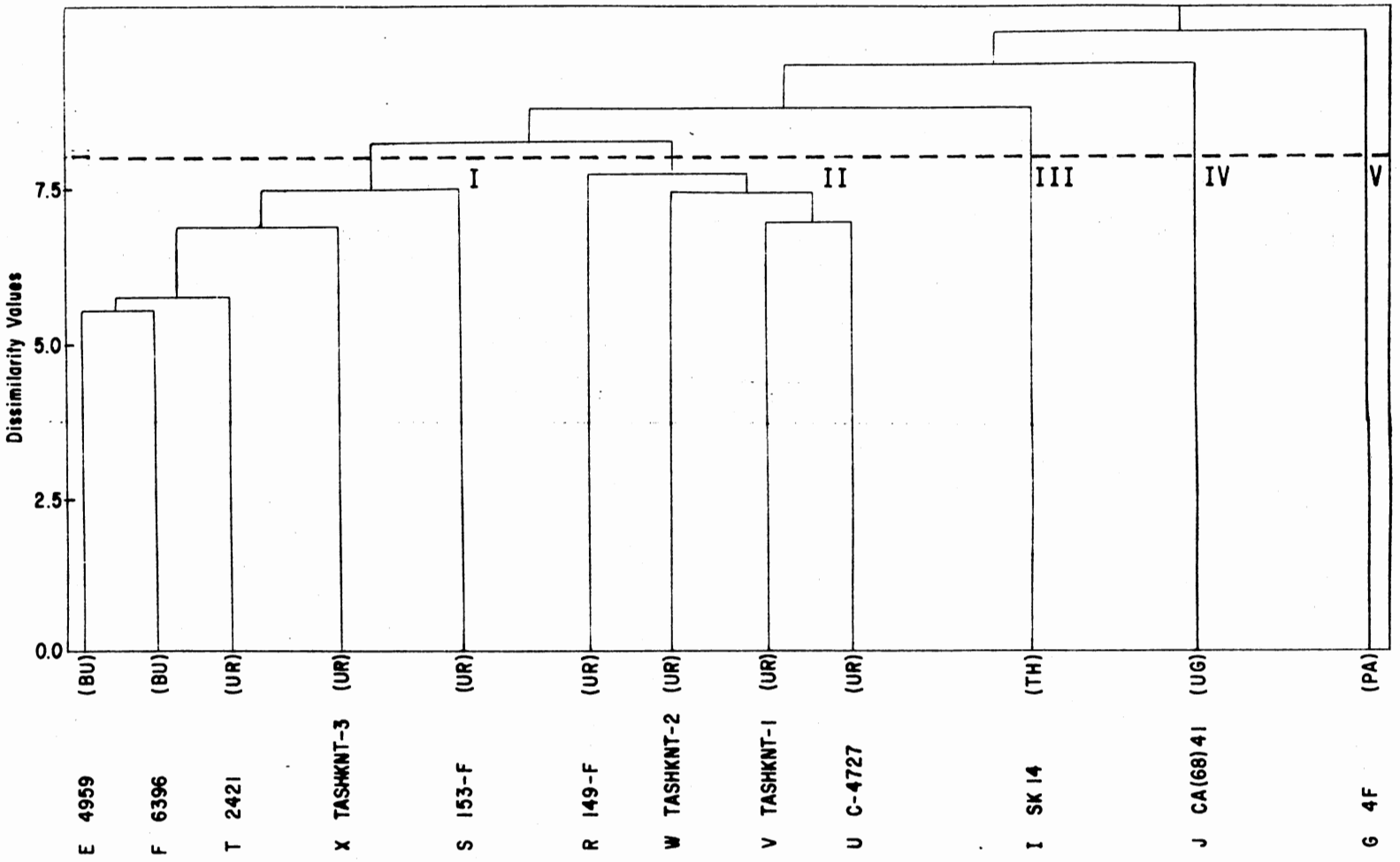

Fig. 3. Dendrogram representing relationships among 12 cultivars from Europe, Asia, and Africa.

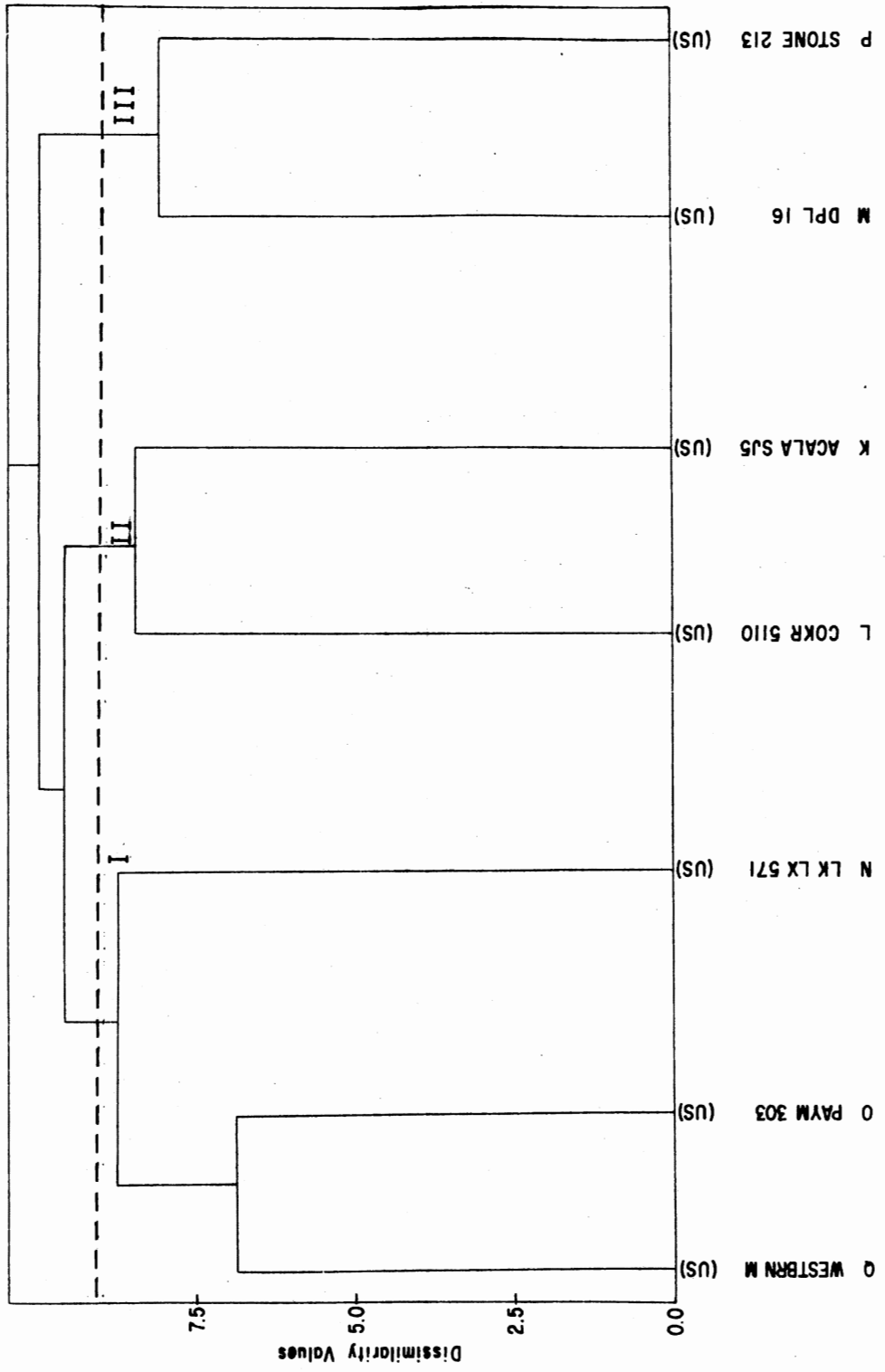

Fig. 4. Dendrogram representing relationships among seven cultivars from the United States.

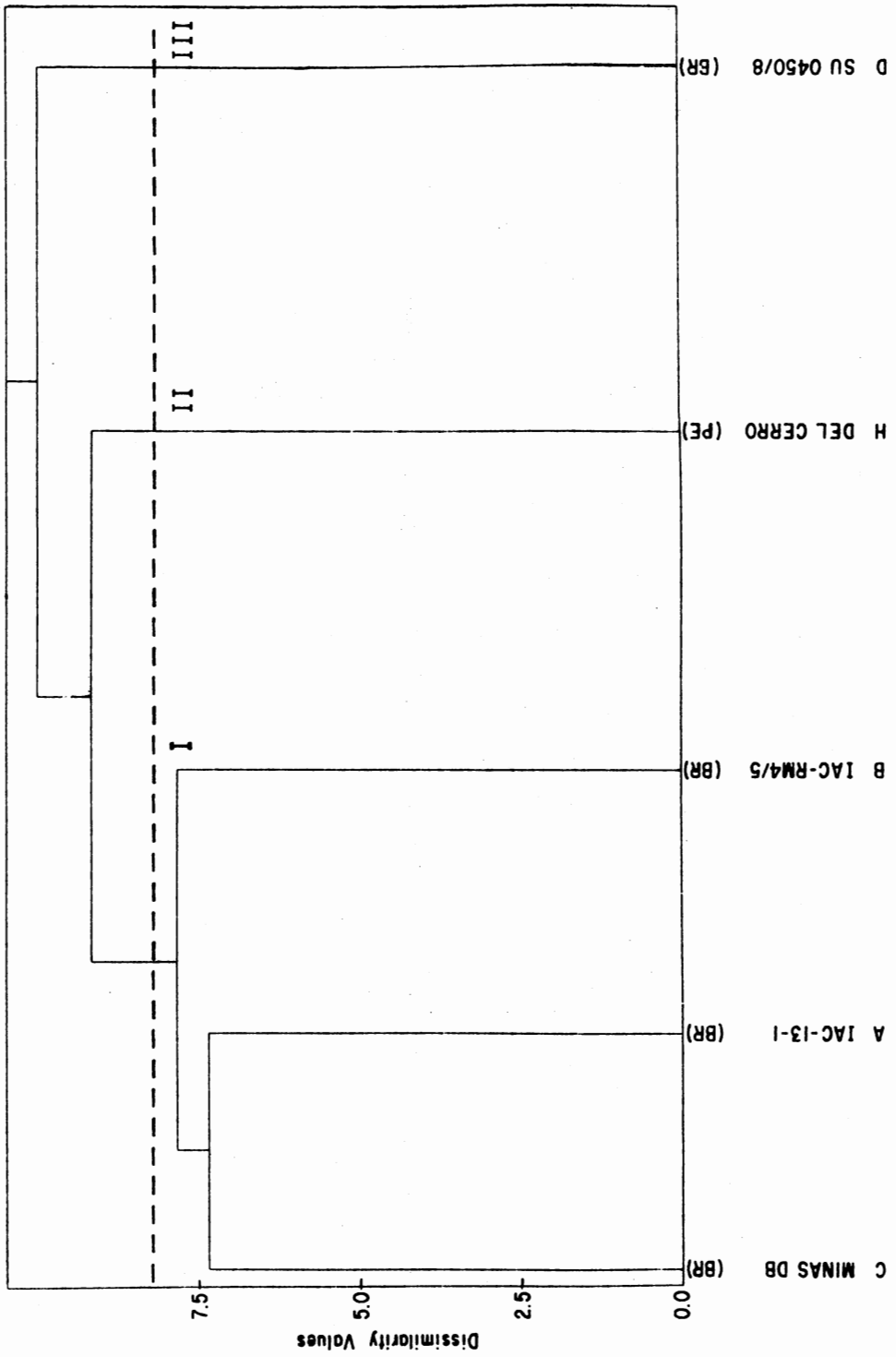

Fig. 5. Dendrogram representing relationships among five cultivars and strains from South America.

APPENDIX

(Tables 4 Through 7)

Table 4. Dissimilarity matrix generated by pairwise computation of generalized Euclidean distances among the 19 entries over 52 characters used to obtain Fig. 2.

Identification		E	F	G	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X
E 4959	(BU)	0.00†																		
F 6396	(BU)	2.21	0.00																	
G 4F	(PA)	4.49	3.69	0.00																
I SK 14	(TH)	4.61	4.07	4.01	0.00															
J CA(68)41	(UG)	4.10	3.27	4.77	2.50	0.00														
K ACALA SJ5	(US)	14.80	14.87	15.24	14.37	14.61	0.00													
L COKR 5110	(US)	14.60	14.43	14.88	13.98	14.20	3.57	0.00												
M DPL 16	(US)	13.72	13.44	13.67	13.07	13.43	5.71	4.11	0.00											
N LK LX 571	(US)	14.87	14.61	14.95	14.77	15.18	6.90	5.60	5.24	0.00										
O PAYM 303	(US)	13.04	12.94	13.66	12.93	12.85	5.30	4.08	3.95	5.65	0.00									
P STONE 213	(US)	14.15	13.94	14.44	14.01	14.20	5.60	4.31	14.16	5.75	4.07	0.00								
Q WESTBRN M	(US)	13.23	12.91	13.40	13.33	13.58	7.36	5.66	5.13	4.50	4.24	5.65	0.00							
R 149-F	(UR)	3.43	2.61	4.87	3.49	2.69	14.51	14.06	13.10	14.80	12.65	13.69	13.12	0.00						
S 153-F	(UR)	4.73	3.55	2.41	4.17	4.84	15.29	14.80	13.68	14.59	13.61	14.47	13.08	5.17	0.00					
T 2421	(UR)	1.58	2.89	4.40	4.65	4.67	15.03	14.74	13.72	14.78	13.09	14.18	13.19	4.19	4.50	0.00				
U C-4727	(UR)	3.69	2.17	4.44	3.44	2.34	14.70	14.19	13.25	14.78	12.93	13.94	13.13	1.56	4.39	4.44	0.00			
V TASHKNT-1	(UR)	3.81	2.40	3.93	2.91	2.32	14.79	14.24	13.19	14.79	12.94	14.02	13.10	1.66	4.03	4.39	1.06	0.00		
W TASHKNT-2	(UR)	4.52	3.26	5.03	3.16	2.70	14.47	13.98	13.15	14.54	12.86	13.98	13.08	2.23	4.79	5.20	1.64	1.77	0.00	
X TASHKNT-3	(UR)	3.58	2.48	3.36	2.34	2.59	14.76	14.27	13.20	14.68	13.00	14.01	13.11	2.42	3.28	3.76	1.94	1.45	2.46	0.00

†Only the lower half of the original matrix is presented here.

Table 5. Dissimilarity matrix generated by pairwise computation of generalized Euclidean distances among the 12 entries over 52 characters used to obtain Fig. 3.

Identification		E	F	G	I	J	R	S	T	U	V	W	X
E 4959	(BU)	0.00†											
F 6396	(BU)	5.54	0.00										
G 4F	(PA)	10.82	11.97	0.00									
I SK 14	(TH)	9.86	10.46	10.91	0.00								
J CA(68)41	(UG)	11.37	11.86	12.41	12.77	0.00							
R 149-F	(UR)	9.07	8.05	14.06	11.01	13.11	0.00						
S 153-F	(UR)	8.65	7.02	13.46	11.73	13.68	8.66	0.00					
T 2421	(UR)	5.98	5.71	11.43	10.28	11.92	10.42	9.20	0.00				
U C-4727	(UR)	8.45	7.58	13.24	12.28	12.17	7.95	8.07	9.69	0.00			
V TASHKNT-1	(UR)	9.72	8.96	13.95	12.26	14.12	7.40	9.25	11.03	6.85	0.00		
W TASHKNT-2	(UR)	8.59	7.65	13.74	10.93	12.16	8.40	8.58	9.74	7.64	7.60	0.00	
X TASHKNT-3	(UR)	8.38	7.04	12.23	10.23	11.69	7.71	8.15	8.52	7.91	7.28	7.46	0.00

†Only the lower half of the original matrix is presented here.

Table 6. Dissimilarity matrix generated by pairwise computation of generalized Euclidean distances among the seven entries over 52 characters used to obtain Fig. 4.

Identification		K	L	M	N	O	P	Q
K ACALA SJ5	(US)	0.00†						
L COKR 5110	(US)	8.42	0.00					
M DPL 16	(US)	11.62	8.77	0.00				
N LK LX 571	(US)	10.87	8.67	11.03	0.00			
O PAYM 303	(US)	10.13	8.91	9.94	9.89	0.00		
P STONE 213	(US)	12.49	9.60	8.04	11.01	9.93	0.00	
Q WESTBRN M	(US)	11.94	10.19	10.16	9.38	6.86	10.31	0.00

†Only the lower half of the original matrix is presented here.

Table 7. Dissimilarity matrix generated by pairwise computation of generalized Euclidean distances among the five entries over 52 characters used to obtain Fig. 5.

Identification		A	B	C	D	H
A IAC-13-1	(BR)	0.00†				
B IAC-RM4/5	(BR)	8.66	0.00			
C MINAS DB	(BR)	7.33	7.46	0.00		
D SU 0450/8	(BR)	10.63	11.82	9.61	0.00	
H DEL CERRO	(PE)	10.92	10.51	9.89	12.77	0.00

†Only the lower half of the original matrix is presented here.

VITA

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Doctor of Philosophy

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