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To the Graduate Council:

I am submitting herewith a dissertation written by Robert Frank McGuire entitled "A Numerical Taxonomic Study of Chara zeylanica and Related Species." I recommend that it be accepted in partial fulfillment of the requirements for the degree of Doctor of Philosophy, with a major in Botany.

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A NUMERICAL TAXONOMIC STUDY OF CHARA ZEYLANICA
AND RELATED SPECIES

A Dissertation
Presented to
the Graduate Council of
The University of Tennessee

In Partial Fulfillment
of the Requirements for the Degree
Doctor of Philosophy

by
Robert Frank McGuire

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ABSTRACT

Eighteen clones of Chara zeylanica and closely related species were selected from the charophyte collection of V. W. Proctor, Texas Technological University, Lubbock. All of the clones were C. zeylanica Klein ex Willd. sensu R. D. Wood. By a recent taxonomic revision of the C. zeylanica complex by V. W. Proctor, D. G. Griffin III, and A. T. Hotchkiss, one of these (X-066) was C. rusbyana Howe, one (369) was C. foliolosa Muhl. ex Willd. (= C. sejuncta Braun), one (X-029b) was C. martiana Br. ex Wallman, two (406 and X-103) were C. haitensis Turpin, and 13 (415, X-008, X-027, X-039, X-041, X-064, X-076, X-251, X-351, X-115, X-180, H, and W-1) were C. zeylanica Klein ex Willd. H and W-1 were hybrids; namely, H from X-041 and X-180, and W-1 from X-064 and 415.

All of the clones were cultured in soil-water preparations during the Spring and Summer of 1970. Data for 75 characters were collected for each of the 18 clones. Means, standard deviations, and maximum and minimum values were calculated by use of a computer program. Means were used as the primary guide for the assignment of character states.

Three sets of simple matching coefficients were tabulated. The first set involved 50 nonratio characters from morphological data. The second set involved 25 ratio characters and 19 independent nonratio characters. The third set involved all 75 characters. From each of the three sets of simple matching coefficients, a dendrogram was drawn. The

unweighted-pair group method using arithmetic averages was used in the construction of the dendrograms.

The results of this study supported the proposed classification by Proctor, Griffin, and Hotchkiss and differed from the classification by Wood; therefore, the conclusions are written with reference to the former classification. There was as much divergence among the 13 C. zeylanica clones as there was among the five clones which have been considered other species. All the C. zeylanica clones were more similar to one another than they were to any of the non-C. zeylanica clones.

X-066, 369, and X-029b appeared to be separate species. X-029b had a chromosome number of 28, while both X-066 and 369 had chromosome numbers of 14. Evidence indicated that X-103 and 406, both of which had a chromosome number of 56, were the same species. This study provided definite evidence that there was more than one species among the 13 C. zeylanica clones studied. One of the better criteria for separating the C. zeylanica clones was chromosome number, since those clones with a chromosome number of 28 tended to be separated from those with a chromosome number of 42. There were strong indications to suggest that X-064 was a separate species from all the other clones, X-027 and X-115 were members of the same species, and X-008 and X-251 were members of the same species. X-064, X-027, and X-115 had a chromosome number of 42, while X-008 and X-251 had a chromosome number of 28. There was also very good evidence to indicate that H, X-076, 415, and X-041 were the same species. X-180, X-039, and X-351 were likely members of the same species as this latter group of four clones,

but there was some evidence that X-180 may be more closely related to X-008 and X-251 and that X-351 might be a separate species. H, X-076, 415, X-041, X-180, X-039, and X-351 had chromosome numbers of 28. W-1 appeared to be a new species created in the laboratory. Evidence from this study showed that the parents of W-1, X-064 and 415, were morphologically dissimilar. The creation of the partially self-fertile W-1 hybrid with a chromosome number of 70 establishes need for further investigation into the relationships between the two groups of C. zeylanica clones with chromosome numbers of 42 and 28.

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I. INTRODUCTION

The charophytes, or stoneworts, are aquatic cryptogams. Botanical authorities generally have agreed that the charophytes have a relationship to the Chlorophyta, the green algae. Smith (1950) and Wood and Imahori (1965) placed the charophytes in the class Charophyceae of the Chlorophyta, while Fritsch (1935, 1944) placed them in the order Charales of the class Chlorophyceae. In view of complex vegetative and gametic structures, Groves and Bullock-Webster (1924) and Zaneveld (1940) placed the charophytes in the division Charophyta phylogenetically below the level of the Bryophyta and above the Chlorophyta. The classifications of Silva (1962) and Bold (1967) also placed the charophytes in the division Charophyta.

The charophytes are described as having an erect, verticillately branched thallus with apical growth and are differentiated into nodes and internodes. Whorles of branches of limited growth develop at each node. Sexual reproduction is oogamous, and the gametangia are enclosed within a jacket of sterile cells. The general morphology and life history of the charophytes have been summarized by Fritsch (1935), Smith (1950), Horn af Rantzien (1956), Bold (1967), and Scagel et al. (1967).

Wood (1962) divided the single family, the Characeae, of the Charophyceae into six genera. These six genera are Lychnothamnus, Chara, Lamprothamnium, Nitellopsis, Nitella, and Tolypella. Of the 19 Chara species listed by Wood (1962), Chara zeylanica has been studied comprehensively by Wood and Imahori (1964, 1965) from both field and herbarium

material. Chara zeylanica and related species have also been studied with respect to chromosome number and breeding data by Hotchkiss (1958), Griffin (1965), McCracken, Proctor, and Hotchkiss (1966), and Proctor and Wiman (in press).

A detailed taxonomic history of C. zeylanica and related species has been recorded by Griffin (1965), Wood and Imahori (1965), and Proctor, Griffin, and Hotchkiss (in press). Chara zeylanica has also been thoroughly investigated with regard to developmental morphology by Sundaralingam (1954). Chara zeylanica is widespread in the tropical regions and in the temperate regions of the western hemisphere (Wood and Imahori, 1965; Proctor, Griffin, and Hotchkiss, in press). Descriptions and the geographical distribution of the species of the C. zeylanica complex have been reported by Daily (1953), Griffin and Proctor (1964), Horn af Rantzien (1950), Imahori and Sinha (1964), Kasaki (1964), Pal et al. (1962), Proctor and Wiman (in press), Robinson (1906), Tindall (1966), Wood and Muenscher (1956), Wood and Imahori (1964, 1965), and Zaneveld (1940). Wood and Imahori (1965) provided a comprehensive bibliography of earlier reports of studies of all the charophytes.

Two Taxonomic Views of the Chara zeylanica Complex

All of the organisms included in this study were Chara zeylanica Klein ex Willd. sensu Wood. By Wood's (1962) classification, C. zeylanica is the only species under the section Grovesia, subsection Willdenowia. Wood and Imahori (1965) listed the following five characteristics as sufficient to delimit C. zeylanica from all the other charophytes:

1. Coronula of five cells in one tier.
2. Branchlets simple, i.e., undivided.
3. Stipulodes in two tiers, well developed.
4. Axial cortex essentially three corticated (triplostichous).
5. Lowest branchlet segment without cortication (gymnopodous).

Of the organisms which have these five characteristics, there are monoecious-conjoined forms, monoecious-sejoined forms, and dioecious forms. Wood concluded that these forms differ by only minor infraspecific fluctuations; therefore, he grouped them all under the name of C. zeylanica.

Proctor and Wiman (in press) and McCracken, Proctor, and Hotchkiss (1966) stated objections to the uniting of all the monoecious-conjoined forms, monoecious-sejoined forms, and dioecious forms as a single species. Griffin and Proctor (1964), Griffin (1965), and Proctor and Wiman (in press) presented sufficient information for the division of the monoecious-conjoined forms into two distinct species--those with eight-plated antheridia (C. haitensis Turpin) and those with four-plated antheridia (C. zeylanica Klein ex Willd.). Also, McCracken, Proctor, and Hotchkiss (1966) gave evidence for considering the dioecious form, C. rusbyana Howe, as a separate species.

Proctor, Griffin, and Hotchkiss (in press) proposed that the series Gymnobasalia Zaneveld (subsection Willdenowia Wood) be divided into seven species rather than the one species which Wood (1962) proposed. Proctor, Griffin, and Hotchkiss (in press) delimited members of the series Gymnobasalia Zaneveld as those which possess a double row of well-developed stipulodes, triplostichous cortication of the

branchlets and main axis, and branchlets with the lowest segment ecorticate. Additional morphological characters considered necessary by Proctor, Griffin, and Hotchkiss (in press) for distinguishing among the seven species of the series Gymnobasalia and the chromosome numbers of the seven species are listed in Table I. The taxonomic relationships among five of the species listed in Table I were investigated in the present study. These five species were C. rusbyana Howe, C. foliolosa Muhl. ex Willd. (= C. sejuncta Braun), C. martiana Br. ex Wallman, C. haitensis Turpin, and C. zeylanica Klein ex Willd.

Review of Numerical Taxonomic Literature in Phycology

Since the mid-1950's many numerical taxonomic studies have been done, especially in the fields of zoology and microbiology. Sokal and Sneath (1963) reviewed many of the earlier studies and presented an extensive discussion of the methods and procedures used in a numerical taxonomic study.

Gilmartin (1963) listed and briefly commented on some of the current numerical taxonomic works from the field of botany. Of those listed, only one, a paper by Ducker, Williams, and Lance (1965) concerning the taxonomy of the genus Chlorodesmis, dealt with algae. They pointed out the problems of the rather poorly defined limits of the species within the genus and collected data on six characters from 14 specimens. Their data were then subjected to conventional statistical methods and a dendrogram was drawn. Their conclusions strongly suggested a single genus with four species, C. caespitosa J. Agardh, C. comosa Harvey and Bailey, C. major Zanardini, and C. bulbosa (Womersley) Ducker.

TABLE I

MORPHOLOGICAL CHARACTERS SUFFICIENT FOR THE SEPARATION OF THE SEVEN SPECIES OF THE GENUS CHARA, SERIES GYMNOBASALIA AND THEIR CHROMOSOME NUMBERS*

Species	Characters	Chromosome Number (n=)
<u>C. zeylanica</u> Klein <u>ex</u> Willd.**	Plants monoecious-conjoined Antheridia tetrascutate, (rarely varying from 3-8)	28, 42
<u>C. haitensis</u> Turpin**	Plants monoecious-conjoined; Antheridia octoscutate	56, 42
<u>C. cienegaensis</u> Tindall	Plants monoecious-sejoined; Antheridia distal and octoscutate; Bract cells verticillate; Oogonia proximal	14
<u>C. martiana</u> Br. <u>ex</u> Wallman**	Plants monoecious-sejoined; Antheridia octoscutate; Bract cells unilateral; Antheridia and oogonia at essentially alternate branchlet nodes; Plants larger than <u>C. foliolosa</u>	28
<u>C. foliolosa</u> Muhl. <u>ex</u> Willd. (= <u>C. sejuncta</u> Braun)**	Plants monoecious-sejoined; Antheridia octoscutate; Bract cells unilateral; Antheridia and oogonia at essentially alternate branchlet nodes; Plants smaller than <u>C. martiana</u>	14
<u>C. rusbyana</u> Howe**	Plants dioecious; Antheridia octoscutate; Bract cells short and unilateral	14

TABLE I (continued)

Species	Characters	Chromosome Number (n=)
<u>C. kenoyeri</u>	Plants dioecious; Antheridia octoscutate; Bract cells long and verticillate	14

*Data for this table came from a paper by V. W. Proctor, D. G. Griffin III, and A. T. Hotchkiss, A synopsis of the genus Chara, series Gymnobasalia (subsection Willdenowia Wood). Amer. J. Bot. (in press).

**Species included in this study.

A second paper from numerical taxonomy which also dealt with the Chlorophyta was written by McGuire (1969). McGuire compiled from previously published data 73 characteristics for each of 17 species of Chlorococcum. Matching coefficients were calculated, and a dendrogram was constructed using the unweighted-pair group method. Besides showing the relative relationships among the 17 species of Chlorococcum, questions were raised about the taxonomic relationship between the species of genus Tetracystis and the genus Chlorococcum.

Few numerical taxonomic studies exist in the field of phycology; however, Whitton (1967, 1969) stated that the only long-term hope for sorting out the present taxonomic chaos of the blue-green algae will be by the use of numerical taxonomy.

The Problem

In the past few years, there has been a trend to go beyond alpha taxonomies, which deal with only a few key morphological characters, for distinguishing one species from another. These new trends have emerged as a result of the constantly more elaborate development and increasingly popular usage of electronic computers and the advancing complexity and quantity of taxonomic data. These two factors were inevitably drawn together to help bring clarity to complex and often controversial taxonomic groups which until recently have been distinguished by purely alpha taxonomic characters. The charophytes are certainly not an exception to biological groups which possess a controversial taxonomy. There are two somewhat widely diverse views of the classification of

Chara zeylanica and its related species, those of Wood (1962) and Proctor, Griffin, and Hotchkiss (in press).

Since there were conflicting classifications of the species of the Chara zeylanica complex and since the methods and equipment for a numerical taxonomic investigation of a number of charophyte species (or clones) existed, there was sufficient justification for a numerical taxonomic investigation of the C. zeylanica complex.

The central purpose of this study was to investigate the relationships among selected clones of the C. zeylanica complex, to evaluate current classifications of the group on the basis of morphological characters and chromosome number, and to present guidelines for a presumably more natural classification of the organisms involved.

II. METHODS OF PROCEDURE

Steps used in this study of Chara zeylanica and closely related species are listed below.

1. Selection of the specimens
2. Definition, selection, and measurement of characters
3. Coding of characters
4. Calculation of affinity values (resemblance coefficients)
between specimens
5. Clustering analysis
6. Conclusions from data analysis
7. Recommendations

These steps are similar to seven basic steps generally used in numerical taxonomic studies as outlined by Sokal and Sneath (1963).

Selection of Clones

Eighteen clones of Chara zeylanica Klein ex Willd. sensu Wood (1962) were selected from the charophyte culture collection of V. W. Proctor, Texas Technological University, Lubbock, Texas. Each of the clones had an assigned clone-collection number. These collection numbers have appeared in several publications and studies, including those by Hotchkiss (1958), Griffin (1965), Proctor, Griffin, and Hotchkiss (in press), and Proctor and Wiman (in press). Voucher specimens of the 18 clones from this study, as well as many of the clones from Proctor's collection, have been placed in the herbaria of New York Botanical Gardens (NY) and the Berlin Botanical Gardens (B).

Proctor, Griffin, and Hotchkiss (in press) recently revised the classification of the Chara zeylanica complex. According to their revision, the 18 clones included in this study were members of five separate species. One of the clones was Chara rusbyana Howe, one was C. foliolosa Muhl. ex Willd. (= C. sejuncta Braun), one was C. martiana Br. ex Wallman, two were C. haitensis Turpin, and the remaining 13 clones were C. zeylanica Klein ex Willd. Of these last 13 clones, two of them, H and W-1, were hybrids created from crosses of other C. zeylanica clones in the laboratories at Texas Technological University; namely, H from X-041 and X-180, and W-1 from X-064 and 415. Unless otherwise stated, the classification referred to in the remainder of this study is that in the sense of Proctor, Griffin, and Hotchkiss (in press). A listing of the 18 clones involved in this study, the collector of each clone, the date of collection, and the location and a brief description of the collection site is given in Table II.

Selection of Characters

Character selection was based upon a search of the literature on the charophytes to find the types of characters which were used to distinguish Chara zeylanica from closely related species. A list of characters was composed primarily from the rather extensive descriptions by Wood and Imahori (1964, 1965); however, character descriptions from other references were also considered, including those of Daily (1953), Fritsch (1935), Griffin (1965), Groves and Bullock-Webster (1924), Kasaki (1964), Pal et al. (1962), and McCracken, Proctor, and

TABLE II

COLLECTION DATA ON 18 CLONES OF CHARA, SERIES GYMNOBASALIA
(SUBSECTION WILLDENOWIA WOOD)

Clone	Collector	Date of Collection	Location and Description of Collection Site
<u>C. rusbyana</u> <u>Howe</u>			
X-066	C. C. Carl de Donterberg	19 March 1964	Entre Rios, Argentina, arroyo cerca del Palmarcito de Yatay al norte de Colon
<u>C. foliolosa</u> <u>Muhl. ex Willd.</u> (= <u>C. sejuncta</u> <u>Braun</u>)			
369	G. Joiner	17 September 1960	Washington Co., Texas, USA, from a small pond (earthen tank)
<u>C. martiana</u> <u>Br. ex Wallman</u>			
X-029b	V. W. Proctor	August 1961	Beni, Bolivia, from a small, muddy overflow pond, on the bank of the Rio Mamore, ca. 15 miles due west of Trinidad
<u>C. haitensis</u> <u>Turpin</u>			
406	F. R. Horne	14 October 1960	San Patricio Co., Texas, USA, from Big Lake, Welder Wildlife Refuge

TABLE II (continued)

Clone	Collector	Date of Collection	Location and Description of Collection Site
<u>C. haitensis</u> Turpin			
X-103	V. W. Proctor	28 August 1965	Merida, Venezuela, from a small canal traversing city park at Lagunillas
<u>C. zeylanica</u> Klein ex Willdenow			
415	V. W. Proctor	25 November 1960	Jim Wells Co., Texas, USA, from a windmill pond (concrete)
X-008	V. W. Proctor	June 1960	Yucatan, Mexico, from among mangrove swamps, near Progreso
X-027	D. G. Griffin III	June 1961	Hyde Co., North Carolina, USA, from Lake Mattamuskeet, National Wildlife Refuge
X-039	H. Harry	27 July 1961	Puerto Rico, from a lime sink pond, between Hatillo and Arecibo
X-041	K. Imahori	3 November 1961	Kibagata, Japan
X-064	B. S. Vaidya	15 February 1964	Baroda, India, from Ajwa Lake

TABLE II (continued)

Clone	Collector	Date of Collection	Location and Description of Collection Site
<u>C. zeylanica Klein ex Willdenow</u>			
X-076	B. S. Vaidya	15 March 1965	Ahmedabad, India, from a village pool at "Pepar," near the village of Modasar, the latter ca. 40 miles from Ahmedabad
X-251	A. T. Hotchkiss	5 November 1968	Northern Territory, Australia, from a waterfall pool, north of West Baines River Crossing
X-351	Y. Lipkin	December 1969	Atlit, Israel, from a nearby small pool in a stream (coordinates: 144/235)
X-115	D. Vital and B. V. Skvortzov	18 April 1965	Southern Brazil
X-180	E. Cabral de Oliverira	May 1967	Espirito Santo, Brazil, from a small rocky pond, near sea coast, 30 km north of Piuma
H	(A self-sterile hybrid, which was synthesized in the greenhouse at Texas Technological University in the autumn of 1968 by V. W. Proctor and F. H. Wiman. The hybrid is from a cross of X-041 and X-180, the female parent being the first listed.)		
W-1	(A partially self-fertile hybrid, which was synthesized in the greenhouse at Texas Technological University in the autumn of 1968 by V. W. Proctor and F. H. Wiman. The hybrid is from a cross of X-064 and 415, the female parent being first listed.)		

Hotchkiss (1966). A list of the 75 selected characters used in this study is given in Table III.

Characters which had the same character state for all 18 clones were not included in this study or in the list in Table III. Characters which would help to distinguish one clone from another were stressed in selecting characters.

The degree of incrustation was eliminated since it depended heavily upon the environment and less upon the genotype. Also, such terms as heavily, moderately, slightly, and very slightly, which have been used to describe the degree of incrustation, may be useful in a strictly descriptive study; but more concrete measurements are desirable for numerical taxonomic character states.

Plant height had to be eliminated as a character since Chara plants in culture tend to grow to the top of the water level of the container in which they are growing, especially when the container is as confining as a one-gallon jar.

Data for the type of oospore membrane was not obtained. This character was used by Griffin (1965) in helping to separate what is now known as C. zeylanica from C. haitensis. Proctor, Griffin, and Hotchkiss (in press) do not list type of oospore membrane in their key for distinguishing species of the series Gymnobasalia.

In a few cases, characters for which data were obtained were eliminated from the analysis. These characters either had the same character state for all clones or had character states which varied so rarely and/or inconsistently that their taxonomic value for separation

TABLE III

METHODS OF OBTAINING DATA FOR 75 CHARACTERS FOR 18 SELECTED
CLONES OF CHARA ZEYLANICA AND RELATED SPECIES

Character	Method of Obtaining Data for Character
<u>Set I: Characters from General Vegetative Structures</u>	
Internode length	Measured in millimeters
Main axis diameter	Measured in microns under low-power (100 X) magnification of a calibrated microscope
Spine cell length	Measured in microns under low-power (100 X) magnification of a calibrated microscope
Spine cell width	Measured in microns under low-power (100 X) magnification of a calibrated microscope
Ratio of spine cell length to spine cell width	Calculated as a ratio of the characters involved
Upper stipulode length	Measured in microns under low-power (100 X) magnification of a calibrated microscope
Upper stipulode width	Measured in microns under low-power (100 X) magnification of a calibrated microscope
Ratio of upper stipulode length to upper stipulode width	Calculated as a ratio of the characters involved
Lower stipulode length	Measured in microns under low-power (100 X) magnification of a calibrated microscope
Lower stipulode width	Measured in microns under low-power (100 X) magnification of a calibrated microscope
Ratio of lower stipulode length to lower stipulode width	Calculated as a ratio of the characters involved

TABLE III (continued)

Character	Method of Obtaining Data for Character
Ratio of upper stipulode length to lower stipulode length	Calculated as a ratio of the characters involved
Branchlet length	Measured in millimeters
Branchlet diameter	Measured in microns under low- power (100 X) magnification of a calibrated microscope
Ratio of branchlet length to branchlet diameter	Calculated as a ratio of the characters involved
Ratio of internode length to branchlet length	Calculated as a ratio of the characters involved
Number of branchlets per node	Observed and counted structures under a dissecting microscope
Number of segments per branchlet	Observed and counted structures under a dissecting microscope
Number of corticated segments per branchlet	Observed and counted structures under a dissecting microscope
Number of ecorticated terminal segments per branchlet	Observed and counted structures under a dissecting microscope
Basal cell length	Measured in microns under low- power (100 X) magnification of a calibrated microscope
Basal cell width	Measured in microns under low- power (100 X) magnification of a calibrated microscope
Ratio of basal cell length to basal cell width	Calculated as a ratio of the characters involved
Ratio of upper stipulode length to basal cell length	Calculated as a ratio of the characters involved

TABLE III (continued)

Character	Method of Obtaining Data for Character
Terminal segment length	Measured in microns under low-power (100 X) magnification of a calibrated microscope
Terminal segment width	Measured in microns under low-power (100 X) magnification of a calibrated microscope
Ratio of terminal segment length to terminal segment width	Calculated as a ratio of the characters involved
<u>Set II: Characters from Gametangia and Closely Associate Vegetative Structures</u>	
Bracteole length	Measured in microns under low-power (100 X) magnification of a calibrated microscope
Bracteole width	Measured in microns under low-power (100 X) magnification of a calibrated microscope
Ratio of bracteole length to bracteole width	Calculated as a ratio of the characters involved
Bractlet length	Measured in microns under low-power (100 X) magnification of a calibrated microscope
Bractlet width	Measured in microns under low-power (100 X) magnification of a calibrated microscope
Ratio of bractlet length to bractlet width	Calculated as a ratio of the characters involved
Anterior bract cell length	Measured in microns under low-power (100 X) magnification of a calibrated microscope
Anterior bract cell width	Measured in microns under low-power (100 X) magnification of a calibrated microscope

TABLE III (continued)

Character	Method of Obtaining Data for Character
Ratio of anterior bract cell length to anterior bract cell width	Calculated as a ratio of the characters involved
Ratio of anterior bract cell length to branchlet diameter	Calculated as a ratio of the characters involved
Ratio of bracteole length to anterior bract cell length	Calculated as a ratio of the characters involved
Ratio of bractlet length to anterior bract cell length	Calculated as a ratio of the characters involved
Posterior bract cell length	Measured in microns under low- power (100 X) magnification of a calibrated microscope
Posterior bract cell width	Measured in microns under low- power (100 X) magnification of a calibrated microscope
Ratio of posterior bract cell length to posterior bract cell width	Calculated as a ratio of the characters involved
Ratio of anterior bract cell length to posterior bract cell length	Calculated as a ratio of the characters involved
Number of bract cells per node	Observed and counted structures under a dissecting microscope
Gametangia type	Observed under a dissecting microscope
Oogonium length	Measured in microns under low- power (100 X) magnification of a calibrated microscope
Oogonium width	Measured in microns under low- power (100 X) magnification of a calibrated microscope

TABLE III (continued)

Character	Method of Obtaining Data for Character
Ratio of oogonium length to oogonium width	Calculated as a ratio of the characters involved
Ratio of bracteole length to oogonium length	Calculated as a ratio of the characters involved
Ratio of bractlet length to oogonium length	Calculated as a ratio of the characters involved
Ratio of anterior bract cell length to oogonium length	Calculated as a ratio of the characters involved
Number of oogonia per branchlet	Observed and counted structures under a dissecting microscope
Location of oogonia	Observed under a dissecting microscope
Coronula height	Measured in microns under low- power (100 X) magnification of a calibrated microscope
Coronula width, at base	Measured in microns under low- power (100 X) magnification of a calibrated microscope
Ratio of coronula height to coronula width	Calculated as a ratio of the characters involved
Width of an oogonium convolution	Measured in microns under high- power (200 X) magnification of a calibrated microscope
Number of convolutions per oogonium	Observed and counted structures under low-power (100 X) magnification of a compound microscope
Antheridium diameter	Measured in microns under low- power (100 X) magnification of a calibrated microscope

TABLE III (continued)

Character	Method of Obtaining Data for Character
Number of antheridia per branchlet	Observed and counted structures under a dissecting microscope
Location of antheridia	Observed under a dissecting microscope
Number of shield cells per antheridium	Observed and counted structures under low-power (100 X) magnification of a compound microscope
Diamond shield cell length	Measured in microns under low-power (100 X) magnification of a calibrated microscope
Diamond shield cell width	Measured in microns under low-power (100 X) magnification of a calibrated microscope
Ratio of diamond shield cell length to diamond shield cell width	Calculated as a ratio of the characters involved
Triangular shield cell basal length	Measured in microns under low-power (100 X) magnification of a calibrated microscope
Triangular shield cell height	Measured in microns under low-power (100 X) magnification of a calibrated microscope
Ratio of triangular shield cell basal length to triangular shield cell height	Calculated as a ratio of the characters involved
Shield cell type	Observed under low-power (100 X) under a compound microscope
<u>Set III: Characters from the Oospores</u>	
Oospore length	Measured in microns under low-power (100 X) magnification of a calibrated microscope

TABLE III (continued)

Character	Method of Obtaining Data for Character
Oospore width	Measured in microns under low-power (100 X) magnification of a calibrated microscope
Ratio of oospore length to oospore width	Calculated as a ratio of the characters involved
Number of ridges per oospore	Observed and counted structures under low-power (100 X) magnification of a compound microscope
Fossa width	Measured in microns under high-power (200 X) magnification of a calibrated microscope
<u>Set IV: Chromosome Number</u>	
Chromosome number	Chromosome counts supplied by V. W. Proctor. Counts made by V. W. Proctor and M. Grant in the laboratories at Texas Technological University, Lubbock, Texas

of the 18 clones involved was doubtful. These characters are briefly discussed in the following paragraphs.

The main axis of all 18 clones was essentially three corticated. Many of the clones, however, had short regions of two and/or four cortication. When variations of this type occurred, it was usually on only a small portion of an internode and was not always consistent in this variation from internode to internode of even the same specimen of the same clone.

All the clones with the exceptions of X-027 and X-115 had branchlets which were three corticated, the same as the main axis. X-027 had ecorticated branchlets, and X-115 had branchlets which were irregularly two and three corticated.

Chara zeylanica was described by Wood and Imahori (1965) as having a single ecorticated basal segment per branchlet, and this was found to be true for all the clones studied with the exceptions of X-027, X-351, and X-180. X-027 had ecorticated branchlets, as stated above, while X-351 and X-180 had a few entirely ecorticated branchlets and a few branchlets with two ecorticated basal segments. The presence of two ecorticated basal segments as opposed to one ecorticated basal segment could perhaps be of value if the former were found to exist in a clone which did not have the majority of the branchlets with a single ecorticated basal segment.

With the exceptions of 369 and X-029b, all of the spine cells were pointed at the apex. In these two cases, a few cells were rounded at the apex, especially toward the central region of the internode.

The number of spine cells per locus was one for all clones except X-064, H, and W-1. In a few cases for each of these latter clones, two spine cells were found per locus. This character was too rare to be of much taxonomic value.

The number of gametangia which occur at a node has been used by Pal et al. (1962), Wood and Imahori (1965), and other botanists as a taxonomic character for distinguishing among various species of the charophytes. In a few cases, five of the clones (X-066, 415, X-008, X-251, and X-115) had two oogonia per node; and in a few cases, three clones (X-103, X-008, and X-115) had two antheridia per node. The occurrence of two antheridia or oogonia per node was so infrequent that these characters were not considered to be of taxonomic value for separating the 18 selected clones of the Chara zeylanica complex.

Methods of Culturing

All the clones studied were cultured in the greenhouse at Texas Technological University during the Spring and Summer of 1970. The plants were cultured in soil-water preparations. The soil used was Amarillo fine sandy loam and was obtained from a cotton field in Lubbock County, Texas, near the campus of Texas Technological University. The soil had a pH of approximately 7.5 and an organic content of about 1 percent.

Soil was placed in large metal trays and autoclaved for 1.5 hours at 121 degrees centigrade under 15 pounds of pressure. About 1.0 to 1.5 inches of autoclaved soil was added to the bottom of clean (not autoclaved) wide-mouth one-gallon jars. The jars were filled

within one inch of the top with tap water, which was local well water from Lubbock County. An hour or two was allowed for the soil to settle before adding small vegetative segments of a selected Chara clone.

All 18 clones studied had previously been cultured by Proctor and others from oospores or vegetative material; and once established, they had been continually maintained. The cultures used in this study were started with vegetative material from these established clones. Usually three to five small (about 2-5 cm) apical pieces of a selected clone were used to start the new culture. After being broken from the parent culture, the small apical pieces were placed upright in the mud with the basal end in the soil to a depth of about 1 cm or less. Approximately four to five weeks were allowed before any vegetative characters were measured and a week or two longer before the first data from the gametangia were obtained.

The greatest type of contamination with this type of culturing was from other species, especially from filamentous green algae. One way in which the contamination level was kept low was to keep the soil depth at not more than 1.0 to 1.5 inches since the greater the amount of soil the higher the probability for further alga contamination. To help control the development of filamentous green algae, two to four snails (Helisoma trivolvis) were placed in the culture within two or three days after the culture was started. These snails reproduced fairly rapidly and, in most cases, kept the filamentous algae under control. The snails do not feed on the charophytes. When the filamentous green algae grew faster than the Chara, the Chara plants

were unsuitable for use in obtaining data for analysis. When this occurred, fresh cultures were started.

With most of the clones, three or four cultures yielded more than sufficient material for obtaining data. On April 4, 1970, two cultures of each clone were started, with the exceptions of the hybrids, H and W-1. On April 15, 1970, an additional culture was started for those clones which had considerable contamination or were growing rather slowly; these included cultures of X-066, 369, X-029b, 415, X-027, X-039, and X-115. On April 27, 1970, an additional culture was started for each clone, again with the exceptions of the hybrids. The cultures of the hybrid W-1 were started on April 1, 1970. A single culture of the H hybrid was used; it was started on January 24, 1969. The cultures were allowed to grow through the Spring and Summer of 1970, with the first data obtained around the middle of April and the last during August.

Methods of Obtaining Data

To aid in obtaining the data, the characters were divided into four sets. The sets were as follows: (1) characters from general vegetative structures, (2) characters from gametangia and closely associated vegetative structures, (3) characters from the oospores, and (4) chromosome number. Table III, page 15, which gives a list of the characters, also indicates to which of these four sets each character belongs.

The chromosome numbers, Set 4, were counted by V. W. Proctor and M. Grant. In so far as was possible, data were obtained first for the general vegetative characters, Set 1, from all clones; then data for

Set 2; and finally data for Set 3. There were exceptions to this routine since not all the cultures grew at the same rate or developed gametangia at the same time or were equally free of contamination. During April and May, 1970, one-half to two-thirds of the data were obtained for each of the 18 clones in the laboratory at Texas Technological University. This data consisted of the measuring of the characters in each set once and then measuring the characters for Set 1 and Set 2 again. During the summer months, data for all three sets and from all 18 clones were obtained again. The final data were obtained in the laboratory at The University of Tennessee from specimens which were sealed in plastic and shipped by air mail from Texas Technological University, arriving at The University of Tennessee within 24 hours after being removed from growing cultures in the greenhouse. When the shipments of Chara specimens arrived, they were immediately removed from the plastic bags and placed in water. They were analyzed within two to three days after their arrival. The clones were shipped at the rate of two or three a week as the clones became mature enough to obtain the desired data. The plant materials on which the final measurements were taken were from cultures started in the Spring of 1970.

Of the data used for any individual character of a certain clone, one-half to one-third of the information came from each replication; for example, with clone X-041, branchlet length data were obtained at three separate times. Approximately 8 to 10 measurements were taken around the middle of April; 5 to 6 measurements were taken around the first of May; and 5 to 6 measurements were taken during June. A total of 20

measurements was used in the calculation of a mean for branchlet length of X-041. These 20 bits of data came from all three measurements. The measurements on a particular clone which were taken at the three different times revealed very little variation for the vegetative characters, and there was no significant variation in the characters obtained from the gametangia and the oospores. The exact number of measurements used for each character for each clone is given in the Appendix.

Characters were also grouped according to the method used to obtain the data. Five methods were used. The methods were as follows: (1) direct observation and/or counting of structures, (2) measurement in microns with a calibrated microscope under low-power (100 X) magnification, (3) measurement in microns with a calibrated microscope under high-power (200 X) magnification, (4) measurement in millimeters, and (5) ratios calculated from pairs of other characters. Each character was assigned to one of the five groups. These assignments are listed in Table III, page 15.

Fifteen characters were obtained by direct observation and/or counting of various structures. Chromosome number was placed in this group of directly observed characters.

In obtaining data for ten of the directly observed characters, a binocular dissecting microscope was used. These ten characters were number of branchlets per node, number of segments per branchlet, number of corticated segments per branchlet, number of ecorticated terminal segments per branchlet, number of bract cells per node, gametangia type, number of oogonia per branchlet, location of oogonia, number of

antheridia per branchlet, and location of antheridia. The observations with the binocular microscope were made at 10 and 20 times natural size. To obtain data for the number of branchlets per node, number of segments per branchlet, number of corticated segments per branchlet, and number of bract cells per node, direct counts were made of these respective structures. Gametangia type was observed as being either monoecious-conjoined, monoecious-sejoined, or dioecious. In counting the number of ecorticated terminal segments per branchlet, the number of ecorticated segments were counted from the tip toward the base of the branchlet; if the branchlet were completely ecorticated, all segments were counted with the exception of the basal segment.

To obtain data for the number of oogonia per branchlet, the number of oogonia per branchlet was counted for 40 branchlets from various specimens of a clone. An average was then calculated. To obtain a value for oogonium location, the nodes at which the oogonia occurred for these same 40 branchlets were also recorded. The nodes of the branchlets were numbered consecutively from the base toward the tip. For example, for X-041, 130 oogonia were found on the 40 branchlets; 37 occurred at first nodes; 39 at second nodes; 38 at third nodes; and 16 at fourth nodes. To obtain a mean oogonium location, the frequency of occurrence was multiplied by the node number for each node which had oogonia. These values were totaled and divided by the total number of oogonia on the 40 branchlets. The procedures which were used for measuring the number of oogonia per branchlet and for finding the mean oogonium location were also used to find the number of antheridia per branchlet and for finding the mean antheridium location.

The data for four other directly observed characters were determined under low-power (100 X) magnification of a compound microscope. The four characters were number of convolutions per oogonium, number of shield cells per antheridium, number of ridges per oospore, and shield cell type. The shield cell type was observed as being either triangular or diamond shaped. Direct counts were made for the number of convolutions per oogonium, number of shield cells per antheridium, and the number of ridges per oospore.

Thirty-one characters were measured with a calibrated microscope (Wild M-11) under low-power (100 X) magnification. The following paragraphs contain a discussion of the procedures used to measure the 31 characters.

The general vegetative characters were obtained from no lower on the plant than the fifth internode. The diameter of the main axis was measured straight across the internode at an angle perpendicular to the corticating cells. In general, the axis diameter tended to be slightly greater near the nodes and smaller at the central region of the internodes.

Structures which were, in general, long and tapered, such as spine cells and upper and lower stipulodes, were measured in length from the apex along a central axis to the base. The width of these same structures was obtained by measuring the diameter of the base of the structure perpendicular to the central axis of length. Other long and tapered structures were terminal segments of branchlets, bracteoles, bractlets, anterior bract cells, and posterior bract cells.

Basal cell length was measured along the central axis of the cell from the location where the branchlets were attached to the main axis to the base of the second branchlet segment. Basal cell width was obtained by measuring the diameter of the central region of the basal cell at an angle perpendicular to the central axis of length.

Branchlet diameter was measured perpendicular to the main axis of length and across the second (or in a few cases the third) node from the basal attachment of the branchlet.

Oogonium length was measured from the basal attachment of the structure to the branchlet node to the base of the coronula along a vertical central axis. Width of the oogonium was obtained by measuring the diameter of the central region of the structure at right angles to the central axis of length.

The coronula height was measured from the base of a selected crown cell to the apex along the central axis of the cell. Coronula width was obtained by measuring across the base of the crown cells and at right angles to the central axis of the length of the oogonium.

The diameter of an antheridium was measured across the center of the structure at an angle perpendicular to the attachment of the antheridium to the branchlet node.

Open antheridial shield cells are commonly found in mature cultures of Chara so there was very little difficulty in obtaining measurements of shield cell length and width. Diamond shield cells were measured in length along the greater central axis and in width along the minor central axis. These two measurements were taken at right angles to each other. Triangular shield cells were measured in

basal length along the side which had the greatest dimension, and then a height was measured perpendicular to this selected base.

Oospores were measured in length along the central axis of length. The width of the oospore was measured in the central region of the oospore and at right angles to the central axis of length.

Two characters were measured in microns under high-power (200 X) magnification of a calibrated microscope (Wild M-11). These two characters were width of a convolution of an oogonium and fossa width. The width of a convolution of an oogonium was measured by selecting a single convolution in the central region of the oogonium and measuring the cell at right angles with the axis of length of the convolution. Fossa width was measured by selecting a central region of an oospore and measuring across the fossa from one oospore ridge to the next and at an angle perpendicular to the main axis of the groove on the oospore.

Two characters were measured in millimeters. These two characters were internode length and branchlet length. The internode length was measured along the main axis from a point where the branchlets were attached at one node to the next node. Branchlet length was measured from the apex of the branchlet along a central axis to the basal attachment of the branchlet to the main axis.

Twenty-five ratio characters were calculated from selected pairs of the characters discussed above. The ratios were calculated by use of a computer program with transformations, BMD01D, Simple Data Description (Dixon, 1967). The ratios are discussed in further detail in Section III.

III. RESULTS AND ANALYSIS OF DATA

Presentation of the Data

The data for 75 characters for each of the 18 selected Chara clones are presented in Tables X-LXXXIV in the Appendix. The characters were grouped according to the method by which the data were obtained. The means, standard deviations, and maximum and minimum values were calculated for data which varied for a particular clone; and character states were assigned. Transformations of data, the means, standard deviations, and maximum and minimum values were calculated by use of a computer program, BMD01D, Simple Data Description (Dixon, 1967).

Characters obtained by direct observation. Fifteen characters were obtained by direct observation and/or counting of various structures of the 18 Chara clones. Of the directly observed characters, eleven yielded data which could be tabulated in such a manner as to give means, standard deviations, and maximum and minimum values. The eleven characters were:

1. Number of branchlets per node
2. Number of segments per branchlet
3. Number of corticated segments per branchlet
4. Number of ecorticated terminal segments per branchlet
5. Number of bract cells per node
6. Number of oogonia per branchlet
7. Location of oogonia

8. Number of convolutions per oogonium
9. Number of antheridia per branchlet
10. Location of antheridia
11. Number of ridges per oospore

Four directly observed characters were of such a nature that calculation of means and standard deviations was not necessary since the data were constant for the character. These four directly observed characters were:

1. Gametangia type
2. Number of shield cells per antheridium
3. Shield cell type
4. Chromosome number

Characters measured under low-power (100 X) magnification.

Thirty-one characters were measured in microns under the low-power magnification of a calibrated microscope. These 31 characters were:

1. Diameter of main axis
2. Spine cell length
3. Spine cell width
4. Upper stipulode length
5. Upper stipulode width
6. Lower stipulode length
7. Lower stipulode width
8. Branchlet diameter
9. Basal cell length
10. Basal cell width

11. Terminal segment length
12. Terminal segment width
13. Bracteole length
14. Bracteole width
15. Bractlet length
16. Bractlet width
17. Anterior bract cell length
18. Anterior bract cell width
19. Posterior bract cell length
20. Posterior bract cell width
21. Oogonium length
22. Oogonium width
23. Coronula height
24. Coronula width, at base
25. Antheridium diameter
26. Diamond shield cell length
27. Diamond shield cell width
28. Triangular shield cell basal length
29. Triangular shield cell height
30. Oospore length
31. Oospore width

The measurements for each of the 31 characters had to be multiplied by the low-power calibration factor of 13.3 to convert the measurements into microns. The transformations or multiplications by 13.3 were performed first; and then means, standard deviations, and maximum and minimum values were calculated.

Characters measured under high-power (200 X) magnification. Two characters were measured in microns under high-power (200 X) magnification of a calibrated microscope. Each measurement had to be multiplied by a calibration factor of 6.7 for the measurement to be in microns. The transformations or multiplications by 6.7 were performed first; then means, standard deviations, and maximum and minimum values were calculated. The two characters measured under high-power magnification were:

1. Width of an oogonium convolution
2. Fossa width

Characters measured in millimeters. Two characters were measured in millimeters; and then means, standard deviations, and maximum and minimum values were calculated. The two characters measured in millimeters were:

1. Internode length
2. Branchlet length

Characters calculated as ratios. Twenty-five characters were calculated as ratios of pairs of other characters. In length-width ratios of the same structures, the cell length was divided by its corresponding width. In so far as was possible, in the case of the upper stipulode length to lower stipulode length ratio, the length of a certain upper stipulode cell was divided by its corresponding lower stipulode cell length. In the case of the ratio of the internode length to branchlet length, two branchlets were measured per internode. Both

of these branchlets were chosen from the node above and adjacent to the measured internode. Each of these branchlet lengths was separately divided into the corresponding internode length. In the ratio of the upper stipulode length to basal cell length, basal cells from the same region in which the upper stipulode cells were attached were used as divisors. For the ratio of the anterior bract cell length to branchlet diameter, the diameter of the second (or in a few cases, the third) node from the basal attachment of the branchlet was divided into the corresponding anterior bract cell length. For six of the ratio characters (bracteole length to anterior bract cell length, bractlet length to anterior bract cell length, anterior bract cell length to posterior bract cell length, bracteole length to oogonium length, bractlet length to oogonium length, and anterior bract cell length to oogonium length), the divisor and dividend were at least from the same specimen of the clone if not from the same branchlet node.

For all 25 characters which were calculated as ratios, the divisions were performed first; and then means, standard deviations, and maximum and minimum values were calculated on the quotients. When the measurements were not in the same units, an additional transformation had to be made before the quotients (ratios) were calculated.

The 25 characters which were calculated as ratios of other characters were:

1. Ratio of spine cell length to spine cell width
2. Ratio of upper stipulode length to upper stipulode width
3. Ratio of lower stipulode length to lower stipulode width
4. Ratio of upper stipulode length to lower stipulode length

5. Ratio of branchlet length to branchlet diameter
6. Ratio of internode length to branchlet length
7. Ratio of basal cell length to basal cell width
8. Ratio of upper stipulode length to basal cell length
9. Ratio of terminal segment length to terminal segment width
10. Ratio of bracteole length to bracteole width
11. Ratio of bractlet length to bractlet width
12. Ratio of anterior bract cell length to anterior bract
cell width
13. Ratio of anterior bract cell length to diameter of branchlet
14. Ratio of bracteole length to anterior bract cell length
15. Ratio of bractlet length to anterior bract cell length
16. Ratio of posterior bract cell length to posterior bract cell
width
17. Ratio of anterior bract cell length to posterior bract cell
length
18. Ratio of oogonium length to oogonium width
19. Ratio of bracteole length to oogonium length
20. Ratio of bractlet length to oogonium length
21. Ratio of anterior bract cell length to oogonium length
22. Ratio of coronula height to coronula width, at base
23. Ratio of diamond shield cell length to diamond shield cell
width
24. Ratio of triangular shield cell basal length to triangular
shield cell height
25. Ratio of oospore length to oospore width

Assignment of Character States

For character state assignments, the characters were grouped according to the method by which the data were obtained. The means of the characters were used as the primary basis for assigning character states.

Characters obtained by direct observation. For four of the directly observed characters (gametangia type, number of shield cells per antheridium, shield cell type, and chromosome number), character states were assigned by simply giving a number to each distinct state of the character. In the case of chromosome number, for example, the character states 1, 2, 3, 4, and 5 were assigned to clones with chromosome numbers of 14, 28, 42, 56, and 70 respectively.

For 10 of the characters which were obtained by direct observation and counting of the structures, the means for each character for each clone were first rounded to the nearest whole number and then character states were assigned to the rounded values. These 10 characters were number of branchlets per node, number of segments per branchlet, number of ecorticated terminal segments per branchlet, number of bract cells per node, number of oogonia per branchlet, location of oogonia, number of convolutions per oogonium, number of antheridia per branchlet, location of antheridia, and number of ridges per oospore. In the case of the number of antheridia per branchlet, for example, the rounded mean number of antheridia per branchlet for any one of the 18 clones was either two, three, or four. If a clone had a rounded average of two antheridia per branchlet, the character state was 1; if a clone had a

rounded average of three antheridia per branchlet, the character state was 2; and if a clone had a rounded average of four antheridia per branchlet, the character state was 3.

In the case of the number of corticated segments per branchlet, five character states were used. The first character state was used for X-027, the only clone which had entirely ecorticated branchlets. The second character state was assigned to those clones which had a rounded mean of 1, 2, or 3 corticated segments per branchlet. The third character state was assigned to those clones with a rounded mean of 4, 5, or 6 corticated segments per branchlet. The fourth character state was assigned to those clones with a rounded mean of 7, 8, or 9 corticated segments per branchlet, and the fifth character state was assigned to those clones which had a rounded mean of 10, 11, or 12 corticated segments per branchlet.

Characters measured under low-power (100 X) magnification. Before assigning character states to the 31 characters measured under low-power magnification, the 31 characters were grouped into five groups based primarily on their similarity in shape and size. The first group had nine characters, all of which were lengths of various long and tapering structures, with the exception of basal cell length. These nine characters were spine cell length, upper stipulode length, lower stipulode length, basal cell length, terminal segment length, bracteole length, bractlet length, anterior bract cell length, and posterior bract cell length. To obtain the data for each of the nine characters, small single-celled structures were measured, with the exception of the

terminal segment length which occasionally had two or three cells per segment. Arbitrary ranges of 200 micron groups were established for all nine characters. In the case of the upper stipulode length, for example, four character states were used. If the mean upper stipulode length were greater than or equal to 400 microns but less than 600 microns, a character state of 1 was assigned. The character state 2 was assigned to those clones with a mean upper stipulode length greater than or equal to 600 microns but less than 800 microns. The character state 3 was assigned to those clones with a mean upper stipulode length between 800 and 1000 microns, and the character state 4 was assigned to those clones with a mean upper stipulode length between 1000 and 1200 microns. A similar procedure was followed for assigning character states for the other eight characters in this group.

Six characters made up the second group of characters measured under low-power magnification. These six characters were main axis diameter, oogonium length, oogonium width, antheridium diameter, oospore length, and oospore width. Measurements of the diameter of the main axis yielded data which were numerically within the ranges of the dimensions of the gametangia and the oospores. For this group of six characters, arbitrary ranges of 100 micron groups were established. An example from this group is oospore length for which three character states were assigned. The first character state was for those clones with a mean oospore length between 500 and 600 microns; the second character state was for those clones with a mean oospore length between 600 and 700 microns; and the third character state was for those clones

with a mean oospore length between 700 and 800 microns. The other four characters in this group had character states assigned in a similar manner.

Seven characters were placed in the third group of characters measured by low-power magnification. The seven characters were branchlet diameter, basal cell width, terminal segment width, diamond shield cell length, diamond shield cell width, triangular shield cell basal length, and triangular shield cell height. In general, these were all widths or diameters of structures with the exceptions of diamond shield cell length and triangular shield cell basal length which were numerically close enough to be placed in this grouping. Arbitrary ranges of 50 micron groups were established. Diamond shield cell width, for example, had four character states. The first character state was for those clones which had no diamond shield cells; the second character state was for those clones which had a mean diamond shield cell width between 200 and 250 microns; the third character state was for those between 250 and 300 microns; and the fourth character state was for those between 300 and 350 microns.

Two characters made up the fourth group of characters measured under low-power magnification; they were coronula height and coronula width. The ranges were in groups of 25 microns each; otherwise, the assignment of the character states followed the same procedure which was used for the first three groups.

The fifth and final group of the characters measured under low-power magnification was made up of seven characters. These characters

were all widths of various structures. The seven characters were spine cell width, upper stipulode width, lower stipulode width, bracteole width, bractlet width, anterior bract cell width, and posterior bract width. The lengths of these seven characters were also placed together in group one. Groups of 20 microns were established for assigning character states. The procedure for character state assignment was the same as for the first three groups.

Characters measured under high-power (200 X) magnification. Only two characters, width of a convolution of an oogonium and fossa width, were measured under high-power magnification. The character state ranges were in groups of 10 microns each. In the case of the width of a convolution, four character states were used. The first character state was assigned to those clones which had a mean convolution width between 30 and 40 microns, the second to those between 40 and 50 microns, the third to those between 50 and 60 microns, and the fourth character state to those with a mean width between 60 and 70 microns.

Characters measured in millimeters. Internode length and branchlet length were the two characters which were measured in millimeters. The character state ranges were in groups of 10 millimeters each. With the internode length, for example, three character states were used. The first character state was assigned to those clones with a mean internode length between 10 and 20 millimeters, the second character state to those with a mean length between 20 and 30 millimeters, and the third character state to those with a mean internode length between 30 and 40 millimeters.

Characters calculated as ratios. The characters measured as ratios were divided into six groups for assignment of character states. These groups were separated from one another by the numerical magnitude of the mean ratios and by the types of characters forming the ratios.

The first group contained a single character, the ratio of branchlet length to branchlet diameter. The character state assignments were based on ranges of 20 units each.

The second group consisted of three characters. These were the ratios of bracteole length to bracteole width, bractlet length to bractlet width, and anterior bract cell length to anterior bract cell width. The arbitrary character state ranges were three units each.

The third group consisted of six characters. These were the ratios of spine cell length to spine cell width, upper stipulode length to upper stipulode width, lower stipulode length to lower stipulode width, basal cell length to basal cell width, terminal segment length to terminal segment width, and posterior bract cell length to posterior bract cell width. Character state assignments were based on ranges of two units each. In the ratio of spine cell length to spine cell width, for example, four character states were used. The first character state was assigned to those clones whose mean ratio was between 2 and 4, the second character state to those with a mean ratio between 4 and 6, the third character state to those with a mean ratio between 6 and 8, and the fourth character state to those with a mean ratio between 8 and 10.

Eight characters made up the fourth group of characters which were calculated by means of ratios. The eight characters were the ratios

of bracteole length to anterior bract cell length, anterior bract cell length to branchlet diameter, upper stipulode length to lower stipulode length, upper stipulode length to basal cell length, bractlet length to anterior bract cell length, anterior bract cell length to posterior bract cell length, bracteole length to oogonium length, and bractlet length to oogonium length. The character state assignments were based on ranges of one unit each. Using arbitrary character state ranges of one unit was the same as rounding each mean ratio to the nearest whole number and assigning character states.

Two characters made up the fifth group of characters calculated by means of ratios. These two characters were the ratios of internode length to branchlet length and anterior bract cell length to oogonium length. Character state assignments were based on the mean ratios with arbitrary character state ranges of 0.5 units, or by rounding each mean ratio to the nearest one-half before character states were assigned.

The sixth and final group of characters calculated from ratios had five characters. These were oospore length to oospore width, triangular shield cell basal length to triangular shield cell height, diamond shield cell length to diamond shield cell width, coronula height to coronula width, and oogonium length to oogonium width. Character states were assigned on the basis of mean ratios with arbitrary character state ranges of 0.2 each. For the ratio of oogonium length to oogonium width, for example, three character states were used. The first character was assigned to those clones with a mean ratio between 1.2 and 1.4, the second to those with a mean ratio between 1.4 and 1.6, and the third to those with a mean ratio between 1.6 and 1.8.

Coefficients of Similarity

The 75 characters were regrouped into three sets in order to calculate the coefficients of similarity. These groups are referred to as Set 1, Set 2, and Set 3. Set 1 was composed of the 31 characters which were not themselves ratios but their data were used in the calculation of the ratio characters. The characters in Set 1 were:

1. Internode length
2. Spine cell length
3. Spine cell width
4. Upper stipulode length
5. Upper stipulode width
6. Lower stipulode length
7. Lower stipulode width
8. Branchlet length
9. Branchlet diameter
10. Basal cell length
11. Basal cell width
12. Terminal segment length
13. Terminal segment width
14. Bracteole length
15. Bracteole width
16. Bractlet length
17. Bractlet width
18. Anterior bract cell length
19. Anterior bract cell width

20. Posterior bract cell length
21. Posterior bract cell width
22. Oogonium length
23. Oogonium width
24. Coronula height
25. Coronula width, at base
26. Diamond shield cell length
27. Diamond shield cell width
28. Triangular shield cell basal length
29. Triangular shield cell height
30. Oospore length
31. Oospore width

Set 2 contained 25 characters which were calculated as ratios of various pairs of characters from Set 1. The characters in Set 2 were:

1. Ratio of spine cell length to spine cell width
2. Ratio of upper stipulode length to upper stipulode width
3. Ratio of lower stipulode length to lower stipulode width
4. Ratio of upper stipulode length to lower stipulode length
5. Ratio of branchlet length to branchlet diameter
6. Ratio of internode length to branchlet length
7. Ratio of basal cell length to basal cell width
8. Ratio of upper stipulode length to basal cell length
9. Ratio of terminal segment length to terminal segment width
10. Ratio of bracteole length to bracteole width
11. Ratio of bractlet length to bractlet width

12. Ratio of anterior bract cell length to anterior bract cell width
13. Ratio of anterior bract cell length to branchlet diameter
14. Ratio of bracteole length to anterior bract cell length
15. Ratio of bractlet length to anterior bract cell length
16. Ratio of posterior bract cell length to posterior bract cell width
17. Ratio of anterior bract cell length to posterior bract cell length
18. Ratio of oogonium length to oogonium width
19. Ratio of bracteole length to oogonium length
20. Ratio of bractlet length to oogonium length
21. Ratio of anterior bract cell length to oogonium length
22. Ratio of coronula height to coronula width, at base
23. Ratio of diamond shield cell length to diamond shield cell width
24. Ratio of triangular shield cell basal length to triangular shield cell height
25. Ratio of oospore length to oospore width

Set 3 contained 19 characters, all of which were independent of Set 1 and Set 2, that is, they were neither characters which were used in the calculation of a ratio nor were they themselves ratios. The characters in Set 3 were:

1. Main axis diameter
2. Number of branchlets per node

3. Number of segments per branchlet
4. Number of corticated segments per branchlet
5. Number of ecorticated terminal segments per branchlet
6. Number of bract cells per node
7. Gametangia type
8. Number of oogonia per branchlet
9. Location of oogonia
10. Width of a convolution
11. Number of convolutions per oogonium
12. Antheridia diameter
13. Number of antheridia per branchlet
14. Location of antheridia
15. Number of shield cells per antheridium
16. Shield cell type
17. Number of ridges per oospore
18. Fossa width
19. Chromosome number

To calculate coefficients of similarity among the clones, the procedure of simple matching coefficients was used. This method was described by Sokal and Sneath (1963). Using standard 80-column computer cards, three cards were punched on a keypunch machine for each clone. The first card had the character states for Set 1; the second card had the character states for Set 2; and the third card had the character states for Set 3. Each card was marked with a clone identification number. In the case of X-066 for Set 1, in the first six columns was punched

WX-066. The W represented Set 1 of the characters, those without ratios but which were later used in pairs to calculate ratios. The same card also had punched on it the character states of Set 1 for the clone X-066. The character state for internode length was punched in column 10, which in the case of X-066 was 1. In column 11 was punched the character state for X-066 for spine cell length. Character states were placed in groups of five across the card. The primary reason for this grouping was to aid in matching and reading the cards. The groups started in columns 10, 20, 30, 40, 50, 60, and 70. Five columns were punched and five columns were skipped in a regular pattern across the card.

After three cards had been punched and checked for each clone, the cards were divided into three decks. The first deck contained the data for Set 1, the second for Set 2, and the third for Set 3. Taking each deck separately, each card within the deck was compared with each of the other cards in that deck. When matching two cards from the same deck, the edges of the cards were held evenly together, and the total number of common punches represented the number of characters for which the two clones had the same character states. With each comparison between two cards of the same deck, the total number of common character punches was counted and recorded. Since in a few cases with the hybrids H and W-1 some missing data occurred, it was necessary with each pair of cards compared to record the number of characters involved. In the comparison of the cards for X-180 and H for Set 1, for example, 16 characters had common character states; but since H had only 29 characters and X-180 had 31 characters, only 29 characters were actually

compared. The similarity coefficient in this example was 16 out of 29. The results of the comparisons for Set 1 of the characters are recorded in Table IV; the results of the comparisons for Set 2 of the characters are recorded in Table V; and the results of the comparisons for Set 3 of the characters are recorded in Table VI.

From the three tables of comparison values (Tables IV, V, and VI), three different sets of similarity coefficients were calculated. The first set of coefficients (Table VII) was calculated by using the comparison data from the characters in Sets 1 and 3, or all the characters which did not involve any ratios. In the case of X-066 with 369, for example, there were 14 matches out of 31 possible matches for Set 1; and there were 11 matches out of 19 possible matches for Set 3. A total of 25 matches out of 50 characters, or a coefficient of 50 percent similarity, between X-066 and 369 existed.

The second set of simple matching coefficients (Table VIII) was calculated by using the comparison data in Sets 2 and 3. In the case of X-066 and 369, for example, there were 19 matches out of 25 possible matches for Set 2 and 11 matches out of 19 possible matches for Set 3. There was a total of 30 positively matched characters out of 44 possible characters which could be matched, or a coefficient of 68 percent similarity, between X-066 and 369.

The third set of simple matching coefficients (Table IX) was calculated by using all three sets of comparison data. In the case of X-066 and 369, for example, there were 14 matches out of a possible 31 for Set 1, 19 matches out of a possible 25 for Set 2, and 11 matches

TABLE IV

THE TOTAL NUMBER OF POSITIVELY MATCHED CHARACTER STATES FOR 31 NONRATIO CHARACTERS
FROM MORPHOLOGICAL DATA FOR 18 CLONES OF CHARA ZEYLANICA AND RELATED SPECIES

Clone	X-066	369	X-029b	406	X-103	415	X-008	X-027	X-039	X-041	X-064	X-076	X-251	X-351	X-115	X-180	H**	W-1
X-066	XX																	
369	14*	XX																
X-029b	14	18	XX															
406	14	20	13	XX														
X-103	13	15	17	17	XX													
415	09	05	04	09	10	XX												
X-008	09	10	08	16	13	13	XX											
X-027	12	11	07	16	08	11	19	XX										
X-039	13	06	07	10	14	14	20	16	XX									
X-041	09	05	04	08	11	23	14	12	19	XX								
X-064	08	05	06	10	11	14	15	09	16	18	XX							
X-076	08	09	06	12	10	18	17	14	14	18	16	XX						
X-251	14	07	09	14	13	12	17	13	17	13	08	10	XX					
X-351	09	08	08	07	07	18	16	11	13	20	16	18	10	XX				
X-115	10	10	09	17	11	16	18	21	16	14	10	18	16	12	XX			
X-180	11	10	09	13	10	14	18	18	16	14	09	17	18	14	19	XX		
H**	07	08	05	09	08	19	17	14	14	17	11	20	11	15	15	16	XX	
W-1	07	10	05	10	09	10	13	12	15	14	13	11	11	11	12	18	10	XX

*The table is read as follows: There were 14 positively matched character states out of 31 possible matches between X-066 and 369.

**The H hybrid had only 29 characters; therefore, the divisor was 29, not 31.

TABLE V

THE TOTAL NUMBER OF POSITIVELY MATCHED CHARACTER STATES FOR 25 RATIO CHARACTERS FROM
MORPHOLOGICAL DATA FOR 18 CLONES OF CHARA ZEYLANICA AND RELATED SPECIES

Clone	X-066	369	X-029b	406	X-103	415	X-008	X-027	X-039	X-041	X-064	X-076	X-251	X-351	X-115	X-180	H**	W-1
X-066	XX																	
369	19*	XX																
X-029b	15	16	XX															
406	08	11	12	XX														
X-103	11	11	07	13	XX													
415	06	07	06	08	11	XX												
X-008	07	04	05	09	12	10	XX											
X-027	11	09	04	08	12	10	09	XX										
X-039	08	06	06	05	10	16	11	10	XX									
X-041	08	05	05	07	11	18	14	10	16	XX								
X-064	05	06	07	11	12	13	13	09	09	15	XX							
X-076	07	07	07	10	12	16	14	09	15	12	12	XX						
X-251	09	06	06	08	10	10	13	12	11	11	09	11	XX					
X-351	05	05	06	08	12	12	13	14	14	14	14	12	11	XX				
X-115	10	08	08	08	13	16	10	11	19	14	09	16	15	12	XX			
X-180	11	08	08	10	10	09	14	12	12	08	10	14	18	10	15	XX		
H**	10	08	06	05	10	12	14	13	16	14	11	16	12	14	13	16	XX	
W-1	05	04	03	07	09	12	10	07	13	13	09	13	10	08	12	10	11	XX

*The table is read as follows: There were 19 positively matched character states out of 25 possible matches between X-066 and 369.

**The H hybrid had only 24 characters; therefore, the divisor was 24, not 25.

TABLE VI

THE TOTAL NUMBER OF POSITIVELY MATCHED CHARACTER STATES FOR 19 NONRATIO CHARACTERS
FROM MORPHOLOGICAL DATA FOR 18 CLONES OF CHARA ZEYLANICA AND RELATED SPECIES

Clone	X-066	369	X-029b	406	X-103	415	X-008	X-027	X-039	X-041	X-064	X-076	X-251	X-351	X-115	X-180	H**	W-1**
X-066	XX																	
369	11*	XX																
X-029b	06	09	XX															
406	06	06	05	XX														
X-103	06	04	10	11	XX													
415	02	03	06	03	04	XX												
X-008	03	03	04	08	05	09	XX											
X-027	01	02	03	02	05	05	06	XX										
X-039	03	03	03	05	02	11	10	07	XX									
X-041	04	05	05	06	01	12	11	06	13	XX								
X-064	02	03	00	07	03	08	09	05	08	11	XX							
X-076	02	02	07	02	04	11	10	10	13	13	07	XX						
X-251	01	02	05	07	06	07	15	05	07	08	09	09	XX					
X-351	02	05	06	05	03	08	09	06	11	10	07	11	07	XX				
X-115	01	01	05	04	05	07	09	12	09	09	07	12	08	08	XX			
X-180	00	02	06	06	06	08	07	06	12	08	05	11	08	13	08	XX		
H**	00	02	07	01	04	11	07	08	12	13	07	15	06	10	09	11	XX	
W-1**	01	01	05	02	03	09	05	05	08	11	08	11	05	07	08	08	12	XX

*The table is read as follows: There were 11 positively matched character states out of 19 possible matches between X-066 and 369.

**The H and W-1 hybrids each had only 17 characters; therefore, the divisor was 17, not 19.

TABLE VII

SIMPLE MATCHING COEFFICIENTS EXPRESSED IN PERCENTAGES FOR 18 CLONES OF CHARA ZEYLANICA
AND RELATED SPECIES BASED ON 50 NONRATIO CHARACTERS FROM MORPHOLOGICAL DATA

Clone	X-066	369	X-029b	406	X-103	415	X-008	X-027	X-039	X-041	X-064	X-076	X-251	X-351	X-115	X-180	H	W-1
X-066	XX																	
369	50*	XX																
X-029b	40	54	XX															
406	40	52	36	XX														
X-103	38	38	54	56	XX													
415	22	16	20	24	28	XX												
X-008	24	26	24	48	36	44	XX											
X-027	26	26	20	36	26	32	50	XX										
X-039	32	18	20	30	32	50	60	46	XX									
X-041	26	20	18	28	24	70	50	36	64	XX								
X-064	20	16	12	34	28	44	48	28	48	58	XX							
X-076	20	22	26	28	28	58	54	48	54	62	46	XX						
X-251	30	18	28	42	38	38	64	36	48	42	34	38	XX					
X-351	22	26	28	24	20	52	50	34	48	60	46	58	34	XX				
X-115	22	22	28	42	32	46	54	66	50	46	34	60	48	40	XX			
X-180	22	24	30	38	32	44	50	48	56	44	28	56	52	54	54	XX		
H	15	22	26	22	26	65	52	48	57	65	39	76	37	54	52	59	XX	
W-1	17	23	21	25	25	40	38	35	48	52	44	46	33	38	42	54	48	XX

*The table is read as follows: The similarity between X-066 and 369 was 50 percent.

TABLE VIII

SIMPLE MATCHING COEFFICIENTS EXPRESSED IN PERCENTAGES FOR 18 CLONES OF CHARA ZEYLANICA
AND RELATED SPECIES BASED ON 25 RATIO CHARACTERS AND 19 INDEPENDENT
NONRATIO CHARACTERS FROM MORPHOLOGICAL DATA

Clone	X-066	369	X-029b	406	X-103	415	X-008	X-027	X-039	X-041	X-064	X-076	X-251	X-351	X-115	X-180	H	W-1
X-066	XX																	
369	68*	XX																
X-029b	48	57	XX															
406	32	39	39	XX														
X-103	39	34	39	55	XX													
415	18	23	27	25	34	XX												
X-008	23	16	20	39	39	43	XX											
X-027	27	25	16	23	39	34	34	XX										
X-039	25	20	20	23	27	61	48	39	XX									
X-041	27	23	23	30	27	68	57	36	66	XX								
X-064	16	20	16	41	34	48	50	32	39	59	XX							
X-076	20	20	32	27	36	61	55	43	64	64	43	XX						
X-251	23	18	25	34	36	39	64	39	41	43	41	45	XX					
X-351	16	23	27	30	34	45	50	45	57	55	48	52	41	XX				
X-115	25	20	30	27	41	52	43	52	64	52	36	64	52	45	XX			
X-180	25	23	32	36	36	39	48	41	55	36	34	57	59	52	52	XX		
H	24	24	32	15	34	56	51	51	68	66	44	76	44	59	54	66	XX	
W-1	14	12	19	21	29	50	36	29	50	57	40	57	36	36	48	43	56	XX

*The table is read as follows: The similarity between X-066 and 369 was 68 percent.

TABLE IX

SIMPLE MATCHING COEFFICIENTS EXPRESSED IN PERCENTAGES FOR 18 CLONES OF CHARA ZEYLANICA
AND RELATED SPECIES BASED ON 25 RATIO CHARACTERS AND 50 NONRATIO
CHARACTERS FROM MORPHOLOGICAL DATA

Clone	X-066	369	X-029b	406	X-103	415	X-008	X-027	X-039	X-041	X-064	X-076	X-251	X-351	X-115	X-180	H	W-1
X-066	XX																	
369	59*	XX																
X-029b	47	57	XX															
406	37	49	40	XX														
X-103	40	40	45	55	XX													
415	23	20	21	27	33	XX												
X-008	25	23	23	44	40	43	XX											
X-027	32	29	19	35	33	35	45	XX										
X-039	32	20	21	27	35	55	55	44	XX									
X-041	28	20	19	28	31	71	52	37	64	XX								
X-064	20	19	17	37	35	47	49	31	44	59	XX							
X-076	23	24	27	32	35	60	55	44	56	61	47	XX						
X-251	32	20	27	39	39	39	60	40	47	43	35	40	XX					
X-351	21	24	27	27	29	51	51	41	51	59	49	55	37	XX				
X-115	28	25	29	39	39	52	49	59	59	49	35	61	52	43	XX			
X-180	29	27	31	39	35	41	52	48	53	40	32	56	59	49	56	XX		
H	24	26	26	21	31	60	54	50	60	63	41	73	41	56	53	61	XX	
W-1	18	21	18	26	29	42	38	33	49	52	41	48	36	36	44	49	47	XX

*The table is read as follows: The similarity between X-066 and 369 was 59 percent.

out of a possible 19 for Set 3. This gave a total of 44 character matches out of a possible 75 characters, or a coefficient of 59 percent similarity between X-066 and 369.

The similarity coefficients from all three sets were calculated with the aid of an electronic calculator and an adding machine.

Calculation and Presentation of the Dendrograms

A dendrogram was calculated for each of the three sets of simple matching coefficients (Tables VII, VIII, and IX). The dendrograms were calculated by the unweighted pair-group method using arithmetic averages (Sokal and Sneath, 1963). A complete 18 by 18 matrix was constructed for each of the sets of coefficients since there were 18 clones involved in each of the sets.

Considering only one set of simple matching coefficients at a time, the highest value in each column of the 18 by 18 matrix was recorded. If clone A had its highest correspondence with clone B and clone B also had its highest correspondence with clone A, then at this common level of similarity A and B were joined together in the dendrogram. However, if A and B did not mutually have the highest level of correspondence, then the relationship between A and B could not be illustrated in the dendrogram until one or more additional matrices were constructed from the data of the original 18 by 18 matrix.

To calculate a second matrix if A and B had not joined, the relationship between A and B did not change and was simply copied from the original matrix. On the other hand, if A and B joined, the relationship between A and B was no longer considered but the new

relationships of the cluster AB to other clones or clusters of clones were considered. To calculate the relationship of the cluster AB to another clone, C, the coefficient for the relationship between A and C and the coefficient for the relationship between B and C were recorded from the original matrix and averaged to give a value for the relationship between the cluster AB and the clone C. The same procedure was followed until all clones of the original matrix were transformed into the second matrix either as clusters or individually. In the second matrix, the highest value in each column was recorded and then additional individual clones and/or clusters of clones were drawn into the dendrogram. If a third matrix or additional matrices were necessary, the values for calculating these matrices were averaged from the coefficients in the first matrix by using the same procedure described for transferring from the original matrix to the second matrix. Additional matrices were calculated until the two clones or groups of clones which were most distantly related had a calculated coefficient of similarity and were thus drawn into the dendrogram.

Three dendrograms were constructed to analyze the data obtained in this study. The first dendrogram (Figure 1) was calculated from characters obtained by measuring and/or counting various structures, but no ratios of these characters were included in the dendrogram. The simple matching coefficients from which the first dendrogram was constructed are given in Table VII, page 54. The second dendrogram (Figure 2) was based on ratios of selected pairs of characters plus those characters which were independent of any of these ratios. The

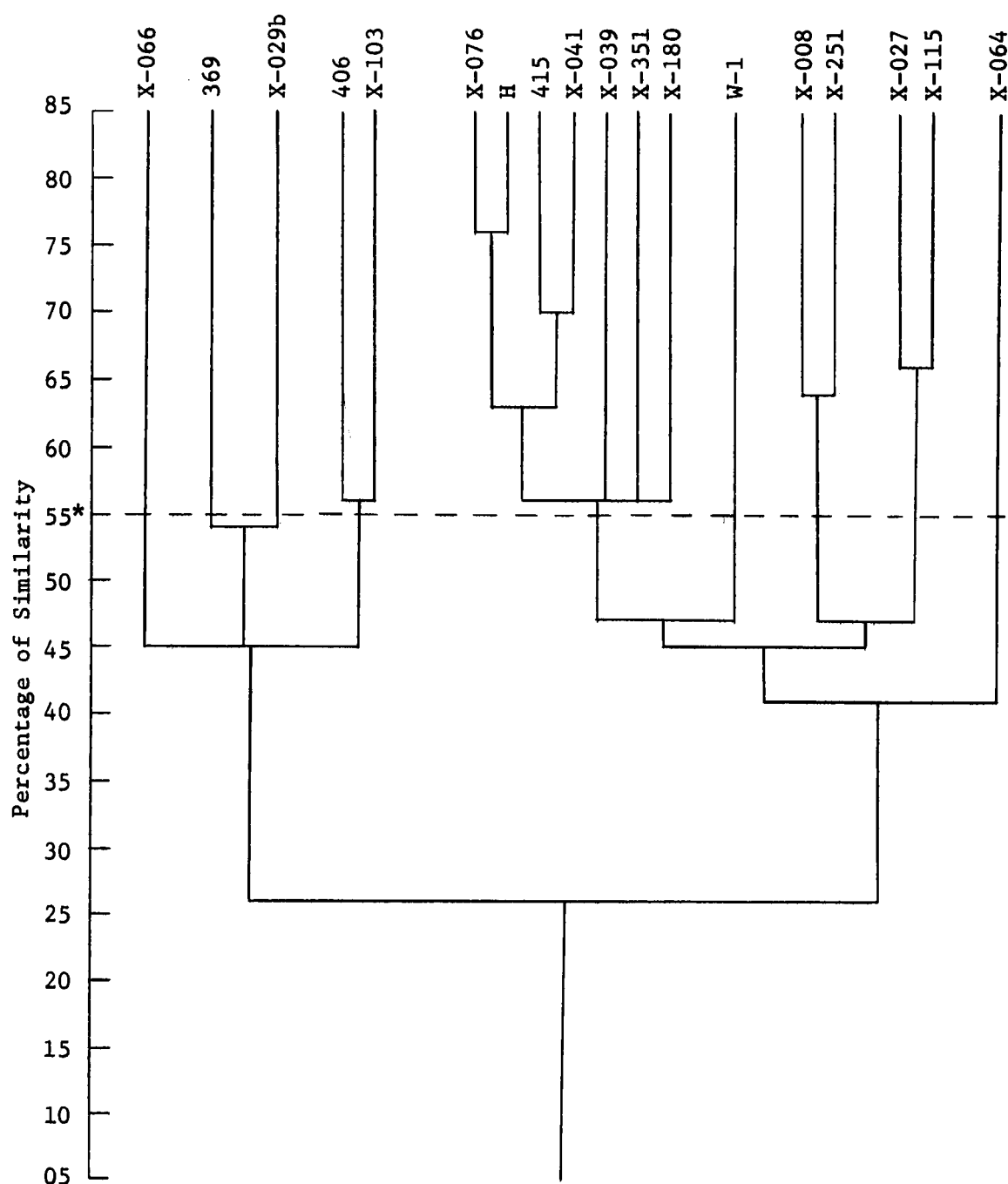


Figure 1. Dendrogram of the relationships among 18 clones of *Chara zeylanica* and related species based on 50 nonratio characters from morphological data.

*Level above which clones grouped together were considered the same species.

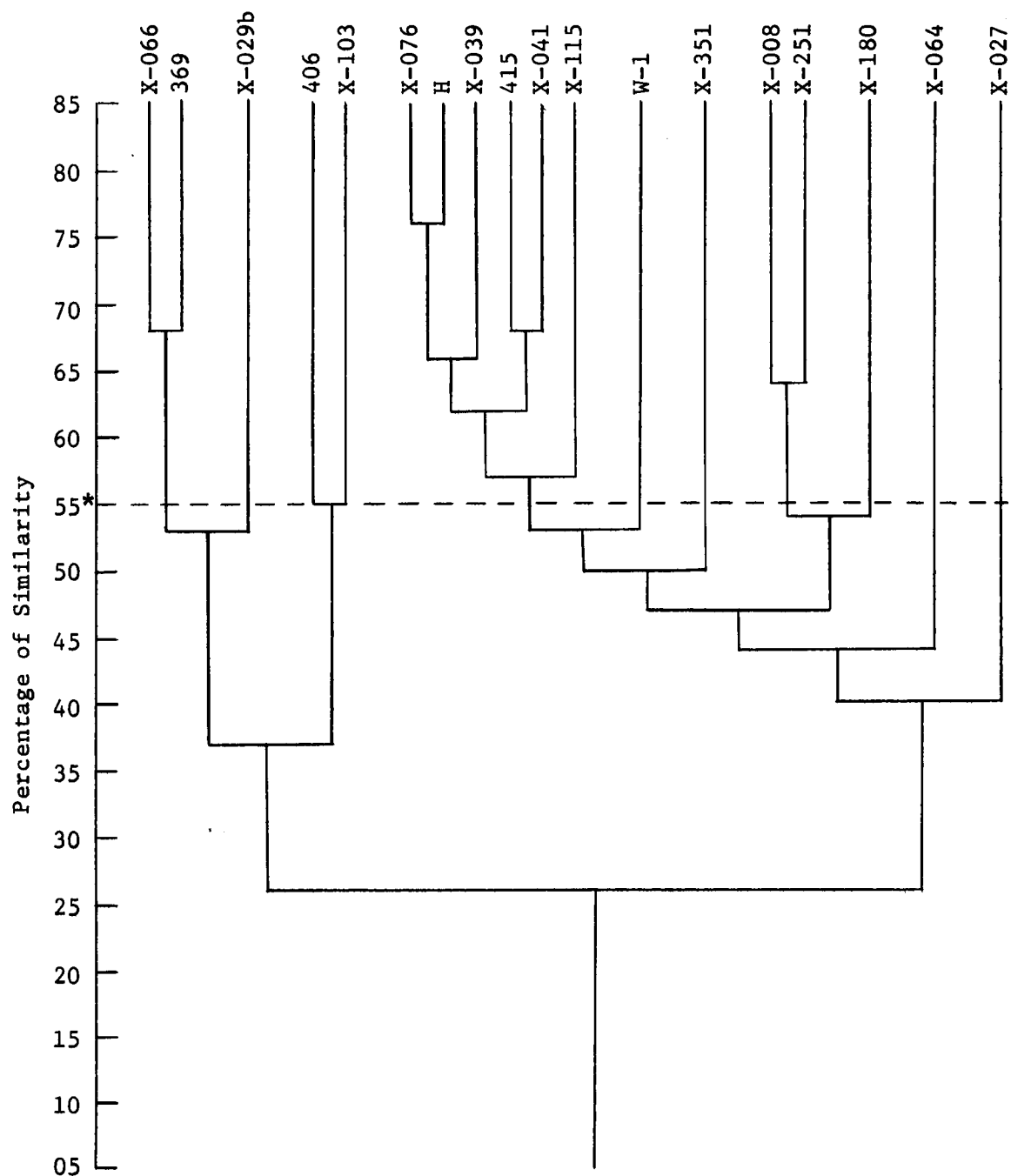


Figure 2. Dendrogram of the relationships among 18 clones of *Chara zeylanica* and related species based on 25 ratio characters and 19 independent nonratio characters from morphological data.

*Level above which clones grouped together were considered the same species.

simple matching coefficients from which the second dendrogram was calculated are given in Table VIII, page 55. The third dendrogram (Figure 3) was constructed by using data from all 75 characters; that is, characters which were ratios, characters which were independent of the ratios, and characters from which the ratios were calculated. The simple matching coefficients from which the third dendrogram was constructed are given in Table IX, page 56. The dendrograms are referred to in the remainder of this study as follows: Figure 1 is called the first dendrogram; Figure 2 is called the second dendrogram; and Figure 3 is called the third dendrogram.

There were 25 characters which were ratios of other characters and 19 characters which were independent of any of the ratios. The remaining group of 31 characters were those which were used in the calculations of the ratios. Of these latter 31 characters, certain characters such as oospore length and spine cell length were used in the calculation of only one ratio, while certain other characters such as upper stipulode length and lower stipulode length were used in the calculations of more than one ratio. Oogonium length was used in four separate ratios, oogonium length to oogonium width, bracteole length to oogonium length, bractlet length to oogonium length, and anterior bract cell length to oogonium length. The use of a character in more than one ratio obviously weighted the final results in those dendrograms in which ratios were used (Figures 2 and 3). The reasons for using ratios in which a single character was used more than once were as follows: (1) Many of the ratios such as bracteole length to anterior

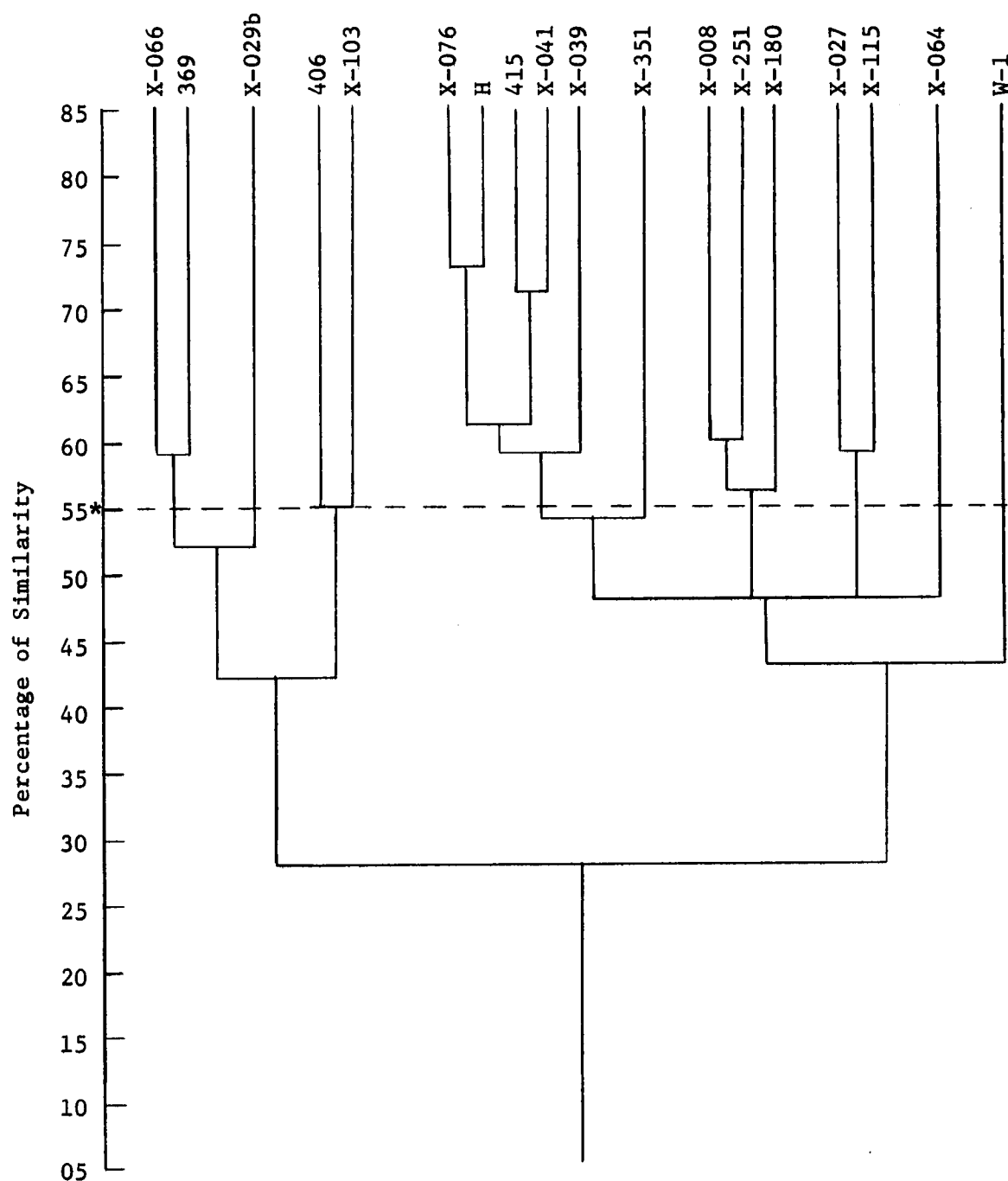


Figure 3. Dendrogram of the relationships among 18 clones of *Chara zeylanica* and related species based on 25 ratio characters and 50 nonratio characters from morphological data.

*Level above which clones grouped together were considered the same species.

bract cell length have previously been included in descriptive studies of the charophytes by Wood and Imahori (1964), Griffin (1965), Pal et al. (1962), and others; and (2) each ratio is a new bit of information. In the same sense that X and a function of X are not the same, neither is the raw data and the ratio the same; however, there is dependence of the ratio upon the raw data in the same manner that there is dependence of the function of X upon X. Ratios and the characters from which they were derived were not used in the same dendrogram, except in the third dendrogram which included all 75 characters. The ratios yielded information which otherwise would have been overlooked.

Sokal and Sneath (1963) and Sneath (1961) expressed the usefulness of assigning a specific taxonomic rank to certain similarity levels in a dendrogram. In this study a line representing the species level above which all clones which were grouped together were considered to be the same species and those which were not grouped together were considered to be different species was drawn on each dendrogram. Sokal and Sneath (1963) indicated that the criteria for taxonomic rank of one group of organisms will not necessarily be the same for another group of organisms even though both groups have been studied by the same or similar numerical taxonomic methods. A species level line was drawn on each of the three dendrograms at the 55 percent level of similarity. To have drawn a line above this point would have tended to further separate the Chara zeylanica clones as well as the two Chara haitensis clones. To have drawn a line below the 55 percent level would have grouped together clones which were quite diverse morphologically and genetically.

Since characters which were identical for all clones were omitted and only characters which varied from clone to clone were used in the calculation of the dendrograms, clones which had at least a 55 percent level of similarity appeared to be the same species. A horizontal broken line was drawn on each of the three dendrograms to represent the level above which clones grouped together were considered the same species.

IV. DISCUSSION

The results of this study supported the proposed classification by Proctor, Griffin, and Hotchkiss (in press) and differed from the classification by Wood (1962); therefore, the conclusions are written with reference to the former classification. According to the relationships among the 18 clones illustrated in the three dendrograms (Figure 1, page 59; Figure 2, page 60; and Figure 3, page 62), there was as much divergence among the 13 Chara zeylanica clones as there was among the five clones which have been considered other species. All the C. zeylanica clones were more similar to one another than they were to any of the non-C. zeylanica clones. Although the discussion includes information from all three dendrograms, perhaps the first dendrogram (Figure 1) presented the most valid view of the taxonomic relationships among the clones studied since each of the characters was independent of the others in the sense that no ratio characters were involved in the construction of the first dendrogram.

As illustrated in the first dendrogram (Figure 1), X-066 (C. rusbyana) was sufficiently different from all the other clones to be considered a different species. The greatest correspondence of X-066 was 45 percent of similarity with the cluster of 369, X-029b, 406, and X-103. As illustrated in the second dendrogram (Figure 2) and also in the third dendrogram (Figure 3), X-066 appeared to be fairly closely related to 369. The level of similarity of X-066 to 369 was 68 percent in the second dendrogram and 59 percent in the third dendrogram. X-066

and 369 are likely not as closely related as suggested by the second and third dendrograms even though they both have the same chromosome number of 14. McCracken, Proctor, and Hotchkiss (1966) tried unsuccessfully to bring about crosses between X-066 and 369 which further suggests that the two clones are separate species. A closer relationship may exist between X-066 and 369 than is implied by the first dendrogram; but with the present information, the two clones are considered separate species.

The relationship of X-066 to the cluster of 369, X-029b, 406, and X-103 was higher in similarity than was its relationship to any of the C. zeylanica clones, as shown in all three of the dendrograms. In the first dendrogram, X-066 joined with 369, X-029b, 406, and X-103 at the 45 percent level of similarity, which is below the 55 percent species rank. In the second dendrogram, X-066 first joined 369 at a level of 68 percent similarity; then X-066 and 369 joined with X-029b at a level of 53 percent similarity; and finally X-066, 369, and X-029b joined with X-103 and 406 at a level of 37 percent similarity. In the third dendrogram, X-066 first joined 369 at a 59 percent level of similarity; then X-066 and 369 joined X-029b at a 52 percent level of similarity; and finally X-066, 369, and X-029b joined 406 and X-103 at a 42 percent level of similarity.

According to all three dendrograms, X-066 is widely removed from any of the C. zeylanica clones. As shown in Table VII, page 54, X-066 had a similarity relationship to X-039 of 32 percent, which was the highest relationship of any of the 13 C. zeylanica clones to X-066. As shown in Table VIII, page 55, X-066 was more closely related to X-027 and X-041 than to any of the other C. zeylanica clones; the relationship

was only 27 percent in each case. As shown in Table IX, page 56, X-066 was more closely related to X-027, X-039, and X-251 than to any of the other C. zeylanica clones; the relationship was 32 percent in each case.

According to the information presented in the first dendrogram, 369 (C. foliolosa) was considered to be sufficiently different from the other clones to be a separate species. By this same dendrogram, 369 was most closely related to X-029b at a level of 54 percent similarity. There was evidence of a possible relationship between 369 and X-066 according to the second and third dendrograms. Also, as explained above and as illustrated in all three of the dendrograms, 369 was more closely related to X-066, X-029b, X-103, and 406 than it was to any of the C. zeylanica clones.

According to all three dendrograms, X-029b (C. martiana) was sufficiently different from the other clones to be considered a separate species. X-029b was most closely related to 369 at a level of 54 percent similarity according to the first dendrogram; however, according to the second and third dendrograms, X-029b was about as closely related to X-066 as it was related to 369. By all three dendrograms, X-029b, X-066, and 369 were more closely related to X-103 and 406 than to any of the C. zeylanica clones.

According to the information in all three dendrograms, X-103 and 406 were sufficiently related to be considered the same species, C. haitensis. This relationship agrees with the classification of Proctor, Griffin, and Hotchkiss (in press). Griffin (1965) and Griffin and Proctor (1964) indicated that there was a great morphological

similarity between clones of C. haitensis and C. zeylanica. According to the results in the current study, X-103 and 406 were more closely related to X-066 (C. rusbyana), X-029b (C. martiana), and 369 (C. foliolosa) than to any of the C. zeylanica clones; however, this study did support the separation of the species of C. zeylanica and C. haitensis.

This study gave definite evidence that there was more than one species among the 13 C. zeylanica clones studied. The clones X-064, X-115, and X-027, which had a chromosome number of 42, were rather widely separated from the C. zeylanica clones which had a chromosome number of 28 and from W-1 which had a chromosome number of 70.

X-027 and X-115 appeared to be sufficiently related to each other (66 percent similarity according to the first dendrogram and 59 percent similarity according to the third dendrogram) to be the same species. In the second dendrogram, X-027 and X-115 were somewhat more remote in similarity; but from the data in Table VIII, page 55, from which the second dendrogram was calculated, they had 52 percent similarity. The breeding data which were obtained by Proctor and Wiman (in press) also showed evidence that X-027 and X-115 were closely related.

A very low relationship existed between X-064 and X-027 and between X-064 and X-115, even though all three had a chromosome number of 42. From Proctor and Wiman's (in press) breeding data, crosses involving X-064 and X-027 created only darkening of the oospores. In crosses between X-115 and X-064, a few of the oospores germinated; and in the case where the X-115 was a female parent, some of the plants survived the germinal stage. It is possible that X-064, X-027, and

X-115 are the same species; but evidence from the present study tended to indicate two separate species. X-027 and X-115 appeared to be members of the same species, and X-064 appeared to be an independent species. According to the first dendrogram, X-064, X-027, and X-115 were below the 55 percent species line of similarity with all of the other C. zeylanica clones.

Evidence was given in all three dendrograms that X-008 and X-251 were sufficiently related to be regarded as the same species. The first and second dendrograms revealed a 64 percent similarity between X-008 and X-251 while the third dendrogram revealed a 60 percent similarity. The chromosome number for both of these clones was 28. The first dendrogram revealed that X-008 and X-251 were more closely related to X-027 and X-115 at 47 percent similarity than to any of the other C. zeylanica clones. Since the relationship of 47 percent was low, X-008 and X-251 were sufficiently different from X-027 and X-115 according to both chromosome number and morphological data to be considered separate species. The relationship of X-008 and X-251 with each of the other C. zeylanica clones was below 50 percent similarity, which was sufficiently low to question the feasibility of placing X-008 and X-251 with the other C. zeylanica clones.

The hybrid W-1, which was a cross between X-064 and 415, appeared to be a new species created in the laboratory. W-1 was not as closely related to its parents as might have been expected since the percentages of similarity were only 44 percent with X-064, the female parent, and 40 percent with 415, the male parent (Table VII, page 54). The

relationship between the parents, X-064 and 415, was only 44 percent similarity. According to all three dendrograms, X-064 was widely separated from all the other C. zeylanica clones; thus, the creation of the partially self-fertile hybrid W-1 establishes need for further investigation into the relationships between the two groups of C. zeylanica clones with chromosome numbers of 42 and 28, since X-064 had a chromosome number of 42 and clone 415 had a chromosome number of 28 while W-1 had a chromosome number of 70.

According to all three dendrograms, X-076 was highly similar to H, and 415 was highly similar to X-041. According to the first dendrogram, X-076 and H had a 76 percent similarity while 415 and X-041 had a 70 percent similarity. The four clones--X-076, H, X-041, and 415--had common similarities at levels of 61 percent or higher, according to all three dendrograms. Also, the breeding data of Proctor and Wiman (in press) supported a relatively high relationship between 415 and X-041. According to the data in the first dendrogram, these four clones were related to X-180, X-039, and X-351 at a level of 56 percent similarity. There was not complete agreement in the information from the second and third dendrograms concerning the placement of X-180, X-039, and X-351 with X-076, H, 415, and X-041. In the second and third dendrograms, there was evidence to indicate that X-180 may be more closely related to X-008 and X-251 and that X-351 might be a separate species. Proctor and Wiman's (in press) breeding data gave evidence that X-180, 415, and X-041 were closely related. Their data also showed that X-180, 415, and X-041 were more closely related to each other than they were related to

X-115, X-027, X-076, or X-064. According to the first dendrogram, the self-sterile H hybrid had 63 percent similarity to X-041, the female parent, and 56 percent similarity to X-180, the male parent. X-041 and X-180 had 56 percent similarity. The chromosome number for each of the clones X-076, H, 415, X-041, X-039, X-180, and X-351 was 28. Thus, there was reliable evidence to indicate that X-076, H, 415, and X-041 were members of the same species, and there was somewhat weaker evidence to indicate that X-039, X-180, and X-351 also belong to this same species.

In summary, the results from this study were interpreted as supporting the classification of the Chara zeylanica complex by Proctor, Griffin, and Hotchkiss (in press) and clearly differing from that by Wood (1962). Based on Figure 1, page 59, nine taxa were distinguished among the 18 clones by drawing a phenon line at the 55 percent level of similarity. These groups of clones are listed below with their respective chromosome numbers.

1. X-066, N = 14
2. 369, N = 14
3. X-029b, N = 28
4. X-103 and 406, N = 56
5. X-076, H, 415, X-041, X-039, X-351, and X-180; N = 28
6. W-1, N = 70
7. X-008 and X-251, N = 28
8. X-027 and X-115, N = 42
9. X-064, N = 42

In the sense of Wood's (1962) classification, all nine of the groups are Chara zeylanica. With respect to the classification of Proctor, Griffin, and Hotchkiss (in press), there are five groups among these 18 clones, the first four of which agree with the findings in this study. These five groups are:

1. X-066, Chara rusbyana
2. 369, Chara foliolosa
3. X-029b, Chara martiana
4. X-103 and 406, Chara haitensis
5. X-076, H, 415, X-041, X-039, X-351, X-180, W-1, X-008,
X-251, X-027, X-115, and X-064; Chara zeylanica

More recently, Proctor and Wiman (in press) have questioned the placing of all 13 of the clones in the fifth group under the single name of Chara zeylanica. Their conclusions were based primarily on breeding data and chromosome counts. This study supports their conclusions in that the clones which are more difficult to hybridize differ morphologically.

Additional attempts at hybridization among the C. zeylanica clones should help to clarify the relationships among these clones. A future numerical taxonomic study in which both breeding data and morphological data are used should reveal considerable insight into the natural taxonomic relationships among the species of the Chara zeylanica complex.

V. SUMMARY

Eighteen clones of Chara zeylanica and closely related species were selected from the charophyte collection of V. W. Proctor, Texas Technological University, Lubbock. All of the clones were C. zeylanica Klein ex Willd. sensu Wood (1962). By a recent taxonomic revision of the C. zeylanica complex by Proctor, Griffin, and Hotchkiss (in press), one of these (X-066) was C. rusbyana Howe, one (369) was C. foliolosa Muhl. ex Willd. (= C. sejuncta Braun), one (X-029b) was C. martiana Br. ex Wallman, two (406 and X-103) were C. haitensis Turpin, and 13 (415, X-008, X-027, X-039, X-041, X-064, X-076, X-251, X-351, X-115, X-180, H, and W-1) were C. zeylanica Klein ex Willd. H and W-1 were hybrids; namely, H from X-041 and X-180 and W-1 from X-064 and 415.

All of the clones were cultured in soil-water preparations in wide-mouth one-gallon jars during the Spring and Summer of 1970. Data for 75 characters were collected for each of the 18 clones. Means, standard deviations, and maximum and minimum values were calculated for data which varied for a particular clone; a computer program was used for the calculations. Means were used as the primary guide for the assignment of character states.

The characters were divided into three sets. The first set included 31 characters which were measurements of various morphological structures. The second set included 25 characters which were simple two-character ratios of various characters of the first set. The third set included 19 characters which were from observations and/or

measurements and which were independent of either of the first two sets. A data deck was punched for each of the three sets of characters. Each deck had 18 cards, one for each clone. On each card was punched the assigned character states for that clone. Each character had a preassigned card column. When any two cards from one deck were held evenly together, the number of common punches equalled the total number of characters for which these two clones had common character states.

Three sets of simple matching coefficients were tabulated. The first set (50 characters) involved all the characters with the exception of the ratios. The second set involved 44 characters, the ratios and those 19 characters which were independent of the ratios. The third set involved all 75 characters; that is, characters which were ratios, characters which were independent of the ratios, and characters from which the ratios were calculated. From each of the three sets of simple matching coefficients, a dendrogram was drawn. The unweighted-pair group method using arithmetic averages was used in the construction of the dendrograms.

The results of this study supported the proposed classification by Proctor, Griffin, and Hotchkiss (in press) and differed from the classification by Wood (1962); therefore, the conclusions concerning the 18 clones studied are written with reference to the former classification. There was as much divergence among the 13 C. zeylanica clones as there was among the five clones which have been considered other species. All the C. zeylanica clones were more similar to one another than they were to any of the non-C. zeylanica clones.

X-066, 369, and X-029b appeared to be separate species, with a questionable exception of the relationship of X-066 to 369. X-029b had a chromosome number of 28, while both X-066 and 369 had chromosome numbers of 14. Evidence indicated that X-103 and 406, both which had a chromosome number of 56, were the same species. This study provided definite evidence that there was more than one species among the 13 C. zeylanica clones studied. One of the better criteria for separating the C. zeylanica clones was chromosome number, since those clones with a chromosome number of 28 tended to be separated from those with a chromosome number of 42. There were strong indications to suggest that X-064 was a separate species from all the other clones, X-027 and X-115 were members of the same species, and X-008 and X-251 were members of the same species. X-064, X-027, and X-115 had a chromosome number of 42, while X-008 and X-251 had a chromosome number of 28. There was also very good evidence to indicate that H, X-076, 415, and X-041 were the same species. X-180, X-039, and X-351 were likely members of the same species as this latter group of four clones, but there was some evidence that X-180 may be more related to X-008 and X-251 and that X-351 might be a separate species. H, X-076, 415, X-041, X-180, X-039, and X-351 had chromosome numbers of 28. The self-sterile H hybrid was morphologically similar to both of its parents, X-041 and X-180. W-1 appeared to be a new species created in the laboratory. Evidence from this study showed that the parents of W-1, X-064 and 415, were morphologically dissimilar. The creation of the partially self-fertile W-1 hybrid with a chromosome number of 70 establishes need for further investigation

into the relationships between the two groups of C. zeylanica clones with chromosome numbers of 42 and 28.

Additional attempts at hybridization among the C. zeylanica clones should help to clarify the relationships among these clones. A future numerical taxonomic study in which both breeding data and morphological data are used should reveal considerable insight into the natural taxonomic relationships among the species of the Chara zeylanica complex.

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APPENDIX

TABLE X
DATA AND CHARACTER STATES FOR THE NUMBER
OF BRANCHLETS PER NODE

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	13.92	0.86	25	15	12	6
369	10.48	1.05	25	12	9	2
X-029b	10.08	0.76	25	11	9	2
406	10.60	1.00	25	12	9	3
X-103	13.56	1.08	25	15	12	6
415	10.16	1.07	25	12	8	2
X-008	11.96	0.84	25	14	10	4
X-027	9.56	0.82	25	11	8	2
X-039	10.88	0.78	25	12	10	3
X-041	10.28	1.21	25	12	8	2
X-064	8.84	0.75	25	10	8	1
X-076	9.96	0.84	25	11	8	2
X-251	8.80	0.76	25	10	8	1
X-351	9.84	0.94	25	11	8	2
X-115	11.12	0.88	25	12	10	3
X-180	11.16	1.07	25	13	9	3
H	10.16	1.14	25	12	8	2
W-1	8.80	0.87	25	10	8	1

*A character state was assigned to each mean rounded to the nearest whole number. A mean of 9 was assigned character state 1; 10 was assigned character state 2; 11 was assigned character state 3; 12 was assigned character state 4; 13 was assigned character state 5; and 14 was assigned character state 6.

TABLE XI
DATA AND CHARACTER STATES FOR THE NUMBER
OF SEGMENTS PER BRANCHLET

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	12.82	1.77	40	16	9	8
369	13.22	1.44	40	15	10	8
X-029b	7.83	1.75	40	11	4	3
406	10.15	1.39	40	12	8	5
X-103	9.63	0.87	40	11	8	5
415	7.68	1.00	40	9	5	3
X-008	9.25	0.90	40	11	7	4
X-027	5.93	0.86	40	7	4	1
X-039	7.70	0.72	40	9	6	3
X-041	8.10	0.67	40	9	7	3
X-064	8.88	0.72	40	10	8	4
X-076	8.05	1.11	40	10	6	3
X-251	9.25	1.53	40	11	6	4
X-351	7.03	0.95	40	8	4	2
X-115	7.13	0.72	40	8	6	2
X-180	7.88	0.88	40	9	6	3
H	8.00	0.68	40	9	7	3
W-1	7.53	1.06	40	9	6	3

*A character state was assigned to each mean rounded to the nearest whole number. A mean of 6 was assigned character state 1; 7 was assigned character state 2; 8 was assigned character state 3; 9 was assigned character state 4; 10 was assigned character state 5; 11 was assigned character state 6; 12 was assigned character state 7; and 13 was assigned character state 8.

TABLE XII
DATA AND CHARACTER STATES FOR THE NUMBER
OF CORTICATED SEGMENTS PER BRANCHLET

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	10.67	2.02	40	14	5	5
369	11.22	1.44	40	13	8	5
X-029b	5.30	2.28	40	9	0	3
406	8.15	1.39	40	10	6	4
X-103	6.95	1.04	40	9	5	4
415	4.88	1.16	40	7	2	3
X-008	6.30	1.11	40	9	4	3
X-027	(branchlets entirely ecorticated)					1
X-039	3.40	0.93	40	6	2	2
X-041	5.63	0.81	40	7	4	3
X-064	6.88	0.72	40	8	6	4
X-076	4.15	1.56	40	8	2	3
X-251	6.48	1.88	40	9	2	3
X-351	1.83	1.28	40	4	0	2
X-115	4.33	1.02	40	6	2	3
X-180	2.30	1.49	40	6	0	2
H	3.88	0.65	40	5	2	3
W-1	5.10	1.26	40	7	3	3

*A character state was assigned to each mean rounded to the nearest whole number. Ecorticated branchlets were assigned character state 1; the means of 1, 2, and 3 were assigned character state 2; 4, 5, and 6 were assigned character state 3; 7, 8, and 9 were assigned character state 4; and 10, 11, and 12 were assigned character state 5.

TABLE XIII

DATA AND CHARACTER STATES FOR THE NUMBER OF ECORTICATED
TERMINAL SEGMENTS PER BRANCHLET

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	1.15	0.43	40	3	1	1
369	1.00	0.00	40	1	1	1
X-029b	1.53	0.72	40	3	1	2
406	1.00	0.00	40	1	1	1
X-103	1.60	0.55	40	3	1	2
415	1.80	0.65	40	3	1	2
X-008	1.95	0.75	40	3	1	2
X-027	4.93	0.86	40	6	3	5
X-039	3.30	0.88	40	5	1	3
X-041	1.45	0.50	40	2	1	1
X-064	1.00	0.00	40	1	1	1
X-076	2.90	0.87	40	5	1	3
X-251	1.78	0.77	40	4	1	2
X-351	4.15	1.03	40	7	2	4
X-115	1.80	0.72	40	3	1	2
X-180	4.45	1.06	40	7	2	4
H	3.13	0.88	40	5	2	3
W-1	1.43	0.59	40	3	1	1

*A character state was assigned to each mean rounded to the nearest whole number. A mean of 1 was assigned character state 1; 2 was assigned character state 2; 3 was assigned character state 3; 4 was assigned character state 4; and 5 was assigned character state 5.

TABLE XIV
DATA AND CHARACTER STATES FOR THE NUMBER
OF BRACT CELLS PER NODE

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	7.00	1.00	15	9	6	3
369	6.33	0.72	15	7	5	2
X-029b	6.53	0.52	15	7	6	3
406	7.20	0.68	15	8	6	3
X-103	7.13	0.64	15	8	6	3
415	5.47	0.52	15	6	5	1
X-008	6.47	0.52	15	7	6	2
X-027	5.53	0.52	15	6	5	2
X-039	5.67	0.62	15	7	5	2
X-041	6.47	0.52	15	7	6	2
X-064	5.73	0.46	15	6	5	2
X-076	5.73	0.46	15	6	5	2
X-251	5.53	0.52	15	6	5	2
X-351	5.53	0.64	15	7	5	2
X-115	5.67	0.49	15	6	5	2
X-180	5.87	0.35	15	6	5	2
H	5.60	0.51	15	6	5	2
W-1	5.27	0.46	15	6	5	1

*A character state was assigned to each mean rounded to the nearest whole number. A mean of 5 was assigned character state 1; 6 was assigned character state 2; and 7 was assigned character state 3.

TABLE XV
DATA AND CHARACTER STATES FOR THE NUMBER
OF OOGONIA PER BRANCHLET

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	3.28	0.96	40	5	1	2
369	3.35	1.49	40	7	1	2
X-029b	1.95	0.75	40	4	1	1
406	2.85	1.17	40	5	1	2
X-103	2.33	1.02	40	4	1	1
415	3.35	0.66	40	4	2	2
X-008	3.45	1.06	40	5	1	2
X-027	1.65	0.48	40	2	1	1
X-039	3.05	0.93	40	4	1	2
X-041	3.25	0.71	40	4	2	2
X-064	3.73	0.72	40	5	2	3
X-076	1.90	0.71	40	3	1	1
X-251	3.70	0.84	30	6	2	3
X-351	2.03	0.92	40	4	1	1
X-115	2.45	0.85	40	4	1	1
X-180	2.00	0.78	40	3	1	1
H	1.75	0.87	40	3	1	1
W-1	1.63	0.77	40	4	1	1

*A character state was assigned to each mean rounded to the nearest whole number. A mean of 2 was assigned character state 1; 3 was assigned character state 2; and 4 was assigned character state 3.

TABLE XVI
DATA AND CHARACTER STATES FOR THE LOCATION OF OOGONIA

Clone	Mean Node for Oogonia Location	Standard Deviation	Number of Oogonia/ Number of Branchlets	Maximum Node for Oogonia	Minimum Node for Oogonia	Character State*
X-066	3.7	1.23	131/40	7	2	4
369	4.2	1.86	134/40	9	1	4
X-029b	2.4	1.19	78/40	5	1	2
406	3.3	1.13	114/40	6	2	3
X-103	3.0	0.86	93/40	5	1	3
415	2.2	1.01	134/40	4	1	2
X-008	2.6	1.20	138/40	6	1	3
X-027	1.4	0.50	66/40	2	1	1
X-039	2.3	0.99	122/40	4	1	2
X-041	2.3	1.01	130/40	4	1	2
X-064	2.5	1.17	149/40	5	1	3
X-076	1.9	0.71	76/40	3	1	2
X-251	3.1	1.16	111/30	5	1	3
X-351	2.3	0.89	81/40	5	1	2
X-115	1.9	0.84	98/40	4	1	2
X-180	1.9	0.70	80/40	3	1	2
H	1.9	0.70	70/40	3	1	2
W-1	2.2	0.84	65/40	4	1	2

*A character state was assigned to each mean rounded to the nearest whole number. A mean of 1 was assigned character state 1; 2 was assigned character state 2; 3 was assigned character state 3; and 4 was assigned character state 4.

TABLE XVII
DATA AND CHARACTER STATES FOR THE NUMBER
OF CONVOLUTIONS PER OOGONIUM

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	12.73	0.59	15	14	12	2
369	12.47	0.52	15	13	12	1
X-029b	12.33	0.72	15	13	11	1
406	13.67	0.90	15	16	13	3
X-103	14.73	0.80	15	16	14	4
415	15.00	0.76	15	16	14	4
X-008	14.20	0.77	15	15	13	3
X-027	15.20	1.01	15	17	14	4
X-039	14.73	0.70	15	16	14	4
X-041	14.27	0.80	15	15	13	3
X-064	14.33	0.49	15	15	14	3
X-076	13.33	0.49	15	14	13	2
X-251	13.80	0.68	15	15	13	3
X-351	11.93	0.70	15	13	11	1
X-115	14.33	0.98	15	16	13	3
X-180	15.33	0.72	15	17	14	4
H	15.47	0.52	15	16	15	4
W-1	16.27	0.46	15	17	16	5

*A character state was assigned to each mean rounded to the nearest whole number. A mean of 12 was assigned character state 1; 13 was assigned character state 2; 14 was assigned character state 3; 15 was assigned character state 4; and 16 was assigned character state 5.

TABLE XVIII
DATA AND CHARACTER STATES FOR THE NUMBER
OF ANTHERIDIA PER BRANCHLET

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	2.90	0.87	40	5	1	2
369	3.10	1.41	40	6	1	2
X-029b	2.10	0.87	40	4	1	1
406	2.83	1.13	40	5	1	2
X-103	2.30	0.97	40	4	1	1
415	3.33	0.66	40	4	2	2
X-008	3.35	1.17	40	6	1	2
X-027	1.68	0.47	40	2	1	1
X-039	3.00	0.96	40	4	1	2
X-041	3.03	0.66	40	4	2	2
X-064	3.48	0.64	40	4	2	2
X-076	1.85	0.77	40	3	1	1
X-251	3.53	0.68	30	5	2	3
X-351	2.63	1.03	40	5	1	2
X-115	2.40	0.87	40	4	1	1
X-180	2.10	0.84	40	3	1	1
H	1.60	0.78	40	3	1	1
W-1	2.20	0.76	40	4	1	1

*A character state was assigned to each mean rounded to the nearest whole number. A mean of 2 was assigned character state 1; 3 was assigned character state 2; and 4 was assigned character state 3.

TABLE XIX
DATA AND CHARACTER STATES FOR THE LOCATION OF ANTHERIDIA

Clone	Mean Node for Antheridia Location	Standard Deviation	Number of Antheridia/ Number of Branchlets	Maximum Node for Antheridia	Minimum Node for Antheridia	Character State*
X-066	4.1	1.00	116/40	6	2	4
369	5.1	1.93	124/40	9	1	5
X-029b	2.7	1.16	84/40	5	1	3
406	3.3	1.11	113/40	6	2	3
X-103	3.0	0.84	92/40	5	2	3
415	2.3	1.01	133/40	4	1	2
X-008	2.6	1.21	134/40	6	1	3
X-027	1.4	0.49	67/40	2	1	1
X-039	2.3	0.98	120/40	4	1	2
X-041	2.3	0.97	121/40	4	1	2
X-064	2.4	1.09	139/40	5	1	2
X-076	1.9	0.72	74/40	3	1	2
X-251	3.0	1.17	106/30	5	1	3
X-351	2.3	0.96	105/40	5	1	2
X-115	1.8	0.84	96/40	4	1	2
X-180	1.9	0.71	84/40	3	1	2
H	2.0	0.66	64/40	3	1	2
W-1	2.0	0.86	88/40	4	1	2

*A character state was assigned to each mean rounded to the nearest whole number. A mean of 1 was assigned character state 1; 2 was assigned character state 2; 3 was assigned character state 3; 4 was assigned character state 4; and 5 was assigned character state 5.

TABLE XX
DATA AND CHARACTER STATES FOR THE NUMBER
OF RIDGES PER OOSPORE

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	11.00	0.65	15	12	10	1
369	11.40	0.51	15	12	11	1
X-029b	10.60	0.51	15	11	10	1
406	12.00	0.65	15	13	11	2
X-103	13.07	0.70	15	14	12	3
415	13.47	0.52	15	14	13	3
X-008	12.53	0.52	15	13	12	3
X-027	12.87	0.83	15	14	12	3
X-039	14.00	0.76	15	15	13	4
X-041	11.93	0.80	15	13	11	2
X-064	12.33	0.49	15	13	12	2
X-076	12.53	0.52	15	13	12	3
X-251	12.53	0.52	15	13	12	3
X-351	10.60	0.63	15	12	10	1
X-115	13.07	0.70	15	14	12	3
X-180	14.53	0.52	15	15	14	5
H	(self-sterile)					
W-1	(too few oospores for data)					

*A character state was assigned to each mean rounded to the nearest whole number. A mean of 11 was assigned character state 1; 12 was assigned character state 2; 13 was assigned character state 3; 14 was assigned character state 4; and 15 was assigned character state 5.

TABLE XXI
DATA AND CHARACTER STATES FOR THE
GAMETANGIA TYPE

Clone	Gametangia Type			Character State*
	Dioecious	Monoecious-sejoined	Monoecious-conjoined	
X-066	X			1
369		X		2
X-029b		X		2
406			X	3
X-103			X	3
415			X	3
X-008			X	3
X-027			X	3
X-039			X	3
X-041			X	3
X-064			X	3
X-076			X	3
X-251			X	3
X-351			X	3
X-115			X	3
X-180			X	3
H			X	3
W-1			X	3

*Clones which had dioecious gametangia were assigned character state 1; clones which had monoecious-sejoined gametangia were assigned character state 2; and clones which had monoecious-conjoined gametangia were assigned character state 3.

TABLE XXII
DATA AND CHARACTER STATES FOR THE NUMBER OF
SHIELD CELLS PER ANTHERIDIUM

Clone	Number of Shield Cells Per Antheridium	Character State*
X-066	8	3
369	8	3
X-029b	8	3
406	8	3
X-103	8	3
415	4	1
X-008	4	1
X-027	3, 4, 5, 6, 7	2
X-039	4	1
X-041	4	1
X-064	4	1
X-076	4	1
X-251	4	1
X-351	4	1
X-115	3, 4, 5, 6, 7	2
X-180	4	1
H	4	1
W-1	4	1

*Clones which had 4 shield cells were assigned character state 1; clones which had 3, 4, 5, 6, or 7 shield cells were assigned character state 2; and clones which had 8 shield cells were assigned character state 3.

TABLE XXIII
DATA AND CHARACTER STATES FOR THE
SHIELD CELL TYPE

Clone	Shield Cell Type			Character State*
	Diamond	Diamond and Triangular	Triangular	
X-066			X	3
369			X	3
X-029b			X	3
406			X	3
X-103			X	3
415	X			1
X-008	X			1
X-027		X		2
X-039	X			1
X-041	X			1
X-064	X			1
X-076	X			1
X-251	X			1
X-351	X			1
X-115		X		2
X-180	X			1
H	X			1
W-1	X			1

*Clones with diamond-shaped shield cells were assigned character state 1; clones with both diamond-shaped and triangular-shaped shield cells were assigned character state 2; and clones with triangular-shaped shield cells were assigned character state 3.

TABLE XXIV
DATA AND CHARACTER STATES FOR THE
CHROMOSOME NUMBER

Clone	Chromosome Number	Character State*
X-066	14	1
369	14	1
X-029b	28	2
406	56	4
X-103	56	4
415	28	2
X-008	28	2
X-027	42	3
X-039	28	2
X-041	28	2
X-064	42	3
X-076	28	2
X-251	28	2
X-351	28	2
X-115	42	3
X-180	28	2
H	28	2
W-1	70	5

*Clones which had a chromosome number of 14 were assigned character state 1; clones which had a chromosome number of 28 were assigned character state 2; clones which had a chromosome number of 42 were assigned character state 3; clones which had a chromosome number of 56 were assigned character state 4; and clones which had a chromosome number of 70 were assigned character state 5.

TABLE XXV
DATA AND CHARACTER STATES FOR THE
MAIN AXIS DIAMETER

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	673.5	65.14	25	798.0	571.9	3
369	769.3	60.67	25	891.1	691.6	4
X-029b	616.6	81.44	25	864.5	505.4	3
406	557.5	51.79	25	665.0	465.5	2
X-103	693.2	45.80	25	771.4	611.8	3
415	467.1	30.55	25	545.3	412.3	1
X-008	555.9	36.83	25	611.8	492.1	2
X-027	481.5	53.61	25	598.5	399.0	1
X-039	493.2	35.80	25	598.5	438.9	1
X-041	441.0	18.68	25	492.1	412.3	1
X-064	474.0	85.75	25	611.8	359.1	1
X-076	437.8	26.30	25	492.1	399.0	1
X-251	511.4	16.97	20	532.0	478.8	2
X-351	518.7	38.39	25	598.5	465.5	2
X-115	482.5	52.58	25	571.9	412.3	1
X-180	549.0	49.84	25	638.4	438.9	2
H	431.5	44.95	25	532.0	385.7	1
W-1	478.3	39.24	25	532.0	412.3	1

*Character states were assigned to the means of the axis diameter as follows: 400 to 500 microns, character state 1; 500 to 600 microns, character state 2; 600 to 700 microns, character state 3; and 700 to 800 microns, character state 4.

TABLE XXVI
DATA AND CHARACTER STATES FOR THE
SPINE CELL LENGTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	376.0	160.7	41	704.9	133.0	2
369	147.2	112.4	42	452.2	26.6	1
X-029b	121.1	99.1	29	385.7	26.6	1
406	338.5	152.4	44	704.9	93.1	2
X-103	262.0	98.9	57	465.5	79.8	2
415	268.9	143.8	32	545.3	79.8	2
X-008	361.6	198.2	47	917.7	93.1	2
X-027	364.0	176.4	41	718.2	119.7	2
X-039	559.3	416.3	58	1756.0	93.1	3
X-041	487.1	193.3	43	798.0	133.0	3
X-064	464.3	187.4	46	891.1	146.3	3
X-076	157.3	47.7	41	266.0	66.5	1
X-251	355.0	158.3	39	651.7	133.0	2
X-351	183.2	60.8	40	372.4	66.5	1
X-115	260.6	237.9	37	1077.0	66.5	2
X-180	227.0	130.4	44	571.9	53.2	2
H	180.2	62.2	44	319.2	79.8	1
W-1	662.0	336.1	54	1436.0	106.4	4

*Character states were assigned to the means of the spine cell length as follows: 0 to 200 microns, character state 1; 200 to 400 microns, character state 2; 400 to 600 microns, character state 3; and 600 to 800 microns, character state 4.

TABLE XXVII
DATA AND CHARACTER STATES FOR THE
SPINE CELL WIDTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	58.39	14.83	41	106.4	39.9	1
369	57.32	12.63	42	79.8	26.6	1
X-029b	50.91	15.52	29	79.8	26.6	1
406	58.94	10.88	44	79.8	39.9	1
X-103	58.57	9.69	57	79.8	39.9	1
415	57.77	13.35	32	79.8	26.6	1
X-008	57.16	12.38	47	79.8	39.9	1
X-027	62.61	12.70	41	79.8	39.9	2
X-039	63.98	13.52	58	93.1	39.9	2
X-041	64.64	14.39	43	93.1	39.9	2
X-064	70.55	14.26	46	106.4	39.9	2
X-076	49.63	9.87	41	66.5	39.9	1
X-251	59.68	13.60	39	93.1	26.6	1
X-351	50.54	9.14	40	66.5	39.9	1
X-115	59.31	14.23	37	93.1	39.9	1
X-180	51.99	8.99	44	66.5	39.9	1
H	52.29	11.26	44	79.8	26.6	1
W-1	69.21	15.37	54	106.4	39.9	2

*Character states were assigned to the means of the spine cell width as follows: 40 to 60 microns, character state 1; and 60 to 80 microns, character state 2.

TABLE XXVIII
DATA AND CHARACTER STATES FOR THE
UPPER STIPULODE LENGTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	876.5	87.36	20	1024.0	758.1	3
369	728.2	48.80	20	851.2	665.0	2
X-029b	803.3	115.60	20	1104.0	665.0	3
406	683.6	111.90	20	864.5	532.0	2
X-103	865.2	137.60	20	1051.0	611.8	3
415	798.0	112.50	20	1051.0	571.9	2
X-008	685.6	98.82	20	904.4	585.2	2
X-027	670.3	72.77	20	837.9	532.0	2
X-039	819.3	142.40	20	1170.0	625.1	3
X-041	863.2	89.05	20	1051.0	718.2	3
X-064	1087.0	204.80	20	1436.0	784.7	4
X-076	494.8	55.53	20	598.5	399.0	1
X-251	956.1	57.76	9	1024.0	837.9	3
X-351	831.2	169.00	20	1077.0	425.6	3
X-115	684.9	113.90	20	904.4	558.6	2
X-180	579.9	72.90	20	731.5	438.9	1
H	708.2	83.77	20	864.5	505.4	2
W-1	1184.0	72.52	20	1343.0	1037.0	4

*Character states were assigned to the means of the upper stipulode length as follows: 400 to 600 microns, character state 1; 600 to 800 microns, character state 2; 800 to 1000 microns, character state 3; and 1000 to 1200 microns, character state 4.

TABLE XXIX
DATA AND CHARACTER STATES FOR THE
UPPER STIPULODE WIDTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	99.75	8.07	20	119.7	93.1	2
369	77.14	6.96	20	93.1	66.5	1
X-029b	99.08	20.00	20	146.3	79.8	2
406	92.43	10.98	20	119.7	79.8	2
X-103	84.45	6.51	20	93.1	79.8	2
415	89.77	7.32	20	106.4	79.8	2
X-008	90.44	8.19	20	106.4	79.8	2
X-027	80.46	6.79	20	93.1	66.5	2
X-039	92.43	10.10	20	119.7	79.8	2
X-041	89.11	13.71	20	133.0	66.5	2
X-064	91.77	10.48	20	119.7	66.5	2
X-076	77.14	11.09	20	93.1	66.5	1
X-251	96.06	12.93	9	106.4	79.8	2
X-351	75.14	11.64	20	93.1	53.2	1
X-115	82.46	5.46	20	93.1	79.8	2
X-180	89.77	10.46	20	106.4	79.8	2
H	82.46	11.09	20	93.1	66.5	2
W-1	94.43	12.87	20	133.0	79.8	2

*Character states were assigned to the means of the upper stipulode width as follows: 60 to 80 microns, character state 1; and 80 to 100 microns, character state 2.

TABLE XXX
DATA AND CHARACTER STATES FOR THE
LOWER STIPULODE LENGTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	498.7	72.53	20	625.1	359.1	2
369	349.8	42.30	20	452.2	292.6	1
X-029b	353.8	67.87	20	478.8	212.8	1
406	307.2	34.49	20	412.3	252.7	1
X-103	429.6	83.13	20	532.0	292.6	2
415	463.5	43.64	20	545.3	412.3	2
X-008	397.7	58.52	20	518.7	332.5	1
X-027	266.0	75.97	20	412.3	119.7	1
X-039	483.5	73.01	20	665.0	372.4	2
X-041	478.1	53.11	20	558.6	359.1	2
X-064	498.1	86.03	20	665.0	399.0	2
X-076	209.5	29.23	20	252.7	146.3	1
X-251	598.5	75.82	9	731.5	518.7	2
X-351	331.8	80.09	20	532.0	159.6	1
X-115	375.1	88.07	20	492.1	186.2	1
X-180	304.6	44.82	20	359.1	199.5	1
H	346.5	75.05	20	532.0	199.5	1
W-1	800.7	98.83	20	1024.0	651.7	4

*Character states were assigned to the means of the lower stipulode length as follows: 200 to 400 microns, character state 1; 400 to 600 microns, character state 2; 600 to 800 microns, character state 3; and 800 to 1000 microns, character state 4.

TABLE XXXI
DATA AND CHARACTER STATES FOR THE
LOWER STIPULODE WIDTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	102.40	9.75	20	119.7	93.1	3
369	80.46	10.98	20	93.1	53.2	2
X-029b	94.43	17.21	20	119.7	66.5	2
406	83.79	13.02	20	106.4	66.5	2
X-103	82.46	10.21	20	93.1	66.5	2
415	77.80	8.92	20	93.1	66.5	1
X-008	83.79	8.74	20	93.1	66.5	2
X-027	63.84	6.96	20	79.8	53.2	1
X-039	81.13	7.35	20	93.1	66.5	2
X-041	76.47	10.46	20	93.1	66.5	1
X-064	83.79	16.20	20	119.7	66.5	2
X-076	66.50	7.47	20	79.8	53.2	1
X-251	113.80	21.15	9	133.0	79.8	3
X-351	72.48	11.80	20	93.1	53.2	1
X-115	69.82	11.31	20	93.1	53.2	1
X-180	75.81	8.74	20	93.1	53.2	1
H	73.81	10.98	20	93.1	53.2	1
W-1	84.45	9.91	20	106.4	66.5	2

*Character states were assigned to the means of the lower stipulode width as follows: 60 to 80 microns, character state 1; 80 to 100 microns, character state 2; and 100 to 120 microns, character state 3.

TABLE XXXII
DATA AND CHARACTER STATES FOR THE
BRANCHLET DIAMETER

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	406.3	44.11	20	518.7	359.1	6
369	347.8	42.78	20	425.6	292.6	4
X-029b	375.7	23.98	20	412.3	319.2	5
406	348.5	27.49	20	385.7	292.6	4
X-103	364.4	30.33	20	412.3	292.6	5
415	224.8	17.21	20	252.7	186.2	2
X-008	287.9	17.41	20	319.2	252.7	3
X-027	196.8	13.74	10	212.8	172.9	1
X-039	283.3	17.84	20	305.9	252.7	3
X-041	264.7	14.89	20	279.3	239.4	3
X-064	268.7	33.87	20	332.5	212.8	3
X-076	222.8	20.64	20	266.0	199.5	2
X-251	329.8	26.69	15	412.3	292.6	4
X-351	256.0	22.37	20	292.6	226.1	3
X-115	224.8	19.73	20	252.7	199.5	2
X-180	279.3	21.58	20	319.2	239.4	3
H	208.1	7.81	20	226.1	199.5	2
W-1	252.0	24.21	20	292.6	212.8	3

*Character states were assigned to the means of the branchlet diameter as follows: 150 to 200 microns, character state 1; 200 to 250 microns, character state 2; 250 to 300 microns, character state 3; 300 to 350 microns, character state 4; 350 to 400 microns, character state 5; and 400 to 450 microns, character state 6.

TABLE XXXIII
DATA AND CHARACTER STATES FOR THE
BASAL CELL LENGTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	711.1	111.70	15	877.8	465.5	2
369	607.4	61.91	15	691.6	505.4	2
X-029b	960.3	226.60	15	1277.0	665.0	3
406	451.3	33.90	15	505.4	399.0	1
X-103	519.6	44.81	15	585.2	438.9	1
415	861.0	223.70	15	1290.0	545.3	3
X-008	539.1	102.00	15	691.6	385.7	1
X-027	1722.0	631.80	15	2633.0	837.9	7
X-039	721.7	108.80	15	957.6	598.5	2
X-041	838.8	145.60	15	997.5	611.8	3
X-064	448.7	62.68	15	545.3	345.8	1
X-076	516.9	89.20	15	665.0	359.1	1
X-251	916.2	106.50	9	1051.0	784.7	3
X-351	908.8	389.00	15	1596.0	571.9	3
X-115	810.4	115.60	15	1024.0	678.3	3
X-108	647.3	93.19	15	784.7	412.3	2
H	613.6	94.70	15	784.7	465.5	2
W-1	639.3	91.38	15	811.3	452.2	2

*Character states were assigned to the means of the basal cell length as follows: 400 to 600 microns, character state 1; 600 to 800 microns, character state 2; 800 to 1000 microns, character state 3; 1000 to 1200 microns, character state 4; 1200 to 1400 microns, character state 5; 1400 to 1600 microns, character state 6; and 1600 to 1800 microns, character state 7.

TABLE XXXIV
DATA AND CHARACTER STATES FOR THE
BASAL CELL WIDTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	231.4	19.98	15	266.0	199.5	2
369	324.5	17.27	15	345.8	305.9	4
X-029b	335.2	51.07	15	425.6	266.0	4
406	274.9	18.58	15	292.6	239.4	3
X-103	279.3	20.73	15	319.2	239.4	3
415	210.1	37.35	15	266.0	159.6	2
X-008	251.8	24.86	15	292.6	212.8	3
X-027	204.8	25.53	15	252.7	172.9	2
X-039	202.2	28.96	15	252.7	159.6	2
X-041	238.5	17.75	15	266.0	199.5	2
X-064	262.5	31.98	15	305.9	199.5	3
X-076	255.4	16.05	15	279.3	226.1	3
X-251	243.8	22.06	9	266.0	212.8	2
X-351	214.6	20.02	15	252.7	186.2	2
X-115	211.0	38.57	15	266.0	159.6	2
X-180	229.6	33.90	15	292.6	186.2	2
H	166.7	16.57	15	186.2	133.0	1
W-1	219.0	23.51	15	252.7	172.9	2

*Character states were assigned to the means of the basal cell width as follows: 150 to 200 microns, character state 1; 200 to 250 microns, character state 2; 250 to 300 microns, character state 3; and 300 to 350 microns, character state 4.

TABLE XXXV
DATA AND CHARACTER STATES FOR THE
TERMINAL SEGMENT LENGTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	500.1	278.50	15	1463.0	305.9	2
369	271.3	62.75	15	359.1	159.6	1
X-029b	1217.0	566.50	15	2421.0	611.8	6
406	342.3	79.72	15	438.9	252.7	1
X-103	440.7	93.22	15	638.4	279.3	2
415	731.5	264.00	15	1623.0	505.4	3
X-008	519.6	205.50	15	997.5	332.5	2
X-027	438.0	76.64	15	545.3	292.6	2
X-039	504.5	114.90	15	731.5	332.5	2
X-041	699.6	200.00	15	1011.0	412.3	3
X-064	1006.0	471.20	15	2487.0	478.8	5
X-076	428.3	124.00	15	691.6	186.2	2
X-251	500.1	74.87	15	611.8	372.4	2
X-351	834.4	499.10	15	2234.0	332.5	4
X-115	522.2	110.40	15	758.1	359.1	2
X-180	465.5	95.51	15	665.0	292.6	2
H	460.2	241.40	15	1184.0	252.7	2
W-1	751.0	213.60	15	1263.0	545.3	3

*Character states were assigned to the means of the terminal segment length as follows: 200 to 400 microns, character state 1; 400 to 600 microns, character state 2; 600 to 800 microns, character state 3; 800 to 1000 microns, character state 4; 1000 to 1200 microns, character state 5; and 1200 to 1400 microns, character state 6.

TABLE XXXVI
DATA AND CHARACTER STATES FOR THE
TERMINAL SEGMENT WIDTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	107.30	42.20	15	252.7	79.8	2
369	86.89	18.03	15	119.7	53.2	1
X-029b	164.90	26.02	15	226.1	119.7	3
406	90.44	12.52	15	119.7	66.5	1
X-103	89.55	12.78	15	119.7	66.5	1
415	99.31	40.49	15	239.4	66.5	1
X-008	91.33	22.41	15	159.6	66.5	1
X-027	78.91	7.90	15	93.1	66.5	1
X-039	78.03	12.18	15	93.1	53.2	1
X-041	85.12	22.93	15	133.0	53.2	1
X-064	118.80	33.90	15	212.8	79.8	2
X-076	76.25	12.78	15	106.4	53.2	1
X-251	94.87	31.74	15	159.6	66.5	1
X-351	108.20	46.04	15	212.8	66.5	2
X-115	81.57	8.51	15	93.1	66.5	1
X-180	90.44	18.94	15	133.0	53.2	1
H	77.14	16.05	15	119.7	53.2	1
W-1	87.78	9.80	15	106.4	79.8	1

*Character states were assigned to the means of the terminal segment width as follows: 50 to 100 microns, character state 1; 100 to 150 microns, character state 2; and 150 to 200 microns, character state 3.

TABLE XXXVII
DATA AND CHARACTER STATES FOR THE
BRACTEOLE LENGTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	857.8	189.10	20	1077	545	2
369	835.9	91.97	20	998	638	2
X-029b	817.9	154.20	20	1157	545	2
406	698.2	170.30	20	958	333	1
X-103	1234.0	135.20	20	1583	1024	4
415	1164.0	97.11	20	1317	944	3
X-008	954.3	116.30	20	1170	798	2
X-027	945.6	179.70	20	1224	545	2
X-039	1219.0	184.40	20	1649	998	4
X-041	1124.0	124.40	20	1383	825	3
X-064	917.0	121.30	20	1130	652	2
X-076	1011.0	132.60	20	1290	678	3
X-251	1165.0	117.00	15	1383	984	3
X-351	901.1	100.10	20	1117	745	2
X-115	1115.0	129.20	20	1396	904	3
X-180	1107.0	183.60	20	1370	785	3
H	1003.0	121.90	20	1224	718	3
W-1	1497.0	244.10	20	1849	1011	5

*Character states were assigned to the means of the bracteole length as follows: 600 to 800 microns, character state 1; 800 to 1000 microns, character state 2; 1000 to 1200 microns, character state 3; 1200 to 1400 microns, character state 4; and 1400 to 1600 microns, character state 5.

TABLE XXXVIII
DATA AND CHARACTER STATES FOR THE
BRACTEOLE WIDTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	81.79	6.51	20	93.1	66.5	3
369	83.12	7.32	20	106.4	79.8	3
X-029b	88.44	7.81	20	106.4	79.8	3
406	87.11	16.42	20	119.7	66.5	3
X-103	87.11	10.10	20	106.4	66.5	3
415	58.52	7.96	20	79.8	53.2	1
X-008	66.50	6.10	20	79.8	53.2	2
X-027	75.81	6.25	20	79.8	66.5	2
X-039	73.81	9.13	20	93.1	66.5	2
X-041	59.85	6.82	20	66.5	53.2	1
X-064	82.46	11.09	20	106.4	66.5	3
X-076	59.85	6.82	20	66.5	53.2	1
X-251	94.87	6.87	15	106.4	79.8	3
X-351	65.17	8.52	20	79.8	53.2	2
X-115	72.48	6.79	20	79.8	66.5	2
X-180	66.50	4.32	20	79.8	53.2	2
H	57.85	6.51	20	66.5	53.2	1
W-1	74.48	9.05	20	93.1	66.5	2

*Character states were assigned to the means of the bracteole width as follows: 40 to 60 microns, character state 1; 60 to 80 microns, character state 2; and 80 to 100 microns, character state 3.

TABLE XXXIX
DATA AND CHARACTER STATES FOR THE
BRACKET LENGTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	977.1	166.7	15	1290.0	691.6	2
369	806.0	108.4	15	984.2	665.0	2
X-029b	889.3	145.1	15	1130.0	651.7	2
406	(no bractlets)					1
X-103	(no bractlets)					1
415	(no bractlets)					1
X-008	(no bractlets)					1
X-027	(no bractlets)					1
X-039	(no bractlets)					1
X-041	(no bractlets)					1
X-064	(no bractlets)					1
X-076	(no bractlets)					1
X-251	(no bractlets)					1
X-351	(no bractlets)					1
X-115	(no bractlets)					1
X-180	(no bractlets)					1
H	(no bractlets)					1
W-1	(no bractlets)					1

*Character states were assigned to the means of the bractlet length as follows: no bractlets, character state 1; and 800 to 1000 microns, character state 2.

TABLE XL
DATA AND CHARACTER STATES FOR THE
BRACKET WIDTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	79.80	11.24	15	93.1	66.5	2
369	84.23	6.49	15	93.1	79.8	2
X-029b	88.67	8.21	15	106.4	79.8	2
406	(no bractlets)					1
X-103	(no bractlets)					1
415	(no bractlets)					1
X-008	(no bractlets)					1
X-027	(no bractlets)					1
X-039	(no bractlets)					1
X-041	(no bractlets)					1
X-064	(no bractlets)					1
X-076	(no bractlets)					1
X-251	(no bractlets)					1
X-351	(no bractlets)					1
X-115	(no bractlets)					1
X-180	(no bractlets)					1
H	(no bractlets)					1
W-1	(no bractlets)					1

*Character states were assigned to the means of the bracket width as follows: no bractlets, character state 1; and 80 to 100 microns, character state 2.

TABLE XLI
DATA AND CHARACTER STATES FOR THE
ANTERIOR BRACT CELL LENGTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	463.5	155.60	20	758.1	172.9	1
369	428.3	60.35	20	532.0	305.9	1
X-029b	648.4	116.20	20	851.2	385.7	2
406	508.7	150.30	20	811.3	239.4	1
X-103	910.4	165.50	20	1237.0	625.1	3
415	849.9	115.10	20	1024.0	611.8	3
X-008	733.5	83.48	20	864.5	571.9	2
X-027	588.5	217.90	20	1077.0	212.8	1
X-039	998.8	164.60	20	1370.0	758.1	3
X-041	838.6	116.30	20	1011.0	571.9	3
X-064	843.9	143.80	20	1144.0	625.1	3
X-076	886.4	98.99	20	1130.0	758.1	3
X-251	720.9	191.20	15	1144.0	425.6	2
X-351	690.3	93.34	20	824.6	518.7	2
X-115	899.7	166.50	20	1277.0	558.6	3
X-180	641.1	185.80	20	997.5	266.0	2
H	650.4	192.10	20	904.5	212.8	2
W-1	1125.0	151.70	20	1396.0	811.3	4

*Character states were assigned to the means of the anterior bract cell length as follows: 400 to 600 microns, character state 1; 600 to 800 microns, character state 2; 800 to 1000 microns, character state 3; and 1000 to 1200 microns, character state 4.

TABLE XLII
DATA AND CHARACTER STATES FOR THE
ANTERIOR BRACT CELL WIDTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	69.82	10.46	20	93.1	53.2	2
369	71.82	9.05	20	93.1	53.2	2
X-029b	93.10	8.63	20	106.4	79.8	3
406	69.82	8.49	20	79.8	53.2	2
X-103	69.82	7.32	20	93.1	66.5	2
415	56.52	5.91	20	66.5	53.2	1
X-008	62.51	7.60	20	79.8	53.2	2
X-027	70.49	6.25	20	79.8	66.5	2
X-039	71.82	6.69	20	79.8	66.5	2
X-041	64.50	7.81	20	79.8	53.2	2
X-064	85.12	13.92	20	119.7	66.5	3
X-076	67.16	9.13	20	93.1	53.2	2
X-251	75.37	6.49	15	79.8	66.5	2
X-351	57.85	11.64	20	79.8	39.9	1
X-115	67.83	5.95	20	79.8	53.2	2
X-180	61.84	9.91	20	79.8	53.2	2
H	60.51	8.04	20	79.8	53.2	2
W-1	69.16	5.46	20	79.8	66.5	2

*Character states were assigned to the means of the anterior bract cell width as follows: 40 to 60 microns, character state 1; 60 to 80 microns, character state 2; and 80 to 100 microns, character state 3.

TABLE XLIII
DATA AND CHARACTER STATES FOR THE
POSTERIOR BRACT CELL LENGTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	188.9	83.07	20	359.1	66.5	1
369	119.7	41.39	20	226.1	53.2	1
X-029b	154.9	34.59	20	226.1	93.1	1
406	150.3	65.60	20	385.7	79.8	1
X-103	198.8	145.30	20	665.0	106.4	1
415	269.3	129.10	20	625.1	106.4	2
X-008	319.9	63.78	20	452.2	239.4	2
X-027	250.0	85.93	20	412.3	146.3	2
X-039	391.0	99.47	20	571.9	239.4	2
X-041	266.7	70.44	20	425.6	186.2	2
X-064	243.4	65.03	20	399.0	146.3	2
X-076	217.5	70.68	20	465.5	93.1	2
X-251	416.3	110.30	20	784.7	266.0	3
X-351	250.7	99.08	20	492.1	119.7	2
X-115	405.0	104.90	20	651.7	279.3	3
X-180	331.8	118.40	20	545.3	159.6	2
H	245.4	110.10	20	478.8	119.7	2
W-1	446.2	138.70	20	811.3	279.3	3

*Character states were assigned to the means of the posterior bract cell length as follows: 0 to 200 microns, character state 1; 200 to 400 microns, character state 2; and 400 to 600 microns, character state 3.

TABLE XLIV
DATA AND CHARACTER STATES FOR THE
POSTERIOR BRACT CELL WIDTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	67.16	5.24	20	79.8	53.2	2
369	51.87	10.48	20	79.8	39.9	1
X-029b	67.83	9.55	20	79.8	53.2	2
406	57.85	10.81	20	79.8	39.9	1
X-103	64.50	10.81	20	79.8	39.9	2
415	47.88	6.69	20	53.2	39.9	1
X-008	57.85	6.51	20	66.5	53.2	1
X-027	58.52	9.05	20	66.5	39.9	1
X-039	61.18	9.05	20	66.5	39.9	2
X-041	49.21	9.75	20	66.5	39.9	1
X-064	58.52	9.05	20	79.8	53.2	1
X-076	46.55	10.12	20	66.5	39.9	1
X-251	61.84	10.81	20	79.8	39.9	2
X-351	47.88	6.69	20	53.2	39.9	1
X-115	54.53	8.52	20	66.5	39.9	1
X-180	54.53	8.52	20	66.5	39.9	1
H	58.52	9.05	20	66.5	39.9	1
W-1	59.85	9.15	20	79.8	39.9	1

*Character states were assigned to the means of the posterior bract cell width as follows: 40 to 60 microns, character state 1; and 60 to 80 microns, character state 2.

TABLE XLV
DATA AND CHARACTER STATES FOR THE
OOGONIUM LENGTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	722.2	60.73	20	864.5	625.1	2
369	836.6	45.85	20	917.7	758.1	3
X-029b	753.4	41.23	20	824.6	691.6	2
406	752.1	63.34	20	891.1	665.0	2
X-103	859.8	55.14	20	931.0	758.1	3
415	627.8	54.68	20	718.2	532.0	1
X-008	716.2	81.68	20	824.6	598.5	2
X-027	756.8	73.85	20	931.0	665.0	2
X-039	730.2	52.48	20	824.6	611.8	2
X-041	649.0	63.07	20	771.4	545.3	1
X-064	641.7	54.90	20	758.1	518.7	1
X-076	677.0	90.50	20	824.6	532.0	1
X-251	779.4	38.87	15	851.2	704.9	2
X-351	617.1	63.33	20	731.5	532.0	1
X-115	726.8	83.03	20	864.5	571.9	2
X-180	758.1	53.20	20	891.1	651.7	2
H	609.8	65.48	20	731.5	518.7	1
W-1	904.4	84.69	12	1024.0	798.0	4

*Character states were assigned to the means of the oogonium length as follows: 600 to 700 microns, character state 1; 700 to 800 microns, character state 2; 800 to 900 microns, character state 3; and 900 to 1000 microns, character state 4.

TABLE XLVI
DATA AND CHARACTER STATES FOR THE
OOGONIUM WIDTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	512.7	25.34	20	545.3	425.6	2
369	595.8	18.10	20	625.1	571.9	2
X-029b	606.5	33.54	20	665.0	532.0	3
406	557.9	48.53	20	638.4	465.5	2
X-103	615.1	42.47	20	678.3	532.0	3
415	403.0	26.98	20	438.9	345.8	1
X-008	436.9	32.37	20	492.1	385.7	1
X-027	525.3	34.11	20	558.6	438.9	2
X-039	440.9	43.21	20	532.0	385.7	1
X-041	417.6	38.93	20	478.8	345.8	1
X-064	468.8	13.56	20	505.4	452.2	1
X-076	460.2	42.37	20	505.4	345.8	1
X-251	541.8	13.74	15	571.9	518.7	2
X-351	450.9	31.38	20	492.1	359.1	1
X-115	470.2	28.39	20	532.0	412.3	1
X-180	548.0	33.03	20	611.8	478.8	2
H	468.2	48.93	20	532.0	332.5	1
W-1	569.7	14.82	12	598.5	532.0	2

*Character states were assigned to the means of the oogonium width as follows: 400 to 500 microns, character state 1; 500 to 600 microns, character state 2; and 600 to 700 microns, character state 3.

TABLE XLVII
DATA AND CHARACTER STATES FOR THE
CORONULA HEIGHT

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	130.3	30.39	20	186.2	79.8	3
369	165.6	14.62	20	199.5	146.3	4
X-029b	121.7	15.72	20	146.3	93.1	2
406	188.9	16.49	20	226.1	159.6	5
X-103	150.3	15.01	20	172.9	119.7	4
415	147.0	13.97	20	172.9	133.0	3
X-008	156.3	14.23	20	186.2	133.0	4
X-027	109.7	12.11	20	133.0	93.1	2
X-039	135.7	22.67	20	186.2	93.1	3
X-041	166.9	15.84	20	199.5	146.3	4
X-064	97.7	17.93	20	133.0	66.5	1
X-076	109.1	11.09	20	133.0	93.1	2
X-251	190.6	22.85	15	226.1	146.3	5
X-351	150.3	17.31	20	172.9	106.4	4
X-115	112.4	16.97	20	133.0	93.1	2
X-180	119.0	10.98	20	133.0	83.1	2
H	135.0	12.41	20	159.6	119.7	3
W-1	156.9	21.83	20	199.5	133.0	4

*Character states were assigned to the means of the coronula height as follows: 75 to 100 microns, character state 1; 100 to 125 microns, character state 2; 125 to 150 microns, character state 3; 150 to 175 microns, character state 4; and 175 to 200 microns, character state 5.

TABLE XLVIII
DATA AND CHARACTER STATES FOR THE
CORONULA WIDTH, AT BASE

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	181.5	11.64	20	199.5	159.6	2
369	232.1	9.13	20	239.4	212.8	4
X-029b	237.4	19.43	20	266.0	186.2	4
406	230.1	12.28	20	266.0	212.8	4
X-103	237.4	12.41	20	252.7	212.8	4
415	185.5	10.10	20	199.5	172.9	2
X-008	194.2	9.05	20	212.8	172.9	2
X-027	178.2	14.57	20	212.8	159.6	2
X-039	184.2	19.90	20	212.8	159.6	2
X-041	197.5	9.91	20	212.8	186.2	2
X-064	174.9	8.92	20	186.2	159.6	1
X-076	176.2	8.49	20	186.2	159.6	2
X-251	205.7	13.17	15	226.1	186.2	3
X-351	188.2	6.51	20	199.5	172.9	2
X-115	172.9	14.31	20	199.5	146.3	1
X-180	200.2	10.98	20	212.8	172.9	3
H	198.2	8.52	20	212.8	186.2	2
W-1	208.8	10.66	20	226.1	199.5	3

*Character states were assigned to the means of the coronula width as follows: 150 to 175 microns, character state 1; 175 to 200 microns, character state 2; 200 to 225 microns, character state 3; and 225 to 250 microns, character state 4.

TABLE XLIX
DATA AND CHARACTER STATES FOR THE
ANTHERIDIUM DIAMETER

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	883.1	63.92	20	997.5	811.3	7
369	411.0	15.50	20	438.9	372.4	3
X-029b	451.5	44.94	20	571.9	385.7	3
406	418.9	20.01	20	465.5	372.4	3
X-103	466.8	21.10	20	505.4	425.6	3
415	273.3	15.24	20	292.6	252.7	1
X-008	370.4	17.94	20	412.3	332.5	2
X-027	371.7	13.28	20	399.0	345.8	2
X-039	388.4	20.05	20	452.2	359.1	2
X-041	301.9	18.36	20	345.8	279.3	2
X-064	327.2	15.80	20	359.1	305.9	2
X-076	327.2	25.31	20	385.7	279.3	2
X-251	419.4	26.54	15	465.5	385.7	3
X-351	313.9	21.32	20	359.1	279.3	2
X-115	351.1	30.02	20	425.6	292.6	2
X-180	413.0	19.04	20	452.2	372.4	3
H	324.5	23.40	20	359.1	266.0	2
W-1	367.1	19.01	20	399.0	332.5	2

*Character states were assigned to the means of the antheridium diameter as follows: 200 to 300 microns, character state 1; 300 to 400 microns, character state 2; 400 to 500 microns, character state 3; 500 to 600 microns, character state 4; 600 to 700 microns, character state 5; 700 to 800 microns, character state 6; and 800 to 900 microns, character state 7.

TABLE L
DATA AND CHARACTER STATES FOR THE
DIAMOND SHIELD CELL LENGTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	(no diamond shield cells)					1
369	(no diamond shield cells)					1
X-029b	(no diamond shield cells)					1
406	(no diamond shield cells)					1
X-103	(no diamond shield cells)					1
415	331.2	26.21	20	372.4	279.3	2
X-008	454.2	41.45	20	505.4	385.7	5
X-027	466.2	36.48	20	545.3	412.3	5
X-039	488.1	38.38	20	545.3	412.3	5
X-041	393.7	31.83	20	425.6	332.5	3
X-064	425.6	37.62	20	492.1	332.5	4
X-076	429.6	29.93	20	478.8	385.7	4
X-251	486.8	42.89	15	545.3	425.6	5
X-351	409.0	50.85	20	532.0	305.9	4
X-115	470.8	47.37	15	532.0	385.7	5
X-180	464.2	39.52	20	505.4	332.5	5
H	369.7	36.99	10	412.3	305.9	3
W-1	430.3	23.74	20	465.5	372.4	4

*Character states were assigned to the means of the diamond shield cell length as follows: no diamond shield cells, character state 1; 300 to 350 microns, character state 2; 350 to 400 microns, character state 3; 400 to 450 microns, character state 4; and 450 to 500 microns, character state 5.

TABLE LI
DATA AND CHARACTER STATES FOR THE
DIAMOND SHIELD CELL WIDTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	(no diamond shield cells)					1
369	(no diamond shield cells)					1
X-029b	(no diamond shield cells)					1
406	(no diamond shield cells)					1
X-103	(no diamond shield cells)					1
415	205.5	18.04	20	239.4	172.9	2
X-008	288.6	24.83	20	332.5	239.4	3
X-027	285.3	15.84	20	319.2	252.7	3
X-039	291.9	25.70	20	332.5	239.4	3
X-041	240.7	17.74	20	266.0	212.8	2
X-064	259.3	24.60	20	292.6	212.8	3
X-076	272.6	13.98	20	305.9	252.7	3
X-251	300.6	23.00	20	359.1	266.0	4
X-351	246.7	27.45	20	292.6	199.5	2
X-115	266.0	25.13	15	319.2	226.1	3
X-180	305.9	35.06	20	359.1	239.4	4
H	250.0	21.54	10	279.3	199.5	3
W-1	293.9	14.25	20	319.2	266.0	3

*Character states were assigned to the means of the diamond shield cell width as follows: no diamond shield cells, character state 1; 200 to 250 microns, character state 2; 250 to 300 microns, character state 3; and 300 to 350 microns, character state 4.

TABLE LII
DATA AND CHARACTER STATES FOR THE TRIANGULAR
SHIELD CELL BASAL LENGTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	616.5	46.93	20	758.1	558.6	8
369	327.8	22.95	20	359.1	279.3	2
X-029b	359.1	34.52	20	412.3	292.6	3
406	302.6	42.69	20	425.6	226.1	2
X-103	355.1	21.62	20	399.0	332.5	3
415	(no triangular shield cells)					1
X-008	(no triangular shield cells)					1
X-027	348.5	21.85	5	372.4	332.5	2
X-039	(no triangular shield cells)					1
X-041	(no triangular shield cells)					1
X-064	(no triangular shield cells)					1
X-076	(no triangular shield cells)					1
X-251	(no triangular shield cells)					1
X-351	(no triangular shield cells)					1
X-115	345.8	48.16	10	412.3	279.3	2
X-180	(no triangular shield cells)					1
H	(no triangular shield cells)					1
W-1	(no triangular shield cells)					1

*Character states were assigned to the means of the triangular shield cell basal length as follows: no triangular shield cells, character state 1; 300 to 350 microns, character state 2; 350 to 400 microns, character state 3; 400 to 450 microns, character state 4; 450 to 500 microns, character state 5; 500 to 550 microns, character state 6; 550 to 600 microns, character state 7; and 600 to 650 microns, character state 8.

TABLE LIII
DATA AND CHARACTER STATES FOR THE
TRIANGULAR SHIELD CELL HEIGHT

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	577.9	46.37	20	678.3	492.1	8
369	307.2	32.55	20	385.7	266.0	3
X-029b	321.9	37.52	20	412.3	266.0	3
406	260.7	26.74	20	305.9	212.8	2
X-103	320.5	29.55	20	359.1	239.4	3
415	(no triangular shield cells)					1
X-008	(no triangular shield cells)					1
X-027	388.4	25.58	5	425.6	359.1	4
X-039	(no triangular shield cells)					1
X-041	(no triangular shield cells)					1
X-064	(no triangular shield cells)					1
X-076	(no triangular shield cells)					1
X-251	(no triangular shield cells)					1
X-351	(no triangular shield cells)					1
X-115	292.6	35.47	10	345.8	239.4	2
X-180	(no triangular shield cells)					1
H	(no triangular shield cells)					1
W-1	(no triangular shield cells)					1

*Character states were assigned to the means of the triangular shield cell height as follows: no triangular shield cells, character state 1; 250 to 300 microns, character state 2; 300 to 350 microns, character state 3; 350 to 400 microns, character state 4; 400 to 450 microns, character state 5; 450 to 500 microns, character state 6; 500 to 550 microns, character state 7; and 550 to 600 microns, character state 8.

TABLE LIV
DATA AND CHARACTER STATES FOR THE
OOSPORE LENGTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	511.3	24.61	25	558.6	452.2	1
369	676.2	28.65	25	731.5	625.1	2
X-029b	652.2	24.43	25	691.6	611.8	2
406	650.6	74.84	25	771.4	558.6	2
X-103	684.7	27.72	25	718.2	585.2	2
415	559.7	20.65	25	585.2	505.4	1
X-008	625.1	31.43	25	691.6	558.6	2
X-027	667.7	27.42	25	704.9	625.1	2
X-039	651.7	39.53	25	718.2	571.9	2
X-041	578.8	23.70	25	625.1	518.7	1
X-064	528.3	25.33	25	571.9	478.8	1
X-076	591.6	38.42	25	665.0	518.7	1
X-251	641.7	23.19	20	691.6	611.8	2
X-351	577.2	29.24	25	611.8	532.0	1
X-115	616.1	34.28	25	678.3	532.0	2
X-180	711.8	33.93	25	771.4	638.4	3
H	(self-sterile)					
W-1	726.5	26.54	8	771.4	691.6	3

*Character states were assigned to the means of the oospore length as follows: 500 to 600 microns, character state 1; 600 to 700 microns, character state 2; and 700 to 800 microns, character state 3.

TABLE LV
DATA AND CHARACTER STATES FOR THE
OOSPORE WIDTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	338.4	14.41	25	359.1	305.9	2
369	432.5	19.62	25	465.5	399.0	3
X-029b	438.9	20.68	25	478.8	399.0	3
406	394.2	18.36	25	425.6	359.1	2
X-103	470.8	26.04	25	518.7	385.7	3
415	291.0	16.88	25	319.2	266.0	1
X-008	308.0	19.83	25	345.8	266.0	2
X-027	384.1	15.98	25	412.3	345.8	2
X-039	337.3	22.68	25	372.4	292.6	2
X-041	318.1	17.14	25	345.8	292.6	2
X-064	322.9	21.56	25	359.1	266.0	2
X-076	332.5	23.67	25	359.1	292.6	2
X-251	386.4	15.84	20	412.3	359.1	2
X-351	331.4	24.26	25	385.7	292.6	2
X-115	348.5	26.88	25	399.0	305.9	2
X-180	437.8	41.87	25	532.0	372.4	3
H	(self-sterile)					
W-1	442.2	13.77	8	465.5	425.6	3

*Character states were assigned to the means of the oospore width as follows: 200 to 300 microns, character state 1; 300 to 400 microns, character state 2; and 400 to 500 microns, character state 3.

TABLE LVI
DATA AND CHARACTER STATES FOR THE WIDTH OF AN
OOGONIUM CONVOLUTION

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	60.30	4.20	15	67.00	53.60	4
369	67.00	5.07	15	77.05	60.30	4
X-029b	67.00	4.90	15	77.05	60.30	4
406	57.62	5.10	15	63.65	46.90	3
X-103	60.30	6.07	15	73.70	53.60	4
415	39.98	4.82	15	50.25	33.50	1
X-008	53.82	4.82	15	63.65	43.55	3
X-027	59.18	5.89	15	67.00	46.90	3
X-039	53.82	3.22	15	60.30	46.90	3
X-041	45.34	5.20	15	56.95	36.85	2
X-064	37.74	4.47	15	46.90	33.50	1
X-076	53.15	8.58	15	67.00	40.20	3
X-251	56.95	3.53	10	60.30	50.25	3
X-351	50.25	4.20	15	56.95	43.55	3
X-115	57.84	5.14	15	63.65	46.90	3
X-180	53.82	4.29	15	63.65	46.90	3
H	44.00	3.07	15	46.90	40.20	2
W-1	48.46	3.98	15	56.95	43.55	2

*Character states were assigned to the means of the width of an oogonium convolution as follows: 30 to 40 microns, character state 1; 40 to 50 microns, character state 2; 50 to 60 microns, character state 3; and 60 to 70 microns, character state 4.

TABLE LVII
DATA AND CHARACTER STATES FOR THE
FOSSA WIDTH

Clone	Mean (Microns)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	52.04	3.32	15	60.30	46.90	2
369	70.35	8.40	15	90.45	63.65	4
X-029b	73.03	4.24	15	80.40	67.00	4
406	66.33	7.07	15	77.05	56.95	3
X-103	63.65	3.10	15	67.00	56.95	3
415	46.68	2.36	15	50.25	43.55	1
X-008	56.50	3.98	15	63.65	50.25	2
X-027	57.17	4.98	15	67.00	50.25	2
X-039	55.39	6.68	15	70.35	46.90	2
X-041	54.49	5.29	15	60.30	46.90	2
X-064	47.79	3.22	15	53.60	43.55	1
X-076	56.50	4.17	15	60.30	46.90	2
X-251	57.95	3.18	10	60.30	53.60	2
X-351	61.86	5.50	15	73.70	56.95	3
X-115	57.40	3.98	15	60.30	50.25	2
X-180	60.52	4.10	15	67.00	53.60	3
H	(self-sterile)					
W-1	(too few oospores for data)					

*Character states were assigned to the means of the fossa width as follows: 40 to 50 microns, character state 1; 50 to 60 microns, character state 2; 60 to 70 microns, character state 3; and 70 to 80 microns, character state 4.

TABLE LVIII
DATA AND CHARACTER STATES FOR THE
INTERNODE LENGTH

Clone	Mean (mm)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	19.60	5.19	10	28.0	12.0	1
369	11.20	1.09	10	13.0	9.0	1
X-029b	14.80	4.79	10	26.0	10.5	1
406	18.25	3.72	10	22.0	11.5	1
X-103	27.10	3.40	10	33.0	21.5	2
415	20.90	5.84	10	34.0	14.5	2
X-008	36.45	13.15	10	52.5	12.0	3
X-027	18.50	3.40	10	26.0	14.0	1
X-039	32.50	6.82	10	47.5	24.5	3
X-041	21.25	5.29	10	27.0	11.0	2
X-064	26.00	5.13	10	32.5	18.0	2
X-076	19.55	5.23	10	26.0	11.0	1
X-251	35.36	9.82	7	47.5	20.5	3
X-351	22.75	3.37	10	28.0	18.0	2
X-115	14.55	4.30	10	24.0	9.0	1
X-180	18.45	6.50	10	31.5	11.0	1
H	23.60	5.35	10	33.5	14.0	2
W-1	15.20	4.39	10	23.5	12.0	1

*Character states were assigned to the means of the internode length as follows: 10 to 20 millimeters, character state 1; 20 to 30 millimeters, character state 2; and 30 to 40 millimeters, character state 3.

TABLE LIX
DATA AND CHARACTER STATES FOR THE
BRANCHLET LENGTH

Clone	Mean (mm)	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	17.27	1.71	20	21.0	14.5	2
369	18.77	2.30	20	21.5	13.0	2
X-029b	11.15	2.52	20	16.5	8.5	2
406	12.10	1.21	20	14.5	10.0	2
X-103	15.25	3.78	20	23.0	10.0	2
415	11.27	3.05	20	16.0	7.0	2
X-008	21.67	8.80	20	40.0	9.0	3
X-027	7.28	1.74	20	11.0	4.5	1
X-039	14.37	3.79	20	19.5	9.0	2
X-041	11.50	3.66	20	17.5	4.5	2
X-064	14.20	5.23	20	26.0	7.5	2
X-076	10.15	2.21	20	15.0	6.5	2
X-251	28.46	5.84	14	35.0	16.0	3
X-351	11.55	2.23	20	17.5	8.5	2
X-115	11.97	1.97	20	16.5	9.0	2
X-180	12.90	2.75	20	17.0	8.0	2
H	9.33	2.31	20	13.5	5.5	1
W-1	15.85	4.97	20	23.5	10.0	2

*Character states were assigned to the means of the branchlet length as follows: 0 to 10 millimeters, character state 1; 10 to 20 millimeters, character state 2; and 20 to 30 millimeters, character state 3.

TABLE LX
DATA AND CHARACTER STATES FOR THE RATIO OF THE
SPINE CELL LENGTH TO THE SPINE CELL WIDTH

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	6.35	1.96	41	11.50	2.50	3
369	2.41	1.54	42	6.80	0.75	1
X-029b	2.16	1.08	29	4.83	1.00	1
406	5.64	2.03	44	10.50	1.75	2
X-103	4.39	1.26	57	7.00	1.50	2
415	4.52	1.99	32	9.75	1.75	2
X-008	6.13	2.71	47	13.80	2.33	3
X-027	5.62	2.05	41	10.00	2.25	2
X-039	8.06	4.75	58	19.50	1.75	4
X-041	7.37	2.24	43	11.75	3.00	3
X-064	6.49	2.13	46	11.17	2.20	3
X-076	3.19	0.87	41	5.33	1.67	1
X-251	5.84	1.83	39	9.20	2.20	2
X-351	3.67	1.21	40	7.00	1.67	1
X-115	4.03	2.82	37	11.57	1.25	2
X-180	4.28	2.21	44	10.75	1.33	2
H	3.44	0.92	44	5.00	1.75	1
W-1	9.23	3.63	54	17.50	2.67	4

*Character states were assigned to the means of the ratio of the spine cell length to the spine cell width as follows: 2 to 4, character state 1; 4 to 6, character state 2; 6 to 8, character state 3; and 8 to 10, character state 4.

TABLE LXI
DATA AND CHARACTER STATES FOR THE RATIO OF THE UPPER
STIPULODE LENGTH TO THE UPPER STIPULODE WIDTH

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	8.82	0.96	20	11.00	7.13	2
369	9.51	0.99	20	11.00	7.57	2
X-029b	8.46	2.18	20	11.86	4.73	2
406	7.46	1.26	20	9.29	5.25	1
X-103	10.23	1.35	20	12.33	7.67	3
415	8.93	1.31	20	11.29	6.14	2
X-008	7.66	1.41	20	11.00	5.63	1
X-027	8.41	1.35	20	11.40	5.71	2
X-039	8.88	1.23	20	11.00	6.22	2
X-041	9.80	1.12	20	11.80	7.40	2
X-064	11.84	1.81	20	15.43	9.57	3
X-076	6.47	0.68	20	7.80	5.33	1
X-251	10.13	1.56	9	12.00	7.88	3
X-351	11.21	2.55	20	17.50	7.14	3
X-115	8.28	1.10	20	11.33	7.00	2
X-180	6.50	0.86	20	7.86	5.14	1
H	8.67	1.09	20	10.83	7.29	2
W-1	12.71	1.47	20	15.33	9.60	4

*Character states were assigned to the means of the ratio of the upper stipulode length to the upper stipulode width as follows: 6 to 8, character state 1; 8 to 10, character state 2; 10 to 12, character state 3; and 12 to 14, character state 4.

TABLE LXII

DATA AND CHARACTER STATES FOR THE RATIO OF THE LOWER
STIPULODE LENGTH TO THE LOWER STIPULODE WIDTH

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	4.90	0.79	20	6.29	3.33	2
369	4.41	0.73	20	6.50	3.43	2
X-029b	3.85	1.00	20	6.00	2.67	1
406	3.74	0.62	20	5.00	2.71	1
X-103	5.24	0.99	20	7.40	3.67	2
415	6.01	0.67	20	7.20	4.71	3
X-008	4.76	0.57	20	6.50	4.14	2
X-027	4.16	1.05	20	6.20	1.80	2
X-039	5.97	0.81	20	7.14	4.29	2
X-041	6.33	0.88	20	8.20	4.50	3
X-064	6.04	0.96	20	7.80	4.29	3
X-076	3.19	0.60	20	4.50	2.17	1
X-251	5.35	0.71	9	6.67	4.20	2
X-351	4.62	1.09	20	6.80	3.00	2
X-115	5.38	1.02	20	8.00	2.80	2
X-180	4.05	0.61	20	5.20	2.83	2
H	4.68	0.66	20	5.71	3.50	2
W-1	9.59	1.55	20	12.80	7.14	4

*Character states were assigned to the means of the ratio of the lower stipulode length to the lower stipulode width as follows: 2 to 4, character state 1; 4 to 6, character state 2; 6 to 8, character state 3; and 8 to 10, character state 4.

TABLE LXIII
DATA AND CHARACTER STATES FOR THE RATIO OF THE UPPER
STIPULODE LENGTH TO THE LOWER STIPULODE LENGTH

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	1.78	0.23	20	2.30	1.54	1
369	2.11	0.29	20	2.91	1.59	1
X-029b	2.34	0.52	20	3.32	1.56	1
406	2.25	0.40	20	2.83	1.55	1
X-103	2.05	0.35	20	2.92	1.49	1
415	1.74	0.30	20	2.55	1.34	1
X-008	1.75	0.33	20	2.48	1.31	1
X-027	2.71	0.82	20	5.44	1.90	2
X-039	1.71	0.25	20	2.33	1.26	1
X-041	1.82	0.26	20	2.56	1.54	1
X-064	2.18	0.21	20	2.63	1.87	1
X-076	2.42	0.51	20	3.73	1.78	1
X-251	1.61	0.15	9	1.82	1.40	1
X-351	2.55	0.37	20	3.13	2.03	2
X-115	1.89	0.38	20	3.00	1.38	1
X-180	1.95	0.39	20	2.67	1.31	1
H	2.11	0.36	20	2.79	1.35	1
W-1	1.50	0.20	20	1.77	1.01	1

*Character states were assigned to the means of the ratio of the upper stipulode length to the lower stipulode length as follows: 1.5 to 2.5, character state 1; and 2.5 to 3.5, character state 2.

TABLE LXIV
DATA AND CHARACTER STATES FOR THE RATIO OF THE BRANCHLET
LENGTH TO THE BRANCHLET DIAMETER

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	42.98	6.46	20	58.48	35.17	2
369	54.65	9.11	20	70.28	39.04	2
X-029b	30.08	8.58	20	50.13	21.30	1
406	34.92	4.51	20	46.14	28.52	1
X-103	42.06	10.54	20	61.76	26.85	2
415	50.37	13.95	20	75.19	33.42	2
X-008	74.73	28.86	20	136.70	32.69	3
X-027	37.44	10.63	20	59.08	21.15	2
X-039	50.31	11.22	20	64.94	32.22	2
X-041	43.24	12.58	20	62.66	16.92	2
X-064	52.15	15.51	20	82.71	35.24	2
X-076	46.31	12.71	20	70.49	30.96	2
X-251	87.87	21.07	14	109.60	38.81	4
X-351	45.67	11.42	20	77.40	31.95	2
X-115	54.04	12.18	20	82.71	37.59	2
X-180	46.29	9.74	20	63.91	28.64	2
H	44.88	11.30	20	67.67	25.85	2
W-1	64.01	22.79	20	101.70	37.59	3

*Character states were assigned to the means of the ratio of the branchlet length to the branchlet diameter as follows: 15 to 35, character state 1; 35 to 55, character state 2; 55 to 75, character state 3; and 75 to 95, character state 4.

TABLE LXV

DATA AND CHARACTER STATES FOR THE RATIO OF THE
INTERNODE LENGTH TO THE BRANCHLET LENGTH

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	1.14	0.31	20	1.65	0.65	2
369	0.60	0.09	20	0.85	0.50	1
X-029b	1.32	0.24	20	1.73	0.88	2
406	1.52	0.34	20	2.10	0.85	3
X-103	1.87	0.44	20	2.64	1.04	3
415	1.90	0.39	20	2.83	1.31	3
X-008	1.76	0.57	20	3.00	1.20	3
X-027	2.63	0.57	20	3.80	1.80	4
X-039	2.37	0.58	20	3.30	1.47	4
X-041	1.92	0.38	20	2.88	1.49	3
X-064	1.95	0.39	20	2.40	1.19	3
X-076	1.95	0.44	20	2.60	1.28	3
X-251	1.25	0.21	14	1.47	0.79	2
X-351	2.02	0.39	20	2.74	1.20	4
X-115	1.22	0.34	20	2.18	0.83	2
X-180	1.44	0.42	20	2.31	0.92	2
H	2.62	0.64	20	3.82	1.67	4
W-1	0.99	0.19	20	1.35	0.62	1

*Character states were assigned to the means of the ratio of the internode length to the branchlet length as follows: 0.5 to 1.0, character state 1; 1.0 to 1.5, character state 2; 1.5 to 2.0, character state 3; and 2.0 and above, character state 4.

TABLE LXVI
DATA AND CHARACTER STATES FOR THE RATIO OF THE
BASAL CELL LENGTH TO THE BASAL CELL WIDTH

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	3.09	0.50	15	3.88	2.06	2
369	1.87	0.15	15	2.13	1.65	1
X-029b	2.84	0.40	15	3.64	2.32	2
406	1.65	0.16	15	1.94	1.36	1
X-103	1.87	0.20	15	2.10	1.38	1
415	4.11	0.87	15	6.06	2.90	3
X-008	2.15	0.37	15	2.63	1.53	2
X-027	8.59	3.50	15	14.38	3.94	5
X-039	3.58	0.25	15	3.86	3.06	2
X-041	3.52	0.56	15	4.29	2.56	2
X-064	1.74	0.37	15	2.67	1.24	1
X-076	2.03	0.37	15	2.78	1.50	2
X-251	3.78	0.54	9	4.44	3.00	2
X-351	4.17	1.50	15	6.41	2.65	3
X-115	3.94	0.77	15	5.07	2.74	2
X-180	2.85	0.45	15	3.69	2.07	2
H	3.69	0.51	15	4.70	3.00	2
W-1	2.92	0.26	15	3.23	2.40	2

*Character states were assigned to the means of the ratio of the basal cell length to the basal cell width as follows: 0 to 2, character state 1; 2 to 4, character state 2; 4 to 6, character state 3; 6 to 8, character state 4; and 8 to 10, character state 5.

TABLE LXVII
DATA AND CHARACTER STATES FOR THE RATIO OF THE UPPER
STIPULODE LENGTH TO THE BASAL CELL LENGTH

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	1.22	0.22	15	1.71	0.86	2
369	1.23	0.18	15	1.63	1.02	2
X-029b	0.85	0.21	15	1.30	0.56	2
406	1.52	0.25	15	2.03	1.08	3
X-103	1.67	0.32	15	2.14	1.05	3
415	1.02	0.30	15	1.54	0.55	2
X-008	1.25	0.29	15	1.74	0.88	2
X-027	0.44	0.18	15	0.72	0.26	1
X-039	1.07	0.20	15	1.43	0.79	2
X-041	1.09	0.20	15	1.38	0.80	2
X-064	2.62	0.67	15	3.85	1.73	4
X-076	1.01	0.19	15	1.44	0.69	2
X-251	1.05	0.09	9	1.20	0.96	2
X-351	1.18	0.47	15	1.65	0.48	2
X-115	0.91	0.22	15	1.26	0.63	2
X-180	0.91	0.19	15	1.31	0.67	2
H	1.16	0.26	15	1.54	0.64	2
W-1	1.90	0.38	15	2.81	1.48	3

*Character states were assigned to the means of the ratio of the upper stipulode length to the basal cell length as follows: 0.0 to 0.5, character state 1; 0.5 to 1.5, character state 2; 1.5 to 2.5, character state 3; and 2.5 to 3.5, character state 4.

TABLE LXVIII

DATA AND CHARACTER STATES FOR THE RATIO OF THE TERMINAL
SEGMENT LENGTH TO THE TERMINAL SEGMENT WIDTH

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	4.63	1.24	15	8.17	3.22	2
369	3.18	0.79	15	5.40	2.14	1
X-029b	7.32	3.14	15	14.92	4.60	3
406	3.78	0.70	15	4.71	2.71	1
X-103	4.97	1.01	15	6.86	2.78	2
415	7.55	1.49	15	10.83	4.78	3
X-008	5.76	2.17	15	12.50	4.00	2
X-027	5.58	0.98	15	7.00	3.67	2
X-039	6.49	1.15	15	8.17	4.83	3
X-041	8.38	2.24	15	14.20	5.50	4
X-064	8.39	2.36	15	14.00	5.14	4
X-076	5.80	2.08	15	10.40	2.33	2
X-251	5.64	1.35	15	7.00	2.75	2
X-351	7.74	2.88	15	13.40	2.89	3
X-115	6.43	1.31	15	9.00	4.50	3
X-180	5.20	0.73	15	7.14	4.14	2
H	5.79	1.91	15	9.89	3.80	2
W-1	8.56	2.17	15	12.50	6.00	4

*Character states were assigned to the means of the ratio of the terminal segment length to the terminal segment width as follows: 2 to 4, character state 1; 4 to 6, character state 2; 6 to 8, character state 3; and 8 to 10, character state 4.

TABLE LXIX
DATA AND CHARACTER STATES FOR THE RATIO OF THE
BRACTEOLE LENGTH TO THE BRACTEOLE WIDTH

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	10.50	2.24	20	13.50	6.83	2
369	10.09	1.13	20	11.83	8.00	2
X-029b	9.33	1.97	20	13.17	5.86	2
406	8.00	1.38	20	10.29	5.00	1
X-103	14.26	1.58	20	17.17	11.57	3
415	20.14	2.59	20	24.75	14.83	5
X-008	14.44	1.99	20	18.00	11.50	3
X-027	12.56	2.59	20	16.80	6.83	3
X-039	16.58	2.10	20	21.40	13.17	4
X-041	18.93	2.51	20	26.00	15.50	5
X-064	11.25	1.77	20	15.00	8.17	2
X-076	16.98	2.19	20	22.25	12.75	4
X-251	12.28	0.89	15	13.57	10.57	3
X-351	14.05	2.37	20	18.75	10.33	3
X-115	15.48	2.05	20	19.60	12.17	4
X-180	16.63	2.48	20	20.60	13.40	4
H	17.45	2.41	20	23.00	13.50	4
W-1	20.38	4.07	20	27.80	10.86	5

*Character states were assigned to the means of the ratio of the bracteole length to the bracteole width as follows: 6 to 9, character state 1; 9 to 12, character state 2; 12 to 15, character state 3; 15 to 18, character state 4; and 18 to 21, character state 5.

TABLE LXX

DATA AND CHARACTER STATES FOR THE RATIO OF THE
BRACKET LENGTH TO THE BRACKET WIDTH

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	12.36	2.19	15	17.60	10.14	3
369	9.60	1.34	15	12.33	7.14	2
X-029b	10.16	2.18	15	14.17	7.00	2
406	(no bractlets)					1
X-103	(no bractlets)					1
415	(no bractlets)					1
X-008	(no bractlets)					1
X-027	(no bractlets)					1
X-039	(no bractlets)					1
X-041	(no bractlets)					1
X-064	(no bractlets)					1
X-076	(no bractlets)					1
X-251	(no bractlets)					1
X-351	(no bractlets)					1
X-115	(no bractlets)					1
X-180	(no bractlets)					1
H	(no bractlets)					1
W-1	(no bractlets)					1

*Character states were assigned to the means of the ratio of the bractlet length to the bractlet width as follows: no bractlets, character state 1; 9 to 12, character state 2; and 12 to 15, character state 3.

TABLE LXXI

DATA AND CHARACTER STATES FOR THE RATIO OF THE ANTERIOR BRACT
CELL LENGTH TO THE ANTERIOR BRACT CELL WIDTH

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	6.60	1.95	20	11.40	3.25	1
369	6.04	1.09	20	8.00	4.43	1
X-029b	7.01	1.34	20	9.14	4.14	1
406	7.38	2.39	20	12.20	3.60	1
X-103	13.03	1.89	20	17.20	9.40	3
415	15.15	2.42	20	19.25	11.50	4
X-008	11.85	1.58	20	14.50	9.00	2
X-027	8.25	2.59	20	13.50	3.20	1
X-039	13.93	1.90	20	17.17	9.50	3
X-041	13.09	1.88	20	16.75	9.50	3
X-064	10.03	1.62	20	13.60	7.00	2
X-076	13.36	2.03	20	19.00	11.40	3
X-251	9.54	2.26	15	14.33	6.40	2
X-351	12.19	1.92	20	15.50	8.00	3
X-115	13.35	2.71	20	19.20	8.40	3
X-180	10.51	3.05	20	16.25	4.00	2
H	10.76	3.09	20	15.50	4.00	2
W-1	16.40	2.68	20	21.00	10.17	4

*Character states were assigned to the means of the ratio of the anterior bract cell length to the anterior bract cell width as follows: 6 to 9, character state 1; 9 to 12, character state 2; 12 to 15, character state 3; and 15 to 18, character state 4.

TABLE LXXII

DATA AND CHARACTER STATES FOR THE RATIO OF THE ANTERIOR
BRACT CELL LENGTH TO THE BRANCHLET DIAMETER

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	1.15	0.42	20	2.11	0.42	1
369	1.25	0.23	20	1.63	0.74	1
X-029b	1.73	0.30	20	2.18	1.00	2
406	1.47	0.47	20	2.65	0.72	1
X-103	2.53	0.60	20	4.04	1.68	3
415	3.80	0.61	20	5.07	2.71	4
X-008	2.55	0.29	20	2.95	1.87	3
X-027	3.01	1.11	20	5.40	1.00	3
X-039	3.57	0.78	20	5.42	2.48	4
X-041	3.17	0.45	20	3.89	2.15	3
X-064	3.17	0.52	20	4.10	2.13	3
X-076	4.01	0.61	20	5.67	3.25	4
X-251	2.21	0.64	15	3.58	1.29	2
X-351	2.70	0.30	20	3.12	2.17	3
X-115	4.03	0.74	20	5.05	2.21	4
X-180	2.29	0.66	20	3.95	1.00	2
H	3.12	0.91	20	4.33	1.00	3
W-1	4.52	0.82	20	5.88	3.21	5

*Character states were assigned to the means of the ratio of the anterior bract cell length to the branchlet diameter as follows: 0.5 to 1.5, character state 1; 1.5 to 2.5, character state 2; 2.5 to 3.5, character state 3; 3.5 to 4.5, character state 4; and 4.5 to 5.5, character state 5.

TABLE LXXIII

DATA AND CHARACTER STATES FOR THE RATIO OF THE BRACTEOLE
LENGTH TO THE ANTERIOR BRACT CELL LENGTH

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	2.01	0.70	20	4.15	1.71	2
369	1.99	0.33	20	2.78	1.33	2
X-029b	1.30	0.35	20	2.23	0.76	1
406	1.49	0.65	20	3.39	0.76	1
X-103	1.39	0.26	20	2.11	1.02	1
415	1.39	0.21	20	1.85	1.14	1
X-008	1.32	0.23	20	1.95	1.02	1
X-027	1.82	0.89	20	5.19	0.87	2
X-039	1.24	0.18	20	1.57	0.83	1
X-041	1.36	0.22	20	1.91	0.91	1
X-064	1.11	0.23	20	1.62	0.69	1
X-076	1.16	0.21	20	1.53	0.68	1
X-251	1.70	0.37	15	2.59	1.11	2
X-351	1.32	0.20	20	1.71	1.03	1
X-115	1.27	0.23	20	1.74	0.93	1
X-180	1.97	0.99	20	5.15	0.79	2
H	1.72	0.72	20	4.25	1.13	2
W-1	1.36	0.29	20	1.99	0.83	1

*Character states were assigned to the means of the ratio of the bracteole length to the anterior bract cell length as follows: 0.5 to 1.5, character state 1; and 1.5 to 2.5, character state 2.

TABLE LXXIV

DATA AND CHARACTER STATES FOR THE RATIO OF THE BRACKET
LENGTH TO THE ANTERIOR BRACKET CELL LENGTH

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	2.25	0.77	15	3.83	1.04	2
369	1.94	0.36	15	2.52	1.47	2
X-029b	1.45	0.24	15	1.89	1.04	2
406	(no bractlets)					1
X-103	(no bractlets)					1
415	(no bractlets)					1
X-008	(no bractlets)					1
X-027	(no bractlets)					1
X-039	(no bractlets)					1
X-041	(no bractlets)					1
X-064	(no bractlets)					1
X-076	(no bractlets)					1
X-251	(no bractlets)					1
X-351	(no bractlets)					1
X-115	(no bractlets)					1
X-180	(no bractlets)					1
H	(no bractlets)					1
W-1	(no bractlets)					1

*Character states were assigned to the means of the ratio of the bracket length to the anterior bracket cell length as follows: no bractlets, character state 1; and 1.5 to 2.5, character state 2.

TABLE LXXV

DATA AND CHARACTER STATES FOR THE RATIO OF THE POSTERIOR
BRACT CELL LENGTH TO THE POSTERIOR BRACT CELL WIDTH

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	2.82	1.26	20	5.40	1.00	1
369	2.28	0.55	20	3.40	1.25	1
X-029b	2.33	0.63	20	4.00	1.40	1
406	2.59	0.91	20	5.80	1.80	1
X-103	3.16	2.26	20	10.00	1.50	1
415	5.75	3.08	20	15.67	2.50	2
X-008	5.60	1.32	20	8.50	3.60	2
X-027	4.23	1.11	20	6.20	2.40	2
X-039	6.40	1.31	20	8.60	4.00	3
X-041	5.53	1.49	20	9.33	3.40	2
X-064	4.15	0.85	20	5.50	2.75	2
X-076	4.88	2.03	20	11.67	2.33	2
X-251	6.78	1.54	20	11.80	4.67	3
X-351	5.24	1.78	20	9.25	2.25	2
X-115	7.44	1.49	20	10.25	4.40	3
X-180	6.07	1.93	20	10.25	3.00	3
H	4.15	1.58	20	7.20	1.80	2
W-1	7.45	1.95	20	12.20	5.00	3

*Character states were assigned to the means of the ratio of the posterior bract cell length to the posterior bract cell width as follows: 2 to 4, character state 1; 4 to 6, character state 2; and 6 to 8, character state 3.

TABLE LXXVI

DATA AND CHARACTER STATES FOR THE RATIO OF THE ANTERIOR
BRACT CELL LENGTH TO THE POSTERIOR BRACT CELL LENGTH

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	3.05	1.72	20	6.50	0.65	2
369	4.11	1.91	20	9.00	1.88	3
X-029b	4.40	1.32	20	7.71	2.53	3
406	3.71	1.55	20	8.83	1.52	3
X-103	5.82	2.12	20	9.30	1.28	5
415	3.81	1.74	20	8.75	1.28	3
X-008	2.35	0.36	20	3.10	1.71	1
X-027	2.56	1.16	20	5.58	1.17	2
X-039	2.77	1.09	20	5.72	1.64	2
X-041	3.35	0.94	20	5.07	1.50	2
X-064	3.66	1.07	20	6.73	2.46	3
X-076	4.49	1.75	20	10.57	1.66	3
X-251	1.76	0.35	15	2.42	1.17	1
X-351	3.12	1.24	20	6.89	1.60	2
X-115	2.34	0.70	20	4.00	1.43	1
X-180	2.27	1.22	20	4.69	0.61	1
H	3.05	1.46	20	6.00	1.07	2
W-1	2.75	0.88	20	4.24	1.27	2

*Character states were assigned to the means of the ratio of the anterior bract cell length to the posterior bract cell length as follows: 1.5 to 2.5, character state 1; 2.5 to 3.5, character state 2; 3.5 to 4.5, character state 3; 4.5 to 5.5, character state 4; and 5.5 to 6.5, character state 5.

TABLE LXXVII
DATA AND CHARACTER STATES FOR THE RATIO OF THE
OOGONIUM LENGTH TO THE OOGONIUM WIDTH

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	1.41	0.13	20	1.67	1.25	2
369	1.41	0.08	20	1.61	1.27	2
X-029b	1.24	0.06	20	1.37	1.13	1
406	1.36	0.16	20	1.72	1.16	1
X-103	1.40	0.09	20	1.56	1.26	2
415	1.56	0.10	20	1.74	1.38	2
X-008	1.64	0.16	20	1.93	1.28	3
X-027	1.44	0.15	20	1.71	1.24	2
X-039	1.66	0.12	20	1.97	1.42	3
X-041	1.56	0.11	20	1.72	1.32	2
X-064	1.37	0.10	20	1.58	1.15	1
X-076	1.47	0.17	20	1.79	1.16	2
X-251	1.44	0.08	15	1.56	1.33	2
X-351	1.37	0.10	20	1.59	1.17	1
X-115	1.55	0.21	20	1.91	1.18	2
X-180	1.39	0.09	20	1.56	1.26	1
H	1.31	0.13	20	1.68	1.05	1
W-1	1.59	0.14	12	1.79	1.40	2

*Character states were assigned to the means of the ratio of the oogonium length to the oogonium width as follows: 1.2 to 1.4, character state 1; 1.4 to 1.6, character state 2; and 1.6 to 1.8, character state 3.

TABLE LXXVIII

DATA AND CHARACTER STATES FOR THE RATIO OF THE
BRACTEOLE LENGTH TO THE OOGONIUM LENGTH

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	1.20	0.32	20	1.72	0.67	1
369	1.00	0.12	20	1.25	0.72	1
X-029b	1.09	0.20	20	1.52	0.73	1
406	0.94	0.25	20	1.25	0.37	1
X-103	1.44	0.19	20	1.75	1.16	1
415	1.87	0.24	20	2.40	1.39	2
X-008	1.35	0.23	20	1.87	0.98	1
X-027	1.25	0.24	20	1.75	0.72	1
X-039	1.67	0.22	20	2.10	1.39	2
X-041	1.75	0.25	20	2.14	1.07	2
X-064	1.44	0.25	20	1.97	1.06	1
X-076	1.51	0.24	20	2.02	1.06	2
X-251	1.50	0.19	15	1.77	1.16	2
X-351	1.47	0.20	20	1.82	1.10	1
X-115	1.56	0.32	20	2.23	1.20	2
X-180	1.46	0.24	20	1.82	1.05	1
H	1.65	0.19	20	2.08	1.23	2
W-1	1.64	0.38	12	2.13	1.01	2

*Character states were assigned to the means of the ratio of the bracteole length to the oogonium length as follows: 0.5 to 1.5, character state 1; and 1.5 to 2.5, character state 2.

TABLE LXXIX
DATA AND CHARACTER STATES FOR THE RATIO OF THE
BRACKET LENGTH TO THE OOGONIUM LENGTH

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	1.39	0.32	15	2.06	0.80	2
369	0.96	0.13	15	1.17	0.72	2
X-029b	1.18	0.23	15	1.57	0.86	2
406	(no bractlets)					1
X-103	(no bractlets)					1
415	(no bractlets)					1
X-008	(no bractlets)					1
X-027	(no bractlets)					1
X-039	(no bractlets)					1
X-041	(no bractlets)					1
X-064	(no bractlets)					1
X-076	(no bractlets)					1
X-251	(no bractlets)					1
X-351	(no bractlets)					1
X-115	(no bractlets)					1
X-180	(no bractlets)					1
H	(no bractlets)					1
W-1	(no bractlets)					1

*Character states were assigned to the means of the ratio of the bractlet length to the oogonium length as follows: no bractlets, character state 1; and 0.5 to 1.5, character state 2.

TABLE LXXX

DATA AND CHARACTER STATES FOR THE RATIO OF THE ANTERIOR
BRACT CELL LENGTH TO THE OOGONIUM LENGTH

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	0.65	0.23	20	1.16	0.25	1
369	0.51	0.08	20	0.63	0.37	1
X-029b	0.86	0.17	20	1.17	0.51	1
406	0.68	0.21	20	1.06	0.33	1
X-103	1.07	0.25	20	1.53	0.71	2
415	1.37	0.25	20	1.75	1.00	2
X-008	1.04	0.16	20	1.38	0.73	2
X-027	0.78	0.27	20	1.43	0.27	1
X-039	1.36	0.17	20	1.73	1.07	2
X-041	1.30	0.18	20	1.55	1.00	2
X-064	1.33	0.27	20	1.83	0.96	2
X-076	1.33	0.23	20	1.77	1.00	2
X-251	0.93	0.27	15	1.54	0.54	1
X-351	1.12	0.13	20	1.37	0.87	2
X-115	1.25	0.27	20	1.85	0.72	2
X-180	0.85	0.25	20	1.34	0.35	1
H	1.06	0.29	20	1.48	0.41	2
W-1	1.23	0.26	12	1.67	0.85	2

*Character states were assigned to the means of the ratio of the anterior bract cell length to the oogonium length as follows: 0.5 to 1.0, character state 1; and 1.0 to 1.5, character state 2.

TABLE LXXXI

DATA AND CHARACTER STATES FOR THE RATIO OF THE
CORONULA HEIGHT TO THE CORONULA WIDTH

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	0.71	0.14	20	1.00	0.50	2
369	0.71	0.07	20	0.94	0.61	2
X-029b	0.52	0.08	20	0.69	0.39	1
406	0.82	0.08	20	0.94	0.65	3
X-103	0.63	0.06	20	0.76	0.56	2
415	0.79	0.08	20	0.93	0.67	2
X-008	0.81	0.07	20	0.93	0.67	3
X-027	0.62	0.05	20	0.75	0.54	2
X-039	0.74	0.10	20	1.00	0.58	2
X-041	0.85	0.08	20	1.00	0.73	3
X-064	0.56	0.12	20	0.83	0.36	1
X-076	0.62	0.05	20	0.71	0.54	2
X-251	0.93	0.14	15	1.14	0.69	3
X-351	0.80	0.10	20	1.00	0.57	3
X-115	0.65	0.07	20	0.77	0.54	2
X-180	0.60	0.06	20	0.67	0.44	2
H	0.68	0.06	20	0.79	0.60	2
W-1	0.76	0.13	20	1.00	0.59	2

*Character states were assigned to the means of the ratio of the coronula height to the coronula width as follows: 0.4 to 0.6, character state 1; 0.6 to 0.8, character state 2; and 0.8 to 1.0, character state 3.

TABLE LXXXII

DATA AND CHARACTER STATES FOR THE RATIO OF THE DIAMOND
SHIELD CELL LENGTH TO THE DIAMOND SHIELD CELL WIDTH

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	(no diamond shield cells)					1
369	(no diamond shield cells)					1
X-029b	(no diamond shield cells)					1
406	(no diamond shield cells)					1
X-103	(no diamond shield cells)					1
415	1.62	0.12	20	1.79	1.39	3
X-008	1.58	0.16	20	2.06	1.36	2
X-027	1.64	0.13	20	1.95	1.41	3
X-039	1.68	0.20	20	2.06	1.39	3
X-041	1.64	0.12	20	1.88	1.45	3
X-064	1.65	0.13	20	1.95	1.41	3
X-076	1.58	0.10	20	1.75	1.43	2
X-251	1.61	0.17	15	1.86	1.33	3
X-351	1.67	0.20	20	2.07	1.28	3
X-115	1.77	0.14	15	2.00	1.45	3
X-180	1.53	0.16	20	1.90	1.36	2
H	1.48	0.12	10	1.63	1.30	2
W-1	1.47	0.11	20	1.75	1.27	2

*Character states were assigned to the means of the ratio of the diamond shield cell length to the diamond shield cell width as follows: no diamond shield cells, character state 1; 1.4 to 1.6, character state 2; and 1.6 to 1.8, character state 3.

TABLE LXXXIII

DATA AND CHARACTER STATES FOR THE RATIO OF THE
TRIANGULAR SHIELD CELL BASAL LENGTH TO THE
TRIANGULAR SHIELD CELL HEIGHT

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	1.07	0.08	20	1.24	0.93	3
369	1.08	0.13	20	1.30	0.81	3
X-029b	1.13	0.13	20	1.48	1.00	3
406	1.17	0.20	20	1.78	0.96	3
X-103	1.12	0.13	20	1.44	0.93	3
415	(no triangular shield cells)					1
X-008	(no triangular shield cells)					1
X-027	0.90	0.09	5	1.00	0.78	2
X-039	(no triangular shield cells)					1
X-041	(no triangular shield cells)					1
X-064	(no triangular shield cells)					1
X-076	(no triangular shield cells)					1
X-251	(no triangular shield cells)					1
X-351	(no triangular shield cells)					1
X-115	1.18	0.09	10	1.30	1.05	3
X-180	(no triangular shield cells)					1
H	(no triangular shield cells)					1
W-1	(no triangular shield cells)					1

*Character states were assigned to the means of the ratio of the triangular shield cell basal length to the triangular shield cell height as follows: no triangular shield cells, character state 1; 0.8 to 1.0, character state 2; and 1.0 to 1.2, character state 3.

TABLE LXXXIV
DATA AND CHARACTER STATES FOR THE RATIO OF THE
OOSPORE LENGTH TO THE OOSPORE WIDTH

Clone	Mean	Standard Deviation	Number	Maximum Value	Minimum Value	Character State*
X-066	1.51	0.07	25	1.71	1.37	1
369	1.57	0.08	25	1.77	1.41	1
X-029b	1.49	0.07	25	1.60	1.31	1
406	1.65	0.19	25	1.97	1.39	2
X-103	1.46	0.05	25	1.52	1.35	1
415	1.93	0.10	25	2.15	1.75	3
X-008	2.04	0.13	25	2.30	1.80	4
X-027	1.74	0.11	25	2.04	1.57	2
X-039	1.94	0.15	25	2.23	1.70	3
X-041	1.82	0.10	25	2.09	1.69	3
X-064	1.64	0.08	25	1.85	1.50	2
X-076	1.78	0.10	25	2.00	1.59	2
X-251	1.66	0.07	20	1.78	1.55	2
X-351	1.75	0.14	25	2.05	1.43	2
X-115	1.78	0.13	25	2.00	1.50	2
X-180	1.64	0.13	25	1.96	1.45	2
H	(self-sterile)					
W-1	1.64	0.07	8	1.73	1.51	2

*Character states were assigned to the means of the ratio of the oospore length to the oospore width as follows: 1.4 to 1.6, character state 1; 1.6 to 1.8, character state 2; 1.8 to 2.0, character state 3; and 2.0 to 2.2, character state 4.

VITA

Robert Frank McGuire was born October 8, 1937, in Greeneville, Tennessee, as the second son of Mr. and Mrs. D. S. McGuire. He received his elementary and secondary education in the Greene County School System. He received his Bachelor of Arts degree from Union College, Barbourville, Kentucky, with majors in biology and mathematics in 1960. He received the Master of Science degree from The University of Tennessee in 1964 with a major in botany and a minor in mathematics.

He was married to the former Gertrude Mynear of Carlisle, Kentucky, on June 16, 1962.

His professional experience includes teacher of secondary mathematics in the Fort Knox Dependent School System, Fort Knox, Kentucky, instructor of science and mathematics at Eastern Kentucky University, Richmond, and graduate teaching assistant in botany at The University of Tennessee, Knoxville.

Professional and honorary organizations in which he holds membership include Iota Sigma Nu, Sigma Xi, The University of Tennessee Arboretum Society, and the American Institute of Biological Sciences. During the Summer of 1968, he received a National Science Foundation Summer Traineeship; and during the year of 1970, he received an NDEA fellowship.