

## CHAPTER 3.1

# PLANKTON COMMUNITIES OF THE COORONG, LOWER LAKES AND MURRAY MOUTH

SOPHIE C. LETERME<sup>1,3</sup>, ROD OLIVER<sup>2</sup>, RUSS SHIEL<sup>2</sup>, DEEVESH HEMRAJ<sup>1</sup>, MIKE GEDDES<sup>2</sup>, DEBORAH FURST<sup>2</sup>, KANE ALDRIDGE<sup>2</sup>, THOMAS BARNES<sup>2</sup> AND SCOTTE O. WEDDERBURN<sup>2</sup>

### INTRODUCTION

The Coorong, Lower Lakes and Murray Mouth (CLLMM) region is quite biodiverse, due to highly variable environmental conditions over a relatively small area. The varying environmental conditions create a broad array of habitats due to physical (i.e. presence of structure), chemical (i.e. variations in water quality/salinity) and biological (i.e. presence of aquatic macrophytes) factors (Chapters 2.7 & 2.10). As such, the region is well known for the presence of a diverse array of biota, particularly bird and fish taxa. However, other biota such as plankton are also abundant and diverse in the region for the same reasons as higher trophic order animals. Plankton are a diverse group of microorganisms that live in water, ranging from unicellular organisms smaller than 0.2  $\mu\text{m}$  (femtoplankton) to multicellular organisms up to 20 cm (macroplankton) (Table 3.1.1).

Autotrophic planktonic organisms, such as Cyanobacteria and microalgae, photosynthesise like plants and produce their own food from inorganic compounds, such as nutrients and minerals, using energy captured from sunlight. The importance of nutrients, cyanobacteria and microalgae to aquatic ecosystems has been well documented in the literature, and consequently they have been monitored across the CLLMM region since the 1970s, although

**Table 3.1.1** Range of size for different types of plankton.

Type of Plankton	Size range	Type of organisms
Femtoplankton	<0.2 $\mu\text{m}$	viruses
Picoplancton	0.2 to 2 $\mu\text{m}$	bacteria and cyanobacteria
Nanoplankton	2 to 20 $\mu\text{m}$	small phytoplankton such as small diatoms and dinoflagellates
Microplankton	20 to 200 $\mu\text{m}$	most phytoplankton and small zooplankton such as foraminifers, protozoans, rotifers
Mesoplankton	200 $\mu\text{m}$ to 20 mm	large zooplankton such as copepods, ostracods, cladocerans and larvae of invertebrates, such as barnacles, crabs, molluscs
Macroplankton	20 mm to 20 cm	amphipods, shrimps, jellyfish and larvae of fish

1 College of Science and Engineering, Flinders University, Sturt Road, Bedford Park SA 5042.

2 School of Biological Sciences, The University of Adelaide, Adelaide SA 5005.

3 Email: sophie.leterme@flinders.edu.au.

irregularly and inconsistently. Also important are heterotrophic planktonic organisms, such as the zooplankton that feed on other microorganisms, e.g. bacteria and phytoplankton, as well as smaller zooplankton. The monitoring of zooplankton communities in the CLLMM region only started in 2010.

Plankton are dispersed by flowing water or transported between water bodies or regions by animals (Havel & Shurin 2004). They provide a crucial source of food for larger organisms, such as bivalves (e.g. cockles, oysters) and fish (e.g. sandy sprat, Tamar goby, small-mouthed hardyhead). The ubiquity of plankton in aquatic ecosystems, and their importance in terms of biomass and production, make them a critical component of food webs and carbon cycling. In particular, they contribute to the availability and cycling of nutrients, and they also influence the pathway of matter transfer to higher trophic levels.

The intense anthropogenic modification of the CLLMM region — largely through the alteration and reduction of flows by barrages, locks and weirs; catchment activities influencing water quality; and climate change — has seen large environmental and hence ecological changes (Lester & Fairweather 2009; Paton & Bailey 2014; Dittmann et al. 2015; Leterme et al. 2015). Therefore, an understanding of the ecosystem, including plankton, is critical in order to assess the impact of changes and to aid management into the future. The aim of this chapter is to provide an overview of our current understanding of the plankton communities in the CLLMM region, and their variations over time. Shifts in community composition may reflect natural seasonal or annual cycles in environmental conditions, such as meteorology or flow, which reoccur over longer periods of time. Such influences may form recognisable patterns in community composition that are considered representative of different habitats. In contrast, large and persistent changes in plankton community composition may reflect major shifts in environmental conditions, and are likely to impact communities of higher organisms, often detrimentally, as the planktonic food resources are altered in their type, time of occurrence and food value. Management aimed at sustaining the environmental status of the region needs to be able to identify when shifts in planktonic community composition are sufficiently extreme and persistent to reflect site degradation, as well as to have sufficient knowledge of the environmental conditions responsible for changes in order to understand how they could be improved by management actions. This review demonstrates that, despite quite extensive information for some areas of the CLLMM region, especially the Lower Lakes, our knowledge of the plankton communities is still rudimentary, and for some areas poor.

Typically, time series of changes in community composition are compared with parallel changes in environmental conditions in order to try and recognise links. Although simple in concept, the identification of such links is often difficult in practice because so many parameters vary simultaneously, so that identification of the driving variables generally requires complex statistical analyses to confirm associations. Even when this is achieved, if the time series do not include periods not impacted by external influences, then identifying a plankton community that might be a target for management actions is still fraught with difficulties. Sometimes a 'space for time' substitution approach can be helpful, where changes in the plankton communities across sites are associated with differences in the environmental conditions. It is then assumed that if the environmental conditions changed to match those observed at a particular site, the same community composition would occur. The reliability of these analyses can be undermined

if sites are not fundamentally equivalent apart from the changing environmental parameter of interest. As this is not always the case, multivariate methods are generally required to tease apart the differences between sites.

This chapter draws on both time series analyses and ‘space for time’ substitution analyses in order to ascribe the variations in plankton communities in the CLLMM region, their responses to changing environmental conditions, and the attempts made to identify major environmental drivers that could help guide the development of management strategies.

## PLANKTON BIOTA

### Viruses and bacteria

Viruses are ubiquitous and abundant in aquatic ecosystems but, most importantly, they play a fundamental role in structuring the plankton food web, primarily by killing bacteria, cyanobacteria and phytoplankton. Through this process, viruses impact plankton diversity in aquatic ecosystems. However, the dynamics of viruses and their response to environmental changes are still understudied and poorly understood. Viruses and bacteria have been studied in the Goolwa Channel and the Coorong wetland in 2009 and 2010. Along the Coorong wetland, their communities became increasingly abundant towards Salt Creek, with the abundance of viruses increasing from  $9.0 \times 10^6$  cells mL<sup>-1</sup> (at the Murray Mouth) to  $2.5 \times 10^8$  cells mL<sup>-1</sup> (at Salt Creek). Viruses found in hypersaline systems such as Salt Creek are described by the term ‘Halovirus’. Similarly, bacterial abundances range from  $2.1 \times 10^6$  to  $2.4 \times 10^8$  cells mL<sup>-1</sup> along the Coorong wetland (Schapira et al. 2009; Pollet et al. 2010). The composition of bacterial communities along the Coorong wetland seemed to be mainly driven by salinity (Schapira et al. 2009).

### Cyanobacteria

Cyanobacteria are photosynthetic bacteria that form significant surface blooms. They are able to do so because they contain gas-filled spaces within the cells that provide a degree of buoyancy. In calmer conditions these cells can float upwards in the water column to the well-illuminated surface layers, where they can photosynthesise and grow prolifically, provided that nutrients and other cellular requirements are also met. In some cases, the gas-vacuolated cyanobacteria can regulate their buoyancy and alter their position in the water column in order to balance their growth requirements. For example, they may move away from the damaging excessive light intensities at the very surface in order to progressively access more nutrient-enriched layers once nutrients in the surface layers have been depleted. Light intensity, nutrient availability and the intensity of turbulent mixing are the major environmental factors that influence the success of the bloom-forming cyanobacteria. Under conditions where surface blooms occur, further concentration of the cells can occur if they are pushed downwind and then accumulate against a lee shore. In these circumstances, exceptionally thick layers of phytoplankton may occur, providing concentrations of cells that, if contacted or imbibed by humans or animals, could be damaging to health.

There has been a long history of cyanobacterial blooms in the region, with one of the first ever detailed scientific accounts of toxic cyanobacteria reported in a paper in *Nature* in 1878

by George Francis, Adelaide assayer and chemist (Francis 1878). This described animal deaths attributed to ingestion of *Nodularia spumigena* by stock watering at Lake Alexandrina. The water level was very low in 1878, and during calm conditions with high water temperatures a bloom floated to the Lake surface and was blown to the shoreline where horses, cattle and sheep ingested the material, resulting in several hundred animals dying. In the 1990s blooms of *N. spumigena* again came to the attention of the public, and following confirmation of toxicity, the water supply was switched to a local reservoir and recreational use of the Lake was restricted.

Salinity and cyanobacteria in the lower River Murray are responsible for degrading the water quality to a point where it negatively impacts both the Lower Lakes and Coorong ecosystems and the water supply for irrigation and domestic supply. Cyanobacteria present a toxic threat to wildlife but also have implications for the entire food chain, as they affect the sustainable biomass of higher order organisms. In 2007, the highest cyanobacterial abundance ( $1.3 \times 10^6$  to  $1.4 \times 10^6$  cells mL<sup>-1</sup>) was recorded at salinity conditions ranging between 8.0% and 11.0%, north and south of Parnka Point (Schapira et al. 2010). Aldridge et al. (2012) found that in response to large water inflows into the Coorong in 2010-2011, first the phytoplankton community was dominated by Cyanobacteria, but as the flow continued, the abundance of Chlorophyta (green algae) and Bacillariophyta (diatoms) increased. Thus, it was assumed that the phytoplankton community was shifting towards one that would have greater nutritional benefits for the Coorong ecosystem.

## Microalgae

The CLLMM water quality monitoring programs operated by the Department of Environment, Water and Natural Resources (DEWNR) used the NATA-registered laboratory of the Australian Water Quality Centre for identification and enumeration of the phytoplankton. Other research programs operated by Flinders University have used Microalgal Services (Victoria), an Australian laboratory with high-level expertise in identification and monitoring of marine phytoplankton. Different regions of the CLLMM have been monitored for different lengths of time: Lake Alexandrina from 1983; the Goolwa Channel, which is a part of Lake Alexandrina, from 2005; Lake Albert from 1997; and the Coorong only from 2006. Specific research projects have provided earlier data but only for short periods of time. In total the monitoring programs have identified 185 different phytoplankton species in 140 different genera. Even in the Coorong, despite the short period of monitoring, 131 different taxa have been identified. Most of the major phytoplankton groups are represented, with a wide array of attributes (Table 3.1.2). Consequently, as environmental conditions change, so the community composition of the phytoplankton changes to be dominated by taxa that are more suitable to the changing growth conditions.

Cyanobacteria and microalgae are critical components of aquatic food webs, their photosynthetic production providing a major food supply. Occasionally, when growth conditions are suitable, excessive growths of those photosynthetic organisms can result in 'blooms' that can cause a range of water quality problems. A high concentration of those organisms can be aesthetically displeasing, especially when forming a 'pea-soup' appearance in areas used for recreational and water sport activities. In some cases, contact with contaminated

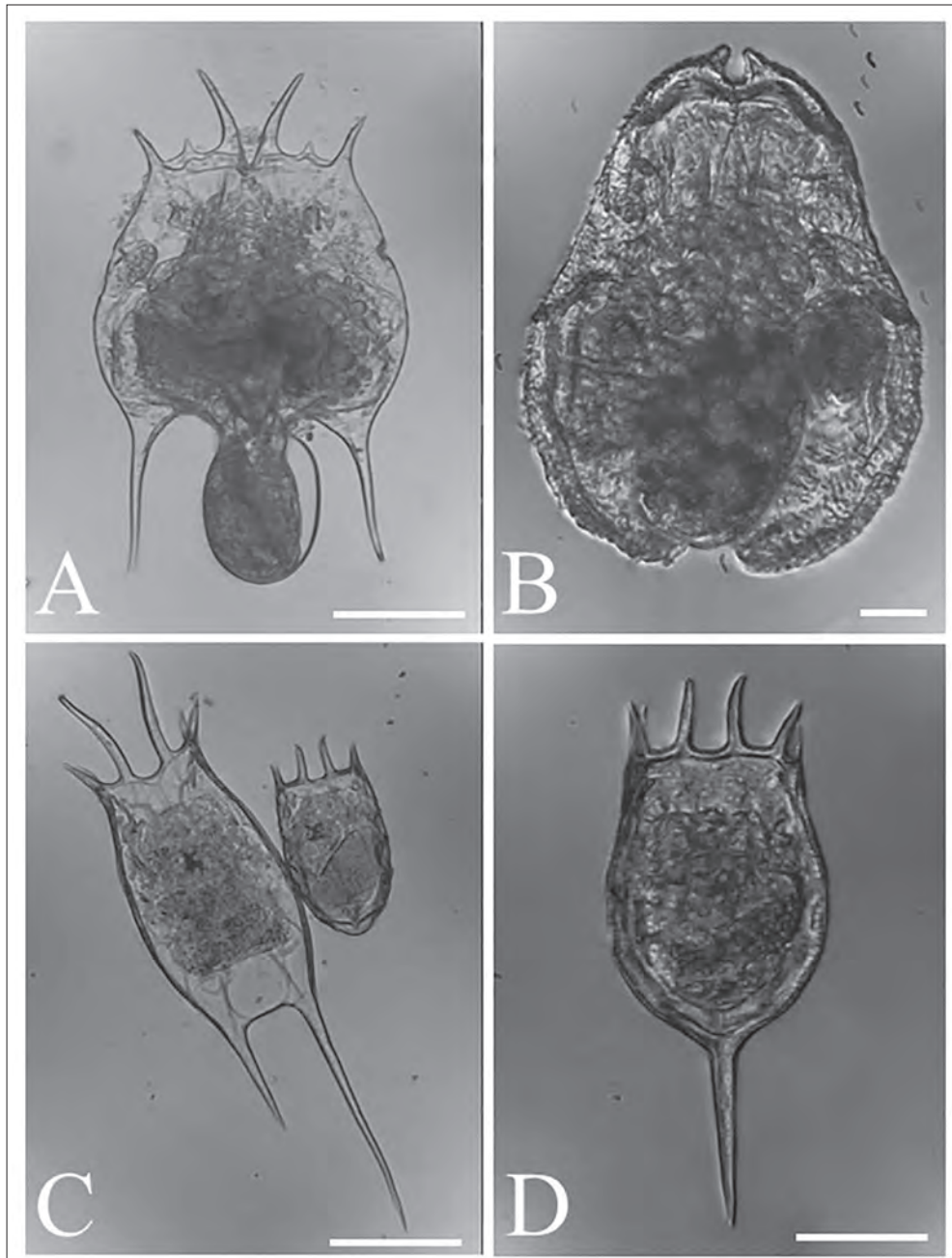
**Table 3.1.2** Phytoplankton taxa observed in the CLLMM region.

Taxa	Common name	Attribute/Characteristics
Bacillariophyceae	Diatoms (single-celled, chain-forming cells)	Cell surrounded by a frustule largely made of silica (SiO <sub>2</sub> ); two halves fit together like a pillbox
Chlorophyta	Green algae (single-celled, filamentous or colonial)	Widely distributed, pigments similar to terrestrial vegetation
Dinophyta	Dinoflagellates (single-celled, flagellated mixotrophs)	Some species present cellulose plates on top of the cell membrane that constitute the armour of the 'armoured' dinoflagellates
Cyanophyta	Cyanobacteria (also called blue-green algae)	Can be single-celled, filamentous or colonial
Cryptophyta	Cryptophytes (flagellated single celled)	Possess at least 2 flagella for locomotion
Chrysophyceae	Chrysophytes (Golden-brown algae)	Mostly in the open ocean, are part of the nanoplankton
Charophyta	Charophytes (filamentous and desmids)	Mostly in hard fresh to brackish water with very limited flow
Euglenophyta	<i>Euglena</i> (flagellated single-celled)	Mostly freshwater; no true cell wall but bound by a pellicle made of proteinaceous strips which give the cell its shape

water can be unhealthy. Large blooms often produce taste and odour compounds, especially when they begin to decay, reducing the usefulness of the water resource for consumptive purposes. Problems with consumptive use are exacerbated by the increased difficulty of treating the water. The large mass of cells readily blocks filters and requires increased chemical treatment to meet drinking water standards. In many cases these problems are annoying, but for some groups of species, especially some of the cyanobacteria and dinoflagellates, blooms can be far more problematic because some have the added attribute of toxin production. A variety of different toxins are produced by the various phytoplankton, with effects ranging from skin irritation to acute diarrhoea, neurotoxicity and liver damage, with the potential to cause death in some extreme cases.

## Zooplankton

Zooplankton are a critical part of any aquatic ecosystem, including the Murray-Darling river system, where they are an important source of food for fish (e.g. Cheshire 2010; Wedderburn et al. 2013), but they also consume and control bacteria (e.g. *Brachionus* spp.; Fig. 3.1.1). There are a high number of species and endemism in Australia. For example, there are almost a thousand Rotifera species in Australian inland waters, with at least 15% endemic to Australia (Shiel & Koste 1986). Rotifera is one of the most diverse microfaunal groups in floodplains of the Murray, but only 10 rotifer species could be considered widespread in the system (Shiel et al. 1998). In spring surveys of 112 temporary floodplain waters on River Murray tributaries by Shiel et al. (1998), ephemeral pool microfaunal assemblages were distinct from those of adjacent permanent billabongs, which is apparently a function of, or response to, habitat heterogeneity (Shiel et al. 1998). In the Murray-Darling Basin, zooplankton species diversity is inversely related to salinity (Shiel 2002).



**Figure 3.1.1** Rotifer species of the Murray-Darling river system (courtesy of Russel Shiel).  
 (A) *Brachionus quadridentatus* (scale bar: 47  $\mu\text{m}$ ) (C) *Keratella slacki* and *Keratella lenzi* (scale bar: 80  $\mu\text{m}$ )  
 (B) *Brachionus keikoa* (scale bar: 12  $\mu\text{m}$ ) (D) *Keratella cochlearis* (scale bar: 39  $\mu\text{m}$ ).

## IMPACT OF ENVIRONMENTAL CHANGES

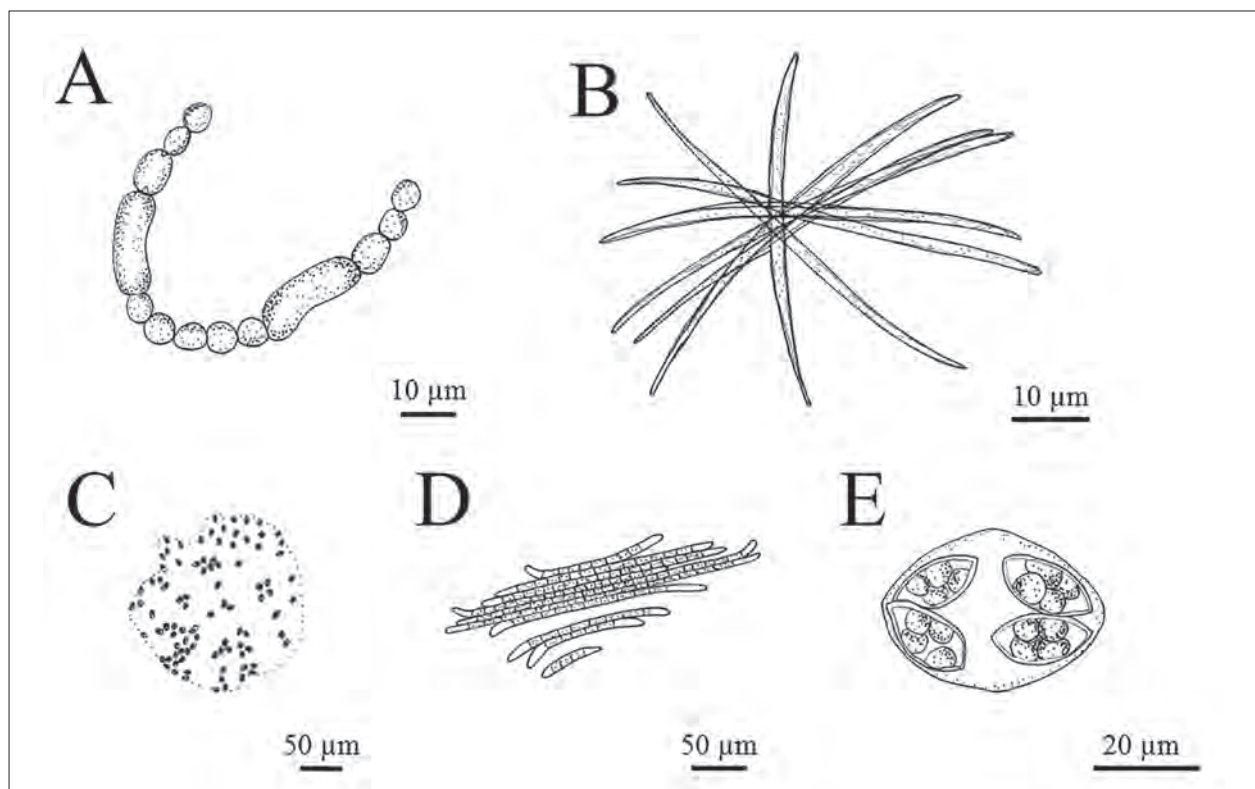
### Lower Lakes — Lake Alexandrina and Lake Albert

Before construction of the barrages between the Lower Lakes and the Coorong, the Lower Lakes used to fluctuate between brackish (estuarine) and fresh (lacustrine), depending on river and tide dynamics. Construction of the barrages has removed the influence of tides from the Lower Lakes and, combined with the removal of water (for anthropogenic application), this

has reduced the frequency of flows into the Lower Lakes. As such, when flows are further diminished due to drought, water quality issues eventuate.

The general patterns of occurrence of phytoplankton in the Lakes were reviewed by Aldridge et al. (2012). Although mixed communities of phytoplankton species occur in the Lakes, particular groups are more likely to be dominant under certain conditions. During the periods 1965-1967 and 1972-1973, blooms of cyanobacteria were observed in the Lakes (Geddes 1984). During periods of high turbidity, low light availability and high nutrient availability, the filamentous green alga *Planctonema lauterbornii* seems to dominate the community. In Lake Alexandrina from 1975 to 1978, that species accounted for more than 95% of algal cells (Geddes 1984). The flow of fresh water into the Lake has been associated with changes in the cyanobacteria community composition, and the changes in phytoplankton dominance have been associated with changes in salinity and nutrients (Jendyk et al. 2014; Leterme et al. 2015).

Later, between 1990 and 1995, cyanobacterial blooms of *Nodularia spumigena*, *Anabaena* spp. and *Aphanizomenon* spp. (Fig. 3.1.2) occurred regularly in Lake Alexandrina and Lake Albert, and were associated with extended periods of low freshwater flow, low turbidity, low turbulence and high light availability. More specifically, the blooms of *N. spumigena* in the summer and autumn of both 1990-1991 and 1995 were associated with low flows (<10 000 ML day<sup>-1</sup>), moderate turbidity (<50 Nephelometric Turbidity Units (NTU)), low electrical conductivity (40-100 mS m<sup>-1</sup>) and variable nutrient concentrations (Aldridge et al. 2012). Towards the end of the Millennium Drought, between August 2008 and September 2009, when river inflows were minimal and Lake depths fell to unprecedented levels, both Lake Alexandrina and Lake



**Figure 3.1.2** Cyanobacteria: (A) *Anabaena* sp., (C) *Aphanocapsa* sp. and (E) *Aphanizomenon* sp.; and green algae: (B) *Ankistrodesmus* sp. and (D) *Oocystis* sp.

Albert regularly experienced blooms of *picocyanobacteria*, notably *Aphanocapsa* spp. (Fig. 3.1.2), *Planktolyngbya* spp., *Aphanizomenon* spp. and *Pseudanabaena* spp. (Aldridge et al. 2012). It was also during the extended drought period that the first recorded bloom of *Cylindrospermopsis raciborskii* occurred in the Lower Lakes in 2006 (Cook et al. 2008).

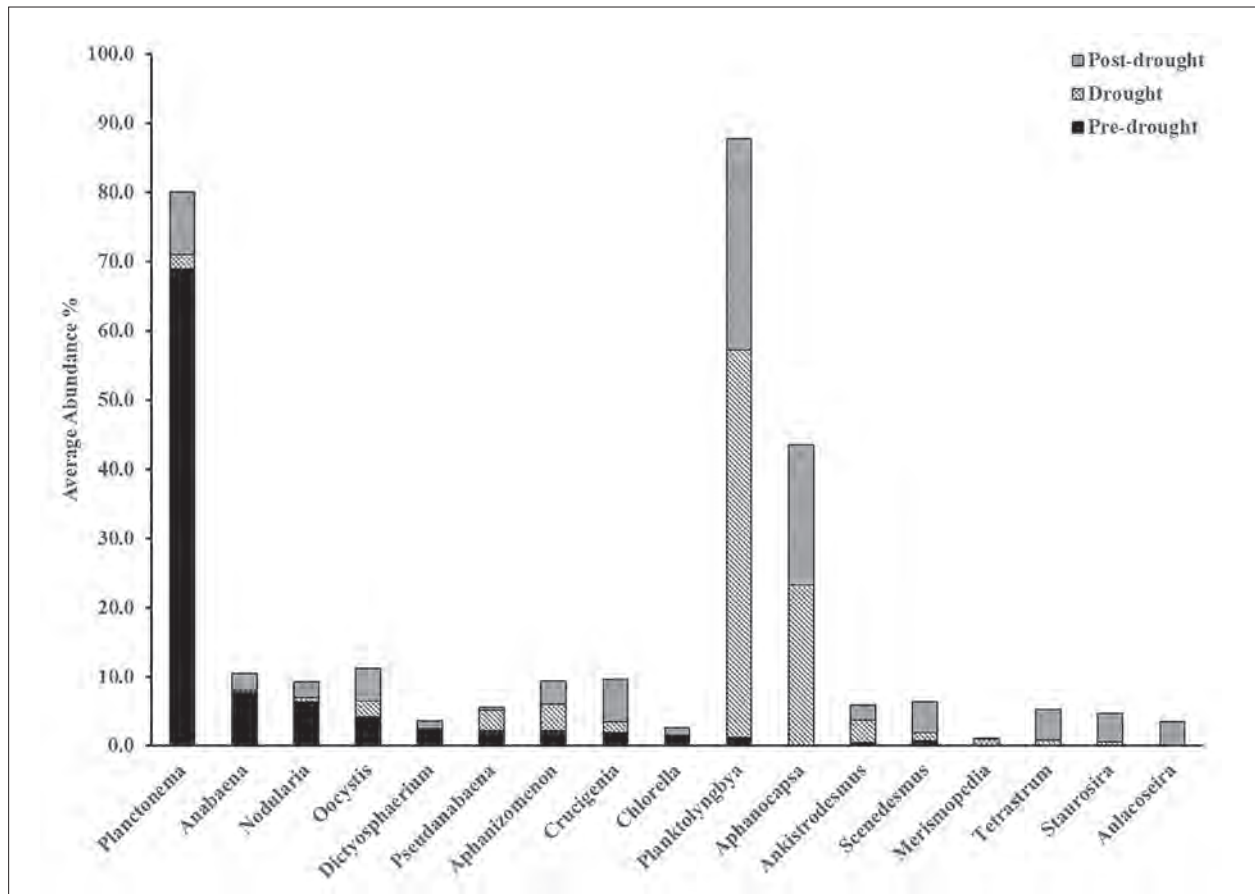
Consistent and reliable long-term monitoring provides the data for developing dependable understanding of the functioning of ecosystems. Monitoring aims to capture the extent of change within a system and provide data amenable to statistical testing. Statistical analysis helps ensure that suggested interactions are reliable and can be used in developing management plans. Monitoring in the CLLMM has been undertaken for different purposes and for different periods of time in the various regions, but in all cases sample collection has been disrupted or altered and this makes statistical analyses difficult. However, overarching data analyses are more powerful and robust than the conceptual linking of individual studies, and recently efforts have been made to extract a standard phytoplankton data set from the DEWNR monitoring program to describe changes in the CLLMM using multivariate analyses (Oliver et al. 2013, 2014). The longest and most continuous monitoring data sets are from Lake Alexandrina, especially from a site near Milang. This has been sampled for phytoplankton since the mid-1970s, although data collection from this site has been disrupted; for example, no monitoring was carried out between 1999 and 2004 due to lack of government funding, which was unfortunate as the decade-long Millennium Drought started at this time.

Multivariate analyses of the data have enabled broad comparisons of community changes — for example, the average concentrations of the genera most responsible for the community changes before, during and after the Millennium Drought (Fig. 3.1.3). The data from Milang capture the major changes in phytoplankton abundance and confirm many of the characteristics previously reported in individual studies. In particular, they show that *Planctonema* spp. were a dominant phytoplankton for the period 1983-1997, but that during this time there were occasional blooms of cyanobacteria, largely of *Nodularia* or *Anabaena*, enhancing their average cell numbers. Monitoring at the site ceased just prior to the drought, but when it recommenced in 2006 during the drought, *Aphanocapsa* spp. and *Planktolyngbya* spp. were common, and their increases and the demise of *Planctonema* were the largest population changes. In 2011, *Planctonema* spp. made a short recovery and returned to dominance during periods of high flows associated with the breaking of the drought, and this is reflected in its contribution to the community composition post-drought (Fig. 3.1.3). However, this was short-lived as flows again declined and the cyanobacteria *Aphanocapsa* spp. and *Planktolyngbya* spp. returned.

These multivariate statistical techniques, which have become available over the last decade as increased computing power has enabled their routine application, provide a means for analysing changes in community composition and relating them to changes in water quality (Oliver et al. 2013, 2014). Such analyses suggest that the major driver of shifts in phytoplankton community composition over the Millennium Drought was the increased salinity of the Lake, a result of reduced inflows of water from the River and the evaporation from the Lake increasing the salt concentration.

Much like smaller planktonic organisms, zooplankton assemblages in the River Murray are reflective of the river water conditions: alkaline (pH 7.5-8.7), turbid (10-225 NTU) and moderately saline (0.2-1.0 g L<sup>-1</sup>; Shiel 1979). All freshwater zooplankton species are sensitive to





**Figure 3.1.3** Average percentage abundance within each period of the microalgal genera accounting for 90% of the change across the pre-drought, drought and post-drought periods in Lake Alexandrina. (Designed by R. Oliver)

salinity increases above  $\sim 4 \text{ g L}^{-1}$  (Shiel & Tan 2013a). In particular, the Murray regime provides more suitable conditions for phytoplankton growth, and thus favours the development of herbivorous microcrustacea with relatively long duration times (Shiel 1986; Shiel & Walker 1984). Downstream weirs and locks on the Murray River provide low- or no-flow conditions and a longer retention time, which permit reconstitution of a microcrustacean assemblage. This is referred to in European studies as the 'age' of the water, with rotifers dominating in waters of low 'age' (e.g. short retention time storages such as Lake Mulwala) and microcrustacean assemblages appearing in waters of greater 'age' (e.g. long retention time storages such as Lakes Dartmouth and Hume).

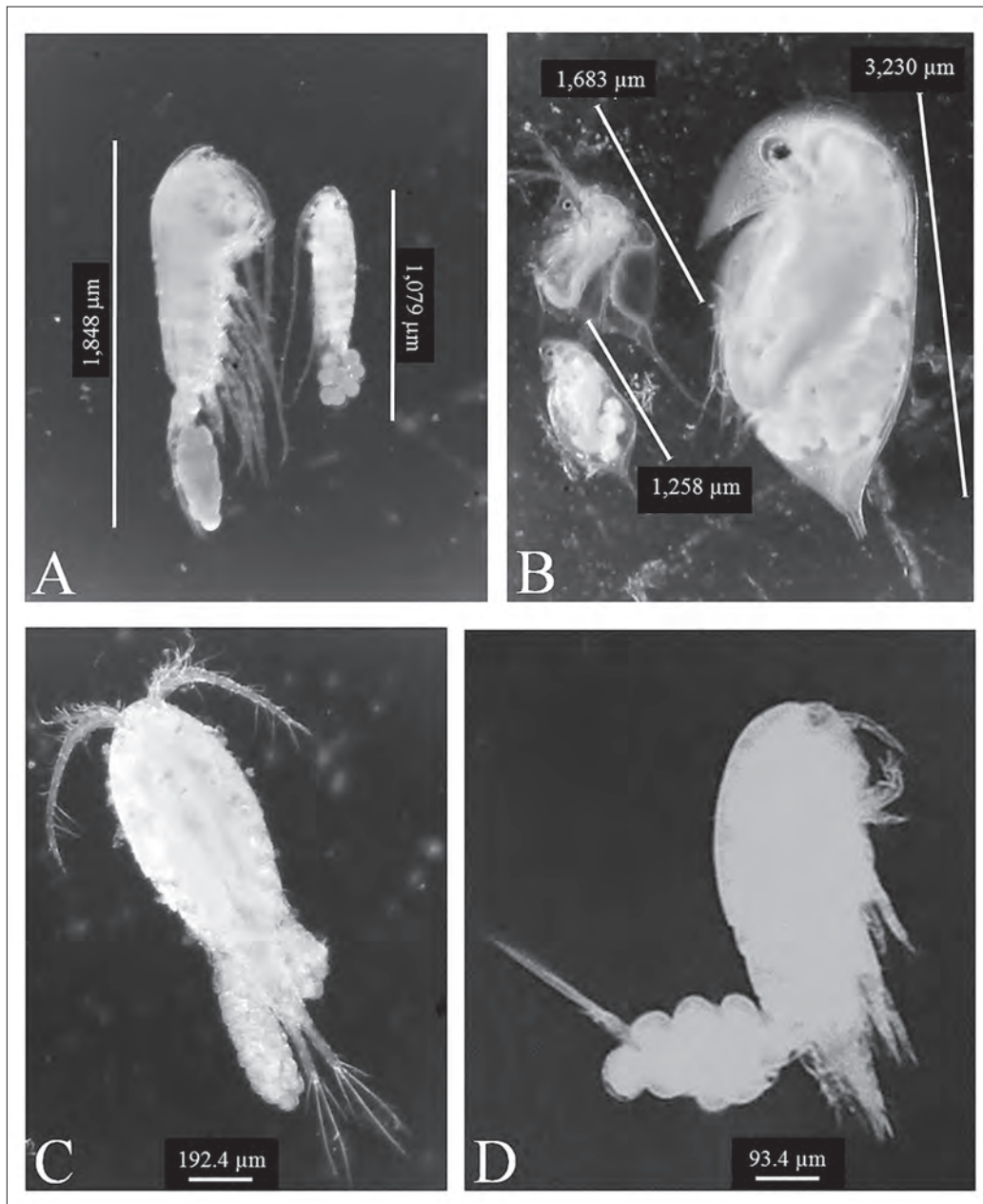
This phenomenon reflects the life cycle of the respective microfauna. At ambient temperatures in Murray River tributaries, rotifers are reproducing in days and microcrustacea in weeks. Rotifers are able to get through their life cycles in the short retention-time storages; microcrustacea are not. The latter require stable conditions for a longer period to reach adult reproductive stages, and are unable to complete life cycles in turbulent or rapid through-flow storages (Shiel 2002). Shiel et al. (1982) noted 133 species of zooplankton in the lower Murray. A mixed assemblage of protists, rotifers and microcrustaceans persists into the lower Murray, with longitudinal changes in species composition during long travel times to the River mouth (Shiel 2002). The persistent microfaunal community reflects disparate contributions

from upstream impoundments, e.g. floodplain waters which may at times have a connection to the River, regions of slow flow such as backwaters or braided channels, waste stabilisation ponds from riverside communities, which may discharge into Murray tributaries — in fact, any standing water which connects to the River at any time (Shiel 2002).

Geddes (1984) also highlighted that there are notable differences between zooplankton assemblages in upstream impoundments of the Murray and Lake Alexandrina (e.g. higher zooplankton biomass), because distinct limnetic species are maintained locally, even though Lake Alexandrina receives femtoplankton from the River Murray and from the tributaries (e.g. Finnis River; Shiel & Tan 2013a). In particular, there is little seasonal pattern for rotifers in the Lower Lakes (Geddes 1984). The size of some zooplankton species (e.g. *Daphnia carinata* up to 5 mm) in Lake Alexandrina is much greater than other parts of their ranges, possibly because high turbidity makes them less prone to predation (Geddes 1984), but this requires testing.

Shiel and Tan (2013a) recorded 207 taxa of zooplankton in the Lower Lakes, Goolwa Channel and the estuarine region of the Coorong in sampling over 2011–2012, with 152 of those taxa recorded in Lake Alexandrina (Fig. 3.1.4). This compares with a total of 28 species recorded in Lake Alexandrina and Lake Albert by Geddes (1984), which partly relates to differences in sampling methods (35 µm mesh versus 158 µm mesh respectively), and also to much lower densities recorded by Geddes (1984). In 2010–2012, Lake Albert had the highest zooplankton densities in the region with 4 000–5 000 individuals L<sup>-1</sup> — the halotolerant *Hexarthra brandorffi* dominated immediately following drought, but was later replaced by freshwater zooplankton species (e.g. the rotifer *Filinia pejleri*; Shiel & Tan 2013a). The return of river flows in 2011 led to a riverine, rotifer-dominated assemblage in Lake Alexandrina, and this assemblage was also reflected in samples taken from the Goolwa Channel and estuarine region of the Coorong at the same time (Shiel & Tan 2013a). Lake Albert differed from Lake Alexandrina in that there was a mix of microcrustaceans, rotifer and protist plankton that was similar to that recorded by Geddes (1984). Shiel and Tan (2013a) found that after high river flows, many zooplankton in the CLLMM region had originated from upstream (e.g. the rotifers *Brachionus angularis* and *Keratella australis* (Fig. 3.1.1)), as previously suggested (Shiel et al. 1982) and recently documented (Furst et al. 2014). The tributaries of Lake Alexandrina and the Goolwa Channel appear to be important sources of zooplankton biomass. For example, Shiel and Tan (2013a) found substantial contributions of microcrustaceans from the Finnis River and Currency Creek.

Lake Albert has an elevated salinity compared with Lake Alexandrina; hence, halotolerant or halophile plankters are present, and assemblages are similar to the marine-influenced North Lagoon of the Coorong (Shiel & Tan 2013b). During freshwater flows through the entrance to Lake Albert (Narrung Narrows), an increase in species richness due to the presence of both riverine and estuarine zooplankton has been recorded (Shiel & Tan 2013b). As well as being diverse compared to other sampling sites in the lower Murray, Lake Albert has been recorded to have the greatest density (4 000–5 000 individuals L<sup>-1</sup>), compared to other lower Murray sites during a monitoring program (Shiel & Tan 2013b). Microcrustaceans, rotifers, copepods and cladocerans have been recorded in Lake Albert. Investigations into Lake Albert zooplankton fauna are few, with only four monitoring reports available in the literature.



**Figure 3.1.4** Zooplankton species.

(A) *Boeckella triarticulata* (left) and *Calamoecia ampulla* (right) sampled in Lake Alexandrina.

(B) *Daphnia* species sampled in Lake Albert. Lower left: *D. galeata*, an invasive species new for the continent. Top left: *D. lumholtzi*. Right: one of the many *D. carinata*, which is a species complex.

(C) *Australocyclops australis* sampled in the River Murray.

(D) *Microcyclops varicans* sampled in Lake Alexandrina.

Images were taken using Dark-Field Light Microscopy. (Micrograph by R. Shiel)

### Murray Mouth/Coorong Lagoon

Monitoring in the Coorong has been restricted to recent times, but has also varied annually along the length of the waterbody. DEWNR and Flinders University, through their respective programs, monitored the Coorong between 2005 and 2016. The three sampling locations monitored in the Murray Mouth region were sampled in 2005/06, 2010/11 and 2012/13, while the northern

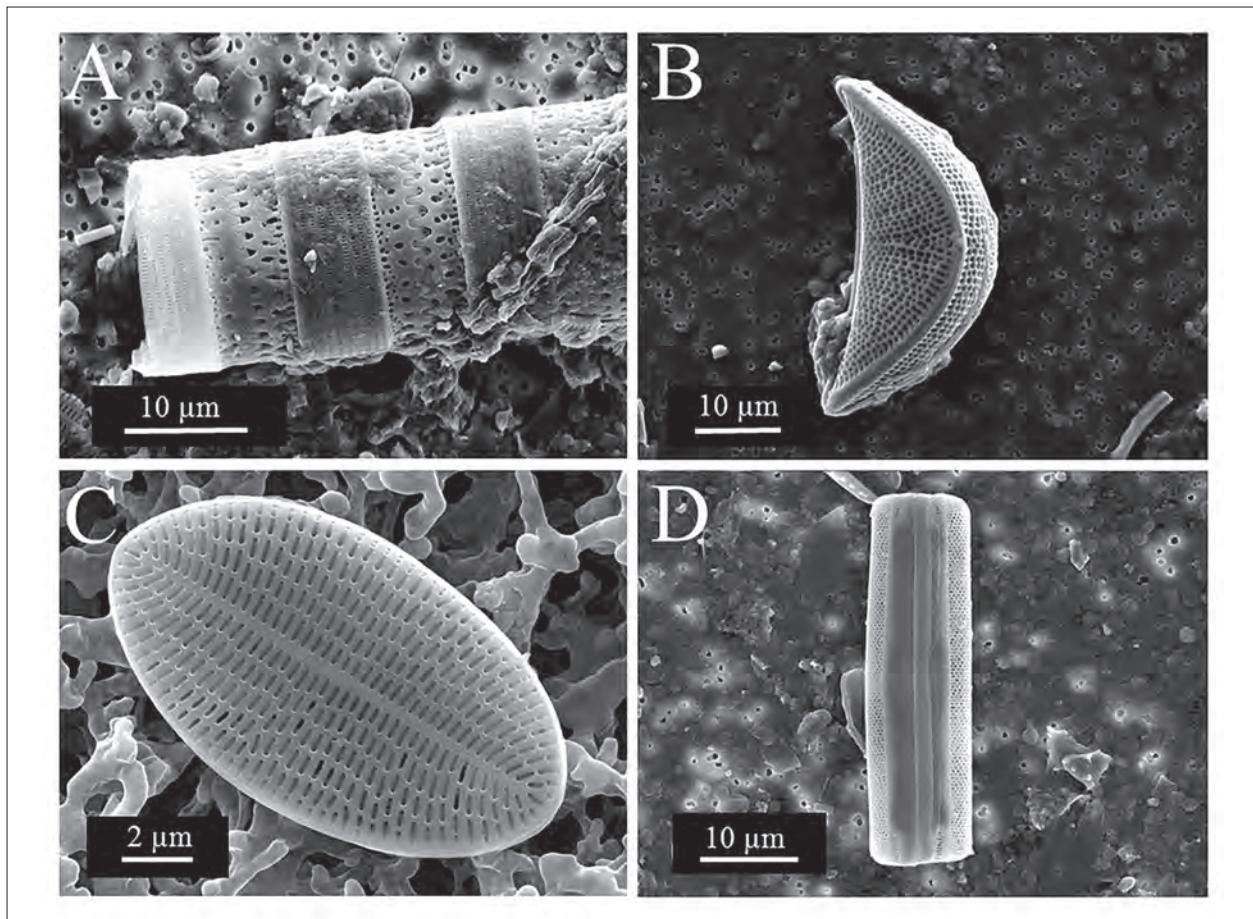
Coorong was sampled in 2010/11 and 2013/14 and the southern Coorong in 2013/14. Flinders University monitored the Coorong between August 2011 and 2013 on a monthly basis. This fragmented sampling regime makes data analyses very difficult. However, multivariate analyses indicated that within each of the sites the changes in phytoplankton composition over time were not significant, while differences between sites were significant. This enabled a snapshot of the longitudinal differences in average phytoplankton community composition at stations along the length of the Coorong over the monitoring period, reflected in average cell abundances for species present in 95% of the samples (Table 3.1.3). Originally in the monitoring data, *Nannochloris* was identified as *Chlorella*, but this was corrected following more detailed taxonomic assessment, and here the *Chlorella* enumerations are attributed to *Nannochloris*.

In the Coorong, phytoplankton has been monitored for its biomass (expressed in Chlorophyll *a*) and its composition. The freshwater inflow into the Coorong varies significantly on a seasonal basis and impacts the salinity levels of the water in the North and South Lagoons. The phytoplankton biomass has been observed to be constantly higher at sites with elevated salinity (Jendyk et al. 2014; Leterme et al. 2015; Hemraj et al. 2017a). The increase in phytoplankton biomass with salinity is associated with the spatial variation in phytoplankton community structure along the system, in particular, with a decrease in taxonomic richness. While salinity is the main driver of the phytoplankton community in the Coorong, the nutrient composition of the different regions (i.e. Goolwa Channel, North and South Lagoons) also affects the community structure along the system.

Jendyk et al. (2014) monitored the phytoplankton communities of the Coorong following the inflow described. Over the two years of monitoring, a total of 52 species of diatoms (Fig. 3.1.5), 27 species of dinoflagellates, 35 species of chlorophytes and 11 species of cryptophytes were identified. The distribution of those species was affected by salinity (Jendyk et al. 2014; Leterme et al. 2015), with chlorophytes dominating brackish locations and diatoms prevailing in hypersaline conditions. While a wide range of phytoplankton species was encountered throughout this study, their origin and/or preferred habitat within the estuary was highly group-dependent. Three distinct populations of phytoplankton were identified as a function of salinity:

1. chlorophyte-dominated populations, indicative of freshwater and low brackish conditions
2. diatom-/dinoflagellate-dominated populations that thrive at higher salinity
3. a transitory or euryhaline population that consists of species encountered throughout the Coorong all year round, and that seems unaffected by seasonal changes in salinity.

The zooplankton assemblages in the estuarine region of the Coorong are more variable than those in the Lakes, being subject to barrage releases and tidal influences; hence they fluctuate between riverine and estuarine microfauna in short periods of time (Shiel & Tan 2013a). Overall, about 85% of zooplankton recorded during high river flows from 2010 to 2012 were riverine in origin rather than being a lacustrine assemblage (Shiel & Tan 2013a). There are likely to be positive food chain effects from the influx of freshwater zooplankton during times of river flows, particularly for small-bodied fish or early life stages of larger fish species (Shiel & Tan 2013b), but in the CLLMM region there are only a few studies in this regard (e.g. Lamontagne et al. 2007; Wedderburn et al. 2013, 2016). During their 2013-2014 survey, Hemraj et al. (2017a) recorded



**Figure 3.1.5** Diatoms.

(A) *Aulacoseira* sp.

(C) *Cocconeis* sp.

(B) *Rhopalodia* sp.

(D) *Grammatophora* sp. sampled in the Coorong.

Images were taken using Scanning Electron Microscopy. (Micrograph by S. Leterme)

30 zooplankton taxa present along the Coorong, with 18 taxa observed in the hypersaline area. The majority of these taxa included rotifers, copepods and invertebrate larvae. Seasonal and spatial variations in populations were apparent, with several species present along the length of the Coorong, while others, such as *Acartia* cf. *fancetti*, were only present in the hypersaline areas, past Parnka Point. Along the Coorong, copepod eggs and nauplii are generally extant throughout the year, although variations in abundances are apparent. However, copepodites and adults are more commonly encountered during periods of higher water levels. As emphasised by Brendonck and De Meester (2003), the structure and dynamics of the egg bank are determined by the life-history characteristics of the species (or local population), the hatching phenology of their resting stages and the characteristics of the habitat. Overlooking the egg bank as an important component of zooplankton communities may lead to erroneous interpretations in the analysis of community and population genetic structure.

### **Influence of river flow on plankton**

Floodplains and other off-channel habitats commonly contain more diverse and abundant zooplankton communities than the river channel itself. Whilst several biotic and abiotic factors



Group	Genus/Species	Monument Road	Halfway	Sugar's Beach	Mundoo Channel barrage	Godfrey's Landing	Murray Mouth	Boundary Creek	Hunter's Creek	Ewe Island	Tauwit- chere	Pelican Point	Mark Point	Long Point	Noona- meena	Parnka Villa	Villa de Yumpa	Jack Point	Salt Creek
Chlorophyta	<i>Dimorphococcus</i>	131	323	267	225	138	11	146	167	171	170	1833	390	217	762	97	103	142	442
Dinophyta	<i>Gymnodinoid &lt;20um</i>	111	198	79	189	74	0	0	725	165	0	0	0	1200	267	0	0	0	0
Cryptophyta	<i>Hemiselmis</i>	0	0	0	0	0	0	0	0	101	23	267	30	0	533	0	0	0	0
Dinophyta	<i>Heterocapsa rotundata</i>	554	1156	474	187	355	0	750	0	7	20	0	18	128	400	82	419	585	1042
Chlorophyta	<i>Kirchneriella</i>	158	238	231	151	705	0	0	0	15	30	433	89	247	275	173	325	202	475
Cryptophyta	<i>Leucocryptos</i>	50	57	61	21	14	0	133	0	2	0	90000	186	37	33	17	17	0	33
Cyanophyta	<i>Merismopedia</i>	0	37	0	17	76	0	0	0	104	16	0	10	0	33	17	8	0	0
Chlorophyta	<i>Monoraphidium</i>	232	587	309	174	80	0	1533	0	8	9	83	27	3	22	12	316	797	783
Bacillariophyceae	<i>Naviculoid</i>	948	1219	627	894	0	1097	14547	3933	389	1357	0	3067	0	0	0	0	0	0
Bacillariophyceae	<i>Nitzschia</i>	2	0	2	93	218	0	0	0	4	34	1400	17508	20	517	133756	13	0	0
Chlorophyta	<i>Oocystis</i>	114	201	365	129	189	10	108	0	26	61	217	95	115	832	33	273	283	867
Chlorophyta	<i>Pediastrum</i>	119	203	1156	121	1979	125	421	100	121	57	283	733	76	267	2035	225	187	767
Cryptophyta	<i>Plagioselmis prolonga</i>	371	404	284	379	96	698	1298	1445	668	916	367	455	198	217	95	0	0	0
Chlorophyta	<i>Planctonema</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cyanophyta	<i>Planktolyngbya</i>	41	3	0	167	11	23	0	0	94	39	53	126	200	147	67	0	0	0
Cryptophyta	<i>Rhodomonas lacustris</i>	207	587	175	265	425	0	75	0	14	17	233	36	208	498	98	336	322	408
Chlorophyta	<i>Scenedesmus</i>	1703	1008	1599	921	0	2486	5345	6217	2703	5145	0	1004	1250	0	7	0	0	0
Bacillariophyceae	<i>Staurisira</i>	53165	1269	2770	4399	0	39980	7750	9480	31241	16464	0	14089	4150	0	313	0	0	0
Cyanophyta	<i>Synechocystis</i>	0	0	0	71	0	0	0	0	0	0	0	59	0	417	0	0	0	0
Bacillariophyceae	<i>Tabellaria</i>	489	123	256	542	182	650	1458	1242	849	1144	1867	376	370	1267	147	0	0	0
Cryptophyta	<i>Teleaulax acuta</i>	463	363	310	424	0	1184	746	2778	2373	2553	0	93	1687	0	0	0	0	0
Chlorophyta	<i>Tetrastrum</i>	0	0	0	0	0	6571	0	0	7250	0	0	13111	0	0	439474	0	0	0

are significant in determining the community composition and abundance, the longer water residence time (WRT) of floodplain habitats is a major factor that determines zooplankton community structure and abundance. In addition to the higher WRTs, ephemeral off-channel sites also generally have highly abundant and species-rich egg banks (Brendonck & De Meester 2003), adding to the significance of these habitats. During times of high flow, floodplains and their conduits, such as those that adjoin the River Murray, transfer a substantial proportion of the biotic production including zooplankton (Furst et al. 2014) back to the River channel.

Due to river regulation and over-extraction, the natural flow regime within the River Murray has been significantly altered (MDBA 2015). This has led to a reduction in the frequency, extent and duration of floodplain inundation, and has thus reduced the transfer of zooplankton from floodplain to main channel habitats.

In the sampling of the CLLMM region during the period of high river flows following the drought in 2010-2011, 70% of the zooplankton taxa were recorded above the barrages in Lake Alexandrina and the Goolwa Channel (Shiel & Tan 2013b). Upper catchment (e.g. Darling River) zooplankton taxa have been recorded in the CLLMM during extended periods of high flows (see Shiel & Tan 2013b). High flows (or at least moderate increases) can also cause localised population booms in the Lower Lakes, when areas that have been dry for a period of time become inundated (Wedderburn et al. 2013). Salinity is influenced by river flows, and variations in salinity also play a role in determining the composition of zooplankton assemblages. For example, during periods of low flow, assemblages in the southern Lower Lakes are dominated by halophilic and estuarine taxa, due to the elevated salinity in such flow conditions. The Coorong estuary is now more marine-influenced since the construction of the barrages, and hence a reduction of freshwater influence (Chapters 2.7 & 2.10). As a result, the Coorong lagoons are often now hypersaline and this elevated salinity likely drives a reduction in species richness (see Shiel & Tan 2013b). Riverine zooplankton communities, including those sourced from upstream floodplains and wetlands, are transported downstream, some eventually reaching the Lower Lakes and Coorong, where they mix with the pre-existing zooplankton communities.

Diversity and abundance of the zooplankton community have been found to be highest during periods of freshwater inflow. The degree to which these freshwater communities mix, influence and persist within the Coorong is dependent upon the dynamic physico-chemistry of the ecosystem, which is driven by the interaction between freshwater discharge, weather and tidal cycles. Interestingly, freshwater zooplankton taxa have been found in the Eastern Indian Ocean, near the Murray Mouth, in times of large freshwater flows through the barrages (Shiel & Aldridge 2011). As well as modifying salinity levels, freshwater flow influences other water quality parameters, including nutrients, organic matter, pH and phytoplankton biomass and species composition. These parameters in turn play a role in determining zooplankton assemblages (Leterme et al. 2015; Hemraj et al. 2017a, b). River flow into the Coorong influences plankton trophic interactions by modifying water quality and habitat complexity (Hemraj et al. 2017b). Changes in plankton community structure (virus, bacteria, nano/picoplankton, phytoplankton and zooplankton) in relation to freshwater flow have been described by Hemraj et al. (2017b). Shifts in plankton interactions from phytoplankton-zooplankton-dominated, during higher water flow, to virus-, bacteria- and nano/picoplankton-dominated, during low water flow, have been documented along the system.



## Consequences for higher trophic organisms

Plankton are a critical support for higher trophic levels, and changes in planktonic community structures and interactions are highly influential on the trophic web. In regards to the diet of fish, studies in the Murray Darling Basin (MDB) have generally considered zooplankton at a coarse (e.g. Balcombe & Humphries 2009) or moderate taxonomic scale only. Zooplankton provide a critical link within aquatic food webs through the ingestion and processing of bacteria, phytoplankton and organic material and as a food source for fish, waterbirds and macro-invertebrates (e.g. *Chaoborus*). In the Coorong, a recent study found that freshwater zooplankton, transported downstream by freshwater discharge, were subsidising the diet of sandy sprat (*Hyperlophus vittatus*), a primary prey item for larger piscivorous fishes (Bice & Zampatti 2015). Moreover, spatiotemporal variation in salinity, pH, dissolved oxygen and phytoplankton biomass has been observed to cause variations in prey diversity for smallmouth hardyhead (*Atherinosoma microstoma*), while temporal variation in prey diversity was observed for sandy sprat and Tamar River goby (*Afurcagobius tamarensis*) in the Murray Estuary and Coorong (Hossain et al. 2017). As a primary prey item for larger piscivorous fishes, increases in food resources and hence production of sandy sprat and smallmouthed hardyhead are likely to benefit the productivity of higher trophic levels throughout the Coorong.

## CONCLUSIONS

Community composition of the plankton in the CLLMM is largely determined by system hydrology, primarily regulated river inflows and water level heights set by infrastructure. Sometimes the hydrological conditions directly impact the plankton communities, but often their effect is through complex influences on physical-chemical water quality conditions, including salinity, turbidity and underwater light availability. The characteristics of flow and water level in the CLLMM are controlled by water resource managers; consequently, so is the condition of the plankton communities that underpin the aquatic food webs. Recent analyses of the Lakes have suggested major shifts in community composition, particularly of phytoplankton, and these are no longer the communities that supported the Lakes during earlier periods. Similarly, in the Coorong, changes in water quality have had major impacts on the plankton, with a critical driver being the management of flows over the barrages. The plankton communities appear to be at a critical juncture, with indications that the system is moving towards a poorer-quality habitat. This sets a major challenge for water resource managers and society as the move to full system management brings with it the mantle of responsibility for its condition. Monitoring programs are critical to cataloguing the changes that are occurring, and to providing the information necessary to understand and manage change. Currently there is no comprehensive monitoring of the plankton of the CLLMM and little support for continued analyses of the historic monitoring data, a situation that will not help future decision makers.

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