Research Report 3

Phytoplankton of the Mallee Tract

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Report Linkages

This individual Research Report forms a component of the larger report:

McCarthy, B., Gawne, B., Meredith, S., Roberts, J. and Williams, D. (2004). Effects of Weirs in the Mallee Tract of the River Murray. Murray-Darling Freshwater Research Centre, Mildura. Report to the Murray-Darling Basin Commission, Canberra.

Introduction

Models of ecosystem function in large rivers assign different levels of importance to the contribution of phytoplankton to the food webs. Both the river continuum concept (Vannote *et al*., 1980) and the flood pulse concept (Junk *et al*., 1989) emphasise the importance of terrestrial-derived carbon to large river food webs. In contrast, the riverine productivity model (Thorp and Delong, 1994) considers organic carbon derived from local autochthonous production to be more "assimilable" to animals. Thorp and Delong (1994) hypothesise that organic carbon production by phytoplankton is likely not the main source of assimilable carbon in the food webs although it may comprise an important contributor to secondary production.

The relative importance of phytoplankton, benthic algae and macrophytes to local autochthonous production remains unclear. Phytoplankton exhibited the greatest in-stream primary production in lowland reaches of the River Murray (at the Hattah site of the Mallee Tract) (Gawne *et al*., 2002). In contrast, Bunn *et al*. (2003) demonstrated that benthic primary production by filamentous algae is the dominant carbon source for the food webs within large, isolated waterholes of the hydrologically-variable Cooper Creek system in Australia's arid zone.

Phytoplankton influence water quality by liberating oxygen through photosynthesis, removing nutrients from the water column and their exudates are important for other biota such as bacteria (Boon *et al*., 1990). Phytoplankton are also an important food source for secondary producers such as zooplankton. Under favourable conditions, some phytoplankton may increase to bloom concentrations (e.g. Sullivan *et al*., 1988; Donnelly *et a*l., 1997; Webster *et al*., 2000) and contribute toxins, tastes and odours to the water column (Jones and Korth, 1995).

In the River Murray alone, over 150 phytoplankton taxa have been identified from weekly sampling conducted from 1980-1985 (Sullivan *et al*., 1988). The Murray-Darling Basin Commission has continued the weekly sampling at points along the River Murray since this time. Data from 1980-1992 was reviewed by Hotzel and Croome (1996) with a particular focus on the dominant alga *Aulacoseira granulata*. Bormans and Webster (1999) utilised this data from 1981-1990 to develop a mechanistic model to explain the distribution of *A. granulata* in the River Murray.

Phytoplankton communities are dynamic and respond to many environmental factors, including light, temperature and nutrients (Sullivan, 1990). Flow is also an important factor, with higher abundances of phytoplankton typically occurring during low flow periods and following an increase in flows due to cell resuspension (Sullivan *et al*., 1988; Bormans and Webster, 1999; Hotzel and Croome, 1996; Webster *et al*., 2000). In the Mallee Tract of the River Murray, patterns of phytoplankton community change were noted between the sites at Euston, Red Cliffs and Merbein (Sullivan *et al*., 1988). The spatial resolution of these sites is such that it is not possible to directly implicate the weirs as being responsible for some of these changes, although their influence has been speculated (Sullivan *et al*., 1988) because of the changed hydraulics in the weir pools.

The greater water depths in the weir pools reduce the flow velocity and provide favourable conditions for thermal and chemical stratification (e.g. Research Report 2; Bormans *et al*., 1997; Sherman *et al*., 1998; Bormans and Condie, 1998). In addition, the greater depths in the weir pools mean that a higher proportion of the water column does not receive light (decrease in photic:aphotic ratio) compared to the free-flowing areas (Research Report 2). These changes are believed to favour some phytoplankton species over others. Cyanobacteria, for example, possess gas vacuoles and can utilise these to adjust their buoyancy. This feature provides this group with a competitive advantage under low flow conditions when they can remain positively buoyant and spend more time within the photic zone. Other phytoplankton, such as diatoms, are negatively buoyant and in conditions of low turbulence may remain below the photic zone for longer periods or settle out of the water column completely (Bormans and Condie, 1998; Sherman *et al*., 1998; Bormans and Webster, 1999).

Within the weir pools of the Mallee Tract, annual monitoring of cyanobacteria since 1996 has in some years recorded elevated concentrations of cyanobacteria, primarily *Anabaena circinalis* (Scholz *et al*., 2003). The cyanobacteria have received considerable attention following the publicity of the world's longest riverine cyanobacteria bloom in the Darling-Barwon River in 1991. This bloom has stimulated increased research into the mechanisms behind these events that continues today (e.g. Oliver *et al*., 1999; Donnelly *et al*., 1997; Sherman *et al*., 1998; Webster *et al*., 2000).

Objectives

This study aimed to examine the effects of weirs on the phytoplankton of the Mallee Tract. The spatial resolution of sampling sites allowed the weir pools and free flowing reaches of river to be separated to examine the effects of the Euston, Mildura and Wentworth weir pools on phytoplankton growth.

Methods

Details of the sampling sites and the three weir pool (WP) and two free-flowing (FF) reaches along the Mallee Tract of the River Murray (Thoms *et al*., 2000) are provided in the Project Report.

Conceptual Design

As a body of water travels along the river, the surrounding physical and chemical environment influences its plankton and water physico-chemistry. The examination of phytoplankton at the upstream and downstream points of the weir pool and free-flowing reaches allows a comparison of the effects of weir pool reaches and free-flowing reaches on phytoplankton (Figure 1).

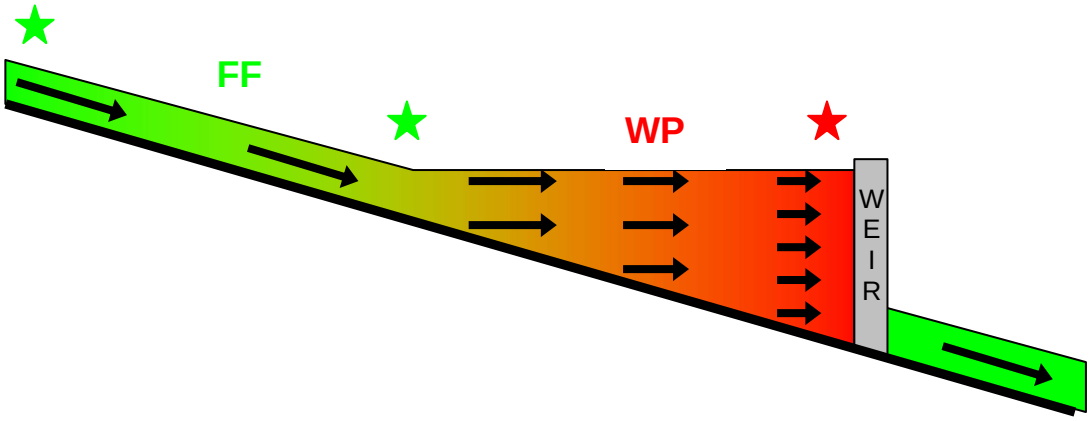

Figure 1. Schematic long section of a weir pool (WP) and free-flowing (FF) reach. Arrows show direction of flow and their lengths reflect the change in flow velocity as river depth increases. The sampling sites (stars) were located so as to allow changes in phytoplankton to be assessed as water passes through the free-flowing and weir pool reaches.

Sample Collection and Processing

At each site a relatively straight section of river was selected and three replicate points were established at approximately 25, 50 and 75% channel width along a transect spanning the river. A vertically integrated water sample was collected at each replicate point by lowering and raising a 12 V bilge pump at a constant rate through the water column and collecting the pumped water in a 25 L container. The bilge pump was positioned inside a shallow bucket to prevent riverbed sediment contaminating the sample when the riverbed was contacted. A 0.6 L sub-sample was taken from each vertically integrated sample to determine phytoplankton species composition and Lugols iodine solution (3 mL) added for preservation. A further 0.5 L sub-sample was taken to determine phytoplankton chlorophyll content as an indicator of phytoplankton biomass.

In the laboratory the samples for species identification and enumeration were gravity settled for at least one week and approximately 90% of the surface water (phytoplankton-free) was drawn off and the volume recorded. The phytoplankton and remaining water were mixed well and the volume recorded. Additional Lugols (3 mL) was added and the sample refrigerated in the dark until analysis. Analysis was conducted at a NATA certified laboratory (WSL Consultants, Richmond) and the precision level of identification was to genera level for minor organisms and species level for dominant taxa. The sample volume at the time of analysis was recorded to allow counts to be converted to cells.mL^{-1} (or 50µm filaments.mL^{-1} for four taxa). Samples from five sites (3 replicates; Yungera Island (FF), Euston (WP), Iraak (FF), Mildura (WP) and Wentworth (WP)) and eight sampling occasions were analysed for phytoplankton community composition (1/8/01 – 16/6/03)(see Project Report for site details).

Chlorophyll samples were refrigerated in the laboratory until processing. Samples were shaken well and a known volume (ca. 500 mL) filtered through a 47 mm Whatman GFC (1.2 µm) filter. The filter with encrusted algae was immersed in a centrifuge tube containing 10 mL of 90% ethanol and the samples stored overnight at 4^{o}C. Samples were heated for 5 min in a water bath (78^{o}C), cooled and centrifuged at 2000 rpm for 15 mins. A 3 mL aliquot was analysed in a spectrophotometer at wavelengths of 665 and 750 nm to determine the total chlorophyll pigment (TCP) (Golterman and Clymo, 1971). The aliquot was then acidified with 0.1 mL of 0.1M HCl and mixed before analysing in at wavelengths of 665 and 750 nm after 90 s to allow the calculation of the viable and non-viable proportions of chlorophyll (APHA, 1995). The protocol of acidification was strictly adhered to as the amount of acid added, degree of mixing, and time after acidification each strongly influence the results. Samples from all eight riverine sites and all 14 sampling trips were examined for chlorophyll.

Statistical Analysis

Multivariate analysis of the phytoplankton community data was conducted with PC-Ord (MjM Software, v4.27). The four taxa counted as 50 µm filaments.mL^{-1} comprised less than 0.04% of the total abundance when combined so were included unmodified in the statistical analyses with the remaining taxa (cells.mL^{-1}). The community data set contained many zeros and was heavily right skewed, so was fourth root transformed to reduce the influence of abundant taxa. The Sorensen (Bray-Curtis) distance measure was adopted in the classification analyses because it is robust and particularly suited to community data sets (both abundance and presence/absence) (Faith *et al*., 1987). The Flexible Beta Group Linkage Method (set at –0.1 due to its ability to recover known groups) was used (Belbin *et al*., 1992). Dendogram details are described in the Main Report.

Univariate analysis was conducted with SYSTAT v9 (SPSS Inc.) on untransformed data (data was normally distributed).

Results

Biomass

Phytoplankton total chlorophyll pigment (TCP) concentrations remained within the range of 16-31 µg.L^{-1} throughout the study period (Figure 2). The viable component of the TCP at each site and time ranged from 74-97%, with a mean (± S.E.) of 85.4 ± 0.4%. The small error bars for each time demonstrate that phytoplankton biomass (as a concentration) remained similar throughout the study reach for a given time.

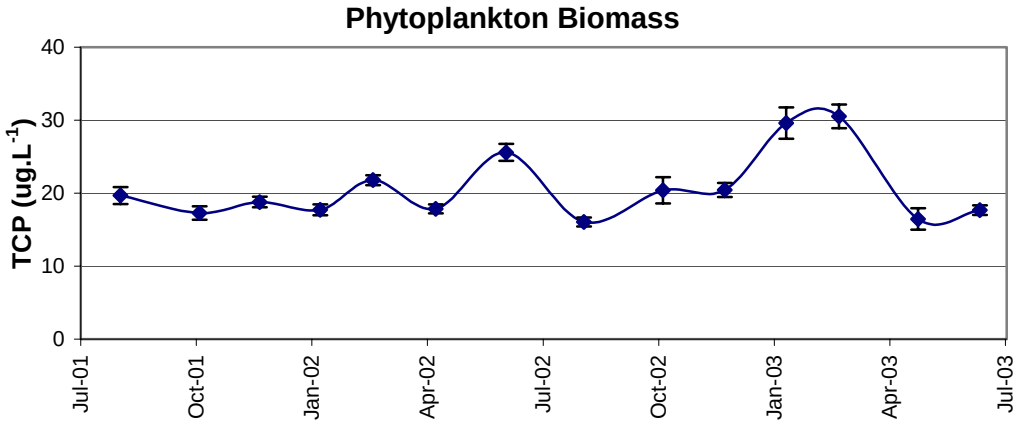

Figure 2. Temporal pattern of phytoplankton biomass measured as total chlorophyll pigment (TCP) in the Mallee Tract, August 2001–June 2003. Error bars = ± 1 S.E.

Mean phytoplankton TCP concentrations increased in the free-flowing reaches (Boundary Bend-Yungera and Hattah-Iraak) and decreases within the weir pools (Figure 3). These changes occurred despite the mean concentrations at the most upstream and downstream sites (Boundary Bend and Wentworth, respectively) remaining very similar (20.5 and 20.4 µg.L^{-1}, respectively). Note that a 1 ug.L^{-1} change in chlorophyll represents ca. 5% change in total phytoplankton biomass.

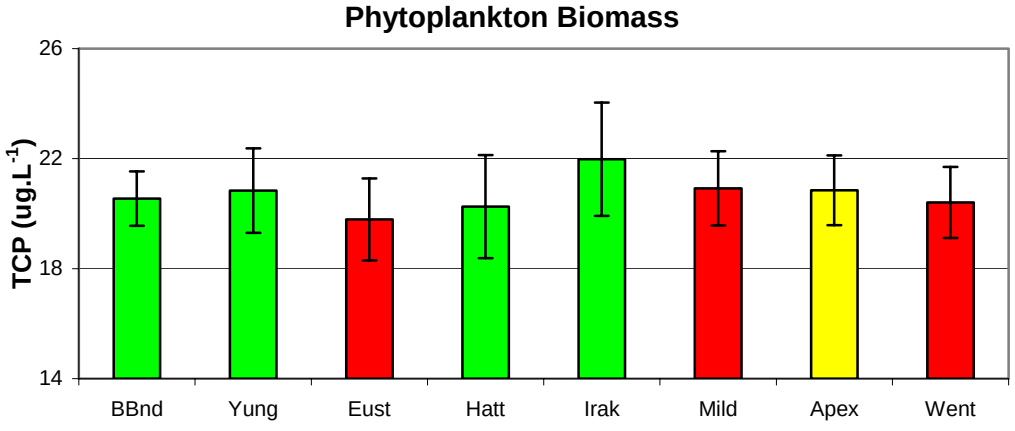

Figure 3. Spatial dynamics of phytoplankton biomass in the Mallee Tract from August 2001-June 2003. Note the scale on the Y-axis. Error bars = ±1 S.E.

The changes in phytoplankton TCP between the upstream and downstream sites of the two free-flowing and three weir pool reaches were calculated to better examine the influence of each reach on phytoplankton chlorophyll (Figure 4A). The change in TCP was also linked to flow on the 14 sampling occasions to estimate the mean daily load of phytoplankton (dry weight) being added or lost to that particular reach. Calculations were based on the

assumption that chlorophyll comprises 1.5% of the dry weight of the organic matter component of algae (APHA, 1995). The mean daily changes in phytoplankton load are shown in Figure 4B.

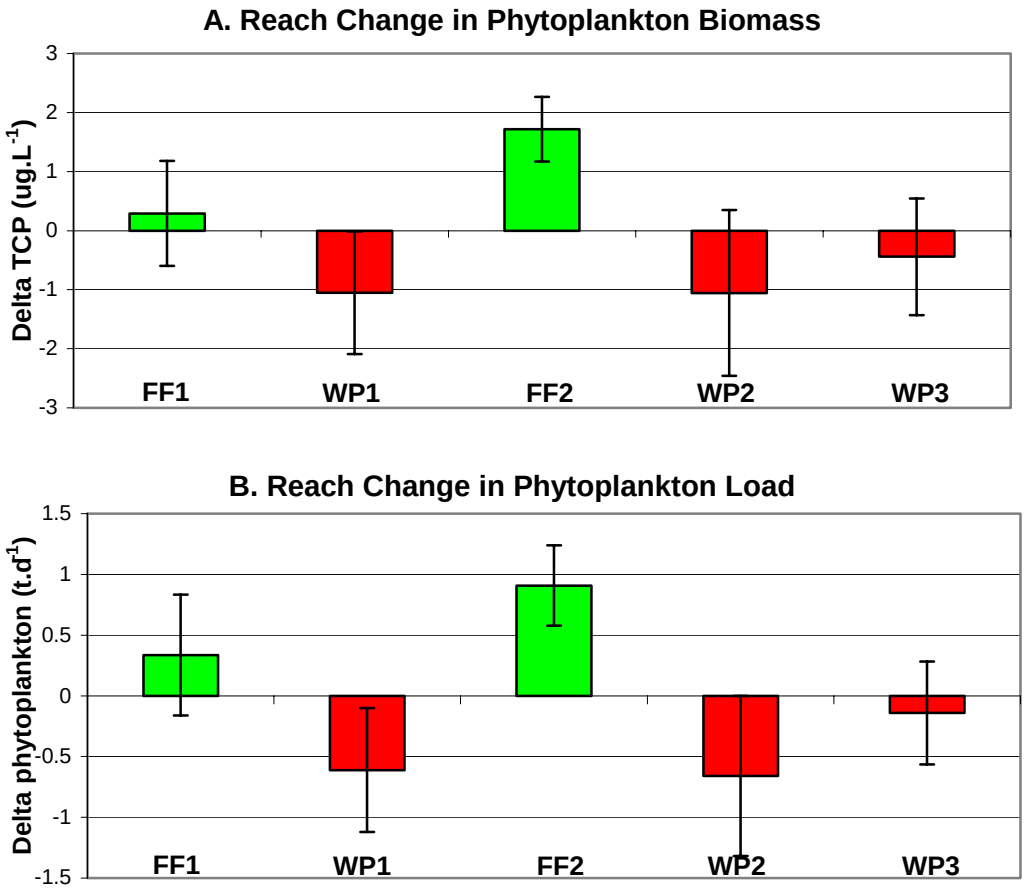

Figure 4. Changes in (A) phytoplankton biomass and (B) phytoplankton load in the free-flowing (green) and weir pool (red) reaches. FF1=BBend-Yung, WP1=Yung-Eus, FF2=Hatt-Iraak, WP2=Iraak-Mda, WP3=Apex-Went. Error bars = ±1 S.E.

Repeated measures ANOVAs were conducted on the change in TCP and phytoplankton loads in the free-flowing and weir pool reaches (Table 1). TCP changes in the free-flowing and weir pool sites were not significantly different to each other (P=0.052) although the statistical power of the analysis was low due to there being only two FF and three WP reaches. Phytoplankton loads, however, were significantly different between the reaches (P=0.036) when flow was taken into account; the interaction term was also significant indicating that the loads responded differently through time for the weir pool and free-flowing reaches (Table 1).

Table 1. Repeated measures ANOVA: WP v FF

Between Subjects		**Phytoplankton TCP**				**Phytoplankton Load**			
Source	**df**	**SS**	**F**	**P**	**G-G**	**SS**	**F**	**P**	**G-G**
REACH (FF v WP)	1	57.855	9.800	0.052		20.048	13.064	0.036	
Error	3	17.711				4.604			
Within Subjects									
TIME	13	75.402	0.511	0.904	0.597	14.401	0.439	0.944	0.648
TIME x REACH	13	377.391	2.558	0.012	0.173	106.283	3.243	0.002	0.120
Error	39	442.521				98.320			

Phytoplankton Taxa: Abundance and Richness

In total, 142 phytoplankton taxa were collected from five sites along the Mallee Tract on eight sampling occasions from August 2001 – June 2003 (Appendix A). Cyanophyta (cyanobacteria), Bacillariophyceae (diatoms) and Chlorophyta (green algae) were the most abundant phytoplankton groups based on mean cell counts, and together comprised over 99.4% of the phytoplankton abundance (Table 2). Phytoplankton taxa richness ranged from 31-62 taxa per sample, with a mean (± S.E.) of 46.2 ± 0.6 taxa. The phytoplankton groups Chlorophyta (green algae), Bacillariophyceae (diatoms) and Cyanophyta (cyanobacteria) also contained the greatest taxa richness (Table 2).

Table 2. Phytoplankton abundance (median and mean) and richness

	Abundance (cells.mL^{-1})		Richness
Phytoplankton Group	**Median**	**Mean ±S.E. (% of total)**	**Mean No. Taxa ±S.E. (% of total)**
Bacillariophyceae	4957	5292 ± 289 (41.7%)	12.7 ± 0.2 (27.4%)
Cyanophyta	2397	6148 ± 1031 (48.5%)	6.9 ± 0.2 (14.9%)
Chlorophyta	1064	1179 ± 61 (9.3%)	22.0 ± 0.3 (47.6%)
Cryptophyta	19	28 ± 2.7 (0.22%)	1.5 ± 0.1 (3.2%)
Euglenophyta	8	11 ± 0.9 (0.09%)	1.8 ± 0.1 (4.0%)
Chrysophyta	3	25 ± 3.7 (0.20%)	0.6 ± 0.1 (1.4%)
Pyrrophyta	2	4 ± 0.6 (0.03%)	0.7 ± 0.1 (1.5%)

Phytoplankton Abundance

The six most abundant taxa are listed in Table 3, with the centric diatoms *Aulacoseira granulata / Aulacoseira ambigua* being the most dominant taxon (both median and mean abundance). It was not possible to separate these two species due to the distinguishing feature - a distinct pore on either side of the valve mantle margin for *A. ambigua* (Sonneman *et al*., 2000) - being indiscernible. It is probable that *Aulacoseira granulata* (previously recorded as *Melosira granulata*) is the most dominant of the two species given that it is typically the most abundant diatom (>90% of diatom abundance) along the River Murray (Sullivan *et al*., 1988; Hotzel and Croome, 1996; Bormans and Webster, 1999).

Table 3. Six most abundant phytoplankton taxa (cells.mL^{-1})

Median abundance		Mean abundance	
Taxa	**Median (% of median total)**	**Taxa**	**Mean ± S.E. (% of mean total)**
Aulacoseira granulata/ambigua	4479 (75.9%)	*Aulacoseira granulata/ambigua*	4723 ± 308 (37.2%)
Aphanocapsa sp.	213 (3.6%)	*Pseudanabaena limnetica*	3234 ± 987 (25.5%)
Anabaena circinalis	180 (3.1%)	*Aphanocapsa sp.*	534 ± 71 (4.2%)
Ankistrodesmus falkatus	164 (2.8%)	*Planktolygbya subtilis*	462 ± 124 (3.6%)
Ankistrodesmus fusiformis	116 (2.0%)	*Anabaena circinalis*	389 ± 50 (3.1%)
Aphanizomenon issatschenkoi	80 (1.4%)	*Aphanizomenon issatschenkoi*	328 ± 55 (2.6%)

Temporal Patterns

Multivariate classification of abundance counts across times (sites pooled) indicated that phytoplankton communities from the same month in consecutive years were most similar to one another with the exception of the August communities (Figure 5). The August 2001 community was most different to all others, and the communities from February were most similar to one another.

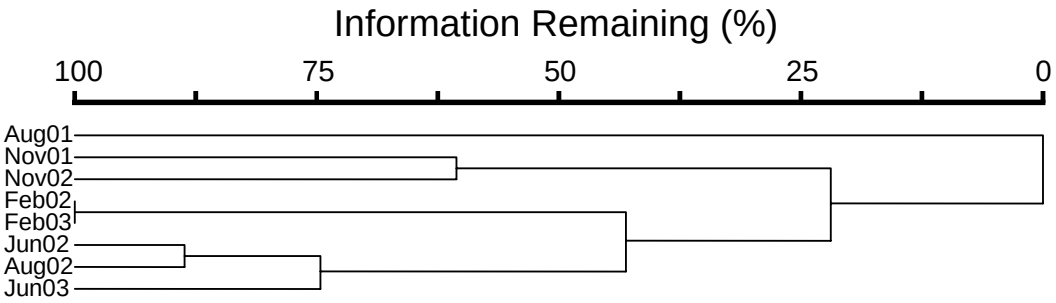

Figure 5. Dendogram of the phytoplankton communities (abundance data) across times.

Bacillariophyceae (diatoms) was the most abundant phytoplankton group for six of the eight sampling times (Figure 6), despite not being most abundant overall (Table 2). The Cyanophyta (cyanobacteria) was the most abundant group overall due to a large bloom of *Pseudanabaena limnetica* in June 2003 throughout the study reach (Figure 6).

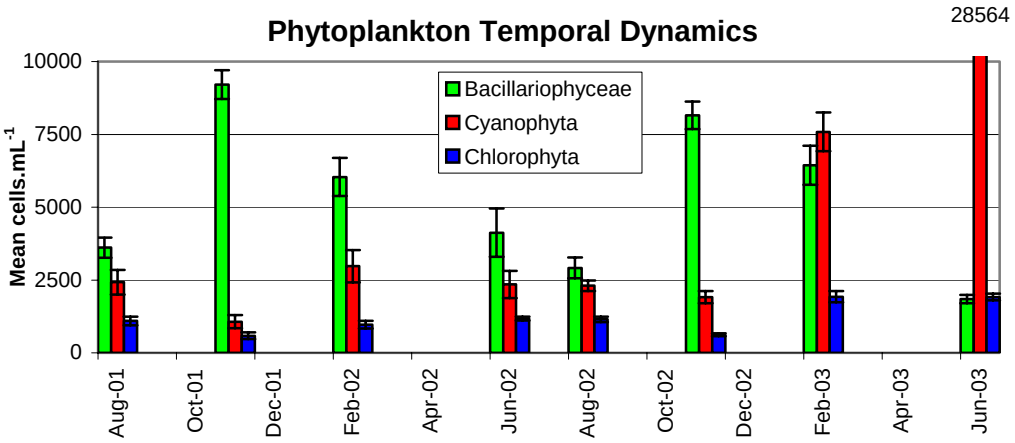

Figure 6. Mean abundances of the three dominant phytoplankton groups, August 2001 – June 2003. Error bars = ± 1 S.E.

Spatial Patterns

Multivariate classification of abundance counts across sites (times pooled) indicated that the greatest sequential change in the phytoplankton community occurred between Iraak (FF) and Mildura (WP) (i.e. within the 56 km Mildura weir pool) (Figure 7). Changes in the phytoplankton community composition also occurred in the Euston weir pool and to a lesser extent in the Wentworth weir pool. In the 175 km free-flowing reach between Euston and Iraak, the phytoplankton community remained essentially unchanged. As this reach is the only free-flowing section encompassed within the study reach examined for phytoplankton community composition (Yungera Island to Wentworth), it is in the weir pools where the changes in the phytoplankton community are occurring.

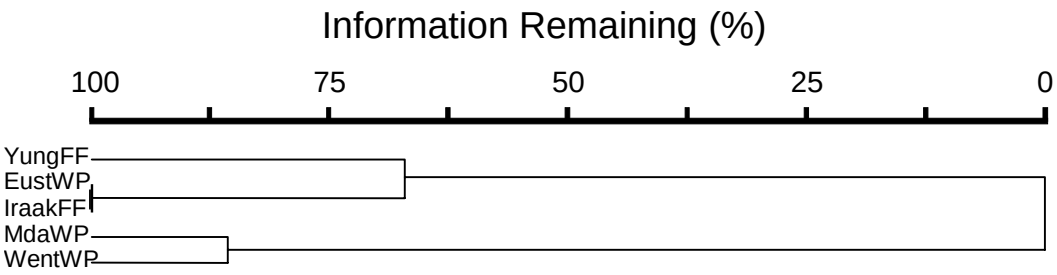

Figure 7. Dendogram of the phytoplankton communities (abundance data) across sites.

Phytoplankton species were grouped into their main phytoplankton divisions (Figure 8) to investigate the changes between sites that the classification analysis revealed. The concentrations of diatoms and cyanobacteria followed opposing trends, with diatom abundance sequentially decreasing and cyanobacteria abundance increasing when passing along the Mallee Tract. The findings are likely explained by the different characteristics of each group: diatoms rely on water turbulence to remain suspended in the water column (Sherman *et al*., 1998; Bormans and Condie, 1998; Bormans and Webster, 1999) and are settling out of the water column in the weir pools, whereas the ability of cyanobacteria to control their buoyancy is providing them with a competitive advantage in the weir pools. A bloom of *Pseudanabaena limnetica* in June 2003 heavily influenced the cyanobacteria data (Table 3), so graphs with and without *P. limnetica* are presented (Figure 8). A graph of median cell counts (not shown) depicted a very similar pattern to Figure 8B.

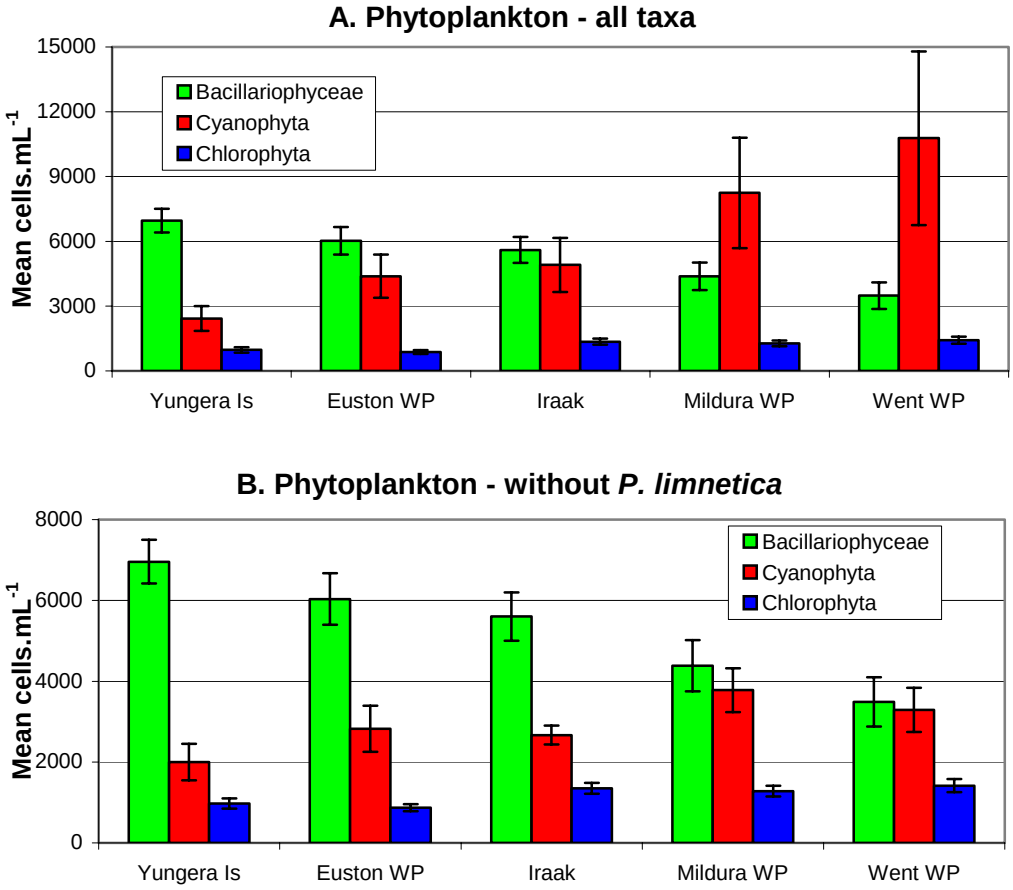

Figure 8. Mean phytoplankton abundance of the main phytoplankton groups at each site for (A) all taxa and (B) with the cyanobacteria *P. limnetica* removed from the data. Error bars = ± 1 S.E.

Phytoplankton Richness

Converting species abundance data to presence/absence removes the influence of abundance and focuses on the changes in taxa between sites. A classification of presence/absence data (Figure 9) revealed that the greatest change in phytoplankton taxa occurred in the Mildura weir pool (Iraak to Mildura). Considerable change in the phytoplankton community occurred in the Euston weir pool (Yungera to Euston), with relatively less taxonomic change along the free-flowing reach from Euston to Iraak. Phytoplankton taxa changed least in the Wentworth weir pool (Mildura to Wentworth), suggesting that the communities had perhaps adapted to the hydraulic conditions of these weir pools.

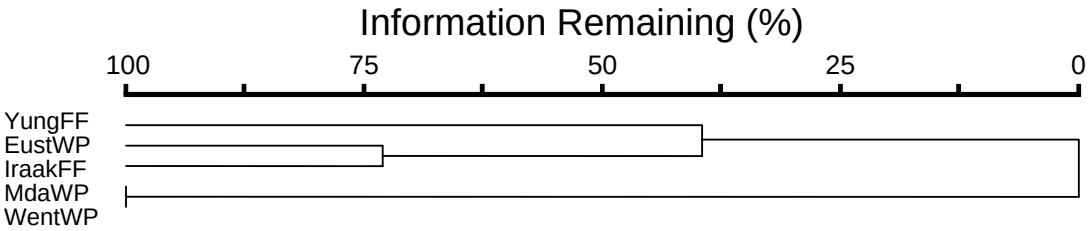

Figure 9. Dendogram of phytoplankton communities (presence-absence) across sites.

Temporal and Spatial Patterns

Chlorophyta was consistently the phytoplankton group with the greatest species richness over both time (Figure 10A) and space (Figure 10B), followed by Bacillariophyceae and Cyanophyta. No clear seasonal changes in taxa richness were evident based on these groupings, with the possible exception of cyanobacteria which exhibited a similar temporal pattern in each year; lowest diversity in November and greatest in June. The groups Euglenophyta, Pyrrophyta, Cryptophyta and Chrysophyta each consistently contained fewer than two taxa and are not depicted.

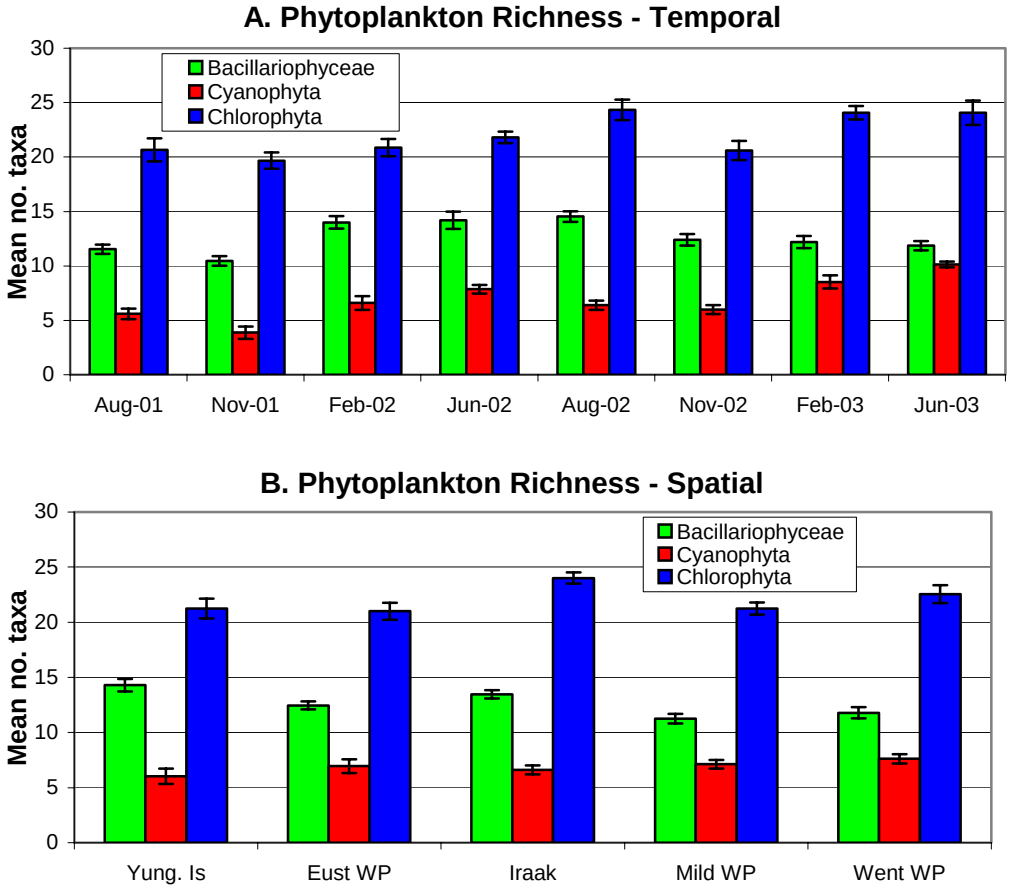

Figure 10. Mean number of taxa per sample over (A) time and (B) space for the three dominant phytoplankton groups. Error bars = ± 1 S.E.

Aulacoseira granulata/ambigua

Aulacoseira granulata /ambigua was highly abundant both temporally (Figure 11A) and spatially (Figure 11B). This taxon was most abundant in November and February of each year but mean concentrations remained above 1000 cells.mL^{-1} on all sampling occasions. Spatially, *Aulacoseira granulata/ambigua* was most abundant at the most upstream site (Yungera Island) and decreased progressively along the Mallee Tract, particularly within each weir pool.

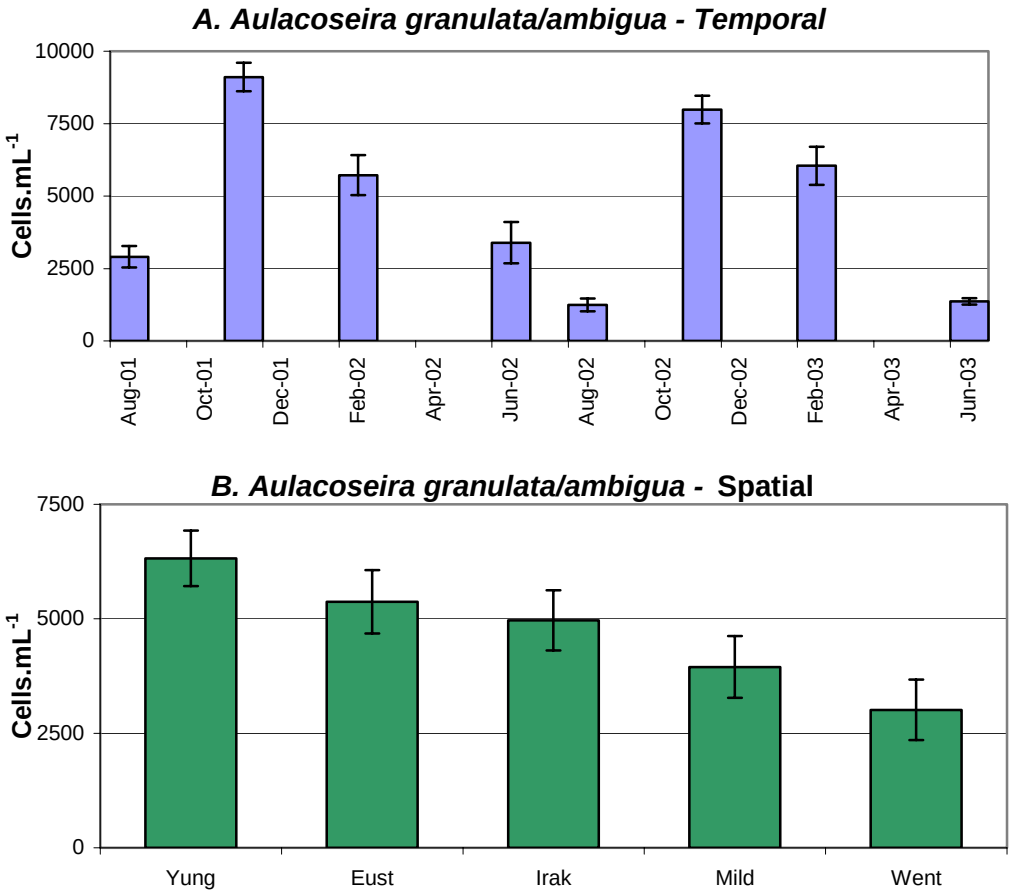

Figure 11. Distribution of *Aulacoseira granulata/ambigua* in (A) time and (B) space along the Mallee Tract of the River Murray. Error bars = ± 1 S.E.

Pseudanabaena limnetica

A large bloom of the cyanobacteria *Pseudanabaena limnetica* occurred in the June 2003 sampling event, with a mean abundance of 16,693 cells.mL^{-1} across all sites. This bloom alone accounted for over 25% of the total phytoplankton abundance recorded throughout the study.

Discussion

Effects of weirs

Changes to the composition of the phytoplankton community occurred along the Mallee Tract, as consistent with the findings of Sullivan *et al*. (1988). Sampling at strategic sites from Yungera Island to Wentworth in this study isolated the weir pools from the free-flowing reaches and revealed that most of this change occurred within the three weir pools, and not the 175 km reach of free-flowing river between Euston and Iraak. Multivariate classification showed that the greatest change in the phytoplankton community (based on abundance data) occurred in the Mildura weir pool, followed by the Euston and Wentworth weir pools. This may be due to the low flows and high residence times of water in the Mildura weir pool in summer as a result of high levels of extraction. As such, river turbulence may have fallen below a threshold to maintain some species in the water column. This raises the question as to why the level of phytoplankton change in the Wentworth weir pool is so low, despite this weir pool receiving the least flow (Research Report 1). A possible explanation is that the phytoplankton community entering the Wentworth weir pool had already undergone considerable community change in the Euston and Mildura weir pools upstream, and the communities now contain species better adapted to the hydraulic environment of the weir pools. The finding of very similar phytoplankton taxa at the Mildura and Wentworth sites supports this.

The progressive decrease in diatoms along the Mallee Tract (particularly *Aulacoseira granulata/ambigua*) and increase in cyanobacteria is further evidence of a phytoplankton community changing in response to the changed hydraulic environment of the weir pools. This transition between species is consistent with other studies examining the dynamics of *Aulacoseira* and *Anabaena* in the Maude weir pool of the Murrumbidgee River (Sherman *et al*., 1998; Bormans and Condie, 1998). The decrease in *Aulacoseira* is also consistent with River Murray studies (Sullivan *et al*., 1988; Hotzel and Croome, 1996; Bormans and Webster, 1999) where the low flow velocity of weir pools is predicted to facilitate shifts in the phytoplankton community. Diatoms are typically negatively buoyant (contain silica in their cell wall) and are reliant on turbulence to maintain their position in the water column. Cyanobacteria generally possess gas vacuoles and hence have an ability to remain positively buoyant; a feature that provides them with a competitive advantage in environments of low flow velocity. Low turbulence may also be predicted to favour mobile flagellates, although this was not evident in this study and these groups remained at low concentrations throughout the study period at all sites.

Weir pools with their relatively low photic:aphotic depth ratios (relative to neighbouring free-flowing areas) and low flow velocity are a challenging environment for phytoplankton reliant on turbulence to maintain their position in the water column. Not only must a phytoplankton remain suspended, but it must also spend sufficient time within the photic zone to undertake photosynthesis. It is probable that the hydraulic conditions likely explain much of the phytoplankton community changes occurring in the weir pools of the Mallee Tract. They may also explain the significant decrease (ca. 5%) in phytoplankton biomass in the weir pools relative to the free-flowing sites. This decrease is generally consistent with measurements of organic material (Research Report 2) demonstrating that some of the organic material deposited on the river bed during the low flow conditions is phytoplankton. The fate of these sedimented cells is largely dependent on their aestivation capabilities (which would differ between species) and the timing of higher flow conditions that may resuspend these cells.

The fate of phytoplankton leaving the Mallee Tract is largely dependent on the inflows from the Darling River (Sullivan *et al*., 1988). The turbidity of the Lower Murray is highly influenced by the discharge and turbidity of the Darling River inflows, and when high results in a large decrease in phytoplankton abundance in the Lower Murray Tract (Sullivan *et al*., 1988).

Flow Considerations

Flow has a strong influence on the diversity and abundance of phytoplankton, with increases in flow resulting in an initial increase in phytoplankton abundance (settled cells become resuspended into the water column) followed by lower abundance during flood events (Sullivan *et al*., 1988; Hotzel and Croome, 1996; Bormans and Webster, 1999). The consecutive years of low flow during the study period (Research Report 1) are likely responsible for the generally similar phytoplankton communities observed at sites for a given time in consecutive years. It is also likely that the total algal biomass during this study period is higher as a result of these low flow conditions. Total chlorophyll pigment remained at least three times greater than the 5 $\mu g.L^{-1}$ trigger value for slightly disturbed lowland rivers of south-east Australia (ANZECC, 2000). Dissolved inorganic phosphorus and nitrogen concentrations also remained low throughout the study (Research Report 2) and may have limited phytoplankton growth.

Seasonal changes in the phytoplankton communities were evident during these low flow conditions, revealing that factors other than flow were producing these differences. Nutrients, hydraulics and climate (particularly sunlight and temperature) all play important roles in structuring the phytoplankton community (Sullivan, 1990). The phytoplankton communities measured during this study – particularly over the winter/spring period – are likely not typical of the Mallee Tract during flood years. Sullivan *et al*. (1988) noted considerable differences in the phytoplankton during the 1982 drought that differed to flood years of 1980-1985. In particular, the winter and spring peaks of *Melosira granulata* (*here Aulacoseira granulata*) were diminished below Euston in 1982. In this study, however, *A. granulata/A. ambigua* remained at relatively high abundance at all sites and times and peaked in spring despite the low flows. Concentrations exceeded 10,000 $cells.mL^{-1}$ at some upstream sites in spring but generally decreased with distance downstream. Mean concentrations over the study period at Wentworth, the most downstream site, remained above 3,000 $cells.mL^{-1}$.

Silica is an important element for diatom development (component of the cell wall) and has been implicated in limiting diatom growth (Sullivan *et al*., 1988). Silica concentrations were not measured as part of this study, although their concentrations in the Mallee Tract based on longer-term monitoring (Mackay *et al*., 1988) are likely not limiting diatom growth (Hotzel and Croome, 1996).

The objective of this study was not to capture in detail the phytoplankton changes over time, as only four sampling times in each of two years were examined. To obtain an accurate depiction of phytoplankton changes, weekly (and expensive) sampling is required (e.g. Appendix 1 of Sullivan *et al*., 1988). However, the analysis of phytoplankton from eight sampling times and five sites allowed the effects of weirs on the phytoplankton community to be examined, and allowed a list of phytoplankton species present in the Mallee Tract during low flow conditions to be obtained. This study was successful in this regard, as it revealed consistent temporal and spatial changes in the phytoplankton community and demonstrated that the greatest changes occurred within the weir pools of the Mallee Tract.

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Appendix A. Phytoplankton taxa of the Mallee Tract

Numbers represent mean abundance (cells.mL^{-1}) of all samples.

Cyanophyta	
Anabaena affinis	173.3
Anabaena aphanizomenioides	280.2
Anabaena circinalis	390.2
Anabaena flos-aqua	187.2
Anabaena solitaria	132.1
Anabaena spiroides	34.4
Anabaena torulosa	4.9
Anabaena sp.	3.6
Aphanizomenon gracile	132.4
Aphanizomenon issatschenkoi	330.7
Aphanocapsa sp.	565.0
Coelosphaerium sp.	84.5
Cyanodictyon sp.	10.6
Cylindrospermopsis raciborskii	14.3
Geitlerinema sp. [fil/ml]	3.2
Lyngbya sp. [fil/ml]	0.1
Merismopedia sp.	4.2
Microcystis sp.	14.3
Oscillatoria sp. [fil/ml]	1.8
Phormidium sp. [fil/ml]	0.1
Planktolygbya contorta	166.1
Planktolygbya subtilis	454.8
Pseudanabaena limnetica	3102.2
Spirulina sp.	4.4
cf *Snowella sp.*	0.7

Euglenophyta	
Euglena sp.	7.0
Phacus sp.	0.2
Strombomonas sp.	1.4
Trachelomonas sp	2.0

Pyrrophyta	
Gymnodinium sp.	0.6
Peridinium inconspicuum	2.3
Peridinium sp.	1.1

Cryptophyta	
Cryptomonas sp.	18.3
Rhodomonas sp.	9.2

Chrysophyta	
Centritractus belenophorus	0.3
Dinobrion sp.	25.5

Chlorophyta	
Actinastrum sp.	117.5
Ankistrodesmus convolutus	5.1
Ankistrodesmus falkatus	226.1
Ankistrodesmus fusiformis	144.0
cf. *Ankyra lanceolata*	6.1
Bothriococcus sp.	5.3
Chlamydomonas sp	7.8
Chlorohormidium sp.	60.7
Lagerheimia sp (Chodatella sp.)	9.6
Closterium aciculare	2.1
Closterium dianae	0.2
Closterium kutzingii	0.8
Closterium macilentum	1.1
Closterium sp.	1.1
Crucigenia sp.	27.9
Coelastrum sp.	2.2
Cosmarium sp.	0.5
Cybotyon sp.	4.7
Dictyosphaerium sp.	36.6
Desmid 1	0.0
Euastrum sp.	0.8
Eudorina sp.	1.8
Fusola sp.	8.0
Golenkiniopsis sp.	6.8
Hyalotheca sp.	0.2
Kirchneriella lunaris	1.7
Kirchneriella obesa	0.7
cf. *Kirchneriella sp.*	1.7
Micrasterias hardyi	1.6
Monoraphidium mirabile	41.3
Mougeotia sp.	135.2
Nephrocitium sp.	1.4
Oocystis gigas	0.6
Oocystis sp.	9.5
Pediastrum duplex	51.7
Pediastrum simplex	1.5
Pediastrum tetras	33.8
Pediastrum sp.	0.8
Quadrigula sp.	0.3
Scenedesmus acuminatus	65.7
Scenedesmus denticulatus	2.9
Scenedesmus dimorphus	23.9
Scenedesmus opoliensis	28.8
Scenedesmus smithii	0.0
Scenedesmus sp.	8.4
Sphaerocystis sp.	16.7
Spirogyra condensata	0.2
Spirogyra sp.	1.1
Spondylosium sp.	0.0
Staurastrum ensiferum	0.6
Staurastrum excavatum	0.4
Staurastrum pinnatum	10.5
Staurastrum playfairi	32.3
Staurodesmus cuspidatus	0.2
Staurodesmus dejectus	0.1
Staurodesmus extensus	8.7
Tetraedron sp.	7.1
Tetrastrum heteracuntum	25.6
Treubaria triappendiculata	5.9
Zygnema sp.	0.5
Green 1	1.7

Bacillariophyceae	
Acanthoceras sp	1.6
Aulacoseira granulata / Aul. ambigua	4634.8
Cyclostephanos tholiformis	1.5
Cyclotella meneghiniana / Stephanodiscus sp.	83.1
Cyclotella setigera	17.7
Melosira sp.	0.6
Urosolenia sp.	1.9
Achnanthes sp.	0.4
Asterionella sp.	117.9
Bacillaria sp.	0.0
Cocconeis sp.	0.1
Diploneis sp.	0.0
Encyonema sp.	0.2
Epithemia sp.	0.0
Eunotia sp.	0.0
Fragilaria sp.	2.7
Gomphonema affine	0.1
Gomphonema lagenula	0.0
Gomphonema parvulum	0.0
Gomphonema sp.	0.0
Gyrosigma attenuatum	1.2
Gyrosigma sp.	1.2
Navicula cf. *cryptocephala*	0.0
Navicula cf. *cryptotenella* / cf *viridula*	21.5
Navicula sp.	0.3
Neidium sp.	0.0
Nitzschia acicularis	22.5
Nitzschia agnita	5.2
Nitzschia clostaerim	19.5
Nitzschia cf. *filiformis*	2.4
Nitzschia cf. *lorenciana (*cf *reversa)*	1.6
Nitzschia palea	1.3
Nitzschia cf *vermicularis*	1.2
Nitzschia sp. 1 (star)	111.6
Nitzschia sp.	17.7
Pinnularia sp.	0.0
Rhoicosphenia sp.	0.0
Rhopalodia sp.	0.2
Surirella sp.	0.1
Synedra acus	137.5
Synedra ulna	0.5
Tryblionella sp.	2.1
Diatom 1	0.0