DOCTORAL DISSERTATION

The Life Cycle of the Centric Diatom
Thalassiosira weissflogii:
Control of Gametogenesis and Cell Size

by
E. Virginia Armbrust

June 1990
The Life Cycle of the Centric Diatom
*Thalassiosira weissflogii:*
Control of Gametogenesis and Cell Size

by

E. Virginia Armbrust

Woods Hole Oceanographic Institution
Woods Hole, Massachusetts 02543

and

The Massachusetts Institute of Technology
Cambridge, Massachusetts 02139

June 1990

Doctoral Dissertation

Funding was provided by the Office of Naval Research and the National Science Foundation through the Massachusetts Institute of Technology.


Approved for publication; distribution unlimited.

Approved for Distribution:

Peter H. Wiebe, Chairman
Department of Biology

Craig E. Dorman
Acting Dean of Graduate Studies
The Life Cycle of the Centric Diatom *Thalassiosira weissflogii*: Control of Gametogenesis and Cell Size

by

ELIZABETH VIRGINIA ARMBRUST

A. B., Stanford University (1980)

Submitted in partial fulfillment of the requirement for the degree of

DOCTOR OF PHILOSOPHY

at the

MASSACHUSETTS INSTITUTE OF TECHNOLOGY

and the

WOODS HOLE OCEANOGRAPHIC INSTITUTION

January 1990

© Massachusetts Institute of Technology

Signature of Author

Joint Program in Oceanography, Massachusetts Institute of Technology/Woods Hole Oceanographic Institution

Certified by

Sallie W. Chisholm
Thesis Supervisor

Accepted by

John J. Stegeman, Chairman, Joint Committee for Biological Oceanography Massachusetts Institute of Technology Woods Hole Oceanographic Institution
List of Figures and Tables

Chapter 1.

Table 1. Summary of induction signals for centric diatoms ..... 35

Chapter 2.

Figures

1. Flow cytometric signature of T. weissflogil under three different light regimes .................................................. 52
2. Flow cytometric signature of an induced population and photo micrographs of the four stages in the formation of male gametes ................................................................. 54
3. Mitotic division and the formation of male gametes as a function of time ......................................................... 58
4. The influence of cell size on the induction of spermatogenesis ................................................................. 62
5. Induction of spermatogenesis as a function of the duration of the dark treatment ............................................. 64
6. Percentages of cells induced to undergo spermatogenesis as a function of time under a range of different light regimes 68
7. Maximum percentages populations induced to undergo spermatogenesis under a range of light regimes ................. 70
8. Distribution of chlorophyll fluorescence of a T. weissflogii population and the sorted samples .............................. 74
9. Percentage of G1 cells in sorted samples and the percentage of the population induced to undergo spermatogenesis ...... 76
10. Schematic of the relationship between the mitotic cycle and responsiveness to an induction signal ......................... 80

Chapter 3.

Figures

1. Cell lineages and initial Coulter volume distributions of T. weissflogii populations .................................................. 98
2. Cell lineages and initial Coulter volume distributions of populations derived from genetically identical cells 100
3. Mean Coulter volume over time of T. weissflogii populations 104
4. Mean Coulter volume over time of T. weissflogii populations 106
5. Mean Coulter volume over time of T. weissflogii populations 108
6. Mean Coulter volume over time of T. weissflogii populations 110
7. Mean Coulter volume and the coefficient of variation over time of a T. weissflogii population .............................. 118
8. Mean Coulter volume and distributions over time during an interval of decreasing cell size ............................. 120
9. Mean Coulter volume and distributions over time during intervals of increasing cell size ..................................... 122
10. Mean Coulter volume over time for populations derived from genetically identical cells ..................................... 124
11. Mean Coulter volume over time for populations derived from genetically identical cells ........................................... 126
12. Mean Coulter volume and population growth rate as a function of time ............................................................. 130

Tables
1. Summary of rates of decrease and increase in mean Coulter volume ........................................................................ 136
2. Summary of correlation coefficients between population doubling times and mean Coulter volume ........................... 138

Appendix.

Figures
1. Procaryotic model of chromosome replication and simulations of DNA distribution per cell ........................................ 147
2. Plot of population average DNA per cell in populations displaying continuous DNA synthesis ................................ 148
3. Representative DNA distributions ............................................................................................................................ 149
4. Duration of cell cycle stages versus doubling time of light limited populations .......................................................... 149
5. Behavior of population transferred to the dark from continuous light ...................................................................... 150
6. Cell division and DNA distributions of a population maintained on a 14:10 L:D cycle ................................................ 150
The predominant mode of reproduction in all unicellular algae is via asexual reproduction. In diatoms, the physical constraints of the cell wall, or frustule, during these mitotic divisions generally result in a decrease in the average cell size of a population over successive generations. The most common manner of breaking this trend of diminishing cell size is through sexual reproduction; meiosis replaces mitosis and the resulting male and female gametes fuse to create a zygote or auxospore which then develops outside the confines of the frustule and forms a post-auxospore cell many times larger than either parent. It is traditionally believed that these newly created large cells are unable to undergo sexual reproduction; theoretically, only cells at the lower end of the size spectrum possess this capability. However, most of the studies concerning diatom life cycles are descriptive and in reality very little is known about what determines if and when a cell will undergo gametogenesis and subsequent zygote formation. The motivation behind this research was a desire to understand more about this "decision making" process in centric diatoms.

Using flow cytometric techniques, I showed that the marine centric diatom, *Thalassiosira weissflogii*, can be induced to undergo spermatogenesis by exposing cells maintained at saturating intensities of continuous light to either dim light or darkness. From zero to over ninety percent of a population can differentiate into male gametes depending upon both the induction trigger and the population examined, regardless of cell size. Through the use of populations representing distinct cell cycle distributions, it was shown that responsiveness to an induction trigger is a function of cell cycle stage; cells in early G1 are not yet committed to complete the mitotic cycle and can be induced to form male gametes, whereas cells further along in their cell cycle are unresponsive to these same cues.

*T. weissflogii* can also undergo sexual reproduction under constant environmental conditions as often as every 120 generations. In the absence of any external induction signals, the ability of a cell to undergo gametogenesis and subsequent auxospore formation is linked with the attainment of an appropriate cell size. However, this permissive size range can vary between isolates and
within a given isolate over time. Moreover, the size of the post-auxospore cells created during these sexual events is also extremely variable; absolute cell size predicts very little about the future conduct of a cell. The unpredictable behavior of these cultures is hypothesized to result from the fact that the genetic composition of a diatom population changes over time. Since diatoms are diploid, each round of sexual reproduction creates genetic diversity, thus enabling the characteristics of a population to undergo frequent transformations.

Thesis Supervisor: Prof. Sallie W. Chisholm
Professor, M.I.T
ACKNOWLEDGMENTS

The experiments are completed, the writing is all done (more or less) and the defense presentation is over. It's finally my turn to write an acknowledgment, the one part of a thesis that everyone reads first - hmmm, let's see ... who all helped this person finish? It's my chance to be just as sappy as I want, to thank as many people as I want, in whatever way I want. So with that as an intro, let's see who all helped Ginger finish.

I'll begin with Penny Chisholm, my advisor and my mentor. The one who taught me a different way of thinking about the ocean, who helped me to believe that studying something just because you think it's neat is perfectly ok, and who was always there when I needed to talk. Penny, it's too complicated to go into all the ways you've helped me through this whole process, so I'll just say thanks. Special thanks also go to Rob Olson. How I've always loved our talks, Rob...about experiments, about science in general, about life. It's great knowing you are ready to help in any way you can. Thanks also to the other members of my committee, Don Anderson and Woody Hastings for all their helpful suggestions and encouragement.

A very special thank you goes to Sheila Frankel for always being there ready to help me fix things, whether it's a piece of equipment or some aspect of my personal life. Sheila, thanks for being such a good friend. And speaking of fixing things for me...Vicki, Christina, thanks for everything.

Erik Zottler also deserves a big thank you. Erik without you, I would know nothing about mini-oceanography, let alone how to get around Senegal. Hey, by the way, I'm still waiting for that motorcycle trip around the world.

I'd also like to thank members of the research group, Brian Binder, Mark Gerath, Jim Bowen, Ena Urbach, and Heidi Sosik for all their help. (P.S. I just have one more version of a few papers that I'd like you to read for me.) And thanks to the extended research group, my friends and colleagues, Brian Palenik, Janet Hering, and Neil Price. Also, thanks to all the UROPs who have helped me collect data. It's been a lot of fun.

And then finally there's my friends who have been incredibly important to me throughout this whole process. A big hug to Lisa Urry and Rosie Salvador who were always there to listen to me complain and to help me to have fun. Special thanks to my support group, Jim Bowen and Deb Backhus. And finally, a very special thank you to Susan Francis who helped me to imagine lot's of possibilities.
Preface

Diatoms are one of the most abundant eukaryotic microorganisms found in the aquatic environment. Due to their photosynthetic capabilities, these ubiquitous organisms are substantial contributors to global primary productivity. And yet, despite their obvious ecological importance, relatively little is known about the details of the physiology of these cells. In fact, studies of the life cycle of diatoms have not progressed beyond the descriptive stage (Chapter 1); very little is understood about what determines if and when a cell will cease asexual reproduction and undergo gametogenesis and subsequent zygote formation. The goal of my thesis was to examine in more detail this "decision making" process.

The marine centric diatom, *Thalassiosira weissflogii*, was used as the model organism for this research due to a serendipitous observation by Vaulot and Chisholm (1987). They found that a portion of a *T. weissflogii* population was induced to undergo spermatogenesis in response to a change in light conditions. What fascinated me about this result was that a majority of the population apparently ignored the induction signal and continued dividing asexually. What differentiated these non-inducible cells from the inducible ones? To address this question, the responsiveness of a cell to an environmental induction trigger was examined as a function of both cell size and cell cycle stage (Chapter 2). I learned that the extent of spermatogenesis displayed by a given population was influenced not by its average cell size as expected but rather by its cell cycle distribution.
This lack of a correlation between cell size and responsiveness to an induction cue was in direct conflict with the work of numerous other researchers. To try to understand the source of this discrepancy, I initiated a systematic examination of the manner in which cell size changed over time in a number of *T. weissflogii* isolates (Chapter 3). In the course of conducting this study I found evidence that the genetic composition of diatom populations varies over time. Thus, the characteristics of these populations can undergo frequent transformations, a feature which must be kept in mind as attempts are made to understand in more detail the physiology of these organisms.

I have also included in this thesis a study which describes cell cycle regulation in the procaryote, *Synechococcus* strain WH-8101, an organism which is unrelated to diatoms and in fact belongs to an entirely different kingdom (Appendix). This work is included here as an example of the fact that an understanding of the behavior of populations of cells requires an understanding of the behavior of the individual cells within the population. This philosophy, the "importance of the individuals", permeates each of the latter studies conducted with *T. weissflogii*.
References

Chapter One

Sexual Reproduction in Centric Diatoms
Introduction

Diatoms (Bacillariophyta) are one of the most abundant groups of aquatic, eukaryotic microorganisms found in nature with approximately 100,000 described species dispersed among over 250 genera (Round and Crawford 1989). These unicellular algae are widely distributed among freshwater and marine habitats in both the plankton and the benthos, in fact "anywhere water drips, collects, or flows there is a diatom microbiota" (Round and Crawford 1989). Due to their dominance in oceanic upwelling zones and the regions of the continental shelves, diatoms are substantial contributors to world net primary productivity (Werner 1977). Moreover, these and other large phytoplankton have recently been hypothesized to play a crucial role in the new production of oligotrophic waters (Goldman 1988).

Despite their obvious ecological importance, however, many of the details of the physiology of these organisms remain mysterious. In an era when model systems such as the budding yeast, *Saccharomyces cerevisiae*, and the freshwater green alga, *Chlamydomonas reinhardtii*, can be genetically manipulated at will through techniques ranging from simple matings to intricate transformations (e.g. Herskowitz 1988, Boynton et al. 1988, Hall 1989), studies of the diatom life cycle have progressed little beyond the descriptive stage. And yet, the sexual cycle of diatoms may be unique among unicellular algae since the vegetative cells are
diploid and thus meiosis precedes gametic differentiation. Moreover, the induction of sexuality in diatoms has traditionally been thought to be linked with the obtainment of an appropriate cell size. If this proves to be true, the diatom life cycle may not only be unique among the phytoplankton but among the entire protist kingdom as well.

Relatively few life cycle studies have been conducted in the 13 years since Drebes's review of diatom sexuality was published (Drebes 1977b). This is perhaps due to the somewhat persnickety nature of diatoms; sexual events serendipitously observed once are frequently hard to replicate. Since 1977, however, research techniques available to scientists have blossomed; for example, painstaking microscopic observations are no longer the only means of detecting sexuality (e.g. Vaulot and Chisholm 1987a, chapter 2). Thus, we may now be able to move beyond simple descriptions of the sexual process and begin to ask more detailed questions. For instance, an understanding of the mechanisms underlying the induction of sexual reproduction in the various diatom species may enable us to someday predict how changing environmental conditions will influence the extent of sexuality and thus the potential for genetic variability in diatom populations in the field.
The diatom literature dating from nearly a hundred years ago overflows with wonderfully detailed descriptions and drawings of the life histories of some of the larger, more easily observed organisms (e.g., Yendo and Ikari 1918, Persidsky 1935, Gross 1937). Towards the end of the nineteenth century, researchers surmised that the unique structure of the diatom frustule imposed potential constraints on its life cycle. An assortment of cell sizes within a given species were generally observed but it was initially unclear whether cells gradually became smaller or larger over successive generations. The diatom frustule is composed of two rigid, unequally sized silica valves, the epitheca and the hypotheca, each attached to a series of silicious girdle bands. MacDonald (1869) and Pfitzer (Rao and Desikachary 1970) simultaneously surmised in what has become known as the MacDonald-Pfitzer hypothesis, that since the valves of the new frustules are created within the confines of the old, each mitotic division results in one daughter cell which is smaller than either her sister or her mother thus causing a gradual decrease in cell size over successive generations.

Some sixty years later, Geitler (1935) reviewed the details of the life cycles of a number of pennate diatom species and defined three distinctive categories of cells (still used today), characterized by their relative cell size. His first category consisted of the largest cells or post-auxospores, generally created
sexually, which were capable only of asexual reproduction. Size diminution of these vegetative cells created the second category, cells characterized by a smaller size range that were capable of both asexual and sexual reproduction. Individuals that passed through this size range without undergoing gametogenesis comprised the third category. These cells were no longer capable of sexual reproduction and simply continued to decrease in size; theoretically this cell line would eventually die. Thus by the early thirties, the foundation of what appear to be the unique features of diatoms had become well established: sexuality and perhaps even cell vigor are intimately associated with cell size.

As pennate diatoms became well characterized and were proven to possess isogamous or morphologically equivalent haploid gametes, arguments flourished as to the exact nature of sexual reproduction in centric diatoms. Flagellated cells which are now known to be sperm were observed (e.g., Gross 1937, Braarud 1939, Subrahmanyan 1946) but it was unclear exactly what role these cells played in the life cycle. For example, Gross (1937) concluded definitively that these "microspores" resulted from either an abnormal division process or the "occasional presence and reproduction in dead diatom cells of flagellates not necessarily of parasitic nature." Another fifteen years of disagreements had to pass before von Stosch (1950), through a detailed examination of field samples, firmly established that centric diatoms are characterized by oogamy, the formation of morphologically dissimilar sperm and eggs.
With the discovery that many diatoms require vitamin B₁₂, the number of bacteria-free clones of diatoms maintained in culture increased dramatically during the fifties and sixties (Lewin and Guillard, 1963). In keeping with this trend, life cycle studies on centric diatoms moved from field observations to laboratory experiments.

Gametogenesis and Zygote Formation

The predominant mode of reproduction in diatoms is mitotic division. However, like many other eukaryotic microorganisms (Sager and Granick 1954, Esposito and Klapholz 1981, Pfiester and Anderson 1987) diatoms can exit the mitotic cycle and undergo gametogenesis. Since diatoms are diploid, meiosis precedes gametogenesis and thus the gametes may be morphologically and physiologically quite distinct from vegetative cells. Moreover, since diatoms are monoecious, each cell can differentiate into either male or female gametes. Drebes (1977b) presents a excellent summary of the numerous possible steps leading to the formation of the sperm, egg, and auxospore. Only a brief review will be presented here.

Spermatogenesis

The first indication of spermatogenesis is a series of specialized mitoses that creates within a single frustule, anywhere from one or two diploid spermatogonia as in Skeletonema costatum (Migita 1967b) to as many as 128 spermatogonia within a single Coscinodiscus pavillardii cell (Findlay 1969). These spermatogonia
may either swell and complete meiosis free of the mother frustule (e. g. French and Hargraves 1985, chapter 2) or else remain enclosed within the frustule until meiosis is completed (e.g. Findlay 1969). As no growth occurs between the successive mitotic and meiotic divisions, a male determined cell of *Lithodesmium undulatum*, for example, can complete four successive mitotic divisions and two meiotic divisions in as little as 12 hours (Manton et al. 1970), an interval comparable to the average doubling time of the vegetative cells of numerous species. The final outcome of these divisions is the creation of four uniflagellated haploid sperm from each spermatogonium. Thus, a *C. pavillardii* cell, for example, can create as many as 512 sperm.

**Oogenesis**

Oogonia, unlike spermatocytes, are formed directly from the vegetative cell with no accompanying reductive mitoses. In the ensuing meiotic divisions, two eggs and two pycnotic or disintegrating nuclei, one egg and a polar body, or one egg and two pycnotic nuclei are formed depending on the species examined (Drebes 1977b). In certain species such as *Stephanopyxis palmeriana* (Drebes 1966) or *Leptocylindrus danicus* (French and Hargraves 1985), the females can be differentiated from vegetative cells since they are slightly elongated and can possess both an enlarged nucleus and an increased number of chloroplasts. In other species such as *Coscinodiscus cocinnus* (Holmes 1967) or *Chaetoceros diadema*
(Hargraves 1972), however, no conspicuous differences between females and vegetative cells are observed.

**Auxospore Formation**

A number of ingenious methods have been devised by different diatom species to facilitate the necessary union of the sperm and egg since the egg is generally still enclosed within her silica frustule. Often, the female bends slightly thus allowing the sperm to enter through a opening between the two valve halves (e.g. von Stosch 1950, Drebes 1966, French and Hargraves 1985). In other instances, the sperm apparently slithers through a bristle opening in the frustule (Drebes 1977b).

Upon fertilization, the developing diploid zygote or auxospore rapidly expands due to a sudden intake of water, squeezing the organelles into a thin layer of cytoplasm within the auxospore periphery (Hoops and Floyd 1979), and then escapes the confines of the mother frustule. At this stage the auxospore is surrounded by an organic wall frequently interspersed with siliceous scales (Crawford 1974, Hoops and Floyd 1979). The protoplasm eventually contracts from the wall and two new silica valves are laid down. Interestingly, an acytokinetic mitotic event (nuclear division without cytokinesis) accompanies the formation of each valve and thus two pycnotic nuclei are created (Drebes 1977b). The auxospore envelope finally ruptures and the newly enlarged "Erslingszelle" or initial cell is released. The relation between the size of the post-auxospore cell and the parent cell can vary (e.g. Rao 1971,
chapter 3), but the newly created cell may be as many as five times as large as either parent (Findlay 1969).

Environmental Induction Signals

Diatoms can be induced to exit the mitotic cycle and undergo sexual reproduction in response to a suite of environmental signals including a sudden change in light intensity, temperature, nutrient status, or salinity (Table 1). The motivation behind many of the early studies on the induction of sexuality was either a manipulation of a given species through its various life cycle stages or a description of a serendipitously observed event rather than an examination of the interaction between a cell and its environment. The appropriate conditions for gametogenesis are often presented simply as recipes and the use of "old" cultures is frequently noted (e.g. Drebes 1966, Rao 1971, Drebes 1972, Hoops and Floyd 1979). Only rarely is the population response to an induction signal quantified, complicating any attempts to evaluate the relative "strengths" of the various induction signals. Thus, it is unclear whether or not the reported range of chemical and physical signals all induce sexual reproduction via a common mechanism.

Light Cues

The duration of the photoperiod is frequently emphasized as an important component of many induction "mixtures". The results obtained with one species, however, are often in direct conflict
with results reported for another species. For example, Steele
(1965) found that only when *Stephanopyxis palmeriana* was maintained
on a 16:8 L:D cycle (rather than a 12:12 or an 8:16 L:D cycle) would
cultures form sexual cells. Similarly, Furnas (1985) reported that
higher proportions of *Chaetoceros curvisetum* cultures underwent
spermatogenesis when maintained on L:D cycles of 16:8 rather than
either 12:12 or 8:16. This preference for sexual reproduction over
asexual reproduction under long photoperiods is exactly the opposite
of what Holmes (1966) found in his systematic study of *Coscinodiscus
cocinnus*. He exposed cultures to sixty-four different light and
temperature combinations at L:D cycles of 16:8, 12:12, and 8:16.
The extent of both spermatogenesis and auxospore formation was
always enhanced under the short photoperiods. This sort of
contradictory behavior unfortunately adds to an apparent
intractability of diatom life cycle studies.

Perhaps a little of the mystery can be removed, however, based
on recent results obtained with the marine diatom, *Thalassiosira
weissflogii*. This diatom can be induced to undergo spermatogenesis
when cells are transferred from saturating levels of continuous
light to either dim light or darkness (chapter 2). Responsiveness
to this induction signal, however, is a function of cell cycle
stage. Only when cells are in early *G_1* can they be induced to
undergo spermatogenesis; cells further along in their cell cycle are
unresponsive to the same induction cues and simply divide
mitotically (chapter 2). If the response of *C. cocinnus*, S.
palmeriana, and C. curvisetum to a change in light conditions is also limited to cells in a particular stage of their cell cycle this may explain some of the conflicting photoperiod results.

In order to predict how the duration of the photoperiod can influence the number of cells induced to undergo gametogenesis, the manner in which light affects cell cycle progression must first be understood. Diatoms posses at least one and more often two light dependent regions, located in G₁ and/or G₂, where continued cell cycle progression requires light (Vaulot et al. 1986, Olson et al. 1986, M. Brzezinski, pers. comm.). Light/dark cycles align the cells cycles of a culture depending on the length of the various cell cycle stages, the location and the duration of the light requiring segments, and the duration of the photoperiod (Vaulot and Chisholm 1987b). The proportion of a population that is induced to undergo gametogenesis under a given photoperiod is a function on the number of cells which are in the appropriate cell cycle stage during induction. If for example, the durations of the light requiring segments differ between Chaetoceros curvisetum and Coscinodiscus concinnus, the cell cycles of these two organisms will be differently aligned to a given light dark cycle and thus different proportions of cells will move through their inducible region during the induction signal and be triggered to undergo sexual reproduction.
**Nutrient Cues**

Two diatoms that have been observed to undergo sexual reproduction in response to nutrient limitation are *Leptocylindrus danicus* (French and Hargraves 1985, 1986) and *Skeletonema costatum* (Davis et al. 1973). *S. costatum* cells can become sexual under silica limited continuous culture conditions. On the other hand, nearly one hundred percent of *L. danicus* populations are induced to undergo sexual reproduction in response to nitrogen limitation. The highly unusual feature of this system, however, is that immediately after zygote formation and cell enlargement, the auxospore always develops into a resting spore. Nitrogen deprivation apparently set into motion two new developmental pathways.

**Salinity Cues**

One final species which holds promise for studying induction signals but has apparently not been examined since the late sixties and early seventies, is an estuarine species, *Cyclotella meneghiniana*. Sexuality in *C. meneghiniana* is triggered by a change in Na⁺ concentrations (Schultz and Trainor 1968, Schultz and Trainor 1970, Rao 1971). Interestingly, only male gametes were formed on a 15:9 L:D cycle whereas in continuous light, all stages in the sexual cycle were formed (Schultz and Trainor 1970) (see section on Sex Determination).
Size and Sexuality

A remarkable feature of the diatom life cycle is that the ability to undergo sexual reproduction is apparently linked to the size of a cell (Drebes 1977b). Over successive generations the mean cell size of a population generally decreases (Rao and Desikachary 1970) and the standard deviation about this mean increases (for exceptions to this general rule of size reduction see for example, Rao and Desikachary 1970, Round 1972, Crawford 1980). It is commonly observed that only when cells obtain a diameter less than about 30-40% of their species' maximum, can they undergo gametogenesis and subsequent auxospore formation (Drebes 1977b). This newly enlarged cell then proceeds along the asexual path until size once again permits sexuality and thus ensuring the periodic nature of diatom sexuality (Lewis 1984).

Evidence

The ideal way to test the relationship between cell size and the ability to undergo gametogenesis is to examine genetically identical population of cells that differ only in their size distributions. This is nearly impossible to do, though, since diatoms are monoecious and thus sexual reproduction can occur in populations originating from a single cell. Von Stosch (1965) circumvented this problem by artificially eliciting size changes through nutritional and other cultural manipulations. He found that newly enlarged cells were not receptive to induction signals,
whereas cells which had been forced instead to decrease abruptly in size were receptive (Drebes 1977b). An examination of the response of cells which have been exposed to extreme conditions, however, is often problematic; the possibility of transient behavior unrelated to absolute cell size can not be eliminated. For example, enlarged cells were obtained by transferring cells to media essentially devoid of silica. Cells discarded their frustules to form "protoplasts" and only formed a new larger, but often misshapen frustule upon a return to silica replete conditions. It is unclear what other physiological changes may have accompanied these conditions.

An alternative method employed to examine the relationship between cell size and sexuality is to periodically remove aliquots from an isolate in the process of size diminution and thus expose populations with different size distributions to a given induction signal. Rao (1971) monitored cell size and susceptibility to a salinity induction signal in Cyclotella meneghiniana for 18 months and found that only cells less than approximately 38% of the maximum formed gametes. However, a single round sexual reproduction and auxospore formation did not always lead to the obtainment of the cells’ maximum size. Instead, at least two size steps were observed; a portion of the cells that had undergone one round of sexual reproduction immediately underwent a second round to form even larger cells.
Similarly, Findlay (1969) followed a isolate of *Coscinodiscus pavillardii* for 15 months and found that sexuality occurred only in cells ranging from 20-63% of the maximum diameter. Although he did not mention the actual proportions of the populations that were induced as the average cell size of the isolate decreased, he did note that sexuality did not occur in all the cells within the inducible range; some cell lines continued dividing vegetatively and eventually died. This heterogeneous response of a population theoretically within the inducible size range has frequently been observed (e.g. Werner 1971) and obviously complicates any simple relationship between cell size and susceptibility to an induction trigger.

In a slight twist to this experimental design, I (chapter 2) isolated a number of *Thalassiosira weissflogii* populations displaying a range of size distributions. In contrast to expectations, no relationship was observed between the average size of the various isolates and the proportion of cells that were induced to undergo spermatogenesis in response to a change in light conditions. In a subsequent follow-up study, I monitored the changes in cell size in these various isolates during approximately two years of exponential growth in constant conditions (chapter 3). Each isolate displayed periodic increases and decreases in mean cell size as expected for populations alternating between asexual and sexual reproduction. However, the overall patterns of cell size change varied dramatically between the various populations despite
the fact that each culture was maintained under identical growth conditions. The only feature common to these patterns was the rate of decrease in mean cell size, a parameter which is apparently determined by the physical constraints of the frustule during asexual reproduction. The rest of the components, i.e., the timing of the sexual episodes, the rate of increase in average cell size and the size of the post-auxospore cells created during a sexual event could vary among isolates and even within a given isolate over time. Both the size at which a cell can undergo sexual reproduction and the size of the post-auxospore cells created during these sexual intervals could display genetic variability. I hypothesized that the extent of variation in the patterns of cell size change exhibited by the different populations resulted from the fact that the genetic composition of a population can vary over time.

Sex Determination

As mentioned previously, diatoms are monoecious and thus each cell can form either male or female gametes. Essentially nothing is known about how this decision making process is achieved in diatoms. The reported environmental cues often differ slightly between males and females (Steele 1965, Holmes 1966, Migita 1967b). For instance, in Melosira moniliformis (Migita 1967) and Skeletonema costatum (Migita 1967b), cells maintained in higher light intensities form females rather than males, whereas in Stephanopyxis palmeriana (Steele 1965), just the opposite is true. Cell size has also been
observed to influence the sex of a cell. For example, in Cyclotella meneghiniana (Rao 1971), cells within the low end of the inducible size spectrum form males whereas the larger inducible cells form females. As with environmental cues, exactly the opposite response can be found in other diatoms; Chaetoceros diadema forms females from small cells and males from larger cells (Hargraves 1972).

Future Studies

Our understanding of those factors which allow a cell to exit the mitotic cycle and undergo sexual reproduction is still quite limited. Although the obtainment of an appropriate cell size is strongly correlated with an ability to respond to environmental cues (e.g. Drebes 1977b), this permissive size range can vary among different isolates of a single species (chapter 3). Moreover, not all the cells within an appropriate size range respond to induction triggers (e.g. Findlay 1969, Warner 1971). For instance, I found that only cells in the G\textsubscript{1} stage of their cell cycle can initiate spermatogenesis in response to a change in light intensities (chapter 2), (see section on Environmental Induction Signals). However, even within this G\textsubscript{1} category, a portion of the cells may still not respond to the induction signal. Other parameters besides cell size or even cell cycle stage must differentiate small inducible cells from small uninducible ones. Could this also be what
differentiates post-auxospores from inducible cells? In Rao's study (1971), what permitted cells to form sequential sets of auxospores?

Many of these types of questions require an understanding of the underlying mechanisms of the induction of sexual reproduction. However, as is apparent from an inspection of Table 1, a common component of sexual cues is some form of environmental stress. This fact makes an assessment of the processes underlying the environmental induction of gametogenesis quite complicated since the cues generally elicit a host of physiological responses, most of which are unrelated to the induction of gametogenesis (e.g. Goodenough 1983). Assuming, however, that certain cells for at least a portion of their life cycle are unresponsive to induction signals (see section on Size Control of Sexuality), details of the physiological changes preceding the onset of gametogenesis can be compared between inducible and these unresponsive cells. Those changes which are unrelated to the induction of gametogenesis will be common to both populations. Early changes found only in the responsive population should be associated with induction.

CONCLUSIONS

Diatoms are apparently unique among the phytoplankton because they are diploid and because they display a gradual decrease in cell size over successive generations. Numerous studies have linked the obtainment of an appropriate cell size with susceptibility to these
induction signals. The fact that often only a portion of the cells within an inducible size range responds to a given signal indicates that other factors besides cell size must control sexuality. It is now clear that the cell cycle distribution of a population upon induction can influence the proportion of cells that can respond to an induction signal. In addition, both the size at which a cell can undergo sexual reproduction and the maximum size of a post auxospore cell can display genetic variability.

Since diatoms are diploid, genetic recombination during sexual reproduction will generate variability in the genotypes and perhaps even the phenotypes of the individual cells within a given population over time. This means that many aspects of the behavior of diatoms may be quite variable, a feature of diatom populations which must be kept in mind as attempts are made to understand the details of the physiology of these organisms.
Table 1. Summary of sexual induction signals reported for a number of centric diatoms.

<table>
<thead>
<tr>
<th>Genus</th>
<th>Species</th>
<th>Induction Signal</th>
<th>Sexual Cells Formed</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Coscinodiscus cocinmus</td>
<td>light</td>
<td>M/A</td>
<td>Holmes 1966</td>
<td></td>
</tr>
<tr>
<td></td>
<td>temp</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>pavillardii</td>
<td>salinity</td>
<td>Findlay 1969</td>
<td></td>
</tr>
<tr>
<td></td>
<td>asteromphalus</td>
<td>temp</td>
<td>Werner 1971</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>light</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Melosira</td>
<td>moniliformis</td>
<td>light (strong)</td>
<td>F</td>
<td>Nigita 1967a</td>
</tr>
<tr>
<td></td>
<td></td>
<td>light (weak)</td>
<td>M</td>
<td></td>
</tr>
<tr>
<td>Stephanopyxis palmeriana</td>
<td>light</td>
<td>M</td>
<td>Steele 1965</td>
<td></td>
</tr>
<tr>
<td></td>
<td>(L:D, 16:8, high intensity)</td>
<td>A</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>(L:D, 16:8 low intensity)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>light (L:D, 14:10)</td>
<td></td>
<td>Drebes 1966</td>
<td></td>
</tr>
<tr>
<td>Thalassiosira weissflogii</td>
<td>light/dark</td>
<td>M</td>
<td>Vaulot &amp; Chisholm 1987</td>
<td></td>
</tr>
<tr>
<td></td>
<td>subsaturating</td>
<td>M</td>
<td>Arambrust et al. 1990</td>
<td></td>
</tr>
<tr>
<td>Skeletonema costatum</td>
<td>light</td>
<td>M/F/A</td>
<td>Migita 1967b</td>
<td></td>
</tr>
<tr>
<td></td>
<td>silica</td>
<td>M/F/A</td>
<td>Davis et al. 1973</td>
<td></td>
</tr>
</tbody>
</table>
Table 1, cont.

<table>
<thead>
<tr>
<th>Genus</th>
<th>Species</th>
<th>Induction Signal</th>
<th>Sexual Cells Formed*</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bytilum</td>
<td>brightwellii</td>
<td>manganese</td>
<td>H/A</td>
<td>Steele 1965</td>
</tr>
<tr>
<td>Lithodesmium</td>
<td>undulatum</td>
<td>fresh medium, temp, light</td>
<td>e.g. Manton &amp; von Stosch 1966</td>
<td></td>
</tr>
<tr>
<td>Cyclotella</td>
<td>meneghiniana</td>
<td>Na⁺ (L:D, 15:9)</td>
<td>H</td>
<td>Schultz &amp; Trainor 1970</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Na⁺ (LL)</td>
<td>A</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Na⁺</td>
<td>H/F/A</td>
<td>Schultz &amp; Trainor 1968</td>
</tr>
<tr>
<td></td>
<td></td>
<td>salinity</td>
<td>H/F/A</td>
<td>Rao 1971</td>
</tr>
<tr>
<td></td>
<td></td>
<td>&quot;old&quot; cultures</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>cryptica</td>
<td>salinity</td>
<td>H/F/A</td>
<td>Schultz &amp; Trainor 1970</td>
</tr>
</tbody>
</table>

| Chaetoceros | curvisetum | light/dark       | H                    | Furnas 1985        |
|            | diadema    | nitrogen         | M/F/A                | French & Hargraves 1985 |
|            | simplex    | light            | A                    | Sato 1967          |
| Bacteriastrium | hyalimum  | temp, light      |                      | Drebes 1972        |
|             |            | "old" cultures  | M/F/A                | Drebes 1967        |
| Leptocylindrus | danicus  | nitrogen         | M/F/A                | French & Hargraves 1985 |
| Attheya    | decora     | light            | M/F/A                | Drebes 1977a       |

* M=male gametes, F=female gametes, A=auxosporic.
References


Chapter 2

Induction of Spermatogenesis in a Centric Diatom: The Role of Light and the Cell Cycle
ABSTRACT

The centric diatom, *Thalassiosira weissflogii* Grun., can be induced to undergo spermatogenesis by exposing cells maintained at saturating levels of continuous light to either dim light or darkness. Using flow cytometry to determine the relative DNA and chlorophyll content per cell, the number of cells within a population which responded to an induction signal was measured. From 0 to over 90% of a population could differentiate into male gametes depending upon both the induction trigger and the population examined, regardless of cell size.

Through the use of synchronized cultures, we demonstrated that responsiveness to an induction trigger is a function of cell cycle stage; cells in early G1 are not yet committed to complete mitosis and can be induced to form male gametes, whereas cells further along in their cell cycle are unresponsive to these same cues. A simple model combining the influence of light on the mitotic cell cycle and on the induction of spermatogenesis has been developed to explain the observed diversity in population responses to changes in light conditions.

Key index words: cell cycle, diatom, light, sexual reproduction
Diatoms, like all unicellular algae, reproduce predominantly via mitotic division. The diatom frustule is generally unable to expand apically during these mitotic divisions resulting in a decrease in the mean cell size of a population and an increase in the standard deviation about this mean over successive generations (MacDonald 1869, Rao and Desikachary 1970, Round 1972). The most common manner of escaping this trend of diminishing cell size is through sexual reproduction. It is commonly believed that once cells reach a diameter less than 30-40% of their species' maximum diameter, they can be induced by an environmental trigger to exit the mitotic cycle and undergo gametogenesis (e.g. Drebes 1977). The resulting male and female haploid gametes combine to create a diploid auxospore which enlarges outside the confines of the parental frustule to produce a cell many times larger than either parent (e.g. Higita 1967, Rao 1971). This newly created cell then proceeds along the asexual pathway until an appropriate trigger once again elicits gametogenesis.

Although the developmental pathways of both spermatogenesis and oogenesis have been well documented in a number of diatom species (von Stosch 1930, Manton et al. 1969a,b. 1970a,b, Drebes 1972.), the underlying mechanisms for triggering these pathways remain elusive. A suite of factors including light (e.g. Drebes 1966, Furnas 1985, Vaulot and Chisholm 1987), nutrients (e.g. Davis 1973, French and Hargraves 1985), salinity (e.g. Schultz and Trainor 1968) and temperature shifts (e.g., Holmes, 1966) have all been
implicated in initiating this switch from asexual to sexual reproduction.

We recently discovered a means of inducing the centric diatom *Thalassiosira weissflogii* to undergo spermatogenesis (Vaulot and Chisholm 1987). Upon the return of a dark arrested population to continuous light, a portion of the cells differentiated into male gametes. The majority of the population, however, apparently "ignored" this cue and continued dividing asexually. This heterogeneous response of diatom populations to an environmental signal has been observed frequently and is often attributed to the non-responsiveness of large cells. However, even within a purportedly appropriate size range, often only a fraction of a culture responds to the cue (e.g. Findlay 1969, Werner 1971). This observation complicates any simple relationship between relative cell size and susceptibility to an induction trigger and suggests that additional factors must underlie the heterogeneous responses of populations. The goal of our study with *T. weissflogii* was to explore responsiveness to an induction signal as a function of both cell size and cell cycle stage.

**MATERIALS AND METHODS**

Clonal isolates of *T. weissflogii* clone Actin (from the Culture Collection of Marine Phytoplankton, Bigelow Laboratories for Ocean Sciences) were obtained by isolating colonies from 2% agar
plates and transferring them to f/2 enriched seawater media (Guillard 1975) with nitrate as the nitrogen source. Cultures of these isolates were obtained whose volumes ranged from approximately 600 to 1200 \(\mu m^3\) (as determined with a Coulter Electronics Model Zm/C256 electronic particle counter). Although Coulter values are determined by assuming that each particle is a sphere, these diameters accurately predicted the apical diameter of cells measured independently with a microscope. Each experiment began with semi-continuous cultures of the various isolates maintained at 20°C in saturating levels of continuous illumination (cool-white fluorescent). In all instances, unless specifically stated, the photon flux density (PPD) was constant at 250 \(\mu E.m^{-2}.sec^{-1}\) as measured with a Biospherical Instruments model QSL100 irradiance meter. A Turner fluorometer was used to monitor daily changes in the in vivo fluorescence of the cultures to determine growth rates (Brand et al. 1981). During the sorting experiments, cell number was determined microscopically with a Fuchs/Rosenthal hemocytometer. A minimum of 300 cells were counted for each sample. For all other experiments, cell number and volume distributions were determined with the Coulter Counter.

To determine DNA content per cell, live samples were stained with 10 \(\mu g.ml^{-1}\) of the DNA fluorochrome Hoechst 33342 (Calbiochem, La Jolla, CA) for at least 10 min and relative DNA and chlorophyll fluorescence were measured with either a microscope based (Olson et al. 1983, Frankel et al. 1988) or a Coulter Epics V flow cytometer.
In both systems, UV excitation was 365 nm and chlorophyll fluorescence emission was measured between 660-700 nm. DNA fluorescence emission (Hoechst 33342) was measured between 430-470 nm on the microscope based flow cytometer and between 418-530 nm on the Epics V. All sorting experiments were conducted using the sorting capabilities of the Epics V.

Because some of the stages in the formation of male gametes are not enclosed within a frustule and are therefore particularly sensitive to the fixation process normally used for DNA analyses (Olson et al. 1983), only live samples were analyzed. This also allowed us to measure chlorophyll fluorescence per cell which increased our ability to discriminate between the various sexual stages. Because the coefficient of variation of DNA measurements is greatly increased in live cells (Olson et al. 1983), however, we could only divide the cell cycle of the vegetative cells into the G₁ and G₂ stages which are assumed to represent a DNA content of 2c and 4c, respectively (where c represents chromosome complement).

A known quantity of preserved nuclei from calf thymocytes (Ortho Diagnostic Systems) was added to each sample to act both as an internal staining standard and to permit a calculation of the density of cells within a given subpopulation. At least 30,000 cells were analyzed for each treatment at a minimum of two separate time points.

The flow cytometric data were stored as two parameter histograms of correlated DNA and chlorophyll fluorescence of either
64 X 64 (Epics V) or 128 X 128 (microscope based) channel resolution. The data generated with either instrument were transferred to an IBM 9000 computer for detailed analysis (Vaulot 1986).

RESULTS

Detection and analysis of spermatogenesis. When T. weissflogii populations were maintained in saturating intensities of continuous light, a typical flow cytometric "signature" of a population revealed that the majority of the cells were located in either the G₁ or G₂ portion of the cell cycle (Fig. 1A); few if any male gametes were produced in these cultures, as shown by a general absence of cells with anything other than two or four complements of DNA. Cells transferred from continuous light to prolonged darkness did not undergo spermatogenesis in the dark, again as indicated by the presence of cells in only the G₁ or G₂ phase of the cell cycle (Fig. 1B). An interruption of growth in continuous light with 12 h of darkness, however, induced a portion of a population to exit the mitotic cell cycle and undergo spermatogenesis (Fig. 1 C-H).

At the end of the 12 h dark interval, the induced and non-induced cells within the population were indistinguishable both morphologically and flow cytometrically (cf. Fig. 1A, C). After 3 h of light exposure, however, a low chlorophyll subpopulation developed creating a distortion in the flow cytometric signature of the vegetative cells (Fig. 1D). Two h later, two subpopulations emerged with lower chlorophyll fluorescence than either the G₁ or G₂
cells; one consisted of cells with a G2 complement of DNA (4c) and the other consisted of cells with twice this amount of DNA (8c) (Fig. 1E). Soon thereafter, the new 4c and 8c subpopulations were well distinguished from the vegetative cells by virtue of the increased chlorophyll fluorescence of the vegetative cells (resulting from the return to continuous light) (Fig. 1F). Twelve h after the return to the light (Fig. 1G), two more subpopulations developed with 2c and 1c DNA contents. By this time, the flux of cells from the vegetative to the low chlorophyll populations was complete and the low chlorophyll cells simply flowed from the 8c to the 1c population. Approximately 30 h after the return to continuous light, the majority of the low chlorophyll cells contained a 1c amount of DNA (Fig. 1H).

Morphological identification of these various subpopulations was obtained using the sorting capabilities of the Epics V flow cytometer. The sorted cells were examined microscopically (Fig. 2) and were found to fit the descriptions in the literature of the male sexual stages (e.g., Drebes 1977). The 8c population corresponded to spermatogonangia containing two 4c spermatocytes within a single frustule (Fig. 2B). The 4c population consisted of naked spermatocytes free of the frustule (Fig. 2C) and the 2c population were small flagellated cells (Fig. 2D). The 1c cells, which are the culmination of this process, were motile sperm (Fig. 2E). The developmental pathway of T. weissflogii adhered to the relatively common hologenous type described by Drebes (1977), since each
Fig. 1. Flow cytometric signatures of relative DNA and chlorophyll fluorescence per cell measured under three different light regimes. A) An exponentially growing population maintained in continuous light and B) transferred to an extended interval of darkness (94.5 h). C-H) Time course of gametic differentiation in a second population that had been transferred to the dark for 12 h and returned to continuous light at t=0 h. The contour levels represent 0.008, 0.012, 0.020, 0.036, 0.064, 0.108, and 0.158% of the total cell number.
Fig. 2. Flow cytometric signature of an induced population containing all four of the stages in the formation of male gametes. The contour levels represent 28, 42, 63, 95, 142, 213, 320 and 480 cells. A) A vegetative cell, B) an 8c spermatogonangium containing two 4c spermatocytes, C) a 4c spermatocyte remaining inside one half of the mother frustule, D) a small 2c cell, and E) a 1c sperm. Scale bars = 10 μm.
meiotic division was accompanied by cytokinesis. This same general
time course of differentiation was observed regardless of the T.
weissflogii isolate examined and is similar to that observed by
Manton et al. (1970b) for Lithodesmium undulatum.

With this understanding, we were able to calculate the number
of cells in a given population that was originally induced to exit
the mitotic cell cycle. At various times after the release of the
population into the light, the number of cells in each of the sexual
stages was determined (Fig. 3A), and the number of vegetative cells
that had therefore been triggered to differentiate into gametes was
calculated according to the following equations:

\[
\begin{align*}
t < 8 \text{ h after release into the light:} & \quad (1) \\
V = (A + B + C/4 + D/8) \\
t > 8 \text{ h after release into the light:} & \quad (2) \\
V = (A + B/2 + C/4 + D/8)
\end{align*}
\]

where \( V \) = the number of vegetative cells that have exited the cell
cycle and are committed to undergo spermatogenesis; \( A, B, C, \) and \( D \) =
the number of 8c, 4c, 2c, and 1c cells, respectively, present within
the population at a given time. These two equations differed
slightly because the 4c flow cytometry signature represented two
different cell types as exemplified by the bimodal distribution in
the number of 4c cells over time (Fig. 3A). Initially, the 4c cell
was derived directly from an induced parent cell and remained
enclosed within the frustules (Eq. 1). A peak in the number of these
cells occurred approximately 6-8 h into the differentiation process (Fig. 3A), at which point the peak declined rapidly as premeiotic DNA synthesis was initiated and the 8c cells were formed. A few hours later, the number of 4c cells again increased as the two naked 4c spermatocytes were released from each spermatogonangium. Thus, the number of these 4c cells reflected one half the number of originally induced cells (Eq. 2). The timing of this transition from 4c cells within the frustule to naked spermatocytes varied only slightly between experiments. However, to ensure that the plateau in the number of induced cells was obtained (Fig. 3B), a minimum of two time points were always analyzed for each treatment.

Through this analysis the proportion of cells that were not receptive to the induction cue was estimated (Fig. 3B). Approximately 3-5 h after the dark induced population was returned to the light, the number of vegetative cells suddenly declined as a portion of the population exited the mitotic cell cycle and initiated spermatogenesis (Fig. 3B). The entrance into gamete formation was fairly synchronous, occurring within a 3-5 h window. After the initial decline in vegetative cell number, asexual division continued at approximately the same rate as before induction (doubling time=10.4 h, Fig. 3B). A plateau in the number of induced cells occurred between 10 and 18 h after the population was returned to the light. The number of induced cells then declined and the sperm began to disappear. The male sexual cells had disappeared from the media approximately 50 h after the dark
Fig. 3. Mitotic division and the formation of the male sexual stages as a function of time in a population induced to undergo spermatogenesis with twelve h of darkness (as described in Fig. 1). t=0 h is the time of the release of the population into continuous light. A) The mean density (of replicate flasks) of each of the stages in the formation of male gametes. B) The number of cells in the original population which continued reproducing asexually (□) and the number of cells which formed male gametes (●). Error bars larger than the symbol size are shown and represent the standard deviation of replicate flasks.
induced population was returned to continuous light. Presumably the sperm simply disintegrated, as no sign of auxospore formation was observed during or for approximately one week after this interval.

*Relationship between cell size and responsiveness to a dark induction signal.* Isolates with mean Coulter volumes ranging from 600 to 1200 μm³ (see Methods) were exposed to 12 h of darkness, and the percentage of each population which underwent spermatogenesis was determined (Fig. 4A). No relationship between the percentage of cells which formed gametes and the mean Coulter volume of a culture was observed. Cultures representing widely different size distributions (Fig. 4B) yielded a comparable percentage of induced cells whereas other cultures representing nearly identical size distributions (Fig. 4C) resulted in very different responses. We concluded that in the isolates we examined, the induction of spermatogenesis was unrelated to cell size. We should note, however, that the average Coulter volume of the largest *T. weissflogii* isolate that we have observed in culture is 2000 μm³ (Armbrust and Chisholm unpubl. data), thus many of the cultures used in this experiment contained cells that were less than the maximum size. Very large cells may be unresponsive to induction signals.

*Influence of dark interval duration on spermatogenesis.* We examined whether the duration of dark exposure influenced the proportion of a culture that was induced to undergo spermatogenesis
by subjecting populations to a range of different light/dark regimes. A culture maintained in continuous light was transferred to the dark for a total of 16 h and subsamples were removed every 2 h and returned to continuous illumination. The resulting percentage of cells induced to undergo spermatogenesis was then determined for each population. Because cell division continues for some time in the dark, the proportion of the population induced to undergo spermatogenesis was normalized to the number of cells present at the end of each dark interval.

Cell division continued for approximately 10 h in the dark (Fig. 5A) until all the cells were blocked in either $G_1$ or $G_2$ (Fig. 1C; Vaulot et al. 1986). Interestingly, the percentage of cells that underwent spermatogenesis also increased as the duration of the dark interval was lengthened to 10 h (Fig. 5B), indicating that cells continued to be induced during the dark period and not simply upon a transfer to darkness. A strong positive correlation was observed between the number of cells that divided during the dark interval and the number of cells that subsequently formed gametes in the light (Fig. 5C). Once cell division stopped in the dark no more cells were induced to undergo spermatogenesis thus suggesting that cell cycle progression during the dark interval is a necessary component of induction.

The role of light intensity. Morphological differentiation did not begin in any of the isolates examined until the dark induced
Fig. 4. The influence of cell size on the induction of spermatogenesis. A) Maximum percentage of populations induced to undergo spermatogenesis as a function of the mean Coulter volume of the population. Each population was induced to undergo spermatogenesis with 12 h of darkness. Closed circles and arrows indicate cultures examined in B and C. Error bars larger than the symbol site are shown and represent the standard error of triplicate flasks. B) The Coulter volume distributions of the two isolates marked "B" in A that displayed a comparable level of induction. Sixty-six percent of a population with a mean Coulter volume of 660 μm$^3$ underwent spermatogenesis; a similar percentage of the population with a much greater mean Coulter volume was induced to form male gametes. C) The Coulter volume distribution of the isolates marked "C" in A. For these two isolates, 7% versus 55% of the populations underwent spermatogenesis even though they displayed the same size distribution.
Figure A shows a scatter plot with % induced on the y-axis and mean Coulter volume (µm^3) on the x-axis. The data points are distributed across the plot, indicating a relationship between the two variables.

Figure B displays two overlaid histograms with relative number of cells on the y-axis and Coulter volume (µm^3) on the x-axis. The histograms are labeled with average volumes: 680 µm^3 and 1194 µm^3.

Figure C presents another pair of histograms, with average volumes: 887 µm^3 and 881 µm^3.
Fig. 5. Induction of spermatogenesis within a single culture as a function of the duration of dark treatment. A) Cell number as a function of time in the dark. The population was transferred from continuous light to darkness at t=0 h, and replicate subsamples were removed from the dark every 2 h and returned to continuous light. B) Maximum percentage of cells induced to undergo spermatogenesis as a function of the amount of time in the dark. The percentage is calculated using the "plateau" region of the induction curve (cf. Fig. 3B). C) Number of cells which divided during the dark interval versus the number of cells which formed gametes after the population was returned to the light. Error bars larger than the symbol size are shown and represent the standard deviation of replicate cultures.
population was returned to the light (Fig. 1) suggesting that light functioned either as an additional signal (Kuhlemeier et al., 1987) which allowed differentiation to proceed, or as a necessary energy source for continued development. To distinguish between these two hypotheses, cells were maintained in 250 μE·m⁻²·sec⁻¹ of continuous illumination (saturating for growth, see below), placed in the dark for 12 h, and shifted to a variety of saturating (Fig. 6A) and subsaturating (Fig. 6B) PFDs. The time course of gamete formation was then determined for each light regime.

To our surprise, we found that a much larger percentage of cells were induced to undergo spermatogenesis when cultures were shifted from darkness to subsaturating rather than saturating PFDs (Fig. 6A, B). Moreover, the dark induced populations that were shifted to a variety of saturating PFDs each formed approximately the same maximum percentage of gametes (Fig. 6A). In contrast, the percentage of cells that formed gametes under subsaturating PFDs was a function of PFD; the higher the PFD (up to saturating levels), the greater the percentage of cells which underwent spermatogenesis (Fig. 6B). Subsaturating light itself appeared to function as an induction signal.

To test this possibility, populations that had been placed in the dark for twelve h and then shifted to a range of PFDs (Fig. 6C, D) were compared with populations shifted directly to these same PFDs without the preceding twelve h of darkness (Fig. 6E, F). Cells shifted directly from saturating to subsaturating PFDs of less than
100 μE·m⁻²·sec⁻¹ were induced to undergo spermatogenesis; a transfer to darkness was not a necessary step (Fig. 6F). Moreover, the magnitude and the time course of the response of each population shifted to subsaturating PFDs was almost identical regardless of whether or not darkness was included as a part of the induction scheme (cf. Figs. 6D, F). In each instance, a peak in the percentage of the population induced to undergo spermatogenesis was observed approximately one day after the cultures were shifted. The maximum percentage of a population induced to undergo spermatogenesis was many times higher in the populations shifted to subsaturating rather than saturating PFDs (Fig. 7) regardless of whether or not dark induction was included. The percentage of cells induced to form gametes increased as the PFD of the shift and thus the growth rate in these new conditions increased (Fig. 7, inset) until saturating PFDs were approached. At this point a drastic decrease was observed in the proportion of the population that underwent spermatogenesis (Fig. 7).

The role of the cell cycle. The dark induction and light intensity experiments suggested that a transfer to dim light or darkness functioned as an induction signal only when cells moved into or through a particular portion of their cell cycle. Populations of cells representing distinct cell cycle stages were necessary to test this hypothesis. Since T. weissflogii cells arrest in both G₁ and G₂ in the dark (Vaulot et al. 1986), in
Fig. 6. Percentages of cells induced to undergo spermatogenesis as a function of time under a range of different light regimes. Populations maintained in 250 µE·m⁻²·sec⁻¹ of light were placed in the dark for twelve h and then shifted to either (A) saturating or (B) subsaturating photon flux densities. The number of cells induced to undergo spermatogenesis was normalized to the number of cells present at the end of the dark interval. C, D) Since subsaturating light can function as an induction signal, the same data as in A and B were normalized to the number of cells present at the time the culture was sampled (note the change in scale) to permit a direct comparison with populations transferred directly to the various saturating (R) and subsaturating (F) PFDs without the accompanying 12 h of darkness. Error bars larger than the symbol size are shown and represent the standard deviation of replicate flasks.
Fig. 7. The maximum proportion of each population described in Fig.
6C, D, E, and F which underwent spermatogenesis when shifted
directly to the various light intensities (□) or first placed
in the dark for 12 h and then shifted (○). Error bars larger
than the symbol size are shown and represent the standard
deviation of replicate flasks. Inset: Steady state growth
rate of T. weissflogii as a function of light intensity.
% Induced

Light Intensity of Shift (μE·m⁻²·sec⁻¹)

Growth Rate (day⁻¹)
contrast to many other phytoplankton (Nelson and Brand 1979), synchronised cultures could not be obtained by maintaining populations on a light/dark cycle. Instead, populations representing a range of cell cycle distributions were obtained using the sorting capabilities of the Epics V. Because chlorophyll content appeared to vary with cell age (Fig. 1A), a number of subpopulations were sorted based on their chlorophyll fluorescence (Fig. 8). To determine in which phase of the cell cycle cells were most responsive to induction, each of these sorted subpopulations was exposed to 2 h of darkness, and the cell cycle distributions were determined at the end of the dark interval. This short period of darkness was used as the cue to minimize the amount of cell cycle progression that occurred during the signal.

The cell cycle distributions of the populations after the dark interval were well correlated with the mean relative chlorophyll fluorescence of the sorted samples (Fig. 9A). Those populations with the lowest mean chlorophyll fluorescence represented populations with the highest proportion of G₁ cells, and those populations with the highest mean chlorophyll fluorescence contained the highest proportion of G₂ cells. A strong correlation between the proportion of cells in G₁ after induction and the percentage of the population which formed gametes in the light was observed (Fig. 9B) indicating that cells in G₁ responded preferentially to the induction cue.
DISCUSSION

We found that the centric diatom, *T. weissflogii*, can be induced to undergo spermatogenesis in response to a decrease in photon flux density. Responsiveness to this cue is unrelated to cell size in the populations we examined. Rather, our evidence strongly suggests that cells preferentially respond to induction signals during a limited portion of their cell cycle. This dependence of developmental options on the location of a cell in its cell cycle has been observed in a number of other eukaryotes (e.g. Kates and Jones 1964, Schmeisser et al. 1973, Pringle and Hartwell 1981, Clegg et al. 1987, Gomer and Firtel 1987, Hoffmeister and Schaller 1987), and translates into an enormous amount of diversity in the behavior of diatom populations under changing light conditions.

The evidence supporting the hypothesis that the susceptibility of a *T. weissflogii* cell to an induction signal is dependent on the cell cycle has several dimensions. First, within a given population, the maximum number of cells that form gametes when returned to the light is proportional to the number of cells that divide in the dark; once cell division stops in the dark, no more cells are triggered to undergo spermatogenesis even if the duration of the dark interval is lengthened (Fig. 5). Cell cycle progression is thus implicated as a necessary component of induction. Second, the use of populations with discrete cell cycle distributions
Fig. 8. A) Distribution of chlorophyll fluorescence per cell of an exponentially growing population. The vertical lines indicate the boundaries of sorting windows. B) Distribution of chlorophyll fluorescence per cell of the sorted samples.
Fig. 9. A) Mean chlorophyll fluorescence of the sorted samples described in Fig. 8 versus the percentage of G_1 cells in each sample after the 2 h dark induction interval. (B) Maximum percentage of each of the sorted subpopulations which underwent spermatogenesis after a 2 hour dark exposure. In (B), samples were analyzed 14 h (O) and 18 h (□) after release into continuous light.
Mean Chlorophyll Fluorescence of Sorted Samples (relative units)

Percent in G₁ after Dark Induction

\( r = 0.855 \)
\( p < 0.001 \)
indicates that the magnitude of a population response is directly related to the number of G₁ cells present within the culture when the dark induction cue is imposed (Fig. 9B). This suggests that G₁ cells are more responsive to the induction signal than cells in other stages of the cycle. Furthermore, the non-zero X axis intercept of Fig. 9B indicates that even within the G₁ population, all the cells are not equally responsive to the cue. Assuming that chlorophyll fluorescence is a measure of cell age (Fig. 9A), younger G₁ cells will be in those populations with the highest proportion of G₁ cells whereas older G₁ cells will be in those populations with the lowest proportion of these cells. This suggests that populations with a high proportion of young G₁ cells are the most responsive to the induction signal. Taken together, these results indicate that, similar to the freshwater alga, Chlamydomonas reinhardtii (Kates and Jones 1964, Schmeisser et al. 1973), T. weissflogii responds preferentially to an induction trigger during an inducible region located in early G₁; cells in the remaining portions of the cycle essentially ignore the signal and continue to divide mitotically (Fig. 10).

To fully explain each of the observed responses of populations to a change in light conditions in terms of this model, the manner in which light affects cell cycle progression must first be examined. The T. weissflogii cell cycle contains two light dependent regions, one in G₁ and another in G₂, where continued cell cycle progression requires light (Vaulot et al. 1986, Olson et al.
The amount of time necessary to traverse these segments increases when light is limiting. In the dark, cell cycle progression ceases completely, and cells arrest in either G₁ or G₂.

With this as a framework, the behavior of populations under a range of light regimes can be interpreted. A key predictor of a population response under a given set of conditions is the number of cells which move through the inducible region. When a culture which has been maintained in exponential growth is transferred to an extended period of darkness, the total number of cells which are past the G₂ but before the G₁ light dependent region determines the maximum number of cells which can move into the inducible region during the dark interval (Fig. 10). The longer the population is maintained in the dark, the greater the number of cells which will move through the inducible region until eventually cell cycle progression ceases in each cell. At this point, all the induced cells will be located in the light dependent region of G₁ (Fig. 10), and one can not further increase the percentage of the population induced to undergo spermatogenesis by extending the dark period (Fig. 5). Since gametic differentiation does not occur until the population is returned to the light (Fig. 1), cells must exit the mitotic cycle somewhere after this G₁ dark arrest point. A burst in the initiation of spermatogenesis is thus observed as the induced cells move out of the light dependent region and exit the cell cycle (Fig. 3B).
Fig. 10. Schematic of the relationship between the mitotic cell cycle and responsiveness to an induction signal. Location of the light dependent segments of the cell cycle is based upon studies by Vaulot et al. (1986). The important features of this model are the relative positions of the various segments rather than the actual durations of each segment.
A major difference between a transfer to darkness and a transfer to subsaturating PFDs is that cell cycle progression eventually ceases in cells kept in the dark, whereas it merely slows in cells maintained in dim light. After a transfer to low light, therefore, each cell within a given population should eventually move through the inducible region; more time will be required for this to occur under more light limiting conditions. The fact that the proportion of cells that undergo gametogenesis does vary with the light intensity of the shift (Figs. 6, 7) therefore indicates that at least one other factor must limit the number of cells which are actually induced. We hypothesize that the apparent "decay" of the cue (Fig. 6) results from the fact that phytoplankton are able to photoadapt to new light conditions (e.g., Falkowski 1980); eventually the shift to low light is no longer sensed as a new light level, and all the cells divide mitotically. The maximum percentage of cells induced to form gametes under subsaturating light will thus be determined by the duration of the cell cycle in the new light conditions relative to the length of time that low light functions as a trigger.

The induction of spermatogenesis in T. weissflogii is undoubtedly more complex than has been described thus far. For example, the slope of Figure 5C indicates that approximately 60% of the cells which divided during the dark interval and thus moved into the inducible region actually formed gametes in the light. Also, the scatter observed in Figure 4A cannot be explained even if the
responses of all our various isolates are plotted against a measure of the number of cells which move into the inducible region (the number of cells which divided during the dark interval). Although a statistically significant positive correlation is obtained (r=0.549, P<.001, data not shown), a great deal of the variability remains unexplained. This cell cycle model can thus predict the responses within a given population, but it is inadequate for predicting the responses between different populations.

Induction of spermatogenesis in T. weissflogii may in fact be a two step process similar to the induction of meiosis in the budding yeast, Saccharomyces cerevisiae (Mitchell 1988). In yeast, nutrient limitation fulfills the first requirement for induction, but only those cells which are heterozygous at the mating locus are actually able to undergo meiosis (Herskowitz 1988). Perhaps movement of cells through the inducible region of G1 in dim light or darkness fulfills the first requirement in diatoms, but as with yeast, the cell must also possess a particular genetic makeup in order to fulfill the second requirement. If this is indeed the case, it may explain the wide range of responses we observed among our various cultures: our method of obtaining the original isolates undoubtedly resulted in genetic differences among these populations. Thus, certain populations may be particularly susceptible to an induction cue whereas others may be relatively unresponsive. Moreover, although diatoms are believed to be monoecious (i.e., both males and females can result from a single clone), we have yet to
observe any evidence of the presence of females in our induced cultures. Perhaps these unresponsive or "sterile males" are actually females awaiting a proper induction signal.

Predictions of the number of cells that will undergo spermatogenesis in response to an induction signal thus require that at least three layers of complexity be taken into consideration: first, the number of cells which move through the inducible region; second, the amount of time that a shift in PFD functions as an induction signal; and third, the number of cells which may be functionally sterile in their response to a change in light conditions.

What are the implications of these results for diatom populations in the field which are exposed to a decrease in PFDs on a daily basis? The maximum extent of gametogenesis in a population depends not only on the presence of an induction signal but also upon the manner in which this signal influences cell cycle progression. If the cell cycles of a population of cells are aligned such that few cells move through the inducible region during the night, for instance, then a minimum number of cells will be induced to form gametes. In this regard, it is interesting to note that in contrast to other eukaryotic phytoplankton, diatoms divide predominantly during the light interval (e.g., Nelson and Brand 1979, Chisholm et al. 1984). Moreover, Chisholm and Costello (1980) found that in T. weissflogii, the timing of the division burst (i.e., an approximation of the interval when cells should move through the
inducible region) on a light/dark cycle varies with temperature, the
duration of the light interval, nutrient status, and even cell size.
Thus, realistic predictions of the extent of sexuality that occurs
in the field require a greater understanding of those factors that
function as induction signals and the manner in which these factors
influence cell cycle progression.

Many thanks to Sheila Frankel and Erik Zettler for their
technical support and to D. Anderson, B. Binder, J. Bowen, W.
Hastings, B. Horvitz, N. Price, and E. Urbach for helpful manuscript
suggestions.

This work was supported in part by National Science Foundation
grants OCE 8316616, OCE 8421041, and 8614488 TO S.W.C. and OCE
8416964 and OCE 8508032 to R.J.O. and by Office of Naval Research
contracts N00014-83-K-0661 to S.W.C. and 84-C-0278 and 87-K-0007 to
R.J.O. and S.W.C.
References


CHAPTER 3

PATTERNS OF CELL SIZE CHANGE IN A MARINE CENTRIC DIATOM
Abstract

During nearly two years of exponential growth, isolates of the centric diatom, *Thalassiosira weissflogii*, displayed periodic increases and decreases in mean cell size as predicted for diatom populations alternating between asexual and sexual reproduction. However, despite the fact that each culture was maintained in constant, identical conditions, the overall patterns of cell size changes displayed by the various populations were unique, complex and unpredictable. The onset of sexual reproduction, the rate of increase in average cell size, and the size of the post-auxospore cells created during a sexual event varied among isolates and even within a given isolate over time; the only constant feature among the various cultures was the rate of decrease in mean cell size. We hypothesize that the extent of the variability exhibited by the various populations results ultimately from the fact that the genetic composition of diatom populations varies over time.
Introduction

Beginning as early as the mid 1800's, studies have indicated that the diatom life cycle is influenced by the unique configuration of its cell wall, a frustule composed of two unequally sized silica valves encircled by a series of siliceous girdle bands (e.g. MacDonald 1869, Geitler 1935, von Stosch 1965, Drabes 1977). Due to the physical constraints of the frustule, each mitotic division creates one daughter cell whose diameter is smaller than that of her sister or her mother by twice the thickness of these girdle bands. For most diatoms, therefore, the mean cell size of a population decreases and the standard deviation about this mean increases over successive generations. Perhaps not surprisingly, though a number of exceptions to this general rule of size reduction have been observed (e.g. Rao and Desikachary 1970, Round 1972, Crawford 1980).

The most common manner of escaping the trend of diminishing cell size is through sexual reproduction (Drabes 1977). In response to a range of environmental cues including sudden changes in light, temperature, salinity or nutrient conditions (e.g. Steele 1965, Drabes 1966, Schultz and Trainor 1968, Furnas 1985, French and Hargraves 1985, Vaulot and Chisholm 1987), diatoms can become sexual; meiosis replaces mitosis and the resulting male and female gametes fuse to form a zygote or auxospore. This auxospore escapes its frustule to create a post-auxospore cell many times larger than either parent (e.g. Findlay 1969). In addition to their new large size, post-auxospore cells apparently also possess an increased
"vigor" since they are often observed to grow at faster rates than those of the relatively small cells from which they were created (Paasche 1973, Costello and Chisholm 1981). An alternative, but rarely observed means of restoring cell size occurs asexually, generally in response to the alleviation of extreme nutrient deprivation. In this circumstance, a vegetative cell simply extrudes its cytoplasm into the surrounding waters and develops a new and much larger frustule (e.g. von Stosch 1965, Drebes 1966, Gallagher 1983, French and Hargraves 1986).

Whether created asexually or sexually, large cells are considered to be incapable of responding to sexual induction signals for several generations, until a permissive size range, approximately 30-40 percent of a species' maximum diameter, is obtained (Drebes 1977). Within this permissive range, an even further refinement of the size control of sexuality has been observed; often, smaller cells appear to preferentially undergo spermatogenesis while larger cells tend towards oogenesis (e.g. Geitler 1952, Migita 1967, Rao 1971, French and Hargraves 1985). Moreover, the signals inducing the cells to undergo either spermatogenesis or oogenesis may differ slightly (Holmes 1966, Drebes 1977). Thus, within an actively growing diatom population there exists an assortment of cell sizes with distinctly different physiologies (e.g. Werner 1971) which makes the study of diatom life cycles extremely complex.
We recently examined whether the putative size requirement for sexual differentiation could account for the proportion of a population that was triggered to undergo spermatogenesis in response to a change in light conditions (Armbrust et al. 1990). To our surprise, we found that for a number of isolates representing a broad range of size distributions, there was no correlation between average cell size and the proportion of a population that could be induced to undergo spermatogenesis. While attempting to interpret these data, we found that no long-term studies existed which described in detail the evolution of cell size in an exponentially growing diatom populations. Although there are many predictions for the change in cell size over time, no data exists on the development of these changes through more than one round of sexuality (e.g. Findlay 1969, Rao 1971). Thus, we initiated a long-term study to document exactly how, under optimum growth conditions and in the absence of external signals, cell size changes in diatom populations over successive generations.

Materials and Methods

Isolates of T. weissflogii Grun. clone Actin (from the Culture Collection of Marine Phytoplankton, Bigelow Laboratories for Ocean Sciences) were obtained by isolating colonies from 2% agar plates and transferring them to f/2 enriched seawater media (Guillard 1975) with nitrate as the nitrogen source. Each isolate was maintained in semi-continuous batch cultures at 20°C and saturating levels of
continuous illumination (250 μE·m⁻²·sec⁻¹, cool-white fluorescent) (Armbrust et al. 1990). After approximately 120 days in exponential growth, new populations were initiated by plating the parent culture and isolating additional colonies (Fig. 1). Each isolate was then split into replicates; at least 10,000 cells were used for each inoculum. Throughout the following discussion, the term isolate rather than clone will be used. Although each population arose from a single cell, diatoms are diploid and genetic recombination during sexual reproduction prevents cultures from remaining genetically homogeneous and thus clonal over time.

In an attempt to obtain genetically identical populations, individual cells from known cell lineages were isolated and cloned. These single cell isolations were obtained by viewing an aliquot of two different cultures through a dissecting microscope and manually picking individual cells from the liquid media. Each of four isolated cells (two from each culture) was transferred to its own well (within a 96-well plate) containing f/2 media. Approximately 24 hours later, each daughter cell was removed from a given well, transferred to its own well, and allowed to develop into a population. In this manner, cultures originating from 15 single cell isolations of known relationships were obtained (Fig. 2). These cultures were also maintained in semi-continuous batch culture at 20°C and 250 μE·m⁻²·sec⁻¹ of continuous light. Cultures descended from the same mother cell were considered to be genetically identical until the onset of sexual reproduction.
Figure 1. Cell lineages and initial Coulter volume distributions of T. weissflogii populations. Each isolate is designated by a number corresponding to its mean Coulter volume ~2 weeks after transfer from colonies on agar plates to liquid medium. The laboratory stock culture was plated and two isolates, 868 and 1724 were isolated and maintained in exponential growth. An aliquot of 868 was plated and two new isolates, 709 and 877 were initiated. In the course of conducting experiments with isolate 868, the average Coulter volume of one experimental flask spontaneously increased suggesting that sexual reproduction had occurred. This newly enlarged population was designated 1147. After approximately 120 days of exponential growth, aliquots of 1724, 877, and 1147 were plated and 6 new isolates, 637, 834, 485, 747, 444, and 920 were initiated. Once each isolate was transferred to liquid media, the population was maintained in exponential growth. In each Coulter volume distribution panel, "initial" refers to the Coulter volume distribution of a population soon after isolation and "subclnd" refers to the Coulter volume distribution of the same population at the time the derivative isolations were made.
Fig. 2. Cell lineage and initial Coulter volume distributions of populations derived from genetically identical cells (A, B, C, D). The four original cells were isolated from replicate cultures of isolate 1724 (1724-1 & 1724-2). The number of branches in a family tree is based on the number of cells observed in each well at the end of 24 hours and indicates the hypothesized number of divisions that occurred before the cells were reisolated. The X in certain circles indicate that some of the reisolated cells did not develop into cultures. The Coulter volume distributions of each population approximately 2-3 weeks after the initial isolation are shown below each tree. The different line types indicate the individual cell lines.
Size distributions and the mean cell size of each population were determined with a Coulter Electronics Model Zm/C256 electronic particle counter. The within-measurement error was estimated by determining the Coulter volume distributions of multiple aliquots of a given population; the mean Coulter volumes of these subsamples varied by less than 5%. The between-measurement error over consecutive days was estimated by determining the extent of the scatter during a linearly decreasing interval of mean Coulter volume. Although random outliers were seen, the greatest persistent scatter observed was approximately 40%; the vast majority of cultures, however, displayed substantially less spread, in many instances an amount comparable to the within measurement error. The coefficient of variation (CV = standard deviation/mean) was determined for each size distribution.

A Turner fluorometer was used to monitor daily changes in the in vivo fluorescence of each culture to determine growth rates (Brand et al. 1981). An innoculum of at least 10,000 cells were transferred to approximately 30 ml fresh media while the in vivo fluorescence was still less than about twenty percent of the maximum fluorescence. Thus, new cultures were inoculated every 2-3 days. Before each transfer, the Coulter volume distribution was determined.
Results

Evolution of mean Coulter volume over time. Coulter volume distributions of a series of isolates representing a broad range of cell sizes and cell lineages (Fig. 1) were monitored for nearly two years to determine the long term trajectories of cell size in T. weissflogii populations. Each isolate displayed periodic increases and decreases in mean cell size. However, the overall patterns of the cell size changes displayed by each culture varied dramatically despite the fact that each population was maintained under identical conditions. The timing, rate of increase, and amplitude of the size oscillations differed between isolates, within a given isolate over time, and even between replicate flasks of a single isolate (Figs. 3-6). For instance, a number of the populations, regardless of their size distribution upon isolation (see Fig. 1), underwent dramatic increases in average cell size early on, only to later undergo smaller, more rapidly occurring oscillations (Figs. 3A, 4A & B, 5B & C). Other isolates maintained a relatively small size throughout the study although increases and decreases in size were still apparent (Figs. 3C, 5A, 6A, B & C). Moreover, the rate of increase in average Coulter volume in the various isolates ranged from a maximum of nearly 23 μm³·cell⁻¹·gen⁻¹ (Fig. 3A) to a minimum of about 1.2 μm³·cell⁻¹·gen⁻¹ (Fig. 4B).
Figs. 3. Mean Coulter volume over time of the *T. weissflogii* isolates presented in Fig. 1. A) Population 1147, was maintained in exponential growth and beginning at t=0 days, the Coulter volume distributions were monitored over time. At t=127 days, the culture was split into replicate flasks (darkened triangles and open circles). B, C) At t=120 days (as indicated by arrow in (A)), 1147 was plated and two new isolates, 920 and 444, were initiated. At t=127 days, these new cultures were split into replicate flasks (darkened triangles and open circles) and the Coulter volume distributions of each were monitored over time.
Mean Coulter Volume ($\mu m^3$)
Figs. 4. Mean Coulter volume over time of the *T. weissflogii* isolates presented in Fig. 1. A) Isolate 1724 was maintained in exponential growth and beginning at $t=0$ days, the Coulter volume distributions were monitored over time. At $t=127$ days, the culture was split into replicate flasks (darkened triangles and open circles). B, C) At $t=120$ days (as indicated by arrow in (A)), 1724 was plated and two new isolates, 834 and 637, were initiated. At $t=127$ days, these new cultures were split into replicate flasks (darkened triangles and open circles) and the Coulter volume distributions of each were monitored over time.
Figs. 5. Mean Coulter volume over time of the *T. weissflogii* isolates presented in Fig. 1. A) Isolate 877 was maintained in exponential growth and beginning at *t*=0 days, the Coulter volume distributions were monitored over time. At *t*=127 days, the culture was split into replicate flasks (darkened triangles and open circles). B, C) At *t*=120 days (as indicated by arrow in (A)), 877 was plated and two isolates, 593 and 747, were initiated. At *t*=127 days, these new cultures were split into replicate flasks (darkened triangles and open circles) and the Coulter volume distributions of each were monitored over time.
Figs. 6. Mean Coulter volume over time of the *T. weissflogii* isolates presented in Fig. 1. A) Isolate 868 was maintained in exponential growth and beginning at t=0 days, the Coulter volume distributions were monitored over time. At t=127 days, the culture was split into replicate flasks (darkened triangles and open circles). B, C) At t=120 days (as indicated by arrow in (A)), 868 was plated and two new isolates, 709 and 877, were initiated. At t=127 days, these new cultures were split into replicate flasks (darkened triangles and open circles) and the Coulter volume distributions of each were monitored over time.
Perhaps the most surprising result of all was that replicate cultures did not always behave as replicates; they consistently "tracked" each other only during the initial downward swing in average Coulter volume (during this interval, the slopes and elevations of the replicate lines were not significantly different, p>0.5, Student's t test). Replicates sometimes diverged when one of the cultures initiated cell enlargement (for example, Figs. 3A & B, 5B & C); the onset of this size increase might (e.g. Figs. 3B, 4) or might not (e.g. Fig. 3A) occur simultaneously in a pair of replicates.

Since diatoms are known to decrease in cell size during mitotic divisions, the intervals of decreasing mean Coulter volume were assumed to reflect a predominance of asexual reproduction. The intervals of increasing mean Coulter volume were assumed to reflect the formation of auxospores, a process that can occur both sexually and asexually. Because none of the cultures experienced nutrient deprivation, asexual cell enlargement (Drebes 1966, Gallagher 1983) was considered an unlikely source of the observed increase in cell size. Moreover, von Stosch (1965) was unable to induce asexual cell enlargement in any of his Thalassiosira species, so this type of auxospore formation may not be possible in this genus. Therefore, for the purposes of our discussion, the intervals of increasing mean Coulter volume are assumed to reflect the sexual formation of auxospores.
The onset of sexual reproduction in each of the various cultures was staggered in time in an unpredictable manner (Fig. 3-6) thus eliminating the possibility that an unintentional and undetected fluctuation in the environment (such as the quality of different batches of seawater) triggered the initiation of these sexual events. Some isolates underwent sexual reproduction and auxospore formation as frequently as every 120 generations (about 2 months, e.g. Fig. 3A) while other populations remained asexual for up to 450 generations (approximately 8-9 months, e.g. Fig. 5B).

The extent of variation observed in the behavior of the various populations despite constant growth conditions, indicated underlying genetic variability among the isolates. Cell lineage (Fig. 1), however, predicted population behavior only slightly better than did the initial size distributions. This is not surprising since each of the original mother isolates had undergone at least one round of auxospore formation and thus sexual reproduction by the time the new daughter isolates were initiated (Figs. 3A, 4A, 5A, 6A). Genetic recombination in these diploid cells during sexual reproduction undoubtedly created the variability in behavior. For example, the average cell size of two isolates, 877 and 868, remained relatively small throughout the study (Figs. 5A, 6A), but only in the 868 lineage did the descendents also remain small (Fig. 6). Descendents of isolate 877 underwent relatively large size increases (Fig. 5). Similarly, the behavior of population 1147, which presumably arose from 868 via sexual
reproduction (Fig. 1), not only contrasted sharply with that of the population from which it was derived, but also with that of its own descendents (Fig. 3). And finally, isolate 1724 which was engaged in auxospore formation when the new isolates were initiated, yielded two populations (834 and 637) one of which was on the downswing of the cycle (Fig. 4B) and the other of which was on the upswing (Fig. 4C), suggesting that the progenitor of 834 had recently undergone sexual reproduction while the progenitor of 637 was still a few generations away.

Against this backdrop of variability, the rate of decrease in mean cell size was relatively constant; on average, cells decreased in Coulter volume by about 8 \( \mu m^3\cdot cell^{-1}\cdot gen^{-1} \) (Table 1). The expected rate of decrease in volume during asexual reproduction can be calculated based on an estimate of the thickness of the girdle bands attached to each frustule half. Li and Volcani (1985) have estimated that the girdle bands of the centric diatom *Ditylum brightwellii*, range from approximately 7 nm to perhaps as much as 15 nm thick (comparable to the thickness of the frustule itself). Assuming that upon mitotic division, the diameter of one daughter cell decreases by twice the thickness of these girdle bands, the volume changes in the *T. weissflogii* cultures should have varied from approximately 2 - 11.5 \( \mu m^3\) per cell per generation (depending on the initial volume used in the calculations). These predictions agree remarkably well with the measured values (Table 1).
The minimum average Coulter volume achieved within a given isolate was generally constant (Figs. 3-6), as would be expected if sexual reproduction was restricted to cells within a permissive size range (e.g. Drebes 1977), but, it should be noted that in one isolate, an upswing was initiated at about 850 \( \mu m^3 \) (Fig. 3A) while in another isolate the upswing began at about 1550 \( \mu m^3 \). This latter value corresponded to a diameter 78% of the eventual maximum diameter (Fig. 4A) and was far in excess of the 30-40% range generally used to define the potential onset of sexuality (Drebes 1977). Moreover, between isolates, the minimum volume ranged from 400 to 700 \( \mu m^3 \). Contrary to other reports (e.g., Migita 1967, Rao 1971), this minimum average cell size did not consistently predict the maximum size obtained once an upswing was completed. Instead, the maximum average size varied greatly and populations underwent anywhere from a 1.2 to a 3.5 fold increase in mean cell size (Table 1). These results implied that at least one of two parameters could differ among populations: either the proportion of cells involved in the formation of auxospores or the maximum size obtained by any given cell.

Coulter volume distributions. The coefficient of variation (CV), an estimate of the extent of dispersion around a mean Coulter volume measurement, was monitored in each culture over time to determine the amount of variability in the size of the individual cells within a population and to estimate whether or not distinct subpopulations remained in a culture once the maximum average
volume was obtained. As each population decreased in average Coulter volume, the spread around the mean increased as would be predicted for populations undergoing asexual reproduction (Rao and Desikachary 1970). As each population began to undergo sexual reproduction, however, the CV decreased such that once the maximum average cell size was obtained, the variation around this new mean was at a minimum (Fig. 7). The minimum CV could vary from 25 to 45 % regardless of either the magnitude of the size increase or the maximum size obtained by the population. However, the spread around the mean volume after a sexual episode was always less than that before the cells initiated sexual reproduction suggesting that by the end of a sexual event a majority of the cells had formed comparably sized post-auxospores.

To determine whether all the cells within a culture were in fact behaving in concert as the CV data suggested, the Coulter volume distributions themselves were examined. During an interval of decreasing mean Coulter volume, populations displayed unimodal size distributions, the CV’s of which gradually increased over time (Fig. 8). During the intervals of increasing mean Coulter volume, the size distribution generally developed into two distinct peaks. Over the course of anywhere from 2 weeks to a month, this bimodal distribution eventually resolved into a new unimodal distribution with a larger mean and a decreased CV (Fig. 9). The maximum size obtained by a cell was not constant and could vary between isolates (Fig. 9), within a single isolate over time (Fig. 9A, C, D), and
even between replicate cultures (data not shown). Therefore, cultures that displayed minor size fluctuations (Figs. 3C, 5A, 6) simply produced smaller post-auxospores than cultures that underwent dramatic oscillations in mean cell size (Figs. 3A, 4A & B, 5B & C).

There was no indication that distinct subpopulations with different size distributions persisted after the maximum average cell size was obtained confirming that all the cells present within the population had undergone cell enlargement by the end of a sexual event. However, it should be noted that it is impossible to determine based on size distributions alone, whether each cell within a population eventually underwent sexual reproduction or only a portion of the cells formed auxospores, the descendents of which then came to dominate the population due to an increased growth rate.

Single cell isolations. An analysis of the possible sources of the variability observed among our various isolates was confounded by the fact that each of the original isolates had undergone sexual reproduction prior to the initiation of replicates and additional isolates (Figs. 3-6). In an attempt to eliminate this complication, a series of cultures derived from genetically identical cousin cells were initiated (Fig. 2) and maintained under the same constant conditions as described previously. The majority of these single cell isolates underwent relatively minor size fluctuations over time (Figs. 10, 11), a behavior that essentially mimicked the minimal size changes observed in the two cultures from
Fig. 7. Mean Coulter volume (darkened triangles) and the coefficient of variation of each volume measurement (open circles) over time for a representative *T. weissflogii* population, 1147. The CV's were smoothed over three measurements.
Figure 8. A) Mean Coulter volume over time of a representative T. weissflogii culture, isolate 747 and B) the Coulter volume distributions during the interval of decreasing mean cell size highlighted in A.
Figure 9. Mean Coulter volume over time of two *T. weissflogii* cultures and their Coulter volume distributions during the intervals of population size increase. A) Mean Coulter volume over time in a population that initially underwent a dramatic, 3.5-fold, increase in average cell size only to later undergo a series of 1.5-fold increases. B) Mean Coulter volume of a population that remained relatively small throughout the study. C, D) Coulter volume distributions over time of intervals indicated by the highlighted regions in A. E) Coulter volume distributions of interval indicated by the highlighted regions in B.
Fig. 10. Mean Coulter volume over time for two sets of populations derived from genetically identical cells of *T. weissflogii* isolate 1724-1 at t=340 days (see Fig. 4A). Each panel represents populations derived from the same grandmother or great-grandmother cell as indicated in Fig. 2. The different symbols represent the four cell lines derived from the original genetically identical cells. The insets are a blow up of the mean Coulter volume (note change in scale) during the first 20 days after the initial isolation.
Fig. 11. Mean Coulter volume over time for two sets of populations derived from genetically identical cells of *T. weissflogii* isolate 1724-2 at t=340 days (see Fig. 4A). Each panel represents populations derived from the same grandmother or great-grandmother cell as indicated in Fig. 2. The different symbols represent the three or four cell lines derived from the original genetically identical cells. The insets are a blow up of the mean Coulter volume (note change in scale) during the first 20 days after the initial isolation.
which these isolates were derived (Fig. 4A, beginning at $t=340$ d). Moreover, the members of each set of replicates initially behaved identically as would be expected of populations composed of genetically identical cells (the slopes and elevations of the replicate cultures were not significantly different for at least twenty days after isolation, $p>0.05$, Student’s $t$ test; see insets Figs. 10, 11). Over time, however, the average cell volume in even these cultures diverged as one of the replicates began to increase in mean Coulter volume; this divergence can be seen most dramatically in Figs. 10B and 11A. Note that the maximum size obtained by populations which were initially genetically identical was not constant implying that over time, the genetic composition of these populations had changed.

Population growth rates. It has repeatedly been shown that post-auxospore cells grow more rapidly than relatively small cells involved in asexual reproduction (e.g., Paasche 1973, Costello and Chisholm 1981). A great deal of scatter was observed in the population doubling times of the $T.$ weissflogii isolates derived here and there was no consistent correlation between average cell size and growth rate regardless of the culture examined (Table 1); in only four out of 22 cultures was the relationship significant. When the growth rate of a culture was examined over time rather than simply with respect to absolute cell size, however, a different picture began to emerge. For those cultures in which the mean cell size remained relatively constant, the population growth rates could
vary dramatically with no apparent predictability (Fig. 12A, B).
However, during intervals in which discernible oscillations in cell size were apparent, the growth rate was correlated with cell size; newly enlarged cells appeared to grow faster than the smaller cells from which they were created (Fig. 12B, C).

Discussion

The control of cell size in populations of the centric diatom, *T. weissflogii*, is a quite complicated process. Numerous isolates of this diatom representing a broad range of size distributions and cell lineages, each displayed complex and unpredictable patterns of cell size change during nearly two years of continuous exponential growth. The only feature common to these various size patterns was the rate of decrease in mean cell size, a value which is determined by the physical constraints of the diatom frustule during mitotic divisions and the minimum cell size achieved within a given culture. The rest of the components, i.e., the timing of the onset of sexual reproduction, the rate of increase in average cell size, and the size of the post-auxospores created during the sexual events varied among populations and even within a given population over time in the absence of any obvious selection pressures. We hypothesize that the variability in the patterns of cell size change exhibited by these cultures results from the fact that the genetic composition of the populations varied over time.
Fig. 12. Mean Coulter volume (open circles) and population growth rate (closed triangles) over time in three isolates of T. weissflogii. The growth rate data were smoothed over three measurements.
In the absence of any discernible environmental triggers, the transition from asexual reproduction to sexual reproduction is apparently linked with the obtainment of an appropriate cell size. However, this permissive size range can vary among different populations and in some instances, even within a given population over time. Thus the relationship between cell size and the capacity to undergo gametogenesis is not absolute; the ability of two comparably sized cells to exit the mitotic cycle and undergo sexual reproduction appears to be determined by the genotypes of these cells. This result may explain our inability to predict the extent of spermogenesis induced in these various isolates (Armbrust et al. 1990).

The size of the post-auxospore cells created during the sexual episodes also varied considerably both within and among the different populations regardless of the size of the cells that underwent gametogenesis. The number of generations that elapse between the completion of one sexual event and the initiation of a new one should be determined by the amount of time necessary for these newly created large cells to reach a permissive size range. Thus, the relative values of these two parameters along with the growth rate of the vegetative cells will determine the frequency of sexual events in diatom populations.

The third factor that varied among the different isolates, the rate of increase in mean cell size, is perhaps the most difficult to interpret. At least two possible scenarios exist for what may have
occurred during the intervals of increasing mean Coulter volume. In the first scenario, all the cells within a population are hypothesized to eventually undergo sexual reproduction and auxospore formation during a given interval of time; the rate of increase in average cell size is thus determined by the size of the post-auxospore cells and the rate of entry of vegetative cells into the permissible size range, i.e., the generation time of these asexual cells. In the second scenario, only a portion of the cells are hypothesized to form auxospores but the generation time of these newly enlarged cells is assumed to be much shorter than that of cells which have not yet undergone sexual reproduction. The amount of time for such a cohort of cells with an increased growth rate to dominate a population can be predicted (Wood 1989). Assuming that in the most extreme case only one post-auxospore cell is created in a population of 10,000 cells with an average growth rate of 1.386 day⁻¹, the growth rate of the post-auxospore would have to be 2.372 day⁻¹ or 1.7 times faster than the other cells for its descendents to represent 99% of the population in 2 weeks and 1.846 day⁻¹ or 1.3 times faster for its descendents to dominate in 1 month. However, if instead of only one cell, 50% of this same population formed auxospores, then the growth rate of these cells would only have to be 1.714 day⁻¹ for this cohort to dominate in two weeks and 1.539 day⁻¹ or 1.1 times faster than average for the descendents of the post-auxospore cells to dominate the population in one month. Thus, if in fact only a portion of a population undergoes sexual
reproduction, replicate cultures may quickly diverge depending on which cohort of cells comes to dominate which culture.

Given any differences in growth rates in pre- and post-auxospore cells, it becomes impossible to determine based on cell size distributions alone, what portion of a population actually formed auxospores. However, regardless of whether or not the entire population or only a fraction of the population undergoes sexual reproduction, by the time the maximum mean cell size is obtained, all the cells remaining within a culture are the descendents of auxospores (Fig. 9). Thus, the genetic composition of a population before the interval of increasing mean Coulter volume will differ from the composition of the population after the sexual event; consequently either the permissive size range or the new potential size of post-auxospores may have changed. Even more genetic variability can be generated in these populations due to the possibility of spontaneous mutations (Lande 1976). As described previously, any cell with a faster than average growth rate can come to dominate a population over time. If this faster growing cell also possesses a mutation that affects the control of cell size, then this new genotype can be propagated throughout the population during the intervals of asexual reproduction.

This study which began as an attempt to describe the development of cell size over time in diatoms, has uncovered some of the wonderful complexity of these populations. The composition of a population of these organisms even in the absence of any selection
pressures is extremely fluid with the potential for frequent alterations of both the genotypes and phenotypes of its members. Even populations that originate from genetically identical cells can rapidly display dramatically different behaviors. Thus, over the course of a year, the characteristics of a population may undergo numerous transformations, a feature which must be kept in mind as attempts are made to understand the details of the physiology of these organisms.

Acknowledgments

Many thanks to Sheila Frankel for her technical assistance, to Dean Jacobsen for his help with the single cell isolations, and to Tina Bartschat for her translations of German articles. The culture work could not have been performed without the help of S. Krolikowski, D. Chen, J. Hwang, T. Helsten, A. Worden and C. Utterback who were supported in part by Sea Grant and the UROP office at MIT.
TABLE 1. Summary of the rates of decrease and increase in mean Coulter volume and the ratio of the maximum volume of a population to the minimum value prior to the initiation of a size increase. All rates reflect the linear regression during an increase or decrease in volume. A generation time of 12 hours was assumed in all calculations.

<table>
<thead>
<tr>
<th>Clone</th>
<th>Rate of Decrease $^{b}$ (µm$^3 \cdot$ cell$^{-1} \cdot$ gen$^{-1}$) X ± SE (n)$^{c}$</th>
<th>Rate of Increase (µm$^3 \cdot$ cell$^{-1} \cdot$ gen$^{-1}$) X ± SE (n)</th>
<th>Max:Min (range)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1147-1</td>
<td>9.8 ± 0.6 (5)</td>
<td>12.1 ± 3.8 (4)</td>
<td>1.6 - 3.5</td>
</tr>
<tr>
<td>-2</td>
<td>8.6 ± 0.6 (6)</td>
<td>10.3 ± 1.4 (5)</td>
<td>1.2 - 2.6</td>
</tr>
<tr>
<td>920-1</td>
<td>8.2 ± 0.8 (6)</td>
<td>4.5 ± 1.8 (5)</td>
<td>1.2 - 1.8</td>
</tr>
<tr>
<td>-2</td>
<td>9.2 ± 0.8 (4)</td>
<td>9.7 ± 3.8 (4)</td>
<td>1.2 - 2.4</td>
</tr>
<tr>
<td>444-1</td>
<td>7.2 ± 0.8 (5)</td>
<td>5.5 ± 1.5 (5)</td>
<td>1.2 - 1.9</td>
</tr>
<tr>
<td>-2</td>
<td>N. A.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>868-1</td>
<td>4.0 ± 0.8 (3)</td>
<td>2.3 ± 0.2 (4)</td>
<td>1.3 - 1.9</td>
</tr>
<tr>
<td>-2</td>
<td>N. A.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>709-1</td>
<td>6.0 ± 2.7 (2)</td>
<td>3.7 ± 1.2 (2)</td>
<td>1.6 - 2.3</td>
</tr>
<tr>
<td>-2</td>
<td>5.6 ± 1.6 (2)</td>
<td>5.3 ± 2.0 (2)</td>
<td>2.3 - 2.5</td>
</tr>
<tr>
<td>877-1</td>
<td>8.4 ± 1.3 (2)</td>
<td>3.6 ± 0.9 (2)</td>
<td>1.8 - 1.9</td>
</tr>
<tr>
<td>-2</td>
<td>N. A.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>877-1</td>
<td>8.4 ± 1.3 (2)</td>
<td>3.6 ± 0.9 (2)</td>
<td>1.8 - 1.9</td>
</tr>
<tr>
<td>-2</td>
<td>N. A.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>593-1</td>
<td>7.2 ± 0.7 (2)</td>
<td>9.6 ± 2.8 (3)</td>
<td>1.7 - 2.0</td>
</tr>
<tr>
<td>-2</td>
<td>9.6 ± 1.8 (4)</td>
<td>8.6 ± 3.0 (4)</td>
<td>1.3 - 2.1</td>
</tr>
<tr>
<td>747-1</td>
<td>8.2 ± 1.1 (2)</td>
<td>10.5 ± 5.1 (2)</td>
<td>1.3 - 2.0</td>
</tr>
<tr>
<td>-2</td>
<td>8.0 ± 0.8 (2)</td>
<td>5.2 ± 0.4 (2)</td>
<td>1.5 - 2.2</td>
</tr>
<tr>
<td>1724-1</td>
<td>16.4 ± 7.6 (4)</td>
<td>9.0 ± 2.9 (3)</td>
<td>1.8 - 2.1</td>
</tr>
<tr>
<td>-2</td>
<td>10.6 ± 0.8 (4)</td>
<td>12.0 ± 3.6 (4)</td>
<td>1.5 - 2.2</td>
</tr>
<tr>
<td>834-1</td>
<td>6.6 ± 1.6 (4)</td>
<td>3.8 ± 1.8 (3)</td>
<td>1.4 - 2.5</td>
</tr>
<tr>
<td>-2</td>
<td>6.4 ± 1.2 (4)</td>
<td>3.6 ± 0.7 (3)</td>
<td>1.3 - 2.4</td>
</tr>
<tr>
<td>637-1</td>
<td>4.8 ± 2.0 (2)</td>
<td>5.5 ± 1.6 (2)</td>
<td>1.6 - 2.2</td>
</tr>
<tr>
<td>-2</td>
<td>10.0 ± 2.8 (3)</td>
<td>5.8 ± 1.5 (4)</td>
<td>1.7 - 1.8</td>
</tr>
</tbody>
</table>
Table 1, cont.

a In reality, generation times ranged from approximately 8-19 hours, which does not influence the conclusions.

b Rates of decrease were multiplied by two since upon division, only one of the two daughter cells is smaller than the its mother.

c \( n \) refers to the number of increases or decreases in average Coulter volume regressed.

d -1 and -2 refer to the two replicate cultures.

e N. A. or not applicable indicates that at least two increasing or decreasing slopes could not be analyzed.
TABLE 2. Summary of correlation coefficients (r) between population doubling times and mean Coulter volume over time for T. weissflogii isolates maintained exponentially in continuous light and constant temperature. Doubling times were determined from three consecutive fluorescence readings. Only those growth rates which were derived from a regression with $r^2 > .990$ were considered for the calculation of the correlation coefficients.

<table>
<thead>
<tr>
<th>Isolate Designation</th>
<th>Replicate 1</th>
<th>Replicate 2</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>r</td>
<td>n</td>
</tr>
<tr>
<td>866</td>
<td>.0268</td>
<td>40</td>
</tr>
<tr>
<td>709</td>
<td>.104</td>
<td>37</td>
</tr>
<tr>
<td>877</td>
<td>.364</td>
<td>30</td>
</tr>
<tr>
<td>593</td>
<td>.213</td>
<td>33</td>
</tr>
<tr>
<td>747</td>
<td>.274</td>
<td>30</td>
</tr>
<tr>
<td>1147</td>
<td>.0396</td>
<td>26</td>
</tr>
<tr>
<td>920</td>
<td>.304</td>
<td>30</td>
</tr>
<tr>
<td>444</td>
<td>.0564</td>
<td>30</td>
</tr>
<tr>
<td>1724</td>
<td>.0149</td>
<td>35</td>
</tr>
<tr>
<td>834</td>
<td>.0439</td>
<td>37</td>
</tr>
<tr>
<td>637</td>
<td>.599*</td>
<td>37</td>
</tr>
</tbody>
</table>

*P < 0.05.
REFERENCES


Appendix

Effect of Light on the Cell Cycle of a Marine Synechococcus Strain
Effect of Light on the Cell Cycle of a Marine Synechococcus Strain

E. V. Araki, J. D. Bowen, R. J. Olson, and S. W. Cushing

Ralph M. Parsons Laboratory, 48-125 Massachusetts Institute of Technology, Cambridge, Massachusetts 02139; and
Biology Department, Woods Hole Oceanographic Institution, Woods Hole, Massachusetts 02543

Received 21 July 1988; accepted 3 November 1988

Light-dependent regulation of cell cycle progression in the marine cyanobacterium Synechococcus strain WH-8110 was demonstrated through the use of flow cytometry. Our results show that, similar to eucaryotic cells, marine Synechococcus spp. display two gaps in DNA synthesis, at the beginning and at the end of the cell cycle. Progression through each of these gaps requires light, and their durations lengthen under light limitation.

Predictions of the physiological responses of individual cells to environmental change require an understanding of cell cycle regulation. The environment affects the progression of cells through their various cell cycle stages and therefore influences the duration of the division cycle. Furthermore, many metabolic processes occur during discrete periods of the division cycle, resulting in limited intervals when cells are able to detect and respond to external stimuli. Thus, a complex feedback system exists between cells and their immediate surroundings. We have shown, for example, that the position of light-dependent arrest points in the cell cycles of two unicellular marine phytoplankton, a diatom and a coccolithophorid, explains the population growth patterns of these organisms on a range of light-dark cycles (25). Similarly, only with the discovery that photosynthesis and nitrogen fixation are restricted to different portions of the cell cycle (26), temporally separating nitrogenous uptake from oxygen evolution (26b) could the presence of nitrogen fixation in populations of unicellular cyanobacteria be adequately explained (26, 27).

Our interest in the cell cycle of marine Synechococcus spp. arose from a desire to understand the observed growth patterns of these cyanobacteria on a diel light-dark cycle. Like many diatoms (27), Synechococcus spp. divide predominantly during the light interval (28) rather than during the dark, a characteristic which sets these two groups of cells apart from most other phytoplankton. A second unusual characteristic of Synechococcus populations is that the frequency of dividing cells becomes constant during the dark interval when cell division is no longer occurring (28), implying that a certain fraction of the population is arrested in the double stage during most of the night.

The freshwater cyanobacterium Anacystis nidulans has been the focus of numerous cell cycle studies (e.g., 10, 24), and yet, cell cycle regulation in related marine species of unicellular cyanobacteria remains virtually unexplored. Prokaryotic cell cycle models based on Escherichia coli predict that DNA will be synthesized continuously throughout the division cycle when the amount of time necessary to complete DNA synthesis and cell division is greater than the generation time of the organism (12; 17, 18, 22). A. nidulans appears to contain multiple copies of its genome at growth rates which, according to the E. coli model, would not necessitate continuous DNA synthesis (23). The minimum doubling time observed for marine Synechococcus strains can be an order of magnitude greater than that of rapidly growing A. nidulans or E. coli populations. These observations raise the question whether the cell cycle characteristics of marine Synechococcus spp. will be more similar in appearance to the prokaryotic model of E. coli or to their rapidly growing prokaryotic relative, A. nidulans, or perhaps instead to the relatively slowly growing eucaryotic cells.

The goals of our study were to describe the DNA cycle of Synechococcus spp. as a function of the growth rate and to examine light-dependent regulation of the cell cycle in order to predict the behavior of populations of cells in their natural environment. Our emphasis was on the elucidation of this coupling between the natural photosynthetic unit and cell cycle progression, rather than on the mechanisms controlling this coupling. The locations of light-dependent processes were identified through the use of flow cytometry, by examining cell cycle responses to light limitation and by determining the arrest points of populations deprived of light (30, 36). Our findings indicate that, similar to eucaryotic cells, the marine Synechococcus spp. displays two gaps in DNA synthesis at each growth rate examined. Moreover, unlike most other unicellular algae, in which only the interval before DNA synthesis is light dependent (27, 30, 33), in the Synechococcus spp., cell cycle progression through each of the gaps in DNA synthesis requires light. For simplicity and in accordance with eucaryotic nomenclature, these two gaps will be referred to as G1 and G2 and the interval of DNA synthesis will be referred to as S.

MATERIALS AND METHODS

Culture conditions. The Synechococcus strain WH-8110, an isolate which lacks phycobilisomes, was obtained from John Waturner at the Woods Hole Oceanographic Institution and was grown in 1/2 enriched seawater medium (16). For the light limitation studies, semicontinuous cultures were maintained in exponential growth for a minimum of 17 generations at 25°C under continuous illumination ranging from 22.4 to 74 microequiv/m^2 s^-1. A Turner fluorometer was used to monitor daily changes in the in vivo fluorescence of the cultures in order to determine growth rates (5).

For the dark arrest experiment, cultures were grown at 1.2°C in continuous light at 70 microequiv/m^2 s^-1 before placement in the dark. During the course of the experiment, changes in the cell number were determined...
with an end-labeled Zeiss microscope. A sample of culture was diluted with filtered seawater to obtain approximately 25 to 50 cells per field and then filtered at a vacuum pressure of less than 135 mm of mercury onto a Nuclepore filter (pore size, 0.2 μm). The filter was then washed with a cover slip and a slide with immersion oil and either frozen or counted immediately. An average of 400 cells per filter was counted. In some experiments the cell number was also monitored with an Epics V flow cytometer (100-nm excitation, 800-nm band emission); a known quantity of standard beads was added to five samples to calculate the amount of sample run through the flow cytometer and thus determine the cell concentration (20).

A series of cultures were also maintained in steady state for 2 weeks on a 14-h light/dark cycle at a light level of 100 μmol photons m⁻² s⁻¹ and a temperature of 20°C. Average population growth rates were determined by monitoring in vivo culture fluorescence at the same time each day to eliminate the effects of diel periodicity on fluorescence yield. During the actual experiment, cell division was monitored by microscopy counts as described above.

Fitting and staining for flow cytometric analysis. In one to ten single cells were harvested by centrifugation at 11,000 × g for 5 min and subsequent removal of all but 0.1 ml of the supernatant. The suspended pellet was then injected through a 24-gauge hypodermic needle into 10 ml of ice-cold absolute methanol and stored at 4°C for a minimum of 2 h to both fix the cells and remove chlorophyll. Samples prepared in this manner remain stable at 4°C for up to 1 year before analysis (29).

In preparation for the flow cytometric analysis of DNA, 1.5 ml of the methanol-fixed sample was centrifuged at 11,000 × g for 5 min. The supernatant was removed, and the pellet was washed once with 2.5 ml of 10% phosphate-buffered saline (PBS, pH 7.4) and suspended in 1 ml of 10% phosphate-buffered saline. By using a modification of the technique of O'Farrell and Donahue (9), propidium iodide (Sigma Chemical Co.; final concentration, 30 μg ml⁻¹) and RNase A (Sigma; final concentration, 0.66 mg ml⁻¹) were added to each sample, and the samples were incubated at room temperature for 2 h. After the 2-h incubation, background stain was removed, if necessary, by first filtering the sample through a Nuclepore filter (pore size, 0.2 μm) and then washing it with 2 ml of 10% phosphate-buffered saline. The washed DNA cells were suspended in 1 ml of 10% phosphate-buffered saline, and analyzed within 4 h with an Epics V flow cytometer.

Flow cytometric analysis. Laser excitation at 514 nm was used to measure simultaneously the forward angle light scatter (FLS), which is an indicator of cell size, and propidium iodide fluorescence emission measured at greater than 590 nm of individual cells. To increase sensitivity, 1 W of laser power was focused to a spot size of 15.5 by 40 μm with a confocal lens system. A total of 20,000 to 50,000 cells per sample were analyzed in this manner. Uniform fluorescent beads (diameter, 0.9 μm; Duke Scientific) were added to each sample as an internal standard to monitor drift in the performance of the flow cytometer and to calibrate each fluorescence and FLS measurement to that samples analyzed on different days could be compared.

The data were stored both as single-parameter DNA fluorescence histograms of 256-channel resolution and as two-parameter histograms of correlated FLS and DNA fluorescence of 64 × 64-channel resolution.

Data analysis. The data generated with the Epics V flow cytometer were transferred to an IBM 9800 computer for detailed analysis (D. Vaulot, Ph.D. thesis, Massachusetts Institute of Technology and the Woods Hole Oceanographic Institution, Cambridge, Mass., 1986). Single-parameter DNA histograms were analyzed by assuming that the two main fluorescence peaks corresponded to GI and G2 cells of either one or two complements of DNA, respectively, and that the region separating these two peaks represented those cells in the process of DNA replication, or the S phase. To calculate the percentage of cells in each of these cell cycle stages, it was assumed that the G1 and G2 peaks displayed Gaussian distributions of DNA fluorescence per cell and that the S phase could be approximated as the sum of a series of Gaussian curves (Vaulot, Ph.D. thesis).

The duration of each cell cycle stage, f, was calculated from the proportion of the population in each stage, Pm, and the doubling time of the population in exponential growth, t_d, according to the equations of Satter et al. (32):

$$f_{G1} = \frac{1}{t_d} \ln \left(1 + \frac{P_{G1}}{P_{G2}}\right)$$

$$f_{G2} = f_{G1} + \frac{1}{t_d} \ln \left(1 + \frac{P_{G2}}{P_{G1}}\right)$$

$$f_{S} = f_{G2}$$

Two-parameter histograms were analyzed by first counting the cells within a given window. Modes and coefficients of variation (CVs) were then calculated for a single parameter of these selected data, finally, the mode of the FLS and DNA fluorescence was transformed from a logarithmic scale to a linear scale, calibrated against the 0.8-μm bead, and expressed in relative units.

Computer model. The general image of cell cycle regulation of procaryotic organisms has been extrapolated from the model for E. coli prepared by Helms and Cooper (17) and summarized in Fig. 1. In their scheme the important determinant of cell cycle behavior is the duration of the division cycle relative to the DNA cycle (Fig. 1A and B). We developed a computer simulation based on this E. coli model (12, 18) to predict the distribution of DNA per cell for prokaryotic populations displaying a range of growth rates (Fig. 1C and D). The use of this general model enabled us to predict how the flow cytometric data would appear if cyanobacteria underwent the "bolus" of E. coli and to place boundaries on the relationship between the cell cycle and the DNA cycle in this species.

The input parameters required for each model condition were the population doubling time, the time necessary for a pair of replication forks to traverse the entire length of the chromosome (the DNA replication time, t_r), the minimum time elapsed between the completion of chromosome replication and cell division (the separation time, t_d), and the CV for the DNA measurement. For slowly growing cells in which the generation time was greater than the amount of time necessary for chromosome replication and septum formation, the duration of either the GI or G2 gap was also needed (G1 = t_r + G2 = t_d + G1 = t_d).

Three assumptions from the E. coli model were central to the formulation of our model. First, it was postulated that each replication fork moved along the chromosome at a constant rate (3, 20). Second, it was assumed that a newly born cell contained a single complement of DNA if the generation time was greater than or equal to the sum of the DNA replication and septation formation times. Third, if the generation time of a cell was less than this sum, then synthesis of a complete chromosome spanned more than a single generation. Newly born cells therefore contained a single complete DNA complement plus one or more partial
complements, the synthesis of which began in a previous generation (Fig. 1B).

To calculate the DNA histogram for an asynchronously growing population, the program first subdivided the cell cycle into a number of increments of constant duration and then calculated the DNA amount for each increment. For slowly growing populations ($t_s = t + D$), G1 cells contained a single DNA complement, G2 cells contained two DNA complements, and cells in the process of chromosome replication contained an intermediate amount of DNA linearly related to the amount of time spent in S relative to the total duration of this phase.

To ascertain the relative amount of DNA in a newly born cell (DNA,~$m$) under fast growth conditions, the number of generations, $m$, which have to be spanned in order to complete the synthesis of an entire chromosome was calculated by rounding up to the nearest integer the ratio $t_s / D$. Based on $m$, DNA,~$m$ was then determined in the following manner. When $m = 1$, a newborn cell contains one complete DNA complement, A. When $m = 2$, a newborn cell contains A amount of DNA in addition to one partial complement, B, the synthesis of which must be completed $D$ minutes before division. Since B must equal 1 at time $t = D$, at time $t = 0$, $B = 1 - (t_s - D)/t_1$ or, upon rearranging, $B = 1 - [(D - t_1)].$ In a similar fashion, when $m = 3$, the DNA content in a newborn cell will be $A = B + 2$ partial complements, C, each with $t_1$, less DNA than B. At time $t = 0$, $C = 1 - [(D - t_1)] - (t_2)$. If $C = 1 - [(D - 2t_1)]$
A continuation of this scheme results in the following general equation for determining the amount of DNA within a newborn cell:

$$\text{DNA}_n = 1 \cdot \sum_j (1 \cdot \{D - t_j + 1\} \cdot c_j)$$

To calculate the DNA amount for each cell cycle increment in a fast-growth case ($t_j < D + 9$), the program determined the time at which replication forks began and ended and synthesis according to the following equations:

- **Start time**: $t_1 = 0$
- **Finish time**: $t_{n+1} = D$
- **Number of replication fork pairs**: $m = t_n - t_1$

These equations were derived by assuming that chromosome replication required $t_j$ minutes, and that cell division occurred $D$ minutes after synthesis occurred. The term $j$ is an index from 1 to $m$ designating each of the sets of complements to be synthesized during the cell cycle. The DNA amount for each increment was calculated based on the DNA amount from the previous increment, the increment duration, the DNA replication time, and the number of active replication forks. Once the DNA amount for each cell cycle increment was known, the relative number of cells within each subdivision was determined according to the equations for the age distribution of an asynchronously growing population (8).

The final processing step was to incorporate into the histogram the experimental error associated with the flow cytometric determination of relative DNA fluorescence per cell. The DNA fluorescence for a given DNA amount was assumed to be a Gaussian distribution with a constant CV (11). The subpopulation within each cell cycle increment was thus also distributed into a Gaussian fluorescence curve according to the DNA amount and the CV. The final distribution of the relative cell number versus the relative DNA fluorescence was therefore assembled by summing the fluorescence contributions from such subpopulations.

**RESULTS**

**Model predictions.** A range of potential distributions of DNA per cell was examined by employing our computer model to simulate both discrete (Fig. 1A and C) and continuous (Fig. 1B and D) DNA replication within exponentially growing populations. The results of the numerical model indicated that a unimodal distribution of DNA per cell could be obtained under a suite of conditions ranging from continuous DNA synthesis to the presence of either one or two gaps, depending on the CV of the DNA measurements. In other words, little can be said about cell cycle regulation if a unimodal distribution is obtained. However, a bimodal distribution of DNA per cell (Fig. 1C) could be obtained only under two circumstances: either two gaps, $G_1$ and $G_2$, existed during the cell cycle or only a single gap, $G_2$, was present after completion of DNA synthesis. It was thus necessary to develop criteria to determine whether a $G_1$ peak would or would not be seen. Our first step was to simulate the DNA distribution of an asynchronous population with a constant DNA synthesis rate, no gaps, and a CV of 0. Since the S phase occupies the entire cell cycle, the ratio of the number of cells entering $S$ to those leaving $S$ is 2. The addition of a $G_1$ peak to this population decreases this ratio to below 2. Since a CV of 0 is unrealistic for flow cytometric measurements of DNA content, we next simulated the DNA distribution of a population with a constant CV of greater than 0 and only the $S$ and $G_2$ stages. Under these circumstances, a measure of the number of cells entering $S$ relative to those leaving $S$ can be obtained by determining the ratio of the maximum peak height to the saddle height between the two peaks. Using our numerical model, we then simulated DNA distributions with a range of CVs and $G_1$ proportions and found that the maximum ratio of the peak height to the saddle height is 2. The $G_1$ distribution is a Gaussian curve, with a peak at a DNA amount less than or equal to the peak of the $S$ distribution (Fig. 1C). The addition of a $G_1$ peak will therefore increase the peak-to-saddle ratio. Thus, if the observed ratio for a population is greater than 2, this bimodal distribution must include a $G_1$ peak. Populations with a $G_1$ phase may have a ratio less than 2 if the error in DNA measurement is high, but populations with a ratio greater than 2 must contain cells in a $G_1$ phase. The presence of gaps in DNA synthesis implies that the duration of the DNA replication cycle is less than that of the division cycle. Thus, a newly born cell would contain a single complement of DNA and no cell would ever possess more than two complements of the genome (Fig. 1A and C). On the other hand, if the DNA replication time is greater than the division cycle, a newborn cell would inherit replication forks from the mother cell and would therefore always contain more than a single complement of DNA (Fig. 1B and D). Moreover, if DNA is synthesized continuously, a positive correlation would exist between the growth rate and the DNA content per newborn cell such that as the growth rate increases, the average DNA content per cell would also increase (Fig. 2).

**Light-limited growth.** To determine whether DNA was synthesized continuously throughout the division cycle and how cell cycle progression was modified as a function of the
growth rate, light-limited *Neurospora crassa* populations were maintained in steady-state growth with doubling times ranging from 11 to 55 h and then analyzed by flow cytometry. Regardless of the growth rate examined, a bimodal distribution of DNA fluorescence, or cell was obtained and the ratio of the left peak height to the height of the small between the peaks was always greater than 2 (Fig. 3). These two foci indicate that the cell cycle of each of these *Neurospora* crassa populations contains a discrete interval of DNA replication divided on either side by a gap in synthesis. This bimodal distribution, reflecting cells with one and two complements of DNA, is apparent in both the single-parameter DNA histograms (Fig. 3A) and the two-parameter histograms of FLS and relative DNA fluorescence (Fig. 3B). Cells in the process of chromosome replication display an intermediate amount of DNA fluorescence, again apparent in both types of histograms (Fig. 3). A critical cell size requirement for the entry of the G1 cells into S is suggested by the increased amount of FLS of the S cells relative to the G1 cells (Fig. 3B). The mode DNA fluorescence of both the U1 and G1 peaks did not differ significantly at each of the various growth rates (Table 1), further suggesting that the DNA copy number does not increase above 2N over this range of growth rates (Fig. 1A and B).

The DNA histograms were further analyzed to determine the steady-state proportion of cells in each cell cycle stage at the various growth rates (a = 1.5 to 3.0 day⁻¹) in order to calculate the duration of each cell cycle stage (see Materials and Methods). We found that the length of the S interval remained constant regardless of the total length of the cell cycle (Fig. 4). The intervals before and after DNA synthesis expanded as growth became more light limited, implying that progression through both of these stages is light dependent. G1, expanded to a greater extent than G2, increasing sixfold as the doubling time increased from 11 to 55 h (Fig. 4).

**Dark arrest and release.** The results of the light limitation experiment imply that cell cycle progression through both G1 and G2 requires light whereas the S interval must be light independent. This suggests that cells placed in the dark should arrest in their cell cycle during G1 or G2 but not S. To test this possibility, cells growing exponentially in continuous light with a doubling time of 11 h were placed in darkness until cell cycling ceased and then returned to continuous light conditions. DNA fluorescence and FLS were examined during both the light and the dark intervals to determine cell cycle dynamics. Cell division appeared to cease immediately upon placement of the population into the dark (Fig. 5A). During the first few hours in the dark, the mode FLS signal of the dark-arrested cells decreased from 0.25 relative FLS units to a minimum of 0.15 (Fig. 5B). This decreased FLS was then maintained throughout the remaining 72 h of darkness. When the population was reexposed to light, the FLS of the cells eventually returned to the pre-dark value of 0.23 relative FLS units.

As predicted from the results of the light limitation experiment, once cell division ceased in the dark (Fig. 5A), cells were blocked in both G1 and G2 (Fig. 5C). For reasons that are not yet clear, the CV of DNA fluorescence of the G2 peak increased in these dark-blocked cells, resulting in an overestimate of the proportion of S-phase cells during the dark interval. We were thus unable to follow the cells in S once cell division ceased in the dark and could not determine unambiguously whether cells were blocked in synthesis in the dark. However, the fact that the percentage of cells decreased in G1 and increased in G2 during the dark when cell division was no longer occurring suggests that cells can progress through S in the dark.

A prolonged dark arrest as in the experiment described above is often used to synchronize populations of cyanobac-
A culture of *Synechococcus* strain WH-8101 growing exponentially in continuous light with a population doubling time of 11 h was placed in the dark for 72 h and then released into continuous light. The darkened bar indicates the duration of the dark interval. The cell number (A), FLS (B), and the percentage of cells in G1, G2, and G0 (C) were measured with a flow cytometer during both the dark and light intervals. Due to the increased CV of the G0 cells in the dark, these DNA distributions were assumed to represent only two cell cycle stages, G1 and G0. Symbols in panel C: (1) G1 cells; (2) G2 cells. In panel B the error bars larger than the symbol size represent the standard deviation for replicate samples.

**FIG. 5.** A culture of *Synechococcus* strain WH-8101 growing exponentially in continuous light with a population doubling time of 11 h was placed in the dark for 72 h and then released into continuous light. The darkened bar indicates the duration of the dark interval. The cell number (A), FLS (B), and the percentage of cells in G1, G2, and G0 (C) were measured with a flow cytometer during both the dark and the light intervals. Due to the increased CV of the G0 cells in the dark, these DNA distributions were assumed to represent only two cell cycle stages, G1 and G0. Symbols in panel C: (1) G1 cells; (2) G2 cells. In panel B the error bars larger than the symbol size represent the standard deviation for replicate samples.

**FIG. 6.** Time course of the cell division (A), FLS (B), and DNA distributions (C) of *Synechococcus* strain WH-8101 over 24 h of a 14-h light/dark cycle. The darkened bar represents the dark interval. In panels A and B the error bars larger than the symbol size represent the standard deviation for replicate samples. In panel C, the contour levels represent the total number of cells analyzed are 0.125, 0.25, 0.5, 0.75, 1.0, 2.5, 5.0, 10, 25, and 50.

When our dark-arrested *Synechococcus* cells were released into the light, however, there was no evidence of synchronous growth. An initial lag was apparent, but once the cells initiated division, exponential growth resumed rapidly (Fig. 5A). Flow cytometry results also confirmed the absence of synchronized growth in the population after reexposure to continuous light at all times after release of the cells into the light, both G1 and G2 cells were present (Fig. 5C). A period never existed when the culture was divided by a single phase, as would be expected in a synchronized culture.

**Diet light/dark cycle entrainment.** An alternative means of synchronizing phytoplankton populations is to maintain cultures on a repeating light/dark cycle (1, 34). Obviously, entrainment of a population to a diet light/dark cycle is very different from an interruption of exponential growth in continuous light with darkness; moreover, a light/dark cycle is the "real world" experience of cells. To expand upon the results of the previous experiments, cell division, FLS, and DNA distributions were measured over 24 h in a *Synechococcus* population entrained to a 14-h light/dark cycle. The cell division pattern for strain WH-8101 observed over this single cycle was similar to that described by Waterbury et al. (38) for a number of cycles in which *Synechococcus* strain WH-7803 divided predominantly during the light interval (Fig. 6A). Over the course of the dark interval, the FLS of the cells declined to its minimum value (Fig. 6B). Upon reexposure to the light, cell division did not begin again for
results, marine cyanobacterium species divide quickly becomes exponential. In contrast to our previous studies on marine cyanobacterium Synechococcus strain BG 4351 and 4352, which were synchronized by placing an asynchronous population in the dark for an extended period (26). In addition, both Hardman et al. (19) and Asato (2) have shown that A. nidulans displays a comparable degree of synchrony in growth upon release into the light after dark exposure. However, Asato (2) and Hardman et al. (19) also describe data which indicate that both G1 and G2 cells are present within A. nidulans populations during the dark arrest; yet somehow, synchronous division is still achieved after the dark block is released. To explain their results, these authors postulated that progression through each cell cycle stage in the light is differentially affected by a previous exposure to darkness (19, 24). A nonuniform effect of darkness on transit through the different cell cycle stages has also been observed in diatoms and was attributed to an interruption of the silicium transport system by darkness (30).

Cell cycle progression through G1 is unconditional in most cell types (21), except for the marine diatoms which are known to have both light- and silicon-dependent block points during this interval (30, 36). The fact that two such fundamentally different organisms as the diatoms and Synechococcus spp. both divide in the light and possess a light requirement at the end of their cell cycle substantiates the hypothesis that a causal relationship exists between the location of light-dependent processes and overall population growth patterns (36).

The actual specifics of the regulation of the cell cycle in Synechococcus spp. are more complicated than has been presented thus far. Theories of cell cycle regulation in prokaryotes rely heavily on the E. coli model put forth by Heinsmeyer and Cooper (15). Cell cycle studies conducted to date with cyanobacteria indicate that apparently these prokaryotes do not always adhere to the rules of the E. coli model. For example, Mann and Curr (25) found that the DNA content of A. nidulans increased up to 16-fold with an increasing growth rate even though the growth rates examined reflected generation times greater than the chromosome replication interval. Under these circumstances, continuous DNA synthesis and multiple replication forks would not be predicted (12, 17). In the study of Mann and Curr (25), the generation time of A. nidulans was approximately 2.3 h, which is about twice its chromosome replication period (19). Similarly, our 11-h doubling time of strain WH-R101 is approximately twice its estimated chromosome replication interval of 5 h (Fig. 4). Yet regardless of the comparable relative growth rates, the DNA content of A. nidulans increased exponentially with an increasing growth rate, while that of WH-R101 did not. An increased genomic content at relatively slow growth rates has also been reported for the marine cyanobacterium Aphanothece quadruplicata, which can pass through up to three copies of its chromosome at generation times of either 7 or 20 h (31), both of which are presumably greater than the synthesis interval in this organism.

In addition, a conflict between cyanobacteria and the E. coli model is that A. nidulans appear to possess both a discrete interval of DNA synthesis (12, 19) and multiple copies of its genome (23). It is difficult to reconcile the existence of multiple copies of the genome and G1 arrest points at generation times greater than the chromosome replication interval. Apparently, the presence of gaps in DNA synthesis and multiple chromosome copies are not mutually exclusive.

If the E. coli model is not a suitable paradigm for the cell cycle behavior of cyanobacteria, perhaps chloroplasts, which have been hypothesized to have a cyanobacterial origin (24), could serve as a more appropriate model. Chloroplasts are known to contain multiple copies of their genome, the number of which varies as the chloroplast develops (4). Little is known, however, about the regulation of the DNA and division cycles within these organisms as well. An enhanced understanding of cell cycle regulation in cyanobacteria could be gained by determining analytically
the relationship between the growth rate and the absolute number of chromosomes per cell. It would then be possible to determine whether marine *Synechococcus* can ever possess both a discrete interval of DNA synthesis and multiple copies of the genome [13, 31, 39].

**ACKNOWLEDGMENTS**

Thanks to Erik Zettler and Sheila Frankel for their always appreciated technical support.

This work was supported in part by National Science Foundation grants OCE 8815679, OCE 8815680, and OCE 8814486 to S.W.C. and OCE 8410664 and OCE 8515012 to R.J.O. and by Office of Naval Research contracts N00014-87-K-0001 to S.W.C. and B-4-C0276 and 87-0007 to R.J.O. and S.W.C.

**LITERATURE CITED**


Attn: Stella Sanchez-Wade
Documents Section
Scripps Institution of Oceanography
Library, Mail Code C-075C
La Jolla, CA 92037

Hancock Library of Biology & Oceanography
Alan Hancock Laboratory
University of Southern California
University Park
Los Angeles, CA 90089-0371

Gifts & Exchanges Library
Bedford Institute of Oceanography
P.O. Box 1006
Dartmouth, NS, B2Y 4A2, CANADA

Office of the International Ice Patrol
c/o Coast Guard R & D Center
Avery Point
Groton, CT 06340

NOAA/EDIS Miami Library Center
4301 Rickenbacker Causeway
Miami, FL 33149

Library
Skidaway Institute of Oceanography
P.O. Box 13687
Savannah, GA 31416

Institute of Geophysics
University of Hawaii
Library Room 252
2525 Correa Road
Honolulu, HI 96822

Marine Resources Information Center
Building E38-320
MIT
Cambridge, MA 02139

Library
Lamont-Doherty Geological Observatory
Columbia University
Palisades, NY 10964

Library
Serials Department
Oregon State University
Corvallis, OR 97331

Pell Marine Science Library
University of Rhode Island
Narragansett Bay Campus
Narragansett, RI 02882

Working Collection
Texas A&M University
Dept. of Oceanography
College Station, TX 77843

Library
Virginia Institute of Marine Science
Gloucester Point, VA 23062

Fisheries-Oceanography Library
151 Oceanography Teaching Bldg.
University of Washington
Seattle, WA 98195

Library
R.S.M.A.S.
University of Miami
4600 Rickenbacker Causeway
Miami, FL 33149

Maury Oceanographic Library
Naval Oceanographic Office
Stennis Space Center
NSTL, MS 39522-5001

Marine Sciences Collection
Mayaguez Campus Library
University of Puerto Rico
Mayaguez, Puerto Rico 00706

Library
Institute of Oceanographic Sciences
Deacon Laboratory
Wormley, Godalming
Surrey GU8 SUB
UNITED KINGDOM

The Librarian
CSIRO Marine Laboratories
G.P.O. Box 1538
Hobart, Tasmania
AUSTRALIA 7001

Library
Proudman Oceanographic Laboratory
Bidston Observatory
Birkcnhead
Merseyside L43 7 RA
UNITED KINGDOM
The goal of this research was to understand what factors determine whether a diatom cell can exit the mitotic cell cycle to undergo gametogenesis and subsequent auxospore formation. Using flow cytometry, I found that the centric diatom, *Thalassiosira weisflogii*, could be induced to undergo spermatogenesis by exposing cells maintained in continuous light to either dim light or darkness. The use of populations representing distinct cell cycle distributions indicated that cells in early G1 could be triggered to form male gametes, whereas cells further along in their cell cycle were unresponsive to these same cues. The size distributions of numerous isolates maintained under identical conditions were examined over time to determine the relation between cell size and the ability to undergo sexual reproduction. Each isolate underwent periodic increases and decreases in mean cell size as expected for populations alternating between asexual and sexual reproduction. However, the timing of the onset of sexual reproduction, the rate of increase in mean cell size, and the size of the post-auxospores created during a sexual event varied among isolates and within a given isolate over time. This variable behavior was hypothesized to occur because the genetic composition of diatom populations varies over time.

### Document Analysis

**a. Descriptors**

1. diatoms
2. sexual reproduction
3. cell size

**b. Identifiers/Open-Ended Terms**

### Security Class (This Report)

**UNCLASSIFIED**

**No. of Pages**

152