NUMERICAL CLASSIFICATION OF THE GENUS CYNODON

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INTRODUCTION

Present-day classifications of <u>Cynodon</u> recognize twelve species
in the genus. These accepted species, however, still show great varia-
bility within themselves and at the same time give a large number of
intermediate forms among them making it difficult at times for the taxo-
nomist to assign an unclassified plant to any species. Very often, this
difficulty results in misclassification.

Realizing the "confused taxonomy" of <u>Cynodon</u>, Hurcombe earlier
attempted to revise the genus. After a series of cytological and
morphological studies of the cultivated species of <u>Cynodon</u> (1946, 1947,
1948), she was able to present definite characters that would distinguish
one species from another. In 1949, Bogdan published a paper on how to
differentiate <u>C</u>. <u>plectostachyus</u> from <u>C</u>. <u>dactylon</u>. According to his
treatment, plants described by Hurcombe as <u>C</u>. <u>plectostachyus</u> would be
classified as <u>C</u>. <u>dactylon</u>.

The often lack of agreement between the results of two classifica-
tions has long been a problem not only in the taxonomy of <u>Cynodon</u> but
in those of practically all organisms. Modern taxonomists attribute
this situation to the fact that most classifications are based on sub-
jective opinions of the investigators. In recent years, a number of
workers, dissatisfied with the existing taxonomic procedures, have tried
to devise more objective methods of classification. They have proposed
the quantification of taxonomy, that is, using mathematical procedures

in classification. With this new method, it is believed that two investigators working independently on two organisms can arrive at the same conclusion concerning the relationship between these two organisms (Sokal and Sneath, 1963).

This study attempts to apply the quantitative or numerical approach of classification to *Cynodon* with the hope of being able to correct any misclassifications that have been done in the genus in the past.

REVIEW OF LITERATURE

One of the earliest attempts to apply the numerical methods to
taxonomy was made in 1898 by Heincke who used a measure of phenetic
distance to distinguish between races of the herring (Sokal and Sneath,
1963). Then as the science of biometry progressed, people began to
recognize its usefulness to systematics. Fisher, in 1936, developed
a function which would best discriminate two or more populations that
have been measured in some characters. He also presented a method
of determining the probability of misclassification if the specific
nature was judged mainly from the given measurements.

An early statistic related to taxonomic distance, which is a measure
of taxonomic resemblance, was developed by Karl Pearson (1926) for use
in physical anthropology. Noting the difficulty of comparing two races
by treating character differences individually, he proposed what he
termed "a Coefficient of Racial Likeness" which would serve as a single
measure of over-all differences. Pearson's coefficient was later deve-
loped by Mahalanobis (1936) and Rao (1948) in the form of the "Generalized
Distance" statistic which is more applicable to taxonomy.

Several other methods of finding similarities and differences among
taxonomic groups were advocated in the early part of the century but
for some reasons these methods did not succeed. Sokal and Sneath (1963)
believe that the failures of these methods were due to the lack at the
time of computational facilities that would permit the study of adequate

number of characters or taxa.

With the introduction of high speed computers, the interests in
using numerical methods in taxonomy have been renewed. In the last
decade, a sufficiently large number of workers have become engaged
in the numerical or mathematical analyses of taxa that some taxonomists
have regarded these as the "New Taxonomy" of today (Cain, 1958; Ehrlich
and Holm, 1962). Various names have been given to the "New Taxonomy":
Quantitative taxonomy (Michener and Sokal, 1957); taxonometrics (Rogers
and Tanimoto, 1960), numerical taxonomy (Sneath and Sokal, 1962), taxo-
metrics (Hill, 1962), and taximetrics (Rogers, 1963).

The numerical methods have been used with satisfactory results
for a wide range of bacteria, including such genera as _Streptomyces,_
Mycobacterium, Pseudomonas, Lactobacillus, and _Micrococcus_ (for a reivew,
see Sneath, 1962). Andrewes and Sneath (1958) attempted to compare and
if possible, group twenty-five viruses by means of the quantitative
method proposed by Sneath (1957a, 1957b) but were not able to use enough
viruses and characters to obtain more conclusive results.

In zoology, the materials studied range from insects; such as bees
(Michener and Sokal, 1957; Sokal and Michener, 1958; and Rohlf and Sokal,
1962), mosquitoes (Rohlf, 1963), and butterflies (Ehrlich, 1961); to the
human skull (Cain and Harrison, 1960).

The relatively few applications to plants include those of Morishima
and Oka (1960) on rice; Rogers and Tanimoto (1960) on the manioc plant;
Soria and Heiser (1961) on _Solanum;_ and Katz and Torres (1965) on _Zinnia._

The various techniques for quantifying similarities or differences
among taxa that have been employed by different workers have been grouped
by Sokal and Sneath (1963) into three types of coefficients - those of

association, of correlation, and of distance – which have been collec-
tively referred to as coefficient of resemblance or similarity. Sneath
(1957) applied to bacteria a coefficient of association which was first
used in ecology by Jacquard as early as 1908 (Sneath, 1962). The coeffi-
cient which Sneath called Similarity is the ratio of those features pos-
sessed by both of the individuals being compared to those features posses-
sed by at least one of them. He did not consider negative features, that
is, features not possessed by either of the two individuals, in his
coefficient on account of the difficulty of deciding which negative
features to include and which to exclude.

Sokal and Michener (1958) in their study on bees considered using
what they termed "matching coefficients". Each character was divided
into two to eight states and the matching coefficient obtained by getting
the ratio of the number of matches, either positive or negative, in
states for all characters to the sum of matches and mismatches (i.e.,
characters possessed by one but not by the other) which is actually
the total number of characters. The coefficients were not employed,
however, since they distorted resemblances by counting a 3 to 4 mismatch
the equal of a 1 to 7 mismatch and because they would have been more
difficult to handle by the IBM equipment accessible to the workers.

The similarity ratio employed by Rogers and Tanimoto (1960) also
includes negative matches but differs from the matching coefficient
in that it gives mismatches twice as much weight as matches, that is,
the resulting coefficient is actually the ratio of the number of matches
to the sum of the number of matches and twice the number of mismatches
($s_{ij} = \frac{m}{m + 2u}$, where i and j are the individuals being compared, m is

the number of matched pairs, and $\underline{u}$, the number of unmatched pairs).
Later, Rogers and Fleming (1964) revised the method for obtaining the
similarity ratio and arrived at a coefficient which is actually just an
elaborate form of the matching coefficient of Sokal and Michener (1958).

Sokal and Sneath (1963) are of the opinion that negative matches
should be included for those characters that vary within the group
under study and hence agree with Rogers and Tanimoto (1960). They
further believe that also not all positive matches should be considered
in the analysis; those for characters which are invariant in the group
should be excluded.

The method of Rogers and his co-workers makes allowance for char-
acters with more than two states, e.g., quantitative characters. However,
it has the same defect noted by Sokal and Michener in their matching
coefficient: it considers a close character difference (the pair being
compared expressing a character in adjacent states) the same as a wide
character difference (the pair expressing a character in the extreme
states). Realizing the need for some means of expressing the magnitude
of differences in quantitative characters, Kendrick and Proctor (1964)
considered the giving of fractional values to these differences, with
a score of unity for the maximum possible difference. Because of pro-
gramming difficulties that might result from the use of fractions, the
proposal was not tested. Kendrick (1964) then proposed the use of a
number which is divisible by all the possible states of the characters
in an analysis. Since he had suggested that there should not be more
than six states allotted to any character, he gave as an example the
number 60, which is divisible by 1, 2, 3, 4, 5, and 6. A character
which is expressed in the highest state is scored 60 and scored

proportionately less, if expressed in other states, depending on the
number of possible states for that character. He outlined three ways
of making comparisons between organisms with the use of this method of
scoring.

Besides the inability of association coefficients to measure the
degrees of character differences, Sokal and Sneath (1963) have another
objection to their use in multistate characters. They showed that in
such characters the probability of matches to occur becomes greatly
reduced and as a consequence, the values of association coefficients
are also much reduced.

Sheals (1964) discussed and followed the work of Gower (unpublished)
at Rothamsted Experimental Station on general problems of classification
which provides a simple procedure for calculating an index of similarity
that takes into consideration both quantitative and qualitative characters.
For a quantitative character, a similarity value, S, is calculated as follows:

$$S = 1 - \frac{|\bar{x}_i - \bar{x}_j|}{r}$$

where $\bar{x}_i$ and $\bar{x}_j$ are the ranked or absolute measurements of the character
in each of the two taxa compared and r is the observed range of that
character in all the taxa under study. For a qualitative character
or a character with only two states, $\underline{S}$ is simply equal to $\underline{1}$, when it
is a match, and $\underline{S}$ is equal to $\underline{0}$, when it is a mismatch. The index of
similarity between the two taxa is then obtained by dividing the sum of
the similarity values for all the characters by the total number of
characters used in the comparison.

Because of the problems associated with the use of association
coefficients in characters expressed in more than two states, Sokal

and Sneath (1963) recommend the employment of either the correlation

coefficient or the distance analysis for such characters. These two

coefficients, unlike most of the association coefficients that have

been discussed, take into account the magnitude of differences between

taxa for multistate characters.

The correlation coefficient was introducted to numerical taxonomy

by Michener and Sokal (1957) and Sokal and Michener (1958). For lack

of a better means of correlation for their studies on bees, they adopted

the Pearson product-moment correlation coefficient (formula can be

found in any statistics book). The method was then applied by Morishima

and Oka (1960) to the study of rice species, by Soria and Heiser (1961)

to Solanum, and by Ehrlich (1961) to butterflies.

"When the data are arbitrarily coded and the number of states

varies for different characters, the correlations cannot meet the

basic assumptions of the bivariate normal frequency distribution" (Sokal

and Sneath, 1963). To remedy this situation in numerical taxonomy,

Sokal (1961) proposes the standardization of characters, which has

been tried before in other fields. To do this, it is necessary to cal-

culate the mean and standard deviation of each character. The deviation

of the character from the mean is then divided by the standard deviation.

Every character will now have a mean of zero and a variance of unity and

therefore one can say that the variates for each taxon are sampled from

populations with a common mean (zero) and standard deviation (unity).

Rohlf and Sokal (1965) determined the effect of standardization of

characters on the coefficients of correlation and distance. They obtained

slight differences between standardized and unstandardized distances

and markedly reduced average correlation for each matrix of coefficients based on standardized characters.

The use of distance as a measure of taxonomic similarity is not new. It was employed as early as 1898 by Heincke (Sokal, 1961) and quite well studied in the few years that followed (e.g., works of Pearson, Mahalanobis, and Rao).

Sokal (1961) developed a distance formula for numerical taxonomy by the extension of the Pythagorean Theorem in analytical geometry. For n characters, Sokal's formula for the distance squared of taxa 1 and 2 is:

$$\delta_{1,2}^2 = \sum_{i=1}^{n} (X_{i1} - X_{i2})^2$$

where X_{i1} and X_{i2} are the state codes of taxon 1 and taxon 2, respectively, for character i. Knowing that the greater the number of characters involved in the comparison, the greater the distance between taxa would be, he considered it more appropriate to use the mean distance squared which is the result of dividing the above expression by n, the number of characters under consideration. He added that if preferred, the linear distances (i.e., not the squared ones) may be used.

Rogers and Tanimoto (1960) converted their similarity ratios into distances defined as $d_{ij} = -\log_2 S_{ij}$ where i and j are the taxa under consideration and S_{ij}, the similarity ratio between them. As pointed out by the workers, the distance d_{ij} defines what is known in mathematics as a semimetric space. Applied to taxonomic problems, this type of space will mean that two taxa which are both similar or related to a third need not be related to each other.

Rohlf (1963) preferred distances to correlation coefficients for constructing a classification of the genus <u>Aedes</u> for the following reasons: 1) the distances gave similar results for adults and larvae; 2) the relationships given by distances agreed with his subjective impressions of the relationships; and 3) the relationships resulting from distances corresponded more closely to the previous classification of the genus.

Penrose (1952) noting that Mahalanobis' "generalized distance" formula will involve extensive computation when used in studies involving a large number of measured characters, reexamined Pearson's Coefficient of Racial Likeness (C.R.L.) which is easier to calculate. He showed that the C.R.L.; in its reduced form; i.e., C.R.L. $= C^2_H = (d_1^2 + d_2^2 +$ . . . $+ d_m^2)/m$ where $\underline{m}$ is the number of measured characters and $\underline{d}$ is the difference for each character between the two populations being compared; could be broken down into two components, namely, "size" and "shape". The "size distance" between the two populations is $= C^2_Q = \underline{/}(d_1 + d_2 +$ . . . $+ d_m)/\underline{m}\underline{/}^2$ and is therefore a measure of the magnitude of the differences. If C^2_Q is subtracted from C^2_H, what remains is an estimate of the "shape distance" which is therefore a measure of the amount of diversity or variance among the d-values. He stated that when classifying two or more objects, it is normally the shape of the object which enables it to be classified, not its size, except when size differences are extreme; that is, the two objects with zero "shape distance" from one another will be assigned to the same class.

Rohlf and Sokal (1965) also believe that shape is more important than size for estimating over-all similarity but showed that Penrose's

"shape" coefficient is not an adequate measure of similarity in shape
since it is zero, only if the difference between the two organisms is
constant for all the characters, a condition which is very unlikely to
happen. They found that the correlation coefficient is a better measure
of similarity in shape and that Sokal's distance coefficient, like Penrose's,
is more a measure of similarity in size. Based on these findings, they
concluded that correlation coefficients are more appropriate measures
of taxonomic similarity when most characters used in a study are measure-
ments of various parts of an organism.

In a recent paper, Eades (1965) showed that in studies involving
few characters, taxonomic conclusions based on correlation coefficients
can be incorrect, that is, these coefficients can be greater for an
obviously less similar pair than for one with actually greater resemblance.
The correlation coefficient r, he said, can be expressed as

$$r = \pm \sqrt{1 - \frac{1}{s_y^2} \frac{1}{n} \sum_{i=1}^{n} (y_i - y'_i)^2}$$

where s_y is the standard deviation of the y's, n is the number of char-
acters under study, and y' is the value of y predicted from the corres-
ponding value of x and the regression line of y on x. This formula gives
the same answers as those obtained from the formula commonly used in
numerical taxonomy. He further stated that deviation should be measured
not from the regression line but from the line showing a perfect match
between x and y, that is, the line where $y'_i = x_i$. In this case the
correlation coefficient equation becomes:

$$r = \pm \sqrt{1 - \frac{1}{s_y^2} \frac{1}{n} \sum_{i=1}^{n} (y_i - x_i)^2}$$

Comparing this equation with the formula for Sokal's square of the average taxonomic distance which is:

$$\frac{1}{n} \sum_{i=1}^{n} (y_i - x_i)^2$$

it can be noted that the two equations differ by only one variable, namely, s_y^2. This variable according to Eades should not be used in measuring taxonomic resemblance because "it is influenced by such irrevalent things as inverting the scale of measurement for some characters (even though characters are standardized)". On this basis, he concluded that the average taxonomic distance is more appropriate than the correlation coefficient as a measure of taxonomic resemblance, provided the characters are well chosen.

The ordering of states of a character is not always an easy task. It is hard to decide, for example, which of three possible shapes of a leaf should be given the lowest code. Minkoff (1965) noted this difficulty and showed that changing the direction of coding for some characters in a study, that is, when the state first assigned the lowest code is then given the highest code and vice versa, a change in the relationships indicated by correlation coefficients could result. For this reason, he does not consider the correlation coefficient a good statistic for measuring similarity. He believes that the distance coefficient, particularly Mahalanobis' generalized distance, is a better measure since it is not affected by the directionality of coding.

One controversial point in numerical taxonomy is the problem of weighting. A number of workers in this field have emphasized the necessity of giving equal weights to all characters, an idea which was first put forward in the eighteenth century by Michel Adanson. Michener and Sokal (1957) agree that weighting characters is important, but since it is not clear how weighting should be done, one should resort to equal weighting. The main argument of those who do not favor the giving of equal weights to characters is that not all characters are of equal importance. A counter argument of Sokal and Sneath (1963) is that the concept of taxonomic importance has no exact meaning. They stated, among other things, that if "importance" means essential to survival, then the taxonomist can estimate viability, not resemblance.

On the other hand, Kendrick and Proctor (1963) and Kendrick (1964) believe that relative importance can be assessed. To them, characters that depend for their existence on other characters, e.g., hairiness of leaf depends on presence of leaf itself, are less important and hence should be given lesser weights than those independent characters.

Rogers (1964) has nothing against the giving of equal weights to characters, having noted that most non-weighted systems have dealt with organisms in which weighting is really difficult, but justified character weighting for higher plants. He, however, believes that there is a very small difference between the two concepts.

The results of a number of numerical taxonomic studies agreed quite well with those obtained from the classical procedures. Soria and Heiser (1961), who obtained one such good agreement, stated that the new method can therefore provide an excellent check on established taxonomies.

MATERIALS AND METHODS

Several collections from all over the world of all the known species
of <u>Cynodon</u> are grown every year in greenhouses and on the farm at the
Oklahoma Agricultural Experimental Station. Bud materials are collected
for cytological examinations and herbarium specimens are preserved for
morphological studies. The materials used in the present study came
from the 1964 planting. One hundred and eleven accessions, most of
which are <u>C</u>. <u>dactylon</u> obtained from fifteen countries, were examined
morphologically, but due to the difficulty of handling so many data,
a number of the <u>C</u>. <u>dactylon</u> accessions studied were not considered in
the numerical analyses. All the fifteen countries were, however,
represented in the <u>C</u>. <u>dactylon</u> accessions included. Three species,
<u>C</u>. <u>bradleyi</u>, <u>C</u>. <u>magennessii</u>, and <u>C</u>. <u>transvaalensis</u>, were not studied
for lack of good herbarium specimens. The accessions analyzed are listed
in Table I.

Records were taken for thirty-eight morphological characters but
two of these characters were eliminated because they did not vary in
all the 111 accessions examined. Table II shows the remaining 36 char-
acters. Except for the metric characters, nineteen of them, all the
characters were coded.

The morphological studies were made on ten mature plants of each
accession.

TABLE I

CYNODON SPECIES STUDIED

SPECIES	ACCESSION NUMBER	SOURCE
C. arcuatus	10121	Ceylon
	10584	India
C. barberi	10575	India
	10580	India
C. coursii	10127	Malagasy
	10128	Malagasy
C. dactylon	8150	Afghanistan
	8800	Afghanistan
	9233	Ethiopia
	9945a	Turkey
	9946a	Greece
	9951	Afghanistan
	9954a	Iran
	9956	India
	9957	Yugoslavia
	9958	Italy
	9960	Iraq
	10005	India
	10006	Ceylon
	10019	India
	10251b	S. Africa
	10257	S. Africa
	10320	Malagasy
	10339	S. Africa
	10355	S. Africa
	10418	Tanzania
	10694	Australia
	10975	Argentina
C. hirsutus	10272	S. Africa
	10974	Argentina
C. incompletus	10376	S. Africa
	10497	S. Africa
C. leptochloides	10104	Malagasy
	10108	Malagasy
C. plectostachyus	9235	Ethiopia
	10229	Nigeria
C. polevansii	10112	S. Africa

TABLE II

CHARACTERS STUDIED

CHARACTER	REMARKS*
1) Number of Chromosomes**	18 - 27 - 36
2) Rhizome**	present (1) - absent (2)
3) Winter hardiness**	hardy (1) - not hardy (2)
4) Peduncle length	in mm.
5) Peduncle sheath length	in mm.
6) Hair, peduncle sheath	present (1) - absent (2)***
7) Peduncle leaf length	in mm.
8) Peduncle leaf width	in mm./10
9) Hair, upper surface of peduncle leaf	present (1) - absent (2)
10) Type of hair, upper surface of peduncle leaf	short (1) - short and long (2) - long (3)
11) Hair, lower surface of peduncle leaf	present (1) - absent (2)
12) Type of hair, lower surface of peduncle leaf	short (1) - short and long (2) - long (3)
13) First internode length	in mm.
14) First internode sheath length	in mm.
15) First internode leaf length	in mm.
16) First internode leaf width	in mm./10
17) Hair, upper surface of first internode leaf	present (1) - absent (2)
18) Type of hair, upper surface of first internode leaf	short (1) - short and long (2) - long (3)
19) Hair, lower surface of first internode leaf	present (1) - absent (2)
20) Type of hair, lower surface of first internode leaf	short (1) - short and long (2) - long (3)

TABLE II (Cont.)

CHARACTER	REMARKS*
21) Ligule length	in mm./10
22) Hair, ligule	present (1) - absent (2)
23) Number of nodes in axis	ranges from 1 to 7
24) Number of racemes	ranges from 3 to 20
25) Length of longest raceme	in mm.
26) Length of shortest raceme	in mm.
27) Number of spikelets in the longest raceme	ranges from 17 to 110
28) Rachilla produced beyond floret	yes (1) - no (2)
29) Length of lower glume	in mm./10
30) Hair, lower glume	present (1) - absent (2)
31) Length of upper glume	in mm./10
32) Hair, upper glume	present (1) - absent (2)
33) Length of spikelet	in mm./10
34) Length of longest glume/length of spikelet	x 100
35) Hair, sides of lemma above upper glume	present (1) - absent (2)
36) Number of nerves, upper glume	1 - 2 - 3

* Number inside parentheses is the code used.
** Data provided by Dr. J. M. J. de Wet.
*** Hair was considered present when distributed over at least 50% of leaf surface or length of lemma or glume as the case may be.

Computational Procedure:

As can be noted in the Review of Literature, several methods for calculating the similarities or differences among taxonomic groups are available. It can be noted also that none of the three types of coefficients of similarity are perfect. However, it appears that the main defect of the coefficients of association, which is their not being able to measure the degree of individual character differences among groups when multistate characters are involved, can be corrected. At least two methods of calculating association coefficients that take care of the magnitude of differences in multistate characters have already been proposed: the method of Kendrick (1964) and that of Gower (discussed by Sheals, 1965). It was decided to adopt Gower's method since it is simpler than Kendrick's. Moreover, with the former method, actual measurements in a metric character can be used, i.e., the measurements need not be coded.

In the calculation of the indices of similarity, the average of the ten values recorded for every character in every accession was the one used so Gower's formula for the similarity between two taxonomic groups for one character became:

$$S = 1 - \frac{|\bar{x}_i - \bar{x}_j|}{r}$$

where $\bar{x}_i$ and $\bar{x}_j$ were the average values for that character of accessions i and j, respectively, and r equalled the highest average value minus the lowest average value for that character in all the 37 accessions.

The calculated similarity indices were placed in a 37 x 37 matrix (Table III, Results). There are several ways of grouping individuals

based on the matrix of similarity coefficients, the simplest of which is the so-called Cluster Analysis. Among the different methods of cluster analyses that can be employed, Sokal and Sneath (1963) consider clustering by average linkage as the most satisfactory. This was used by Sokal and Michener (1958) and by Soria and Heiser (1961) for analyzing correlation coefficient matrices but according to Sokal and Sneath (1963) it can be applied to the other types of coefficients.

Details of the clustering procedure which was based on the procedures of Sokal and Michener (1958) and Soria and Heiser (1961) are included in the Results.

RESULTS

Comparisons of the thirty-seven accessions with one another yielded
666 similarity indices (Table III). Using the technique of Sokal and
Sneath (1963) for determining the individual significance of association
coefficients, all the 666 similarity indices were found significantly
different from zero at one per cent level.

There are four methods of clustering by average linkage to choose
from, namely, unweighted variable-group, weighted variable-group, unweight-
ed pair-group, and weighted pair-group. Since there is not much evidence
yet that any of these methods is better than the others, it was decided
to adopt the unweighted variable-group method which can easily be employed
with a desk calculator. In this method, more than two members are allowed
to join a cluster during one clustering cycle. This necessitates the setting
of a value which will serve as the limit to which a new member can be
admitted to the group. No formula for determining the statistical signi-
ficance of the difference between two association coefficients has yet
been devised so the limit has to be arbitrarily set. In this study, a
value of 0.05 was first tried but 0.04 was later found to give a better
grouping.

The pair that gave the highest index of similarity in the matrix,
.933, comprised accessions 10272 and 10376, C. hirsutus and C. incompletus,
respectively. These two therefore, were used as the nucleus of the first
clustering cycle. Found closest to 10272 and 10376 was accession 10497,

TABLE III

MATRIX I OF SIMILARITY INDICES AMONG

THIRTY-SEVEN ACCESSIONS OF <u>CYNODON</u>

ACCESSION	8150	8800	9233	9235	9945a	9946a	9951	9954a	9956
8800	.793								
9233	.664	.695							
9235	.523	.478	.635						
9945a	.923	.831	.694	.494					
9946a	.880	.814	.676	.494	.887				
9951	.860	.814	.758	.564	.871	.852			
9954a	.807	.762	.721	.506	.815	.833	.839		
9956	.786	.840	.678	.499	.809	.802	.824	.838	
9957	.887	.864	.721	.519	.911	.907	.908	.846	.824
9958	.869	.856	.730	.553	.873	.895	.893	.865	.834
9960	.859	.792	.709	.491	.891	.864	.805	.806	.784
10005	.796	.764	.645	.424	.786	.723	.735	.745	.743
10006	.837	.829	.633	.432	.838	.796	.803	.793	.798
10019	.768	.872	.746	.515	.794	.766	.760	.718	.800
10104	.690	.740	.631	.596	.669	.678	.766	.665	.733
10108	.693	.701	.687	.662	.694	.688	.787	.677	.700
10112	.807	.789	.754	.543	.825	.754	.764	.751	.744
10121	.690	.703	.684	.624	.677	.673	.778	.672	.731
10127	.692	.760	.700	.515	.692	.740	.778	.749	.805
10128	.736	.775	.689	.499	.724	.740	.794	.745	.750
10229	.568	.495	.641	.792	.567	.583	.607	.543	.517
10251b	.849	.838	.661	.485	.847	.796	.818	.820	.858
10257	.810	.747	.760	.569	.815	.803	.827	.893	.804
10272	.727	.677	.725	.532	.739	.691	.720	.630	.611
10320	.810	.860	.698	.498	.832	.794	.805	.759	.847
10339	.771	.865	.680	.466	.793	.775	.797	.748	.807
10355	.808	.766	.771	.587	.837	.807	.816	.835	.824
10376	.729	.685	.708	.534	.753	.714	.732	.645	.621
10418	.586	.659	.710	.494	.602	.639	.683	.726	.731
10497	.727	.672	.701	.576	.738	.714	.725	.670	.643
10575	.591	.611	.567	.320	.573	.592	.608	.548	.565
10580	.638	.671	.599	.376	.609	.605	.654	.579	.621
10584	.779	.776	.720	.564	.762	.771	.858	.731	.718
10694	.776	.821	.675	.405	.795	.786	.781	.814	.825
10974	.725	.664	.680	.500	.724	.662	.697	.597	.580
10975	.839	.794	.649	.482	.854	.900	.799	.810	.782

TABLE III (Cont.)

ACCESSION	9957	9958	9960	10005	10006	10019	10104	10108	10112
8800									
9233									
9235									
9945a									
9946a									
9951									
9954a									
9956									
9957									
9958	.932								
9960	.831	.841							
10005	.768	.751	.709						
10006	.843	.821	.756	.919					
10019	.818	.790	.762	.812	.795				
10104	.715	.721	.610	.608	.686	.711			
10108	.730	.736	.636	.567	.638	.663	.914		
10112	.811	.806	.817	.764	.774	.823	.634	.655	
10121	.720	.720	.614	.576	.657	.668	.900	.901	.641
10127	.755	.773	.651	.685	.762	.740	.788	.760	.677
10128	.767	.781	.679	.758	.827	.773	.779	.726	.715
10229	.554	.587	.583	.468	.473	.532	.530	.585	.553
10251b	.839	.831	.811	.848	.890	.819	.727	.684	.821
10257	.825	.839	.793	.744	.793	.750	.704	.723	.809
10272	.698	.681	.747	.643	.608	.691	.554	.580	.704
10320	.849	.838	.774	.784	.858	.881	.766	.710	.828
10339	.819	.794	.722	.831	.832	.877	.711	.644	.733
10355	.836	.828	.826	.733	.767	.804	.685	.732	.879
10376	.706	.697	.764	.665	.623	.695	.551	.578	.715
10418	.643	.659	.570	.685	.682	.715	.677	.643	.593
10497	.691	.710	.795	.637	.614	.681	.537	.560	.717
10575	.606	.579	.517	.706	.657	.689	.601	.531	.570
10580	.651	.618	.527	.725	.682	.743	.668	.593	.624
10584	.819	.801	.691	.673	.745	.751	.870	.859	.723
10694	.803	.807	.786	.823	.868	.789	.650	.601	.771
10974	.679	.656	.713	.710	.633	.683	.549	.566	.716
10975	.858	.849	.886	.679	.756	.751	.654	.650	.743

TABLE III (Cont.)

ACCESSION	10121	10127	10128	10229	10251b	10257	10272	10320	10339
8800									
9233									
9235									
9945a									
9946a									
9951									
9954a									
9956									
9957									
9958									
9960									
10005									
10006									
10019									
10104									
10108									
10112									
10121									
10127	.774								
10128	.749	.895							
10229	.566	.538	.538						
10251b	.694	.712	.750	.501					
10257	.717	.755	.761	.604	.820				
10272	.548	.531	.556	.600	.664	.633			
10320	.739	.805	.837	.504	.857	.801	.609		
10339	.673	.768	.798	.513	.807	.730	.645	.810	
10355	.713	.735	.730	.616	.840	.890	.655	.825	.758
10376	.545	.533	.575	.610	.673	.655	.933	.619	.665
10418	.717	.815	.796	.539	.660	.703	.509	.689	.743
10497	.534	.578	.613	.654	.669	.666	.912	.627	.651
10575	.563	.681	.724	.400	.580	.532	.514	.657	.699
10580	.653	.716	.758	.412	.637	.557	.572	.707	.734
10584	.853	.804	.837	.593	.760	.773	.644	.796	.743
10694	.628	.768	.821	.454	.856	.786	.618	.826	.834
10974	.530	.496	.540	.574	.669	.620	.897	.605	.628
10975	.641	.713	.738	.593	.763	.752	.671	.783	.751

TABLE III (Cont.)

ACCESSION	10355	10376	10418	10497	10575	10580	10584	10694	10974
8800									
9233									
9235									
9945a									
9946a									
9951									
9954a									
9956									
9957									
9958									
9960									
10005									
10006									
10019									
10104									
10108									
10112									
10121									
10127									
10128									
10229									
10251b									
10257									
10272									
10320									
10339									
10355									
10376	.681								
10418	.688	.525							
10497	.697	.897	.543						
10575	.537	.540	.699	.476					
10580	.582	.571	.737	.528	.885				
10584	.751	.640	.697	.615	.663	.719			
10694	.787	.618	.723	.662	.644	.647	.698		
10974	.640	.896	.475	.836	.564	.614	.643	.576	
10975	.784	.692	.618	.725	.580	.593	.712	.775	.625

C. incompletus, whose similarities to the pair averaged .905. The drop
in similarity was less than 0.04 so 10497 was admitted to the group 10272-
10376. Accession 10974, C. hirsutus, had an average similarity to 10272-
10376-10497 of .876 so was permitted to join this group. The accession
closest to the now four-membered group was 9960, a C. dactylon from Iraq,
with an average similarity to the four accessions of .755. There was a
drop of more than 0.04 from the group's average similarity index so 9960
was not included in the cluster which is called Group A.

The next highest mutual similarity was between accessions 9957 and
9958, both C. dactylon, so the second cluster was started at these two.
Following the above procedure, six more accessions, all C. dactylon,
joined the group which is called B, namely (in the order of their admit-
tance), 9946a, 9945a, 8150, 9951, 10975, and 9960.

The third nucleus was provided by two more C. dactylon accessions,
10005 and 10006. No other accessions entered this group, however.

The first clustering cycle closed with six more groups formed –
Group D: 10104 (C. leptochloides), 10108 (C. leptochloides), and 10121
(C. arcuatus); Group E: 10127 and 10128 (both C. coursii); Group F:
9954a, 10257, and 10355 (all C. dactylon); Group G: 10575 and 10580 (both
C. barberi); Group H: 10019, 10320, 8800, 10339, 10251b, 9956, and 10694
(all C. dactylon); and Group I: 9235 and 10229 (both C. plectostachyus) –
and four accessions left unadmitted to any group: 9233 (C. dactylon),
10112 (C. polevansii), 10418 (C. dactylon), and 10584 (C. arcuatus).
The four unattached accessions were given the group names J, K, L, and
M, respectively, in the second matrix of similarity indices (Table IV).

As can be seen in Table IV, the highest between-group similarity
index was that of D and M which is .861. The group closest to D and M

TABLE IV

MATRIX II OF SIMILARITY INDICES

GROUP	A	B	C	D	E	F	G	H	I	J	K	L
B	.711											
C	.642	.775										
D	.553	.693	.622									
E	.553	.735	.758	.763								
F	.649	.818	.763	.699	.746							
G	.547	.596	.693	.602	.720	.556						
H	.646	.800	.820	.694	.776	.786	.658					
I	.573	.548	.449	.594	.523	.571	.377	.490				
J	.704	.700	.639	.667	.695	.751	.583	.690	.638			
K	.713	.791	.769	.643	.696	.813	.597	.787	.548	.754		
L	.513	.625	.684	.679	.806	.706	.718	.703	.517	.710	.593	
M	.636	.774	.709	.861	.821	.752	.691	.749	.579	.720	.723	.697

is E. Group E's similarities to the members of groups D and M averaged
.777 which is more than .04 lower than .861 so E was excluded from
the cluster D-M.

The next highest intergroup similarity index was .820 which was
between C and H. Three groups joined this cluster at this cycle:
B, F, and K. The second cycle ended with still five groups unattached
to a cluster.

Table V shows the third matrix of similarities. For the third
clustering cycle, there was only one possible nucleus: E and L, which
have a similarity of .806. The third cycle terminated at cluster
E-L because no other groups qualified for admission to this cluster.

By the end of the fifth cycle all the groups except I had converged
with a similarity value of .637. Group I finally joined them at a
similarity level of .531. Table VI and VII show the fourth and fifth
matrices, respectively.

The results of clustering are presented in the form of a dendogram
(Figure 1).

TABLE V

MATRIX III OF SIMILARITY INDICES

GROUP	A	CHBFK	DM	E	G	I	J
CHBFK	.674						
DM	.573	.702					
E	.553	.750	.777				
G	.547	.620	.624	.720			
I	.573	.522	.590	.523	.377		
J	.704	.701	.681	.695	.583	.638	
L	.513	.667	.684	.806	.718	.517	.710

TABLE VI

MATRIX IV OF SIMILARITY INDICES

GROUP	A	CHBFK	DM	EL	G	I
CHBFK	.674					
DM	.573	.702				
EL	.540	.722	.746			
G	.547	.620	.624	.719		
I	.573	.522	.590	.521	.377	
J	.704	.701	.681	.700	.583	.638

TABLE VII

MATRIX V OF SIMILARITY INDICES

GROUP	A	(DM)(EL)(CHBFK)J	G
(DM)(EL)(CHBFK)J	.647		
G	.547	.630	
I	.573	.536	.377
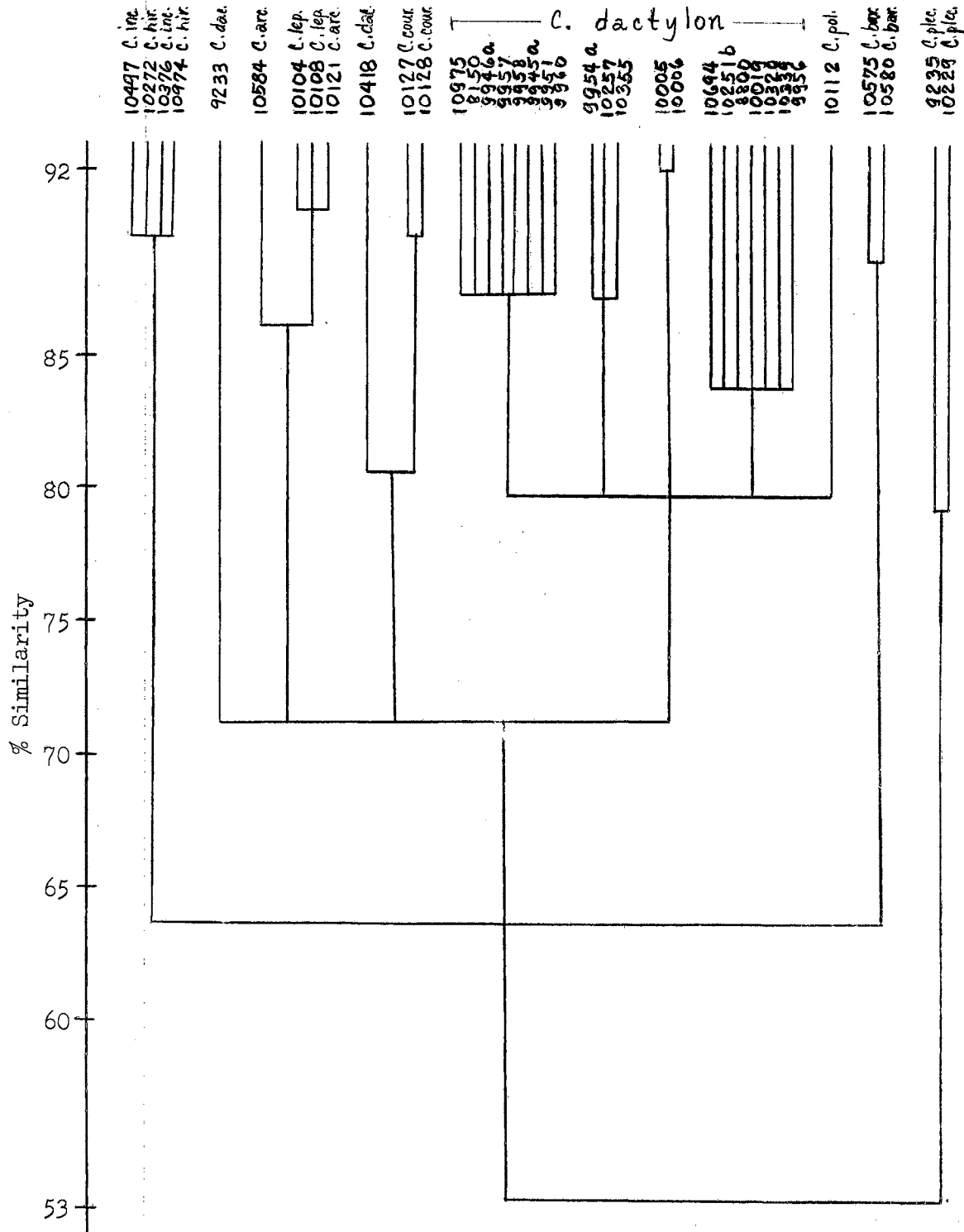
Figure 1. Diagram of Relationships Among Thirty-seven Accessions
of the Genus Cynodon Obtained by the Unweighted
Variable-Group Method.

DISCUSSION AND CONCLUSIONS

The making of a classification out of a dendogram is trouble-
some in practice (Rohlf, 1963). This is more so if not all the known
taxonomic groups, species in this study, have been included in the
study. The taxonomist should try to look for the classification that
will be least altered when the groups that have been left out are added
at a later date. If the study represents a more or less complete sam-
pling of the known taxonomic groups, Rohlf (1963) believes that the phenon
lines, i.e., lines dividing the taxonomic units into new groups, should
be drawn with little regard for the present classification and simply
allowed to cross the longer stems. In the dendogram in Figure 1, the
longest stem separating species is that one which connects C. plectos-
tachyus to the rest of the species; the stem between the 63.7% and 53.1%
similarity levels. In the present study, three species of Cynodon,
which make up 25% of all the recognized species, were not included:
C. bradleyi, C. magennessii, and C. transvaalensis. The phenon line,
therefore, cannot just be drawn across the longest stem. However, if
the descriptions of C. bradleyi, C. magennessii, and C. transvaalensis
appearing in the literature are assumed to be correct, their later
inclusion will not change the relationship of C. plectostachyus to the
rest of the species in the dendogram. Cynodon bradleyi was considered
by Stent (1927) as a natural hybrid of C. dactylon and C. hirsutus.
Hurcombe (1947), however, found it to be a well-defined species. By

Chippindal's (1955) descriptions, C. bradleyi does not seem to differ much from C. hirsutus and C. incompletus. Cynodon magennessii was found by Hurcombe (1947) to be a natural hybrid between C. dactylon and C. transvaalensis. This finding not only shows the closer relationship of C. magennessii to C. dactylon than to the other species in the present study but also indicates the close relationship of C. transvaalensis to C. dactylon. Forbes and Burton (1962) observed a high rate of trivalent formation in the artificial triploid hybrids between C. transvaalensis and tetraploid C. dactylon indicating that there is indeed a great degree of relationship existing between the two species. Thus it can be seen that if ever the later consideration of C. bradleyi, C. magennessii, and C. transvaalensis will affect the structure of the dendogram at all, the effect will likely be above the 63.7% similarity level.

The phenon line can now be placed somewhere between 53.1% and 63.7% similarity levels, say, along the 55% level, and by doing so two distinct groups of species are obtained: one consisting of only the two accessions of C. plectostachyus, 9235 and 10229, which may be called the plectostachyus group and the other comprising the rest of the accessions which may be referred to as the dactylon group.

Sneath and Sokal (1962) state that if the taxonomist desires, he can equate the groups established by numerical taxonomy with genera, tribes, or families, e.g., if the original taxonomic units are species, the new taxa may represent subgenera or genera. It does not seem important, though, whatever rank is given to the plectotachyus group. What appears to be significant is that the numerical analyses of the different

species of Cynodon have proven that C. plectostachyus is quite distinct
from C. dactylon, as contended by Bogdan (1949), or from any other
species and therefore other workers are not justified in confusing this
species with any of the other species.

It can be seen that the dactylon group is not a uniform group but
is made up of distinct smaller groups. One subgroup comprises the
species C. incompletus and C. hirsutus. Some workers identify C. hirsutus
as C. incompletus but Stent (1927) thinks that the two species differ
markedly. The present study shows that the two species are inseparable.
Even the lowering of the significant drop in similarities will not change
the relationship between the two "species" because the pair that give
the highest similarity to each other are a C. hirsutus accession, 10272,
and a C. incompletus accession, 10376. Chippindal (1955) differentiates
the two on the bases of amount of hair on leaves, length of ligule, and
the length of the glumes in relation to the length of the spikelet.
The four accessions used in this study seem separated into two groups
mainly on the basis of the degree of leaf pubescence which is a quite
subjective character.

Another subgroup in the dactylon group combines C. arcuatus and
C. leptochloides. The main criterion used to differentiate the two is
geographical distribution, C. arcuatus being distributed in Asia and C.
leptochloides, in Madagascar. The earlier described species, C. arcuatus,
must have been introduced to Nossible Island where it was given another
name.

Cynodon polevansii forms a subgroup with most of the C. dactylon
accessions included in the present study. Because C. polevansii was

known only on dry sandy regions of South Africa, Stent (1927) suspected
that it was not a true species but the result of a mutation. The $\underline{C}$.
polevansii material used in the present study looks distinctly better
than the original accession which was collected from a saline area in
South Africa so it is probably true that $\underline{C}$. polevansii is not a new
species but one of those earlier described species that has been exposed
to less favorable growing conditions. The dendogram indicates that
that species is $\underline{C}$. dactylon.

The fact that one of the $\underline{C}$. dactylon accessions, 10418, has formed
a subgroup with the two $\underline{C}$. coursii accessions, 10127 and 10128, and
another $\underline{C}$. dactylon accession has formed another distinct subgroup has
shown that $\underline{C}$. dactylon is really a variable and complex species. But
since there are relatively few accessions studied of the other species
it cannot be concluded that these other species are more uniform than
$\underline{C}$. dactylon and so only $\underline{C}$. dactylon needs to be reclassified. It can be
noted that high similarity indices are obtained between accessions coming
from quite close, if not the same, places. The species that give high
within species similarities are represented by accessions obtained from
the same locality, showing that classification within a certain area has
been quite consistent. If it had been possible to include in the study
specimens from a wider range of habitats, the estimates of the variabili-
ties of species like $\underline{C}$. barberi and $\underline{C}$. coursii could have been more relia-
ble. These species might have been found as variable as $\underline{C}$. plectostachyus.

On the average, the classification obtained by the numerical analysis
is in good agreement with the presently accepted classification of Cynodon.
It can be noted, however, that most of the characters used in the present
study are characters used to differentiate the different species of

Cynodon. It has not been intended to give too much weight to these characters. Several other morphological characters have been considered but not very many of these other characters vary in the materials studied. A study which will not confine the choice of characters to morphological characters is probably needed to obtain a more reliable conclusion concerning the correct classification of Cynodon.

Character correlations have not been considered in the present study. There are possibilities that some characters used are inter-correlated. Leaf length, for example, may be correlated to leaf sheath length and internode length, peduncle length to internode length, peduncle length to raceme length, or all these "length" characters may be correlated to one another. If the latter possibility is true, then two accessions which actually are similar in only one character had been scored as similar in no less than six characters. It will be necessary in later studies to investigate character correlations.

The numerical method of classification does not appear entirely non-subjective as proponents of this procedure have claimed. The division of the taxonomic units into groups, for example, still requires the judgment of the investigator. It is, however, a promising method and it is believed that it can provide solutions to some of the pro-blems raised by the classical method.

SUMMARY

In an attempt to correct any misclassification in Cynodon, the
numerical method of classification, which has been successfully used
for a wide range of organisms, was tried on this genus. Thirty-seven
accessions representing nine species of Cynodon were examined for
thirty-six morphological characters. Ten plants represented each
accession but only averages were used in evaluating resemblance or
similarity between every pair of accessions. Similarities were cal-
culated using the formula discussed by Sheals (1964). A grouping
of the thirty-seven accessions based on their similarities to each
other was done using the unweighted variable-group method of Sokal
and Michener (1958).

The diagram of the relationships among the thirty-seven accessions
obtained from the clustering procedure shows the separation of C.
plectostachyus from the rest of the species. It also indicates that
some species should belong to only one taxonomic group, e.g., C. hir-
sutus and C. incompletus should go together and C. leptochloides
should be combined with C. arcuatus. There are indications that some
plants classified as C. dactylon are actually distinct species. Because
of the poor sampling of most of the species, no definite conclusions
could be reached concerning the revisions that should be made in the
existing classification of Cynodon.

LITERATURE CITED

1. Andrewes, C. H. and P. H. A. Sneath. 1958. The species concept among viruses. Nature 182: 12-14.

2. Bogdan, A. V. 1949. Two species of Star grass in Kenya. The East African Agricultural Journal 15: 102-104.

3. Cain, A. J. 1958. The post-Linnaean development of taxonomy. Proc. Linn. Soc. London 170: 234-244.

4. Cain, A. J. and G. A. Harrison. 1960. The phenetic affinity of some hominaid skulls. Proc. Soc. Study Human Biol. May 27, 1960.

5. Chippindall, L. K. A. 1955. A guide to the identification of grasses in South Africa. The Grasses and Pastures of South Africa. Central News Agency Ltd., Johannesburg, Union of South Africa.

6. Eades, D. C. 1965. The inappropriateness of the correlation coefficient as a measure of taxonomic resemblance. Systematic Zool. 14: 98-100.

7. Ehrlich, P. R. 1961. Has the biological species concept outlined its usefulness? Systematic Zool. 10: 167-176.

8. Ehrlich, P. R. and R. W. Holm. 1962. Patterns and populations. Science 137: 652-657.

9. Fisher, R. A. 1936. The use of multiple measurements in taxonomic problems. Ann. Eugen. 7: 179-188.

10. Forbes, I. and G. W. Burton. 1963. Chromosome numbers and meiosis in some *Cynodon* species and hybrids. Crop Science 3: 75-79.

11. Hill, L. R. 1962. Taxometrics Newsletter No. 1.

12. Hurcombe, Ruth. 1946. Chromosome studies in *Cynodon*. S. African J. Science 42: 144-146.

13. Hurcombe, Ruth. 1957. A cytological and morphological study of cultivated *Cynodon* species. J. of S. African Bot. 13: 107-116.

14. Hurcombe, Ruth. 1948. A cytological and morphological study of cultivated Cynodon species. Better Turf Through Research. African Explosives and Chemical Industries Limited and the South African Turf Research Fund, Johannesburg, Union of South Africa. pp. 36-48.

15. Katz, M. W. and A. M. Torres. 1965. Numerical analyses of cespitose zinnias. Brittonia 17: 335-349.

16. Kendrick, W. B. 1964. Quantitative characters in computer taxonomy. In Phenetic and Phylogenetic Classification (Systematics Assoc. Publication No. 6) pp. 105-114.

17. Kendrick, W. B. and J. Proctor. 1964. Computer taxonomy in the Fungi Imperfecti. Can. J. Botany 42: 65-88.

18. Mahalanobis, P. C. 1936. On the generalized distance in statistics. Proc. Nat. Inst. Sci. India 2: 49-55.

19. Michener, C. D. and R. R. Sokal. 1957. A quantitative approach to a problem in classification. Evolution 11: 130-162.

20. Minkoff, E. C. 1965. The effects on classification of slight alternation in numerical technique. Systematic Zool. 14: 196-213.

21. Morishima, H. and H. Oka. 1960. The pattern of interspecific variation in the genus Oryza: its quantitative representation by statistical methods. Evolution 14: 153-165.

22. Pearson, Karl. 1926. On the coefficient of racial likeness. Biometrika 18: 105-117.

23. Penrose, L. S. 1954. Distance, shape, and size. Ann. Engenics 18:337-343.

24. Rao, C. R. 1948. The utilization of multiple measurements in problems of biological classification. J. Royl. Stat. Soc., Ser. B, 10: 159-193.

25. Rogers, D. J. 1963. Taximetrics - New name, old concept. Brittonia 15: 285-290.

26. Rogers, D. J. and H. Fleming. 1964. A computer program for classifying plants. II. A numerical handling of non-numerical data. BioScience 14: 15-28.

27. Rogers, D. J. and T. T. Tanimoto. 1960. A computer program for classifying plants. Science 132: 1115-1118.

28. Rohlf, F. J. 1963. Classification of Aedes by numerical taxonomic methods (Diptera: Culicidae). Annals of the Entomological Society of America 56: 798-804.

29. Rohlf, F. J. and R. R. Sokal. 1962. The description of taxonomic relationships by factor analysis. Systematic Zool. 11: 1-16.

30. Rohlf, F. J. and R. R. Sokal. 1965. Coefficients of correlation and distance in numerical taxonomy. The Univ. of Kansas Science Bull. 45: 3-27.

31. Sheals, J. G. 1964. The application of computer techniques to
     Acarine taxonomy: a preliminary examination with species of the
     Hypoaspis-Androlaelaps complex (Acarina). Proc. Linn. Soc. London
     176: 11-21.

32. Sneath, P. H. A. 1957a. Some thoughts on bacterial classification.
     J. Gen. Microbiol. 17: 184-200.

33. Sneath, P. H. A. 1957b. The application of computers to taxonomy.
     J. Gen Microbiol. 17: 201-226.

34. Sneath, P. H. A. 1962. The construction of taxonomic groups.
     In Ainsworth, G. C. and P. H. A. Sneath (eds.), Microbial Classi-
     fication. 12th Symposium of the Society for General Microbiology
     pp. 289-332. Cambridge Univ. Press, Cambridge. 483 pp.

35. Sneath, P. H. A. and R. R. Sokal. 1962. Numerical taxonomy.
     Nature 193: 855-860.

36. Sokal, R. R. 1961. Distance as a measure of taxonomic similarity.
     Systematic Zool. 10: 70-79.

37. Sokal, R. R. and C. D. Michener. 1958. A statistical method for
     evaluating systematic relationships. Univ. Kansas Sci. Bull. 38:
     1409-1438.

38. Sokal, R. R. and P. H. A. Sneath. 1963. Principles of Numerical
     Taxonomy. W. H. Freeman and Company. San Francisco. 359 pp.

39. Soria, V. J. and C. B. Heiser, Jr. 1961. A statistical study
     of relationships of certain species of the Solanum nigrum complex.
     Econ. Botany 15: 245-255.

40. Stent, S. M. 1927. South African species of Cynodon. Bothalia
     (South Africa National herbarium) II: 274-288.

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