Bird and algal dynamics of two small rivers

Dl Luyt

orcid.org 0000-0002-2852-4733

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Supervisor:	Prof H Bouwman
Co-supervisor:	Dr MS Janse van Vuuren

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ABSTRACT

Algae are widely present in freshwater environments and serve as important primary producers in aquatic ecosystems, where they generate biomass that is transferred to higher trophic levels. Algae respond to environmental variables such as pH, dissolved oxygen, conductivity, temperature, and different inorganic nutrients. The same environmental variables may differ markedly between different river systems, which may have profound effects on the biota of that system. I hypothesised that the algal composition will determine the productivity of a system that will consequently be reflected by the avian composition depending on that system. The effect of algal community composition on the productivity of that system has received much attention; however, the interactions between freshwater phytoplankton and birds have not been well documented. I therefore conducted an in depth study on the avian and algal biodiversity of two small, closely located, rivers water quality factors involved. The hypothesis I tested was that freshwater quality and environmental parameters affect algal community parameters, which, in turn, affect bird community parameters. To investigate this, monthly algae and bird surveys were done and water quality variables were measured monthly over a period of 11 months (July 2016 - May 2017) along the Mooi River (MR) and Wonderfontein Spruit (WFS). Mooi River had four and Wonderfontein Spruit five sites, all within a radius of 15 km of each other. WFS is known to be highly polluted by residential areas and mining activities, while MR has small scale diamond mining and some agricultural influences. I used ANOVA and t-tests (and equivalent non-parametric tests), linear regressions, cluster analyses, PCA - and NMS ordinations, indicator species analyses, ANOSIM, and SIMPER to analyse the data. Comparisons between the rivers showed significant differences for pH, dissolved oxygen, conductivity, phosphorus, sulphate, nitrate, dissolved inorganic nitrogen, and richness and abundance of birds and algae. Although the phosphorus concentrations were significantly higher for MR, nitrogen was much lower than WFS, limiting algal growth potential. Additionally, multivariate results showed that algal and avian composition differed markedly between rivers. Avian biomass and diversity was strongly correlated with algal abundance that was much higher in WFS, most likely due to organic enrichment. I concluded that algal diversity was associated with water quality measurements, and that algal parameters were associated with bird parameters.

Keywords: algal, avian, birds, community composition, dissolved inorganic nutrients, diversity, eutrophic, nitrogen, phosphorus

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ACRONYMS USED IN THE STUDY

ANOSIM	Analysis of Similarity
ANOVA	Analysis of Variance
CBD	Convention on Biological Diversity
COP	Conference of the Parties
DIN	Dissolved Inorganic Nitrogen
DO	Dissolved Oxygen
EC	Electrical Conductivity
EEH	Exploitation Ecosystem Hypothesis
GBA	Global Biodiversity Assessment
ISA	Indicator Species Analysis
IV	Indicator Value
MR	Mooi River
NMS	Non Metric Multidimensional Scaling
OECD	Organisation for Economic Corporation and Development
OFT	Optimal Foraging Theory
OIV	Observed Indicator Value
PAST	Paleontological Statistics
PCA	Principle Component Analysis
SBSTTA	Subsidiary Body on Scientific, Technical, and Technological Advice
SD	Standard Deviation
SIMPER	Similarity Percentage
TDS	Total Dissolved Solids
UNEP	United Nations Environmental Program
WFS	Wonderfontein Spruit

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1.1 RIPARIAN ECOSYSTEMS

1.1.1 Overview

Riparian ecosystems occupy the eco-tone between terrestrial and freshwater aquatic realms. In their broadest sense, riparian ecosystems can be defined as those occurring in semi-terrestrial areas adjacent to water bodies and influenced by freshwaters (Capon *et al*., 2013). The riparian corridor encompasses the stream channel and the portion of the terrestrial landscape between the low- and high-water mark to the point where vegetation might be influenced by elevated water tables or flooding, as well as the ability of soils to hold water (Naiman *et al*., 1993; Nilsson & Berggren, 2000). Therefore, riparian ecosystems could probably be best considered as those assemblages of plant, animal, and aquatic communities whose presence can either be directly or indirectly attributed to factors that are stream-induced or related (Kauffman & Krueger, 1984).

Riparian ecosystems encompass sharp gradients of environmental factors, ecological processes, and plant communities and are consequently difficult to define rigidly. Therefore, it is useful to view it from a perspective that focusses on the ecological linkages between terrestrial and aquatic ecosystems (Gregory *et al*., 1991). Riparian ecosystems can be seen as ecosystems consisting of three-dimensional zones of direct interaction between terrestrial and aquatic ecosystems. The boundaries of these zones extend outward towards the limit of flooding, upward into the canopy of streamside vegetation, and downstream. Riparian ecosystems therefore consist of three spatial dimensions namely; lateral, vertical, and longitudinal (Figure 1.1). These ecosystems, however, are dynamic and undergo changes over time, creating temporal changes in each of the three spatial dimensions (Gregory *et al*., 1991; Kondolf *et al.*, 2006).

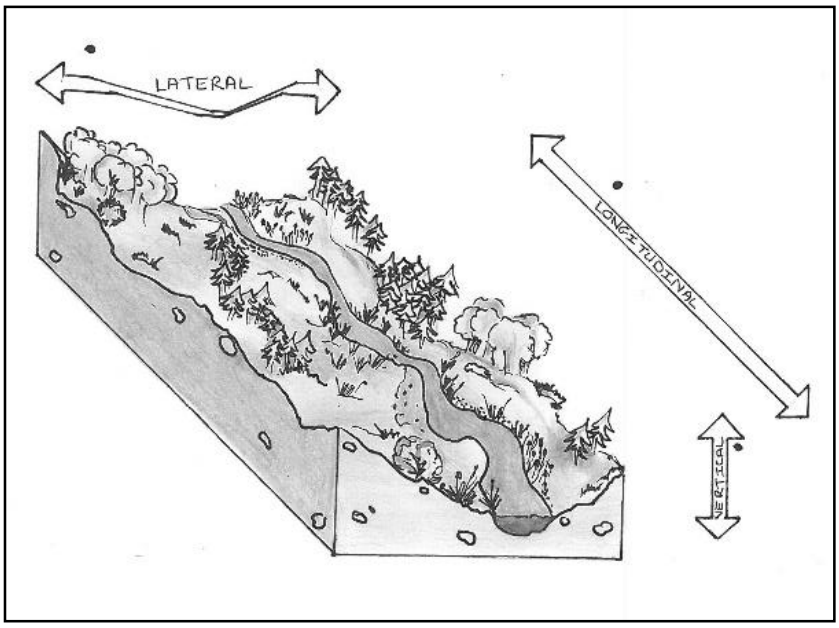

Figure 3.1: Spatial dimensions of a riparian ecosystem (drawn by Carmi Luyt after Eubanks & Meadow, 2002)

1.1.2 Factors affecting riparian ecosystems

Riparian ecosystems are largely influenced by hydrology, geomorphology, and vegetation (Capon *et al*., 2013; Gregory *et al*., 1991; Kauffman & Krueger, 1984). As a result, riparian ecosystems are characterised by the combination of abiotic factors and their interactions that affect the composition of the biotic community. Such abiotic factors include gradient, aspect, topography, soil type, water quality, and elevation (Kauffman & Krueger, 1984). These fluvial and upland geomorphic processes are major determinants of physical and biogeochemical processes in riparian ecosystems (Capon *et al*., 2013). Hydrologic regimes however, are widely considered as the 'master variable' that controls riparian ecosystem structure and function. Changes in precipitation and to a lesser extent evapotranspiration will influence the frequency and intensity of water flow. These have major effects on riparian ecosystems, altering the physical, chemical, and geological components. Accompanying such changes are shifts in water and soil quality as well as the riparian plant community composition (Busch & Smith, 1995; Capon *et al*., 2013).

Vegetation is an important component of a riparian zone, and controls physical conditions in the stream environment. Roots of riparian vegetation have a structural function that stabilises stream banks and protect it from erosion, thereby determining bank morphology. Vegetation also reduces the velocity and erosive energy of stream flow (Belsky *et al*., 1999; Kauffman & Krueger, 1984). In addition, vegetation also contributes to energy input into the aquatic environment by supplying the bulk of detritus that provide the majority of the organic matter necessary to support headwater stream communities (Kauffman & Krueger, 1984). These components and processes regulate the exchange of materials and energy between

adjacent aquatic and terrestrial habitats, which in turn affect ecosystem processes and functions for considerable distances among lateral, vertical, and longitudinal dimensions (Figure 1.1) (Capon *et al*., 2013).

1.1.3 Importance of riparian ecosystems

Riparian ecosystems have a wide range of ecological, socio-economic, and cultural functions, which include, *inter alia*, regulation (exchanges of material and energy), habitat, and production (provision of resources) (Capon *et al*., 2013). Many of these functions have considerable influence on physical, chemical, and biological components (Capon *et al*., 2013; Nilsson & Berggren, 2000). This high value of riparian ecosystem functions, goods, and services are a result of two key characteristics of riparian ecosystems: i) high spatial connectivity; and ii) high levels of environmental heterogeneity (Capon *et al*., 2013).

The interaction of several biotic, environmental, and abiotic factors in riparian zones creates a disproportionately higher number of niches and therefore the density and diversity of organisms are considerably higher in riparian ecosystems when compared with the adjacent upland habitats (Kauffman & Krueger, 1984). This results in a highly productive system which arise from the high soil moisture and fertility levels, created and maintained by the interaction between the hydrologic component and vegetation (Belsky *et al*., 1999). Vegetation is a crucial component of riparian ecosystems and is responsible for:

- Ecosystem functions which include the:
  1. regulation of - climate, water temperature, sediments, nutrients, soils, and topography (Capon *et al*., 2013; Naiman *et al*., 1993);
  2. production and distribution of - food and energy among food webs (Capon *et al*., 2013).
- Providing a filter between the terrestrial and aquatic components, which prevents sediment and terrestrial debris from entering the aquatic system (Kauffman & Krueger, 1984; Nilsson & Berggren, 2000).
- Stream bank stabilisation through a complex root structure and by reducing the erosive potential of water flow (Hickey & Doran, 2004).
- Habitat functions; and because of the combination of higher humidity and lower air temperatures compared with adjacent upland systems (a direct result of riparian vegetation) they serve as:
  - refuge -,
  - breeding -,
  - nursery -, and
  - feeding habitats

for many resident and migrating organisms (Kauffman & Krueger, 1984; Knopf *et al*., 1988).

Despite their enormous ecological, social, and economic importance, riparian ecosystems were regarded as 'sacrifice' areas by land-use managers because of their small surface area until the late 1960s (Belsky *et al*., 1999; Kauffman & Krueger, 1984). Consequently, more than eighty percent of the riparian corridor area of North America and Europe has disappeared in the last 200 years, while the remaining riparian corridors continue to decline (Belsky *et al*., 1999; Naiman *et al*., 1993).

1.1.4 Vulnerability of and threats to riparian ecosystems

As mentioned, riparian ecosystems are highly dynamic in time and space and are adapted to these temporal and spatial changes (Section 1.1). Naiman *et al*. (1993) states that the ecological diversity of riparian corridors is maintained by an active natural disturbance regime that operates over a wide range of spatial and temporal scales. Although riparian ecosystems are adapted to and dependent on continual natural disturbances, they are particularly sensitive to changes in the hydrological cycle (Nilsson & Berggren, 2000).

Riparian ecosystems are subject to a wide variety of threats, which influences the vegetation composition, quality of surface and ground water, and quality of riparian habitat (Hickey & Doran, 2004; Kauffman & Krueger, 1984). Threats include:

1) Damming operations:
    - which now obstructs two-thirds of fresh water on land flowing to the ocean (Nilsson & Berggren, 2000),
    - causing global scale ecological changes in riparian ecosystems (Nilsson & Berggren, 2000),
    - modifying the hydrological regime of rivers which in turn contributes to stream degradation (Belsky *et al*., 1999; Busch & Smith, 1995)
    - which affects the frequency and intensity of flooding,
    - decrease in connectivity attribute of these systems (Kondolf *et al.*, 2006),
    - has major effects on ecosystems upstream (Busch & Smith, 1995):
        - increase in water volume, and
        - inundation of adjacent terrestrial habitat (Nilsson & Berggren, 2000).
    - has major effects on ecosystems downstream (Busch & Smith, 1995):
        - altered river discharge,
        - decreased suspended sediment,
        - channel incision, and
        - floodplain narrowing (Nilsson & Berggren, 2000).

2) Climatic changes:
   - Depends largely on the degree of exposure to climatic stimuli which is considered to experience high levels of exposure,
   - Influence the hydrology mainly by alterations in precipitation, and to a lesser extent evapotranspiration (Capon *et al*., 2013),
   - Significant changes in on-land precipitation on local and regional scales (Milliman *et al*., 2008),
   - Directly affects riparian biota resulting in:
     - physiological responses,
     - behavioural changes,
     - altered phenology,
     - shifts in species distribution, and
     - disrupted symbiotic and trophic interactions (Capon *et al*., 2013).

3) Agricultural and forestry activities:
   - Destruction of vegetation that forms a natural filter between terrestrial and aquatic realms (Belsky *et al*., 1999; Hickey & Doran, 2004),
   - Removal of riparian forest which leads to an increase in stream temperatures (Hickey & Doran, 2004),
   - Pollution of water, mainly from the leaching of fertilisers and pesticides,
   - Degraded surface water quality due to:
     - increased stream-bank erosion,
     - increased contaminant and nutrient loading (Belsky *et al*., 1999; Hickey & Doran, 2004).

4) Grazing by livestock:
   - Damage riparian ecosystems substantially by altering:
     - vegetation,
     - hydrology,
     - stream bank morphology,
     - soil structure, and
     - habitat quality (Belsky *et al*., 1999).

5) Invasive species:
   - Adversely affects riparian ecosystems through both aquatic and terrestrial species,
   - Cosmopolitan phenomenon (Busch & Smith, 1995),
   - 25% of freshwater fish - and 20 aquatic plant species in South Africa (Van As *et al*., 2012), and

- Outcompete indigenous species (Busch & Smith, 1995; Van As *et al*., 2012).

1.2 BIODIVERSITY

1.2.1 History

The term biodiversity was created in September 1986 by Walter G. Rosen during the organisation of the "National Forum on BioDiversity", which was held in Washington DC (Sarkar & Margules, 2002). The concept of biological diversity was present prior to this and Raymond F. Dasmann used the phrase "biological diversity", which appeared as early as 1968 in his book *A Different Kind of Country* (Franco, 2013). Biodiversity, the contracted form of biological diversity, however only appeared in a publication for the first time in 1988. This was in the book *Biodiversity* which brought the results from the National Forum on BioDiversity and is comprised of 60 articles by leading international authorities on the subject that attended the forum (Franco, 2013). Following this forum, the term 'biodiversity' immediately found wide use and in 1993 'biodiversity' appeared as a keyword in abstracts of biological journals seventy-two times, while the first journal with the term in its title; *Canadian Biodiversity*, appeared in 1991 (Sarkar & Margules, 2002).

1.2.2 The Convention on Biological Diversity

The importance of biodiversity is widely accepted. However, the term 'biodiversity' is not well defined, and its use varies between different countries and disciplines (Duelli & Obrist, 2003). De Long (1996) stated that a widely accepted fundamental definition of biodiversity is imperative for the effective communication and cooperation within and among different countries, government agencies, disciplines, organisations and private landowners; and ultimately its conservation. Consequently, using the term in different ways is one of the main obstacles to reaching agreement in problem solving and decision-making (De Long, 1996).

The general lack of information and knowledge regarding biological diversity and the urgent need to develop scientific, technical and institutional capacities to provide the basic understanding on which to plan and implement appropriate measures, were recognised during the Convention on Biological Diversity (CBD), which was launched by the United Nations Environment Program (UNEP) (Heywood, 1995; Franco, 2013). This led to the commission of the Global Biodiversity Assessment (GBA), which is an independent, critical peer-reviewed, scientific analysis of all the current issues, theories and views regarding biodiversity, viewed from a global perspective (Heywood, 1995).

The CBD provides a global legal framework for action on biodiversity, which is governed by the Conference of the Parties (COP) (Secretariat of the Convention on Biological Diversity, 2018). The COP is assisted by the Subsidiary Body on Scientific, Technical, and Technological Advice (SBSTTA), which consists of:

- government representatives (with expertise in relevant fields),
- observers from non-Party governments,
- the scientific community, and
- other relevant organisations.

The SBSTTA is responsible for providing recommendations to the COP on the technical aspects of the implementation of the Convention. During the tenth meeting of the COP, which was held from 18 to 29 October 2010, they adopted a revised and updated Strategic Plan for Biodiversity, including the Aichi Biodiversity Targets for the 2011-2020 period. This Plan provides an overarching framework on biodiversity for the entire United Nations system, and all other partners involved in biodiversity management and policy development. The Aichi Biodiversity Targets consist of 20 targets within five strategic goals:

- Strategic Goal A: Address the underlying causes of biodiversity loss by mainstreaming biodiversity across government and society.
- Strategic Goal B: Reduce the direct pressures on biodiversity and promote sustainable use.
- Strategic Goal C: Improve the status of biodiversity by safeguarding ecosystems, species, and genetic diversity.
- Strategic Goal D: Enhance the benefits to all from biodiversity and ecosystem services.
- Strategic Goal E: Enhance implementation through participatory planning, knowledge management and capacity building (Secretariat of the Convention on Biological Diversity, 2018).

1.2.3 Defining biodiversity

It is apparent that the term biodiversity still lack consistent meaning within the field of natural resource management. One main cause for such inconsistency is because different authorities define biodiversity in fundamentally different ways, focussing on components of biodiversity that is applicable to their discipline. This term is commonly used in the fields of politics and environmental technology, in addition to various scientific disciplines. Biodiversity is often re-defined according to the context and purpose of the author and therefore, most definitions that exist for biodiversity are biased (De Long, 1996; Swingland, 2001).

Recognising the inconsistency of the use of this term, de Long reviewed 85 definitions of biodiversity across different disciplines. These definitions were evaluated based on the following approaches to construct an objective and sound definition of biodiversity (De Long, 1996):

- Definition based on derivation.

- Definition by classification.
- Definition by listing characteristics, properties, qualities and parts.
- Definition by comparison and contrast.
- Definition by operation.

Many of the definitions that were reviewed by De Long, could be replaced by more appropriate terms for example, species richness and species diversity where these definitions for biodiversity were merely a definition of one component of biodiversity (De Long, 1996). Evaluating the definition of biodiversity concerning the abovementioned approaches, de Long (1996) proposed a more comprehensive and objective definition that allows for modification according to the context in which it is used:

> *"Biodiversity is an attribute of an area and specifically refers to the variety within and among living organisms, assemblages of living organisms, biotic communities, and biotic processes, whether naturally occurring or modified by humans. Biodiversity can be measured in terms of genetic diversity, and the identity and number of different types of species, assemblages of species, biotic communities, and biotic processes and the amount (e.g., abundance, biomass, cover, and rate) and structure of each. It can be observed and measured at any spatial scale ranging from microsites and habitat patches to the entire biosphere."*

Although no formal definition of biodiversity is agreed upon, it has recently become widespread practice to define biodiversity in terms of genes, species, and ecosystems (Swingland, 2001; Cardinale *et al*., 2012). During the Convention on Biological Diversity (CBD) a very broad and functional definition of biodiversity was reached, covering three levels:

1. species diversity,
2. genetic diversity, and
3. ecosystem diversity.

Biological diversity is defined as:

> *"the variability among living organisms from all sources including, inter alia, terrestrial, marine and other aquatic ecosystems and the ecological complexes of which they are part; this includes diversity within species, between species and of ecosystems"*. (Secretariat of the Convention on Biological Diversity, 2005; Franco, 2013).

Genetic diversity is reliant on the heritable variation within and between populations of organisms. New genetic variation arises mainly by recombination during reproduction, but can also be a result of gene and chromosome mutations (Swingland, 2001). Genetic diversity

defines the evolutionary potential of a species and is a critical factor that allows populations to adapt to changing environmental conditions, and consequently help to ensure the long-term preservation of biodiversity. Biodiversity at gene level is important, not only for preserving the evolutionary potential of a species, but also for ecosystem functioning (Taberlet *et al*., 2012).

Species diversity refers to the number of different species (species richness) within a community or area, in conjunction with their relative abundance and evenness (Van As *et al*., 2012). However, there are conflicting opinions of what constitutes a species, which has led to the development of a wide array of species concepts. Mayden *et al*. (1997) listed and evaluated 24 different named species concepts with even more alternative definitions. Different species concepts seek to define species in mutually incompatible ways (De Queiroz, 2007; Mallet, 2007). Additionally, not all species have the same ecological importance and therefore species diversity on its own is not deemed satisfactory for determining biodiversity (Swingland, 2001).

Ecosystem diversity can be seen as the variety of ecosystems in an area. While it is possible to define what is in principle meant by genetic and species diversity, it becomes more difficult to do so at ecosystem level (Swingland, 2001). Ecosystems may vary considerably in size and complexity, and often do not have a distinct boundary (TEEB, 2010). Ecosystem diversity refers to the largest unit of biodiversity and encompasses all the genetic and species diversity in that area, including the interactions that exist between them. Because of the complexity of ecosystems, combined with the fact that they can be viewed on different scales, there is not an authoritative index for measuring ecosystem diversity (Swingland, 2001). Consequently, ecosystem biodiversity is often assessed based on three sets of attributes; compositional, structural and functional biodiversity (Duelli & Obrist, 2003). The complexity of all the aspects of biodiversity is illustrated in Figure 1.2.

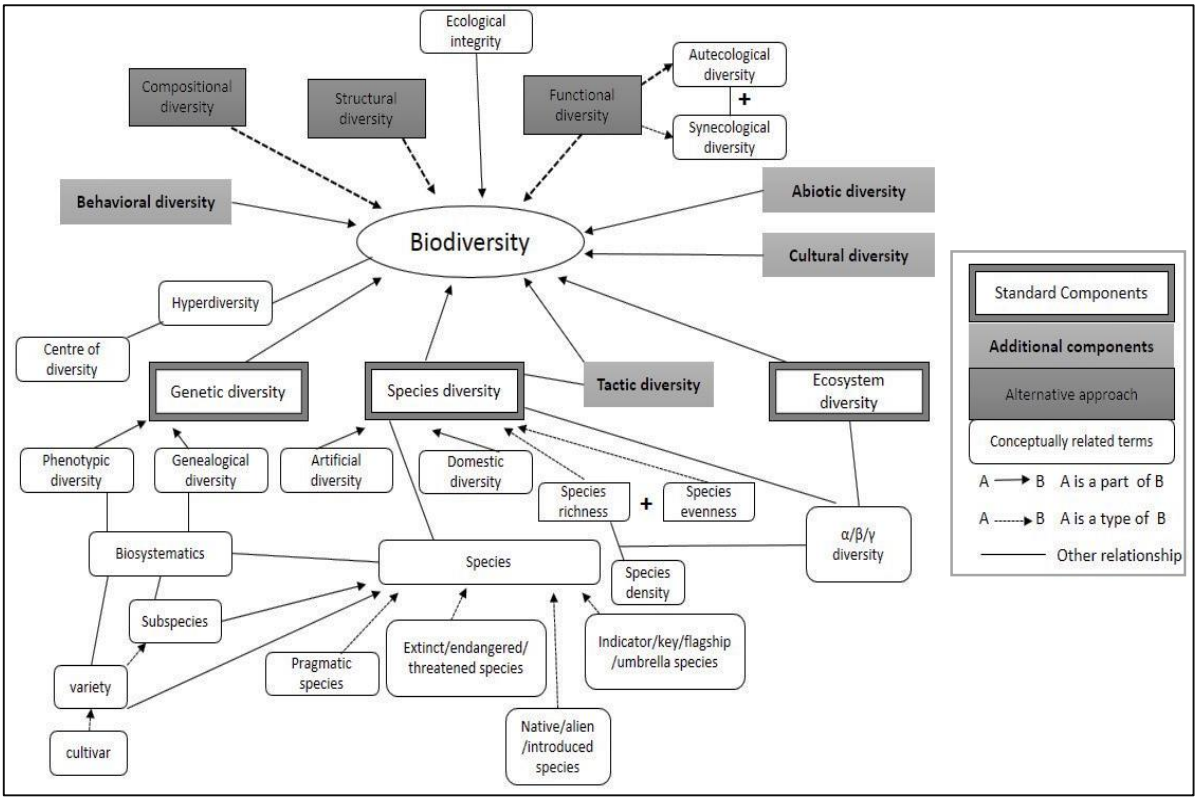

Figure 1.4: Provisional domain tree of biodiversity. Concepts used by various authors to define biodiversity are in square boxes and related concepts in rounded boxes. Type and direction of conceptual relationships are indicated by arrows (after Duelli & Obrist, 2003).

Although the term biodiversity is practically indefinable, it is possible to define different components of biodiversity, as was done by the GBA. This allowed not only for the evaluation of the state of knowledge on biodiversity, but also its role in ecosystem and landscape processes (Cardinale *et al*., 2012). Despite not having a universally accepted standard definition, biodiversity has enjoyed much attention with efforts focussed on the components of biodiversity and the conservation thereof. This is accompanied by a shift in focus, from defining biodiversity to conceptualising biodiversity (Sarkar & Margules, 2002).

1.2.4 Biodiversity conservation

Soon after the 1992 Earth Summit in Rio de Janeiro, interest in understanding how biodiversity loss might affect the dynamics and functioning of ecosystems and the supply of goods and services grew dramatically (Cardinale *et al*., 2012). During the Earth Summit, the term 'Ecosystem Approach' was applied in a policy context for the first time, where it was adopted as an underpinning concept of the Convention on Biological Diversity (Beaumont *et al*., 2007). The ecosystem approach, defined by the Convention on Biological Diversity is a strategy for the integrated management of land, water, and living resources that promotes conservation and sustainable use in an equitable way (Secretariat of the Convention on Biological Diversity, 2005). An ecosystem approach is based on the application of appropriate

scientific methodologies that focus on levels of biological organisation, which includes the structure, processes, functions, and interactions among organisms and their environment. Furthermore, it also recognises that humans, with their cultural diversity, are an integral component of many ecosystems (Secretariat of the Convention on Biological Diversity, 2005).

The ecosystem approach is not a static model, but rather a holistic process for integrating and delivering the three objectives of the CBD, namely: conservation, sustainable use of biodiversity, and equitable sharing of benefits, in a balanced way (Maltby, 2000). The implementation of such a holistic approach contributed towards greater understanding of how biodiversity loss affects the functioning of ecosystems, and in turn affects society (Cardinale *et al*., 2012). Ecosystem functions are ecological processes that control the fluxes of energy, nutrients and organic matter through the environment. This includes primary production, decomposition, nutrient cycling, soil formation, hydrologic cycling, and biological control (Cardinale *et al*., 2012; TEEB, 2010). These ecosystem processes ultimately generate services when they provide utilities to humans (TEEB, 2010).

Ecosystem services are the suite of direct and indirect benefits that ecosystems provide humanity and can be divided into four categories – provisioning, regulating, cultural, and supporting services. Provisioning services involve the production of renewable resources. Regulating services are those that lessen environmental change. Cultural services are the non-material benefits that people obtain through ecosystems. Supporting services are those that are necessary for the production of all other ecosystem services, but do not yield direct benefits to humans (Beaumont *et al*., 2007; Cardinale *et al*., 2012).

1.3 COMMUNITY ECOLOGY

1.3.1 Overview

Community ecology is the field of study concerned with identifying and explaining the patterns of distribution, abundance, and interaction of species that co-occur in time and space (Koide & Fernandez, 2011; Leibold *et al*., 2004; Wiens, 1989). A central goal of ecology is to understand and predict the dynamics of natural communities (Wootton, 1997). Ecological communities are extremely complex systems and to understand their dynamic nature it is necessary to abstract this system into components; consequently achieving a greater understanding of the relationship between the different components (Werner & Peacor, 2003).

Community structure is a key component in the ecology of communities and refers to the particular species present and their relative abundances (Koide & Fernandez, 2011). It is important to note that communities can be viewed on different spatial scales that introduce difficulties with predicting patterns in communities, as these patterns will vary within the scale

of observation (Leibold *et al*., 2004). A second component that influences ecological communities is interactions between species in the community (Werner & Peacor, 2003).

Species in a community are directly affected by the presence of other species, and patterns can be relatively easy to predict when studying the pair-wise interactions between two species in a community (Wootton, 1994). Other species are also affected indirectly by these interactions. These indirect effects indicate that biotic interactions are important to ecological systems. Nutrient cycling, carbon storage, and productivity are important ecosystem functions that results from the interactions between species. It is also important to note that not all species interact in the same way with one another, and the strength of interactions between species is a crucial factor determining community ecology (Werner & Peacor, 2003; Wootton, 1997). Therefore, in order to understand and predict the dynamics of natural systems, studies must focus on communities as opposed to individual species (Koide & Fernandez, 2011; Wootton, 1994).

1.3.2 Ecology of bird communities in wetlands

Local communities that are in close proximity often differ markedly in species composition, while distant communities may be quite similar (Wiens, 1989). This can be explained by the mechanisms leading to a certain composition of species in a community. Species composition of a local community is determined by the addition of species through successful colonisation, and establishment of breeding populations. These species compositions undergo changes in time and space with the addition and removal of certain species, which is caused by various factors (Wiens, 1989). One of the key factors affecting any community is interactions, and these interactions are what makes a community more than just the sum of its different components. Community ecology aims to explain the patterns in the structure and behaviour for multispecies assemblages (Begon *et al*., 2008). Community patterns are therefore, consequences of the species composition, abundances, and distribution of the community, as well as the morphological and behavioural attributes of those species, and the way they relate to the environment (Wiens, 1989).

There are different views on community assembly with emphasis on different aspects of factors and effects, summarised by Wiens (1989a). With regard to avian communities, some downplayed the influences of area, distance and dispersal abilities on colonisation probability, stressing the importance of ecological conditions in the target area in determining which species entered a local community. An environment may be viewed as a large number of dimensions, each representing some resource or factor of importance, on which different species exhibit frequency distributions of performance, response, or resource utilisation. According to this niche theory, ecologically similar species coexist by virtue of niche differences. At the same time, each species has certain minimal requirements on the niche

dimensions. Hence, competitive interactions are of primary importance in adjusting the niche relationships between those species whose ecological requirements were met in a particular area (Wiens, 1989).

Wetlands are diverse habitats, involving diverse and unique biotic communities. Because of this, birds that form part of wetland communities have a variety of anatomical, morphological, and physiological adaptations, allowing them to utilise this unique and rich habitat in an effective manner (Weller, 1999). Avian adaptations to utilise wetland and other aquatic systems are often species specific, which results in increased fitness regarding one or multiple components of community interactions. Ecologists have found that communities might contain as many species as ecologically possible, but this species pool reaches a saturation point, because of competition for limited resources. Species occupying the habitat are therefore those better adapted to exploit the limited resources (Wiens, 1989). Wetland birds have diverse morphological adaptations for specialised feeding on just about any food source, which results in a greater niche breadth. Many bird species are anatomically adapted to diving and swimming, both for foraging and evasion of predators. Physiological adaptations include increased respiratory capacity for species that engage in long-term and deep diving (Weller, 1999).

The ecological tolerances of species dictate the environmental situations they can occupy. How these conditions are met in space determines where the species may occur. The distributional patterns of species therefore, determine the potential memberships of a community. As one move between locations, the boundaries of species ranges are crossed and the composition of the species pool changes. Range boundaries are determined by several factors, including, lack of suitable habitat, competitive interactions between ecologically similar species, absence of critical resources, too small an area to satisfy species needs, and climatic factors causing physiological stress (Wiens, 1989).

Within their geographical ranges, species often have patchy distributions. Factors accounting for distributional patchiness are the same as those that influence range boundaries (Wiens, 1989). Wetlands are naturally patchy within the terrestrial landscape, which alters distribution patterns in different ways. Avian abundance has been shown to be key in the capacity of a species to colonise the available space in a patchy habitat. Species often select the available resources and microhabitats in different ways throughout the wetlands, depending on their behaviour or location for feeding. Because of their dynamic nature, changes in wetland size may alter the avian composition according to alterations in the availability of their respective habitat (Paracuellos, 2006).

1.4 BIRDS

1.4.1 Habitat selection

Birds are extremely mobile and widespread, and therefore they move through a wide variety of habitats of which only certain ones are used for breeding, foraging, or wintering (Cody, 1985). Virtually every aspect of an animal's behaviour is affected by where it lives, whether resident or migratory. The habitat of an animal affects its behaviour, but the behaviour of an animal also affects its choice of habitat (Dugatkin, 2014). The evolution of habitat preferences is determined by a bird's morphological structure and behavioural functions, its ability to obtain food as well as the ability to find suitable shelter in that habitat (Cody, 1985).

Habitat selection can be regarded as one of two types of causation, namely proximate and ultimate. Ultimate causation refers to the evolutionary costs and benefits of using each of a possible range of habitat types; meaning why does a species occur in a range of habitats that it does? Proximate causation refers to the mechanism by which the habitat was selected; meaning what cues do individuals use as indications for habitat choice? (Hutto & Cody, 1985).

According to Hutto and Cody (1985) habitat is defined as a spatially contiguous vegetation type that appears more or less homogenous throughout and is physiognomically distinctive from other such types. Habitat selection is a complex process, influenced by a variety of factors. Such factors include food availability, suitable nesting sites, and presence of other species (Marone *et al*., 1997). These factors are in turn influenced by other factors such as seasonality, for example; in winter food acquisition must figure prominently in decisions regarding space use, since getting food to store fat or merely survive is likely to be the single most important factor affecting habitat selection of non-breeding birds (Hutto & Cody, 1985).

All these factors have led to the development of a theory of habitat selection. This theory assumes that individuals are able to make the best settlement decisions, thus selecting the highest-quality habitats available in a heterogeneous landscape to maximise their fitness (Hollander *et al*., 2011). If two patches of habitat are available, individuals will choose that with more resources. However, higher densities results in lower individual fitness and as individuals settle in the best habitat a density will eventually be reached where individual fitness in the poorer habitat will be equal to that of the better habitat (Whitham, 1980). This theory has been linked to individuals' fitness measures with their habitat choices made over multiple rather than single life-cycle events (Morris *et al*., 2008).

Following the habitat selection theory two predictions were made, that subsequently evolved into two models that involved density dependence, namely: 1) the ideal-free distribution and 2) ideal-despotic distribution models (Jones, 2001; Whitham, 1980). The ideal free distribution model refers to the above scenario in the absence of territorial behaviour

where an individual is free to settle in the habitat of his choice (Whitham, 1980). The ideal-despotic distribution model states that territoriality and dominance are traits that limit the density within a habitat, as individuals that are more dominant will deny less dominant ones access to resources (Jones, 2001; Whitham, 1980). Individuals are however, not always able to directly judge the habitat quality in terms of fitness returns and, instead have to rely on environmental cues to guide their selection (Hollander *et al*., 2011).

Patterns of habitat distribution that we observe are a consequence of decisions made by individual birds in selecting a place in which to establish a breeding territory or overwinter. We may view individuals of a species as possessing an internal image or template of what constitutes a suitable habitat (Wiens, 1989). Habitats that fit the template provide various cues. Such cues that guide decision-making include aspects of habitat and vegetation structure, food availability, edge area, anti-predation shelters, microclimate, and presence of other species, amongst others (Hollander *et al*., 2011; Wiens, 1989). Whether or not an individual selects a habitat based on these cues depends on various factors, which collectively may constrain or distort the optimal pattern determined by the template (Wiens, 1989). Orians & Wittenberger (1991) stated that although selection of a habitat is extremely important, the initial decision of whether to explore a habitat or to continue searching is often made very quickly and usually, based on rather general features of the environment. Cody (1981) assessed the different aspects of habitat selection and found that all factors affecting whether a habitat will be suitable and consequently selected, can be apportioned to three categories, namely, vegetation structure, competitors, and productivity.

Vegetation structure has long been assumed the dominant factor in habitat selection of birds (Karr & Freemark, 1983). The role of vegetation structure in habitat selection of birds was focussed by MacArthur's work (1964) on species diversity, where he made successful predictions of bird diversities based on the equitability of vertical foliage distribution in deciduous woodlands. This led to the realisation that structural aspects of a habitat may be good predictors of the presence of certain species (Cody, 1981). Importantly, some species may also require some non-vegetation structural features; for example, some grebes will only nest in dense vegetation adjacent to deep, open water, while many diving water birds are restricted to certain water depths for foraging or moulting. Bird species often require different vegetational characteristics for cover, breeding, and foraging (Cody, 1981; Hildén, 1965). Differences in habitat selection based on habitat structure are dependent on species-specific structural and functional characteristics. For example, mode of locomotion and behaviour are determined by the morphology of a species, which necessitate a certain type of terrain (Hildén, 1965). Vegetation structure is an especially important factor in the habitat selection of breeding birds, as sufficient shelter for parents and their young against predators, and adverse weather is a basic requirement in decision-making (Hildén, 1965).

Vegetation alone does not always determine where bird species can be found since the presence of competitor- and predator species are important additional constraints. These constraints may be in the form of inter-specific or intra-specific competition (Cody, 1981; Hildén, 1965). Conspecific interactions may render a habitat unsuitable (Cody, 1981). Variation in habitat occupancy by a species is strongly influenced by population density (Wiens, 1989). Where density is low, only optimal habitats are exploited, whereas an increase in density lead to intensified intraspecific competition, forcing some individuals to occupy less suitable habitats (Hildén, 1965; Wiens, 1989). The effect of intra-specific competition on species distribution thus, depends on the existence of an upper limit of population density, which varies with habitat quality (Hildén, 1965). Additionally, allospecific competitors render a habitat unsuitable in a similar manner to conspecifics (Cody, 1981). Competition between species with closely related ecological preferences influences their distribution. Where they overlap, species are more strictly confined to their species-specific optimal environment (Hildén, 1965). Inter-specific aggression and interspecific territoriality are restrictive forces that regulate the use of habitat such that limited resource value of that habitat are maintained (Cody, 1981). Inter- and intraspecific interactions do not always have an adverse effect on habitat selection. The well-known tendency of many ducks, grebes, and waders to nest in larid (Laridae = skuas, jaegers, gulls, skimmers, terns, and noddies) colonies seems originally based on the effective protection against predators that larids provide (Hildén, 1965).

The optimal environment of a species often coincides with the most productive types of their habitat range (Hildén, 1965). The role of productivity, of either standing crop or renewal rate of food supply in the habitat selection process is still speculative (Cody, 1981). Pair density of most species, as well as total abundance of birds, is proportional to the quantity of food available in the environment (Hildén, 1965). There has also been strong evidence that seasonal changes in habitat use by several bird species parallels seasonal differences in food availability (Cody, 1981).

Lastly, habitat selection seems to be not only dependent on relevant factors such as vegetation structure, food availability, nest site requirements, and competition. Birds also appear to be guided by a primary innate reaction released by certain environmental stimuli. This include stimuli of landscape, terrain, nest-, song-, lookout-, feeding-, and drinking sites, and other animals. According to the principle of stimulus summation, not every habitat approved as suitable need possess all the features characteristic of the optimal environment. It is enough that the combined effect of the individual stimuli exceeds the threshold of the settling reaction. Sometimes, single key stimuli outweigh others and in its absence, other stimuli are never sufficient to induce the settling reaction (Hildén, 1965).

1.4.2 Foraging and diet

Foraging behaviour is a critical part of any animal's existence and therefore individuals spend a fair share of their time foraging (Dugatkin, 2014). The food available to birds includes just about any kind of organic material. This great variety of food has led to great variation in adaptations used for feeding (Maclean, 1990). Adaptations allows for certain feeding behaviour and these adaptations will determine the food the individual will consume, as well as the habitat in which an individual will forage. This can be explained in terms of the Optimal Foraging Theory (OFT), which assumes that the most economically advantageous foraging pattern will be selected for a species through natural selection.

The Optimal Foraging Theory attempts to predict the behaviour of animals while they are foraging, and this theory is based on a number of assumptions. Firstly, the contribution of an individual to the next generation depends on its behaviour while foraging, with the contribution being measured genetically or culturally (Pyke, 1984). Secondly, there should be a heritable component to foraging behaviour. Given these two assumptions, the proportion of individuals in a population that forage in ways that enhance their fitness will increase over time and foraging behaviour will therefore evolve (Pyke, 1984). There are various other assumptions for the exact mechanisms of foraging behaviour and the evolution thereof, which will not be discussed in detail in this study. It is however important to note that foraging behaviour will evolve and that the average foraging behaviour will increasingly come to be characterised by those characteristics that enhance individual fitness (Maclean, 1990; Pyke, 1984).

The usage of resources in an environment is central to animal ecology (Johnson, 1980). Resource abundance varies in both space and time. The abundance of a resource in an environment, however, is of less importance to an organism than its availability, because only a portion of those present in an environment will be available at any given time (Johnson, 1980; Wiens, 1989). Most bird species are not specialised in their diet. They will eat whatever can be obtained with the least difficulty (Hildén, 1965). Intra- and interspecific competitors that exploit resources used by other individuals, alter resource abundance. However, if the competitors aggressively preclude access to resources, resource availability is affected (Wiens, 1989).

Resource use is influenced by constraints or predispositions associated with morphology, physiology, and behaviour of the species, coupled with external factors such as availability of alternative food types, spatial relationships among resources, attributes of resources themselves, or competition with other species (Wiens, 1989). For example, limitations of locomotory technique often have the result that access to food, in itself abundant, is difficult (Hildén, 1965). Wetland birds are extremely diverse, reflecting a wide range of

adaptations to this unique habitat (Weller, 1999). Bird species will therefore, select available resources and microhabitats in different ways throughout wetlands (Paracuellos, 2006). A disproportionally large section of wetland bird species are specialists, compared to terrestrial communities.

In light of this wide range of avian adaptations to wetland environments, it might be useful to view foraging and diet through an ecomorphological approach. Darwin stated as early as 1895, that there is a close relationship between the structure of a species and its ecology, and that morphological differences between species, also indicate ecological differences (Wiens, 1989). Adaptations to bird species that inhabit wetland systems include differences in size and structure of the bill, legs and feet, wings, and digestive system (Maclean, 1990; Wiens, 1989). The bill of a bird is equipped with many fine nerve endings that serve to feel and taste food. Many water birds find their food by touch alone, using their bill as a sensitive probe (Maclean, 1990). Adaptations of the digestive system of different birds are in accordance with their diet. The harder the food eaten, the more muscular the stomach and gizzard which is responsible for the fragmentation of food. This process is often assisted by swallowing stones or other hard objects (Maclean, 1990).

The linkage between morphology and ecology seems especially clear when one makes comparisons across a range of related species, sharing a common form of resource exploitation (Wiens, 1989). Many aquatic birds are adapted to diving. Underwater propulsion may be via their feet (grebes, cormorants, darters, and most ducks) or wings (some ducks). These diving specialists all have webbed or lobbed feet, allowing great manoeuvrability under water, however, their terminally placed legs make them rather ponderous on land (Maclean, 1990; Weller, 1999). Grebes and darters can sink underwater without active jump-diving, which is common in ducks and coots (Weller, 1999). Diving in grebes, cormorants and darters differ from ducks and coots in that they use underwater propulsion to actively hunt fish, whereas ducks and coots feed on plant tubers and other vegetation by wading or upending (Maclean, 1990; Weller, 1999). As a result, they have similar morphology adapted for diving. However, they differ in bill shape because they exploit different food resources.

Other birds have adapted to exploit similar food resources but in different ways. These include a wide variety of birds with different body structure. However, because they exploit a similar food resource they have a similar bill shape. Herons, kingfishers and terns all feed on fish and therefore all possess a dagger-like bill, although each bird has a different foraging method (Maclean, 1990). Close morphology-ecology relationships are often most apparent within taxonomically or ecologically restricted groups of species. Bill shape and size, is indicative of the food source a species utilise, while body shape and feet are often indicative of the foraging method used to exploit a certain habitat (Weller, 1999; Wiens, 1989).

Wading species such as Yellow-billed Stork and African Spoonbill hunt by touch alone, snapping prey items disturbed by stirring with their feet, and sweeping of the bill, respectively (Maclean, 1990). Other waders such as ibises and those in the family Scolopacidae, feed by probing. Birds that feed by probing have extremely sensitive touch receptors in their bills, especially at the tip, and locate food items as they move their bill through the substratum (Maclean, 1990; Weller, 1999).

Filter feeding is a specialised feeding adaptation used by flamingos, ducks, and prions. The basic adaptation consist of more or less fine projections, known as lamellae, along the sides of the bill, which allow water through, but keep particles back. The Greater Flamingo has a shallow-keeled bill for filtering out micro-crustaceans, molluscs, and seeds from mud, while the Lesser Flamingo has a deep-keeled bill for filtering much finer blue-green algae and diatoms (Maclean, 1990; Weller, 1999).

Species in the family Rallidae frequent either the shoreward zone in dense vegetation (flufftails, rails, and crakes), while others (gallinules, moorhen, and coots) use deeper and even open water. Foods are highly variable, with seasonal shifts from animal foods to seeds, tubers, and foliage in winter (Weller, 1999).

1.5 ALGAE

1.5.1 Overview

Algae can be described as a loose group of organisms that contain all, or most of the following characteristics:

- aquatic,
- photosynthetic,
- simple vegetative structures without a vascular system, and
- reproductive bodies without a sterile layer of protective cells (Wehr & Sheath, 2003).

Algae consist of both prokaryotic and eukaryotic taxa and cannot be treated as a phylogenetic concept. Consequently, the term ‘algae’ are used to describe a phylogenetically artificial cluster of unrelated groups of organisms. Nonetheless, they still represent an ecologically meaningful group of organisms (McCarthy & Orchard, 2007; Wehr & Sheath, 2003).

Algae can be unicellular, colonial, or multicellular and are an extremely diverse group of organisms. They are present in fresh water and on land, as well as in the ocean and occupy a wide variety of ecological niches (McCarthy & Orchard, 2007; Nabors, 2004). This broad range of habitats occupied by algae is a reflection of their broad evolutionary diversity. Although algae are primarily found in aquatic environments, they do also occur in terrestrial

habitats (McCarthy & Orchard, 2007). Within freshwater ecosystems, algae occur either as free-floating (planktonic) or substrate-associated (benthic) organisms (Bellinger & Sigee, 2010). Most unicellular and small colonial algae are free-living and exist as phytoplankton that floats near the surface of oceans and lakes. Phytoplankton contributes toward half of the world's photosynthesis and serves as the basis of all marine food chains (Nabors, 2004). Although the majority of algae can be described as small unicellular or colonial organisms, which reproduce mainly asexually, they can also occur as multicellular forms with complex cellular differentiation and tissue-level organisation. Sexual reproduction is common in multicellular algae and many species have complex life cycles involving an alternation of generations (Nabors, 2004).

Algae are classified based on a combination of characteristics, including photosynthetic pigments, starch-like reserve products, cell covering, and other aspects of cellular organisation (Wehr & Sheath, 2003). Freshwater algae can be grouped into 10 major divisions or phyla in relation to appearance, biochemical, and cytological characteristics (Bellinger & Sigee, 2010; Wehr & Sheath, 2003). This includes:

- cyanobacteria or blue-green algae (*Cyanophyta*),
- green algae (*Chlorophyta*),
- euglenoids (*Euglenophyta*),
- yellow-green algae (*Xanthophyta*),
- dinoflagellates (*Dinophyta*),
- cryptomonads (*Cryptophyta*),
- chrysophytes (*Chrysophyta*),
- diatoms (*Bacillariophyta*),
- red algae (*Rhodophyta*), and
- brown algae (*Phaeophyta*).

There is enormous variation in the chemical composition of freshwater habitats that algae occupy (Wehr & Sheath, 2003). Freshwater habitats can be divided into two groups namely, lentic and lotic environments. Lotic environments refer to running water, which may vary from a small stream to a large river. Lentic environments refer to standing water, which may vary from a small pond to massive lakes. They include ponds, reservoirs, and lakes and vary in formation, geography, limnology, and size (Wehr & Sheath, 2003).

Aquatic systems can be classified as either oligotrophic, mesotrophic or eutrophic, according to their state of nutrient enrichment (Walmsley, 2000). The trophic state of a lake is regulated by three main factors namely i) the rate of nutrient supply, ii) climate and iii) the shape of the lake basin. Nutrient supply is affected by soils, vegetation, land use-, and management. The amount of sunlight, temperature, and hydrology are important climatic

factors, which influences the trophic state of a lake, while the shape of the lake is determined by the depth, surface area, and volume of the lake (Van As *et al*., 2012; Wehr & Sheath, 2003).

Phytoplankton, are the primary source of organic matter, supporting food webs in freshwater ecosystems (Paerl *et al*., 2001; Zhou *et al*., 2016). The effects of algal biomass on the food web structure in lakes have been well characterised. A shift in phytoplankton composition to a system dominated by cyanobacteria, however, might have profound effects on all trophic levels (Smith, 2003). Blue-green bacteria typically become dominant over other algae species in the phytoplankton of eutrophic systems, as they are adapted to exploiting nutrient-enriched conditions. Although most freshwater algal phyla contain some harmful or otherwise nuisance bloom-forming genera, cyanobacteria is by far the most notorious and problematic (Paerl *et al*., 2001; Smith, 2003). A study by Ndetei & Muhandiki (2005) showed that repeated episodes of Lesser Flamingo mortalities in the Kenyan rift valley lakes were caused by cyanobacteria toxins.

Cyanobacteria are the oldest oxygenic phototrophic inhabitants on earth and therefore, a long evolutionary history has equipped them with numerous physiological, morphological, and ecological adaptations (Paerl *et al*., 2001). They are effective at light harvesting through the formation of accessory pigments and increased cellular chlorophyll (Shapiro, 1990). This tolerance for low light allows them to survive lower in the water column where photosynthetic activity of other algae would be inhibited due to insufficient light (Bellinger & Sigee, 2010). Many cyanobacteria have the capacity to become both positively and negatively buoyant to manipulate their position in the water column. By doing so they avoid photo-inhibition during the early phase of population increase, and allowing them to obtain inorganic nutrients from the hypolimnion (lower layer of water in a stratified lake), when the epilimnion (upper layer of water in a stratified lake) gets depleted (Bellinger & Sigee, 2010; Shapiro, 1990). Cyanobacteria are also uniquely adapted to nutrient deficiencies in two important ways; they are the only phytoplankton group capable of utilising atmospheric nitrogen gas through biological nitrogen fixation, and they are capable of taking up phosphorus in excess of cellular growth requirements and storing it for subsequent use under phosphorus-limited conditions (Paerl *et al*., 2001). Additionally, many genera are resistant to zooplankton grazing, because of their ability to produce toxins (Bellinger & Sigee, 2010; Smith, 2003).

1.5.2 Factors affecting algae

Phytoplankton populations exhibit large temporal variations in response to abiotic factors such as light, temperature, nutrients, and water movement, as well as biotic factors such as grazing, competition, parasitism, and microbial attack. The composition and distribution of algal communities are therefore influenced by physical-, chemical-, climatic-, and ecological factors (Granéli & Turner, 2006).

1.5.2.1 Physiochemical factors

Water quality differs from region to region, because of differences in climate, geomorphology, geology, and soils. Water quality variables can be divided into physical attributes and chemical attributes. Physical attributes include temperature, turbidity, and the concentration of suspended solids. Chemical attributes include pH, conductivity, total dissolved solids (TDS), salinity, individual ions, dissolved oxygen (DO), and nutrients (Dallas & Day, 2004).

All aquatic organisms have a range of temperatures at which optimal growth, reproduction, and general fitness occur (Dallas & Day, 2004). Natural fluctuations in water temperature occur on a daily and seasonal basis, and indigenous organisms are adapted to such fluctuations (Malan & Day, 2002). Temperature also influences other water quality variables. An increase in temperature decreases oxygen solubility, increase the toxicity of certain chemicals, and increase metabolic activity. Water temperature in turn, is influenced by hydrology, climate, vegetation cover, water volume, depth, and turbidity (Dallas & Day, 2004; Hickey & Doran, 2004; Kauffman & Krueger, 1984).

Turbidity can be defined as an expression of the optical property that causes light to be scattered and absorbed, rather than transmitted in straight lines through water. Others, however, define turbidity as the extent to which water appears to interfere with the straight-line transmission of light, i.e. the effect of the presence of suspended particles, and consequently, the effect of dissolved component is not considered (Dallas & Day, 2004). Turbidity determines the degree of penetration by light, and an increase in turbidity decreases vision and photosynthesis (Day *et al*., 1994). As light penetration is reduced, primary production decreases, and food availability to organisms higher in the food chain is diminished (Dallas & Day, 2004). Increases in turbidity may be attributed to land-use practices such as over-grazing, ploughing, and removal of vegetation that leads to an increase in erosion, and increased quantities of suspended solids in water. Increased turbidity is often a consequence of anthropogenic processes such as industrial discharge, mining, and release of domestic sewage. An increase in suspended matter also affects the concentrations of inorganic ions available as nutrients. Phosphate, for example, often binds to such particles which may result in nutrient deficiencies (Dallas & Day, 2004; Malan & Day, 2002).

pH is determined largely by the concentration of hydrogen ions (H^+), and alkalinity by the concentrations of hydroxyl (OH^-), bicarbonate (HCO_3^-), and carbonate (CO_3^{2-}) ions in water (Dallas & Day, 2004). pH may vary naturally from season to season as a result of the rainfall pattern. In productive systems, however, pH may exhibit daily fluctuations due to the competing processes of respiration and photosynthesis (Malan & Day, 2002). A change in pH alters the concentrations of both H^+ and OH^- ions, which affects the ionic and osmotic balance

of aquatic organisms (Dallas & Day, 2004). As H^+ concentrations increase, pH decreases and the solution becomes more acidic. As H^+ concentrations decrease, pH increases and the solution becomes more alkaline. Carbon dioxide dissolves in water to form carbonic acid (H_2CO_3), which, depending on the pH, dissociates to form carbonate, bicarbonate and hydrogen ions (Dallas & Day, 2004). Figure 1.3 illustrates the relationship between pH and the percentage of free carbon dioxide, bicarbonate, and carbonate ions in water. At a pH of 4, all carbon dioxide is present in the form of free CO_2. As pH increases, the proportion of bicarbonate rises to a peak at a pH of 8.3. Thereafter, bicarbonate ions decrease while carbonate ions increase, although, only present in significant quantities at a pH approaching 10 (Dallas & Day, 2004). The pH of natural waters is determined by geological and atmospheric influences (Day *et al*., 1994). pH, and more specifically the concentrations of bicarbonate and carbonate ions directly affect the growth of algae, as it is the main source of carbon used in photosynthesis (Moss, 1973).

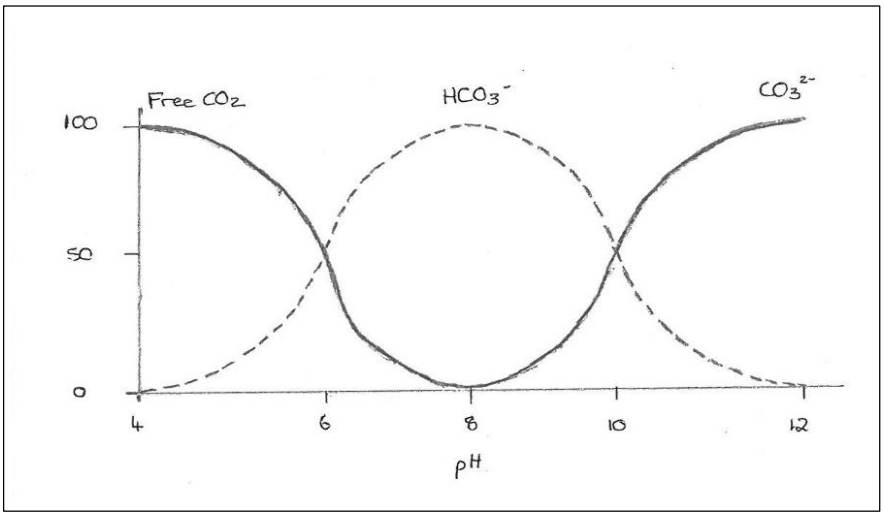

Figure 1.3: The relationship between pH and the percentage of free carbon dioxide, bicarbonate, and carbonate ions in water (after Dallas & Day, 2004).

Material dissolved in water is often measured as total dissolved solids, conductivity, or as salinity. TDS represent the total quantity of dissolved material, organic and inorganic, ionised and unionised, in a water sample. Conductivity is a measure of the ability of a sample to conduct an electrical current. TDS and conductivity usually correlate closely for a particular type of water and can be interconverted (Dallas & Day, 2004; Day *et al*., 1994; Malan & Day, 2002). Salinity refers to the saltiness of water, and for most purposes can be considered to be the same as TDS (Day *et al*., 1994). TDS, as its name suggest, is a measure of the total amount of soluble material in a water sample. The greatest mass of this material in natural waters comprises inorganic ions. Major ions are those that are most common and include the cations Na^+, K^+, Ca^{2+}, and Mg^{2+}, and the anions HCO_3^-, CO_3^{2-}, Cl^-, and SO_4^{2-}. Other, usually

less common, inorganic ions include nutrients such as NO_3^- and PO_4^{3-} and various species of trace metals (Dallas & Day, 2004).

The maintenance of adequate dissolved oxygen concentrations is critical for the survival and functioning of aquatic biotas (Dallas & Day, 2004). The dissolved oxygen content of the water column is therefore a useful indicator of the biotic integrity of an aquatic ecosystem (Malan & Day, 2002). Dissolved oxygen fluctuates diurnally, depending on the relative rates of respiration and photosynthesis of aquatic animals and plants (Dallas & Day, 2004). It is usually lowest near dawn, increasing during the day, peaking in the afternoon, and decreasing at night (Day *et al*., 1994). Factors resulting in an increase in dissolved oxygen include atmospheric re-aeration, increasing atmospheric pressure, decreasing temperature and salinity, and photosynthesis by plants and algae. Factors decreasing dissolved oxygen concentrations include increasing temperature and salinity, respiration of aquatic organisms, decomposition of organic material by microbial organisms, chemical breakdown of pollutants, re-suspension of anoxic sediments, and release of anoxic bottom water (Dallas & Day, 2004; Day *et al*., 1994; Malan & Day, 2002). It is usually a depletion of oxygen that is observed in aquatic ecosystems, although super-saturation may occur in eutrophic waters (Dallas & Day, 2004). The extent to which an organism is affected by dissolved oxygen concentrations is determined by its dependence on water as a medium (Day *et al*., 1994).

Light is an essential source for autotrophic growth and photosynthetic activity. All algae contain chlorophyll *a* that is the major light harvesting pigment. Most algae also contain additional pigments, as different pigments are able to absorb lights of different wavelengths (Nabors. 2004; Singh & Singh, 2015). Light intensity is a critical factor in algal growth and aquatic systems can be limited by light, as well as nutrients (Karlson *et al*., 2009). Consequently, water depth will also have an impact on the productivity of an aquatic system, as an increase in depth will lead to a decrease in light availability. In addition to its primary role as energy source for phytoplankton photosynthesis, light availability also affects water transparency, algal competition, phytoplankton biodiversity, seston (particulate matter suspended in water bodies including plankton, organic detritus, and inorganic material) stoichiometry, and its nutritional quality for zooplankton grazers (Llames *et al*., 2009).

Two types of enrichment occur in aquatic systems, namely, organic enrichment and nutrient enrichment. Organic enrichment is usually of anthropogenic nature. Major sources include domestic sewage, food-processing plants, breweries and vegetable canning, animal feedlots, abattoirs and cattle grazing. The major effects of organic enrichment are a decrease in dissolved oxygen concentrations, an increase in nutrient concentrations, an increase in turbidity, and concentration of suspended solids. Of these, reduced oxygen concentration is considered to have the greatest impact on aquatic biotas (Dallas & Day, 2004).

Nutrients are chemical compounds or elements that can be used directly by plants and algae for growth. Nutrients are mostly inorganic elements that are assimilated, and in conjunction with the process of photosynthesis, are utilised to produce and accumulate organic material in aquatic ecosystems. Algae and aquatic macrophytes require about 20 different elements, and the rate and extent of aquatic plant growth is dependent on the concentration and ratios of nutrients present in the water (Walmsley, 2000). Elements required for normal growth and reproduction in plants and algae include carbon, oxygen, hydrogen, sulphate, potassium, calcium, magnesium, silica, nitrogen, and phosphorus, as well as other nutrients, which are required in much smaller quantities (Dallas & Day, 2004; Day *et al*., 1994). Plant growth, however, is generally limited by the concentration of that nutrient that is present in the least quantity relative to the growth needs of the plant. This is known as the limiting nutrient concept, and nitrogen and phosphorus have been found to be the most common limiting nutrients (Day *et al*., 1994; Walmsley, 2000). Phosphorus occurs most commonly as orthophosphates (PO_4^{3-}), which is the dissolved inorganic form. Nitrogen occurs as nitrate (NO_3^-), nitrite (NO_2^-), and ammonium (NH_4^+) ions (Dallas & Day, 2004).

Lastly, it is important to mention seasonality as a factor, influencing temperature, turbidity, pH, conductivity, light availability, and water volume, amongst others. Seasonality also affects every aspect of other biota that forms part of the aquatic ecosystem.

1.5.2.2 Biotic factors

Aquatic systems often alternate between two possible states: one with submerged macrophytes and relatively few phytoplankton; and another with few submerged macrophytes and abundant phytoplankton. The reason for limited phytoplankton in the presence of macrophytes includes a reduction in nutrient availability, shading, release of allelopathic substances, and greater shelter availability for grazers (Allende *et al.*, 2009). This indicates that interspecific competition may greatly influence algal composition.

Emphasis has often been placed on the role of nutrient supply as a regulator of lake productivity. However, nutrient supply cannot explain all the variation in the primary productivity of the world's lakes. Carpenter *et al*. (1985) argued that the concept of cascading trophic interactions explains differences in productivity among lakes with similar nutrient supplies, but contrasting food webs. The cascading trophic interaction concept, simply put states that a rise in piscivore biomass brings decreased planktivore biomass, increased herbivore biomass, and decreased phytoplankton biomass (Carpenter *et al*., 1985). The development of the trophic cascade theory led to an increased interest in understanding the relative role of zooplankton grazers in controlling algal biomass and species composition (Levine *et al.*, 1999). Ecosystems are usually seen as being controlled by either top-down (consumer-driven) or bottom-up (resource-driven) mechanisms. If an ecosystem is productive

enough to facilitate the existence of vertebrate predators, the "ecosystem exploitation hypothesis" predicts that predators keep the population sizes of herbivorous prey low, enabling plants to grow and reproduce (Mäntylä *et al.*, 2011). According to the exploitation ecosystem hypothesis (EEH):

- Plant biomass reflects the primary productivity of an ecosystem, which is modified and regulated by herbivory
- Herbivore abundance reflects the productivity of plants, and is modified and regulated by predation (Choquenot & Forsyth, 2013).

Carpenter *et al*. (1985) found that productivity at a given trophic level is maximised at an intermediate biomass of its predators. Productivity at all trophic levels and energy flow through the food web, are highest where intensities of predation are intermediate at all trophic levels (Carpenter *et al*., 1985).

Zooplankton often feed selectively, with prey discrimination based on size, shape, toxicity, or nutrient content (Levine *et al.*, 1999). One important paradigm of phytoplankton ecology however, is the existence of low grazing pressures on blue-green algae, which are toxic, of low nutrient content, or too large and filamentous for easy consumption. This increase grazing pressures on other algae and cryptophytes, chrysophytes, and small non-colonial diatoms are among the phytoplankton generally considered most edible (Levine *et al.*, 1999). Additionally, algae form interactions with microbial organisms, other algae, higher plants, and animals. Consortial cyanobacteria-bacteria interactions exist and may promote growth. Many algae are also epiphytic and form endosymbiosis with algae, ferns, and vascular plants (Paerl *et al*., 2001).

1.5.3 Eutrophication

Eutrophication is a traditional ecological term used to describe the process by which a water body becomes enriched with plant nutrients. The most widely accepted definition of eutrophication is: the nutrient enrichment of waters which results in the stimulation of an array of symptomatic changes, amongst which increased production of algae and aquatic macrophytes, deterioration of water quality and other symptomatic changes are found to be undesirable and interfere with water uses (Walmsley, 2000). Eutrophication can either be a natural- or human-induced process. Natural eutrophication is dependent on the geology and natural features of the catchment area. It is not reversible and continues *ad infinitum* but at a very slow rate. Eutrophication related to anthropogenic activities is known as cultural eutrophication, and may be reversible (Dallas & Day, 2004; Walmsley, 2000).

Humans now strongly influence almost every major aquatic system, and their activities have dramatically altered the fluxes of growth-limiting nutrients from the landscape to receiving waters (Smith, 2003). Nutrient enrichment may lead to an imbalance in biological communities;

particularly by an increase in plant communities and associated water quality problems (Dallas & Day, 2004). Aquatic ecosystems can be classified as oligotrophic, mesotrophic, eutrophic, and hypertrophic, based on the state of enrichment of the system. Oligotrophic means the presence of low levels of nutrients with no water quality problems. Mesotrophic refers to systems with intermediate levels of nutrients, with emerging signs of water quality problems. Eutrophic refers to high levels of nutrients and an increased frequency of water quality problems, while hypertrophic refers to excessive levels of nutrients, where plant production is governed by physical factors and water quality problems are almost continuous (Walmsley, 2000).

Considerable limnological research was directed at identifying and quantifying the key nutrients in the eutrophication process in the last 50 years, which contributed greatly to the understanding of nutrients and their impact on the aquatic environment (Walmsley, 2000). Phosphorus has been identified as the chief causative agent of freshwater eutrophication, while nitrogen plays a secondary role, although it may become important at a high level of eutrophication (Paerl *et al*., 2001; Smith, 2003; Walmsley, 2000).

The main driving force of eutrophication is human population growth and associated economic activities (Walmsley, 2000). This has led to the rapid intensification of agriculture, where agricultural fertilisers alone released more than 10 million metric tonnes of nitrogen in 1950, which may exceed 135 million metric tonnes by the year 2030 (Smith, 2003). Human activities make use of numerous products and resources containing bound nitrogen and phosphorus ultimately converting them into available nitrogen and phosphorus that are released into the aquatic environment (Walmsley, 2000).

Anthropogenic sources of nutrients may enter the aquatic environment in two main ways. The first is a point source, which is usually a location of high nutrient concentration, where some form of effluent is discharged directly into a receiving aquatic ecosystem (Dallas & Day, 2004; Walmsley, 2000). Point sources are relatively simple to measure and regulate, and can be controlled by treatment at the source (Dallas & Day, 2004). The second way, in which nutrients enter aquatic systems are known as non-point source or diffuse source. A diffuse source is a location with multiple nutrient sources that are spread over a much larger area and nutrients enter the aquatic environment through leaching and atmospheric depositions (Walmsley, 2000). Diffuse source inputs are often intermittent and linked to seasonal agricultural activities and irregular events such as heavy precipitation (Dallas & Day, 2004).

Nutrient enrichment can have profound effects on the water quality of receiving systems. The most common effect of nutrient enrichment is an increase in the abundance of algae and aquatic plants. The environmental consequences of excessive nutrient enrichment, however, are more serious and far-reaching than nuisance increases in plant growth alone

(Smith, 2003). Additional problems associated with eutrophication include an increased occurrence of nuisance and toxic algal blooms, an increased dominance by blue-green algae, increased occurrence of deoxygenation in bottom waters, increased fish and vertebrate mortality, and changes to ecological community structure and loss of biodiversity (Smith, 2003; Walmsley, 2000). Ecological impacts of eutrophication are reflected through influence on natural biological communities. Ecological components provide one of the most effective treatment systems for eutrophication, through a feature known as natural assimilative capacity. Assimilative capacity however, is dependent on the presence of appropriate biodiversity, and any activity that reduces this biodiversity can result in a reduction of assimilative capacity. The relationship between nutrient inputs and their impact is extremely complex, and the most severe eutrophication problems are experienced in areas where the scale of anthropogenic nutrient inputs far exceeds the capacity of the natural environment to assimilate the waste (Walmsley, 2000).

1.6 AIM, OBJECTIVES AND HYPOTHESIS

1.6.1 Motivation

It was noted from previous aerial surveys (conducted by Bouwman in 2013/14/15 to locate breeding sites) that the avian composition of the Wonderfontein Spruit seemed much more diverse in terms of species richness when compared with the Mooi River. Subsequent flights showed that there were almost no waterbirds in the Mooi River between Klerkskraal Dam and the confluence with the Wonderfontein Spruit, when compared with an equivalent section of the Wonderfontein Spruit. There were almost no water birds at Klerkskraal Dam (except some coots), while many flamingos were observed on the Wonderfontein Spruit, and almost none in the Mooi River. Birds are considered one of the more visible indicators of the total productivity of biotic systems (Weller, 1999). Algae are important primary producers in aquatic ecosystems where they generate biomass, which is the foundation of diverse food webs (Bellinger & Sigee, 2010). The differences between these two rivers might therefore be explained by differences in water quality and concomitant algal composition, which then may affect bird community compositions. Relatively few studies have been done on the interactions between algae and birds. Wootton (1995) investigated trophic cascades between macro-algae, sea urchins, and birds. Some studies have also investigated the interactions between water birds and submerged macrophytes (Perrow *et al*., 1997; Russel *et al*., 2009). However, there seem to be a lack of studies focussing on the interactions between water quality, freshwater phytoplankton, and birds. This project will investigate these relationships.

1.6.2 Hypothesis

Freshwater quality and environmental parameters impact algal community parameters, which, in turn, impact bird community parameters.

1.6.3 Problem statement

Does the algal diversity in riparian ecosystems have an effect on the avian composition of that system?

1.6.4 Aims and objectives

Aim: To conduct an in depth study on the avian and algal diversity of two small rivers and the water quality factors involved.

Objectives:

- Determine the surface area of the water mass of each site.
- Measure the water depth of each site.
- Record the avian and algal diversity of each site, monthly, over a period of a year.
- Compare the water quality of each site, monthly, over a period of a year.
- Analyse the data for correlations using comparative statistics multivariate analysis.

CHAPTER 2: MATERIALS AND METHODS

2.1 STUDY AREA

2.1.1 Location

This study was conducted along the Mooi River and Wonderfontein Spruit (Figure 2.1), situated between the towns of Potchefstroom (North West Province) and Carletonville (Gauteng Province), approximately 10 km north and 15 km north east of Boskop Dam Nature Reserve respectively. Sites representing the Mooi River are situated in the North West Province along a 30 km stretch of river downstream of Klerkskraal Dam, while sites representing the Wonderfontein Spruit are situated in Gauteng along a 20 km stretch of river downstream of Abe Bailey Provincial Nature Reserve.

The Mooi River has three major sub-catchments, which include the Wonderfontein Spruit (WFS) on the north-eastern reach, the Mooi River proper on the northern reach and the Loop Spruit on the eastern reach (Barnard *et al.*, 2013). During the past decade the Mooi River catchment, and the Wonderfontein Spruit in particular, has received much attention regarding significant radioactive and other pollution sources associated with mining activities (Barnard *et al.*, 2013). The Wonderfontein Spruit originates in the Tudor and Lancaster areas south of Krugersdorp.

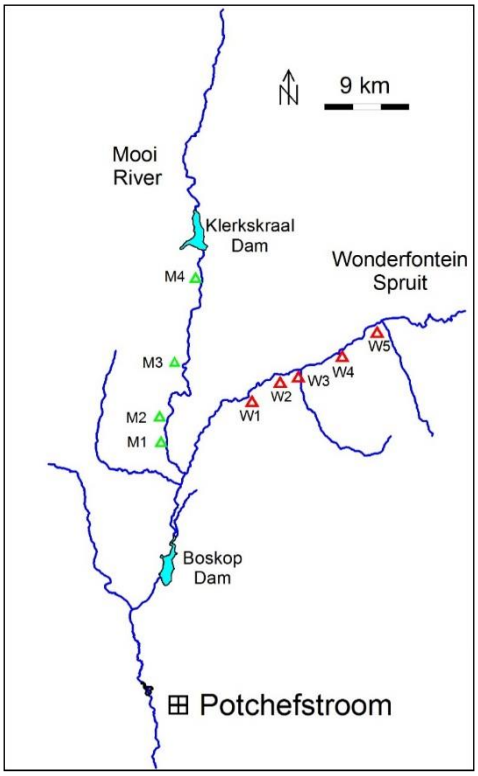

Figure 2.1: Location of the different sites of Wonderfontein Spruit and Mooi River.

2.1.2 Climate and rainfall

South Africa is globally considered a semi-arid country with a mean annual precipitation of 487 mm per year, which is less than the world average of 860 mm per year (Carrim, 2006). This rainfall is also not evenly distributed, with 65 % of the country receiving less than 500 mm of rain per year (Annandale & Nealer, 2011). The study area is mainly located within the Carletonville Dolomite Grassland, with a few sites in the Vaal-Vet Sandy Grassland, which forms part of the Dry Highveld Grassland Bioregion (Mucina & Rutherford, 2006). The Carletonville Dolomite Grassland occur at an altitude of 1 360–1 620 m, within a warm-temperate, summer-rainfall region with an overall mean annual precipitation of 593 mm. Summer temperatures are high, while severe frequent frosts occurs in winter (Mucina & Rutherford, 2006).

2.2 TIME OF STUDY AND SURVEY METHOD

Sampling was carried out on a monthly basis over a period of 11 months, which spanned from July 2016 to May 2017. The sampling period was spread across four seasons, which allowed for the recording of species with seasonal movements, both migratory and nomadic. Surveys were conducted in the first two hours following the first survey, starting between dawn and sunrise to ensure that bird activity were optimal. Surveys took place in the first week of every month, unless hindered by adverse weather conditions. Species were recorded using a point count method with an open radius (see Bibby *et al*., 2000). An open radius was used because sites varied greatly in size and dimensions, and therefore an open radius allowed for the recording of individuals over a range of aquatic, semi-aquatic, and terrestrial habitats, and ensuring that each site consisted of the same habitats to avoid bias. Both birds seen and heard were recorded. Birds were recorded over an eight-minute period, following a two-minute waiting period allowing birds to settle down from any disturbances caused by the observer's arrival. Any birds flying by were not recorded. All surveys were carried out by the same observer and all birds recorded were conveyed to an additional observer to notate on spreadsheets. All surveys were recorded on a voice recorder and used to ensure that all bird species and numbers were correctly documented.

2.3 WATER ANALYSIS

Two water samples of 250 ml each were collected at each site following the bird survey. One sample was to be used for analyses of dissolved inorganic nutrients, which was done

within 24 hours of collection. The second sample was for analysis of algae and the samples were fixated with formalin (1ml/100ml of water) and stored for later analysis.

2.3.1 Water quality variables

Water quality variables that were measured include pH, temperature, dissolved oxygen, and conductivity. This was done on site with a Lovibond SensoDirect 150 Multi Parameter Hand-held Meter.

2.3.2 Dissolved inorganic nutrients

Nutrient concentrations were measured using standard methods for a HACH DR 2800 Spectrophotometer:

- Ammonia, Nitrogen - Salicylate Method (8155).
- Nitrate, Nitrogen - Cadmium Reduction Method (8192).
- Nitrite, Nitrogen - Diazotization Method (8507).
- Phosphorus, Reactive - PhosVer3 Method (8048).
- Sulphate - SulfaVer4 Method (8051).

The nitrite -, phosphorus -, and sulphate methods are EPA accredited and the machine is factory calibrated at the recommended intervals.

2.4 ALGAL SAMPLE ANALYSIS

Phytoplankton identification and enumeration was done by making use of the sedimentation technique using gravity, a method used and validated by North-West University – Potchefstroom Campus (Swanepoel *et al*., 2008).

2.4.1 Algae sample preparation

Before preparation of samples, strict safety precautions were followed:

- The samples were preserved at site by adding 37% formaldehyde solution (formalin) at a ratio of 1:100.
- After preservation, gas vacuoles of cyanobacteria were pressure-deflated to allow them to settle. Deflating was done by placing a subsample in a thick-walled metal container to a volume where there is no air left in the container when closed with a rubber stopper. Pressure was applied by hitting the rubber stopper with a hammer.
- The sample was then shaken to ensure uniform distribution of cells.

- With a calibrated dispenser pipette, 1 ml of the prepared sample was transferred into a sedimentation chamber, and labelled with the sample name and date. It was left to settle for approximately 30 minutes on a surface free of vibrations and disturbances. A new pipette tip was used for each sample to prevent cross contamination.
- The sedimentation chamber was placed on the inverted light microscope and briefly examined for turbidity and density of phytoplankton in the sample.
- In the event of the sample being too turbid or too dense in algal concentration, dilution was done. I started by diluting the known volume of the preserved and deflated sample to half the volume. This was done by adding one part sample by one part distilled water, giving a dilution factor of two. The chamber was re-evaluated for turbidity and density of phytoplankton. If it was still too turbid or dense in algal concentration one part of the diluted sample was added to one part distilled water, giving a dilution factor of four. The chamber was then re-evaluated for turbidity and the process was repeated until phytoplankton cells were visible enough to identify and enumerate accurately.
- If the sample was too low in algal concentration, a greater volume was settled out. This was done by estimating the volume of sample necessary to identify algal taxa without any phytoplankton cells or particles obscuring each other. This was the final volume of sample added to the sedimentation sample.
- The final volume of sample in the sedimentation tube was recorded on the sedimentation chamber.
- The sedimentation chamber was then filled to the top with distilled water and covered with a cleaned cover slip so no air was left in the sedimentation chamber.
- The sedimentation chamber was placed in a humidifier with water in the bottom section to prevent evaporation of sample water.
- The height of the sedimentation chamber determined the appropriate time necessary for phytoplankton to settle. For 1 cm of chamber height, a settling period of 24 hours was allowed.

2.4.2 Algae identification and enumeration

- The sedimentation chamber was removed from the humidifier, with care being taken not to disturb the settled material at the bottom of the sedimentation chamber.
- The sample was placed in the round slot on the microscope table and the inverted light microscope was switched on.

- Identification of phytoplankton was done using 40x magnification.
- The settled phytoplankton was identified and enumerated to genus level. Counting was started on the left hand side of the sedimentation chamber on a line running through the centre of the sedimentation chamber and all phytoplankton in the Whipple grid were identified.
- I moved one grid at a time from left to right, identifying all the phytoplankton genera within the grid, and continued counting in this manner until at least one lane was completed (Figure 2.2).
- A minimum of 200 cells must be counted. If the count was less than 200 cells at the end of the first lane, the sedimentation chamber was rotated to a cross section that has not yet been analysed and continued as above, this time from right to left. These steps were continued until a total greater than 200 cells have been counted. If the 200 cells have been achieved, the lane was finished so that the exact area analysed was known.
- Every phytoplankton cell was counted as one, whether it was part of a colony/filament or not.
- If a cell was located on the edge of the Whipple grid, it was only counted if more than half of the cell was located within the Whipple grid. When cells in a colony/filament were counted, only those cells falling within the Whipple grid were counted.
- Counts were recorded on a well-marked sheet and the sample name, date sampled, date of analysis, amount of lanes enumerated, objective used, the conversion factor, and name of the analyst, was noted.
- The data was then entered into an excel spreadsheet that converted the counts to the amount of algal cells per millilitre (cells/ml).

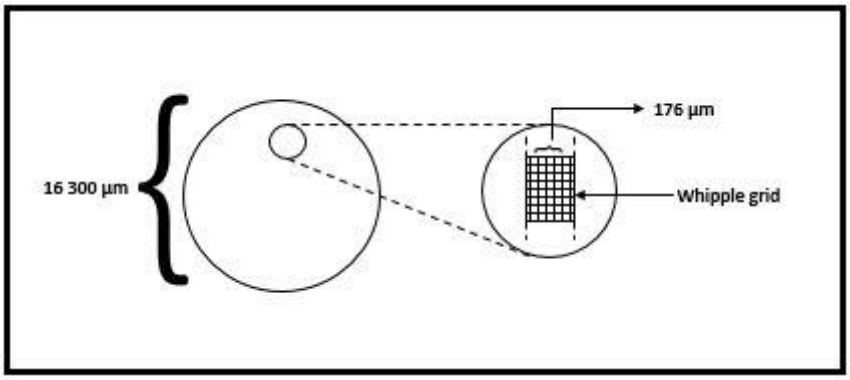

Figure 2.2: Line diagram showing the orientation of lanes and the Whipple grid (after Swanepoel *et al*., 2008).

2.5 DATA ANALYSIS

Statistical analysis of data was done by performing both univariate and multivariate tests. Univariate analyses were done to find differences between rivers, and differences within rivers. Multivariate analysis on the other hand combines differences between rivers and differences within rivers.

2.5.1 Univariate Analysis

Differences between rivers, and differences within rivers (sites) were compared in terms of:

- water quality variables,
- dissolved inorganic nutrients,
- algae, and
- birds.

Microsoft Excel was used to compile data sheets including species lists with abundances per site. Data were processed and refined in Microsoft Excel and all tables in this study were created using this program. The data were then imported into GraphPad Prism 5.0.

T-tests and Mann-Whitney tests were performed to compare Wonderfontein Spruit with Mooi River for the various parameters. One-way Analysis of Variance (ANOVA) and similar Non-parametric tests were performed to compare the means of different sites within each stream to one another, for the same parameters as for t-tests and Mann-Whitney tests. Non-parametric tests were applied for data that were not normally distributed. Values were considered as outliers if they fell outside of three SDs from the mean or median. Any outliers were excluded. Descriptive statistics were compiled by Prism and exported to Excel, where tables were compiled.

2.5.2 Multivariate Analysis

Multivariate analysis was done using PC-ORD. Species-accumulation curves were constructed to evaluate the adequacy of sample size for both bird and algal samples. Cluster analysis was done to classify all sites based on similarity of species composition. This was done for both avian and algal composition.

Nonmetric multidimensional scaling (NMS) was used extensively to identify and interpret patterns in algal and avian community datasets that otherwise would not be seen using univariate techniques. NMS allows you to order your sample units such that their interpoint distances reflect the redundant pattern of covariation observed in your original response data (Peck, 2010). NMS is becoming the most commonly applied free ordination tool for species datasets, because it avoids the assumption of linear relationships among variables,

makes use of rank distances, and allows the use of any distance measure (McCune & Grace, 2002; Peck, 2010). Principal component analysis (PCA) was used where NMS gave unsatisfactory results, for example NMS ordinations with very high stress values.

Indicator Species Analysis (ISA) was used to identify algal and bird species characteristic of a particular stream or site within a stream. ISA allows you to assess the degree to which a species indicates a group based on its constancy and distribution of abundance (Peck, 2010). More specifically, Dufrêne and Legendre's method combines information on the concentration of species abundance and the faithfulness of occurrence of a species in a particular group. A perfect indicator of a group should be both faithful to that group (always present), and exclusive to that group (never occurring in other groups). Indicator values are then tested for statistical significance using a randomization (Monte Carlo) technique (McCune & Grace, 2002).

PAST 3.18 was used to evaluate the significance of similarities or differences between sites and rivers. A One-way Analysis of Similarity (ANOSIM) is a nonparametric test of significant difference between two or more groups, based on any distance measure. ANOSIM works by comparing the distances between groups with distances within groups (Hammer *et al*., 2001). Similarity Percentage (SIMPER) is a simple method for assessing which taxa are primarily responsible for an observed difference between groups of samples (Hammer *et al*., 2001).

CHAPTER 3: RESULTS

3.1 VARIABLES

Water quality variables that were measured include pH, temperature, conductivity (EC), and dissolved oxygen (DO). Additionally, water samples were analysed for dissolved inorganic nutrients, which included phosphorus, sulphate, nitrite, nitrate, and ammonia.

3.1.1 Differences between rivers

T-tests and Mann-Whitney tests (when data were not normally distributed) were done to compare the Wonderfontein Spruit (WFS) and Mooi River (MR) regarding water quality variables and dissolved inorganic nutrients. T-tests and Mann-Whitney tests showed significant differences between means/medians for pH, DO, and EC, but not for temperature. There were also significant differences between the medians of all of the dissolved inorganic nutrients that were analysed except for nitrite and ammonia.

Water quality variables:

pH values for WFS varied between 7.0 - 9.4 with a mean and standard deviation (SD) of 7.9 ± 0.58; while that of MR varied between 6.8 - 8.5 with a mean ± SD of 7.7 ± 0.35 (Figure 3.1a). An unpaired t-test (unequal variances) showed that the mean of WFS was significantly higher than that of MR ($p = 0.042$).

Temperatures for WFS varied between 6.4ºC - 28ºC with a mean and SD of 18 ± 5.3ºC, while that of MR varied between 8.7ºC - 26ºC with a mean and SD of 18 ± 4.7ºC (Figure 3.1b). An unpaired t-test showed that there was no significant difference between the mean of the two rivers ($p = 0.8098$).

Dissolved oxygen concentrations for WFS varied between 2.3 mg/l - 10 mg/l with a mean and SD of 5.7 ± 2.1 mg/l, while that of the MR varied between 1.6 mg/l - 20 mg/l with a mean and SD of 5.0 ± 4.1 mg/l (Figure 3.1c). One value from MR was excluded due to being an outlier as it fell outside three SDs from the median. A Mann-Whitney test showed that there was a significant difference between the medians of the two rivers ($p = 0.0030$).

The conductivity of WFS varied between 0.66 mS - 1.1 mS with a mean and SD of 0.92 ± 0.1 mS, while that of MR varied between 0.30 mS - 0.50 mS with a mean and SD of 0.42 ± 0.059 mS (Figure 3.1d). One value from WFS was excluded as an outlier. An unpaired t-test (unequal variances) showed that the mean of WFS was significantly higher than that of MR ($p < 0.0001$).

Dissolved inorganic nutrients:

Phosphorus concentrations in WFS varied between 0.17 mg/l - 110 mg/l with a mean and SD of 8.2 ± 21 mg/l. Phosphorus concentrations in MR varied between 0.09 mg/l - 131 mg/l with a mean and SD of 17 ± 36 mg/l (Figure 3.2a). A Mann-Whitney test showed that the median of MR was significantly higher ($p = 0.0040$) than that of WFS.

Sulphate concentrations in WFS varied between 100 mg/l - 860 mg/l with a mean and SD of 222 ± 145 mg/l, while sulphate concentrations in MR varied between 0.5 mg/l - 840 mg/l with a mean and SD of 45 ± 148 mg/l (Figure 3.2b). One value from MR was excluded as an outlier. A Mann-Whitney test showed that the median of WFS was significantly higher ($p < 0.0001$) than that of MR.

Nitrite concentrations in WFS varied between 0.0005 mg/l - 0.092 mg/l with a mean and SD of 0.013 ± 0.021 mg/l, while that of MR varied between 0.0005 mg/l - 0.037 mg/l with a mean and SD of 0.0056 ± 0.0065 mg/l (Figure 3.2c). One value from MR was excluded as an outlier. A Mann-Whitney test showed no significant difference ($p = 0.2924$) between the medians of the two rivers.

Nitrate concentrations in WFS varied between 0.005 mg/l - 0.29 mg/l with a mean and SD of 0.056 ± 0.066 mg/l, while nitrate concentrations in MR varied between 0.005 mg/l - 0.06 mg/l with a mean and SD of 0.018 ± 0.013 mg/l (Figure 3.2d). A Mann-Whitney test showed that WFS had a significantly higher median ($p = 0.0008$) than that of MR.

Ammonia concentrations in WFS varied between 0.005 mg/l - 1.5 mg/l with a mean and SD of 0.15 ± 0.35 mg/l, while ammonia concentrations in MR varied between 0.005 mg/l - 0.25 mg/l with a mean and SD of 0.025 ± 0.037 mg/l (Figure 3.2e). A Mann-Whitney test showed no significant difference ($p = 0.4267$) between the medians of the two rivers.

Dissolved inorganic nitrogen (DIN) is the sum of nitrate-nitrogen (NO_3-N), nitrite-nitrogen (NO_2-N) and ammonia-nitrogen (NH_3-N). DIN concentrations in WFS varied between 0.017 mg/l - 1.8 mg/l with a mean and SD of 0.22 ± 0.40 mg/l, while that of MR varied between 0.013 mg/l - 0.26 mg/l with a mean and SD of 0.051 ± 0.044 mg/l (Figure 3.2f). A Mann-Whitney test showed that the median of WFS was significantly higher ($p = 0.0023$) than that of MR.

Table 3.1: Summary of water quality variables and dissolved inorganic nutrients of the two rivers, and associated tests.

	WFS				MR					
Variables	**Min**	**Max**	**Mean**	**SD**	**Min**	**Max**	**Mean**	**SD**	**Test**	**p value ≤ 0.05**
pH	7.0	9.4	7.9	0.58	6.8	8.5	7.7	0.35	Unpaired t test with Welch's correction (Two-tailed)	Yes
Temperature	6.4	28	18	5.3	8.7	26	18	4.7	Unpaired t test (Two-tailed)	No
Dissolved Oxygen	2.3	10	5.7	2.1	1.6	20	5.0	4.1	Mann-Whitney test (Two-tailed)	Yes
Conductivity	0.66	1.1	0.92	0.10	0.30	0.50	0.42	0.059	Unpaired t test with Welch's correction (Two-tailed)	Yes
Nutrients	**Min**	**Max**	**Mean**	**SD**	**Min**	**Max**	**Mean**	**SD**	**Test**	**p value ≤ 0.05**
Phosphorus	0.17	110	8.2	21	0.09	131	17	36	Mann-Whitney test (Two-tailed)	Yes
Sulphate	100	860	222	145	0.5	840	45	148	Mann-Whitney test (Two-tailed)	Yes
Nitrite	0.0005	0.092	0.013	0.021	0.0005	0.037	0.0056	0.0065	Mann-Whitney test (Two-tailed)	No
Nitrate	0.005	0.29	0.056	0.066	0.005	0.06	0.018	0.013	Mann-Whitney test (Two-tailed)	Yes
Ammonia	0.005	1.5	0.15	0.35	0.005	0.25	0.025	0.037	Mann-Whitney test (Two-tailed)	No
Dissolved Inorganic Nitrogen	0.017	1.8	0.22	0.40	0.013	0.26	0.051	0.044	Mann-Whitney test (Two-tailed)	Yes

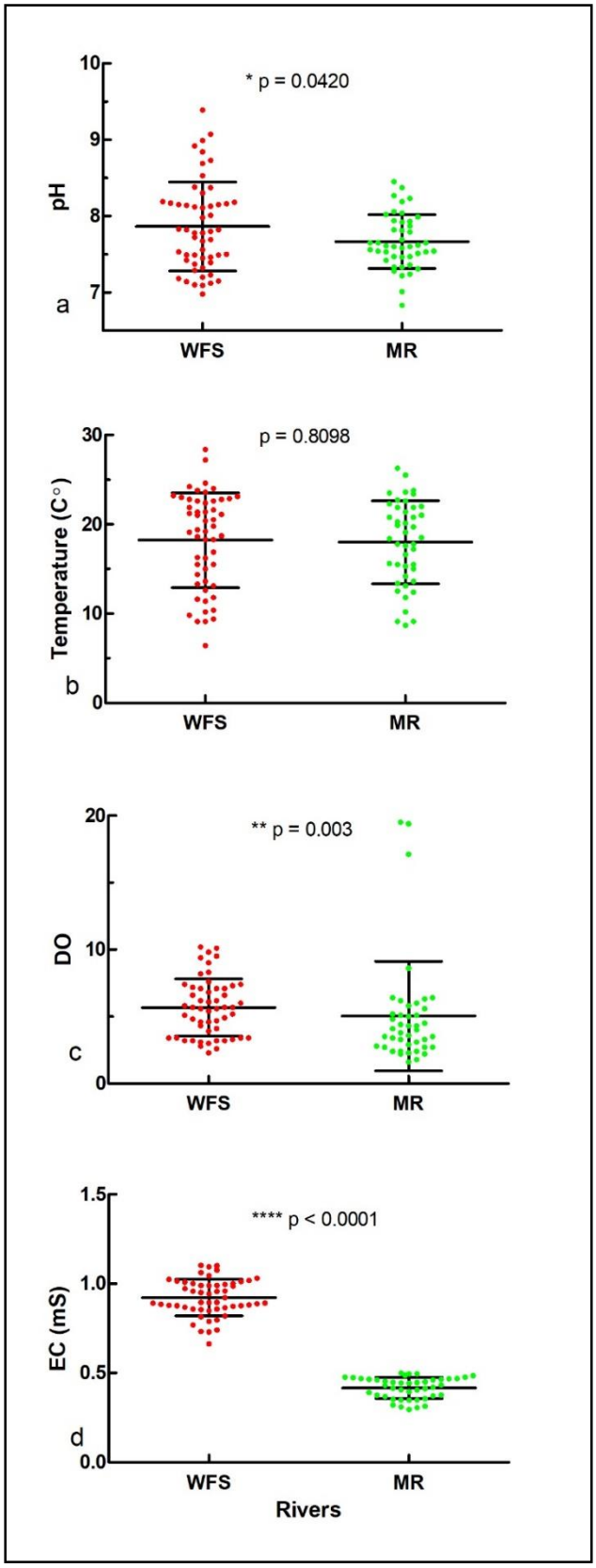

Figure 3.1: T-tests and Mann-Whitney tests of water quality variables of Wonderfontein Spruit and Mooi River (a - pH, b - temperature, c - dissolved oxygen, d - conductivity).

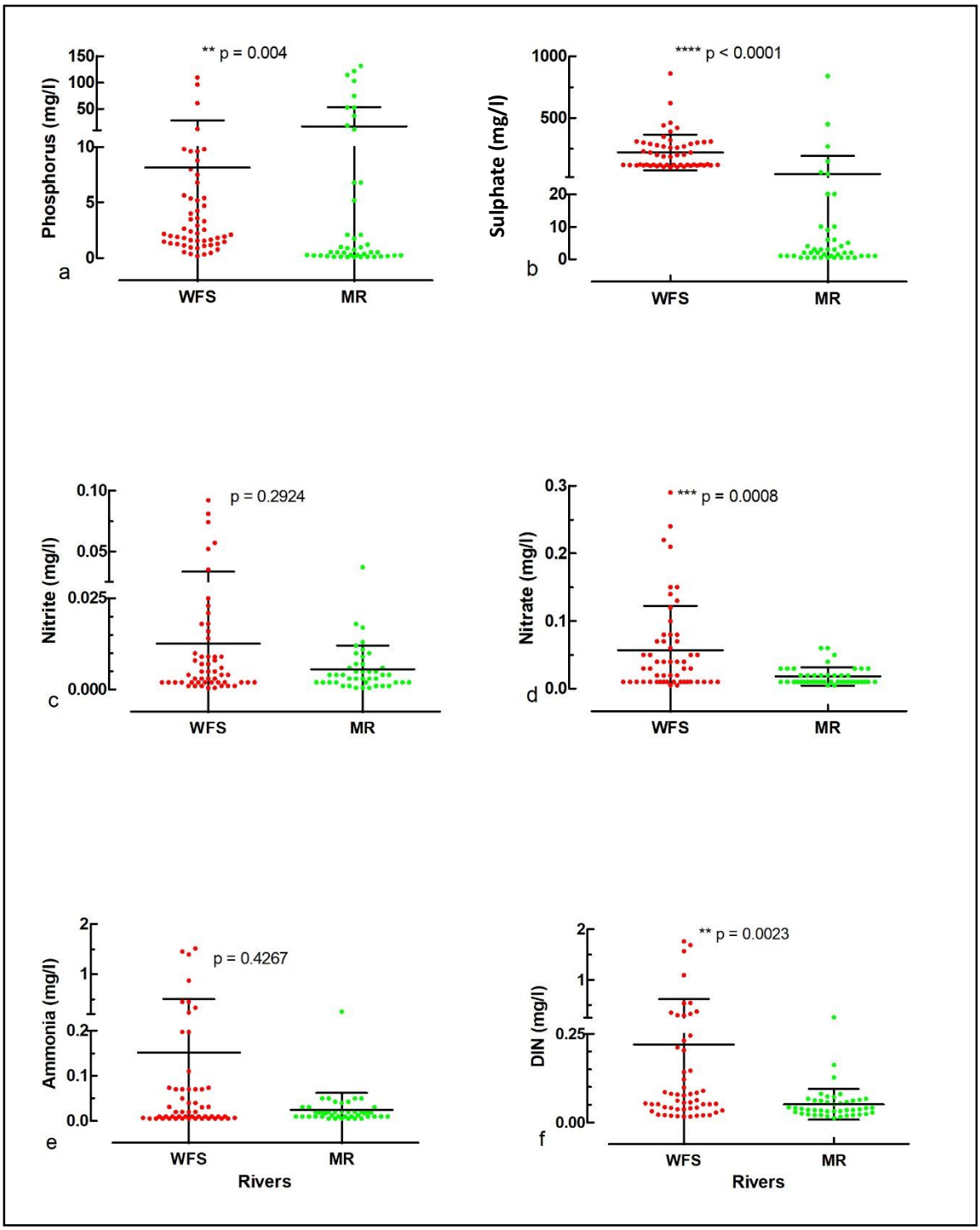

Figure 3.2: T-tests of dissolved inorganic nutrients of Wonderfontein Spruit and Mooi River (a - phosphorus, b - sulphate, c - nitrite, d - nitrate, e - ammonia, f - dissolved inorganic nitrogen).

3.1.2 Differences within rivers

All sites within each river were analysed and compared to one another for the same water quality variables and dissolved inorganic nutrients.

Water quality variables:

For pH of the different sites of WFS, the means varied between 7.6 (W4) - 8.2 (W5) with SD between 0.34 (W4) - 0.79 (W3). A One-way ANOVA showed a significant difference between means ($p = 0.0270$). Bartlett's test showed no significant differences between SD's ($p = 0.0754$). Tukey's multiple comparison test showed a significant difference in the means of W4 and W5 ($p = 0.0441$) (Figure 3.3a). For the different sites of MR, means varied between 7.4 (M4) - 8.1 (M1) with SD between 0.20 (M1) - 0.27 (M4). A One-way ANOVA showed a significant difference between means ($p < 0.0001$). Bartlett's test showed no significant differences between SD's ($p = 0.8335$). Tukey's multiple comparison test showed significant differences between the means of M1 and M2 ($p = 0.0007$), M1 and M3 ($p < 0.0001$), as well as M1 and M4 ($p < 0.0001$) (Figure 3.3b).

For WFS sites, the temperature means varied between 17ºC (W3) - 19ºC (W4, W5) with SD between 4.6ºC (W4) - 7.7ºC (W1). A One-way ANOVA showed no significant difference between means ($p = 0.9499$) (Figure 3.3c). Bartlett's test showed no significant differences between SD's ($p = 0.4640$). For MR sites, the means varied between 17ºC (M2) - 20ºC (M1) with SD between 1.7ºC (M2) - 5.1ºC (M4). A One-way ANOVA showed no significant difference between means ($p = 0.4900$) (Figure 3.3d). Bartlett's test showed no significant differences between SD's ($p = 0.5676$).

For WFS sites, the conductivity means varied between 0.90 mS (W5) - 1.0 mS (W1) with SD between 0.086 mS (W3) - 0.38 mS (W1). A Kruskall-Wallis test showed that there was no significant difference between medians ($p = 0.3224$) (Figure 3.3e). For MR, means varied between 0.34 mS (M4) - 0.45 mS (M1, M2) with SD between 0.028 mS (M4) - 0.052 mS (M3). A One-way ANOVA showed that there were significant differences between means ($p < 0.0001$). Bartlett's test showed no significant differences between SD's ($p = 0.1712$). Tukey's multiple comparison test showed significant differences between the means of M1 and M4 ($p < 0.0001$), M2 and M4 ($p < 0.0001$), and M3 and M4 ($p < 0.0001$) (Figure 3.3f).

Dissolved oxygen means of WFS sites varied between 4.9 mg/l (W2) - 7.2 mg/l (W5) with SD between 1.4 mg/l (W3) - 2.4 mg/l (W1). A Kruskall-Wallis test showed that there was no significant difference between medians ($p = 0.937$) (Figure 3.3g). For MR, means varied between 3.9 mg/l (M3) - 7.2 mg/l (M2) with SD between 1.2 mg/l (M3) - 7.8 mg/l (M2). A Kruskall-Wallis test showed significant differences between medians ($p = 0.0032$). Dunn's

multiple comparison test showed a significant difference between the mean rank of M1 and M4 (p = 0.0015) (Figure 3.3h).

Dissolved inorganic nutrients:

Means of phosphorus for WFS sites varied between 2.1 mg/l (W1) - 14 mg/l (W2) with SD between 1.96 mg/l (W1) - 32 mg/l (W2). A Kruskall-Wallis test showed that there was no significant difference between medians (p = 0.1359) (Figure 3.4a). For MR, means varied between 13 mg/l (M3) - 21 mg/l (M4) with SD between 36 mg/l (M1 - M3) - 41 mg/l (M4). A Kruskall-Wallis test showed that there was no significant difference between medians (p = 0.9995) (Figure 3.4b).

Means of sulphate for WFS varied between 180 mg/l (W5) - 275 mg/l (W1) with SD between 78 mg/l (W4, W5) - 238 mg/l (W1). A Kruskall-Wallis test showed that there was no significant difference between medians (p = 0.9773) (Figure 3.4c). For MR, means varied between 18 mg/l (M2) - 82 mg/l (M3) with SD between 47 mg/l (M2) - 252 mg/l (M3). One value from MR was excluded as an outlier. A Kruskall-Wallis test showed that there was no significant difference between medians (p = 0.1141) (Figure 3.4d).

Means of nitrite for WFS varied between 0.0053 mg/l (W3) - 0.035 mg/l (W2) with SD between 0.0065 mg/l (W3) - 0.035 mg/l (W2). A Kruskall-Wallis test showed a significant difference between medians (p = 0.0352), however, a Dunn's multiple comparison test showed no significant difference between mean ranks (p > 0.05) (Figure 3.4e). For MR, means varied between 0.0053 mg/l (M1) - 0.016 mg/l (M2) with SD between 0.0046 mg/l (M1) - 0.038 mg/l (M2). A Kruskall-Wallis test showed no significant difference between medians (p = 0.8206) (Figure 3.4f).

Means of nitrate for WFS varied between 0.034 mg/l (W3) - 0.094 mg/l (W2), with SD between 0.038 mg/l (W4) - 0.10 mg/l (W5). A Kruskall-Wallis test showed no significant difference between medians (p = 0.1039) (Figure 3.5a). For MR, means varied between 0.015 mg/l (M2, M4) - 0.027 mg/l (M3), with SD between 0.0087 mg/l (M4) - 0.019 mg/l (M3). A Kruskall-Wallis test showed no significant difference between medians (p = 0.2793) (Figure 3.5b).

Means of ammonia for WFS varied between 0.0094 mg/l (W4) - 0.45 mg/l (W2), with SD between 0.010 mg/l (W4) - 0.58 mg/l (W2). A Kruskall-Wallis test showed a significant difference between medians (p = 0.0117). Dunn's multiple comparison test showed a significant difference between the mean rank of W2 and W4 (p = 0.0130) (Figure 3.5c). For MR, means varied between 0.014 mg/l (M2) - 0.044 mg/l (M1), with SD between 0.013 mg/l (M2, M3) - 0.069 mg/l (M1). Kruskall-Wallis test showed no significant difference between medians (p = 0.0541) (Figure 3.5d).

Means of dissolved inorganic nitrogen for WFS varied between 0.049 mg/l (W4) - 0.58 mg/l (W2), with SD between 0.038 mg/l (W4) - 0.65 mg/l (W2). A Kruskall-Wallis test showed a significant difference between medians ($p = 0.0448$). Dunn's multiple comparison test showed a significant difference between the mean rank of W2 and W4 ($p = 0.0209$) (Figure 3.5e). For MR, means varied between 0.044 mg/l (M2) - 0.066 mg/l (M1), with SD between 0.019 mg/l (M4) - 0.067 mg/l (M1). A Kruskall-Wallis test showed no significant difference between medians ($p = 0.3429$) (Figure 3.5f).

Table 3.2: Summary of water quality variables of the different sites of the Wonderfontein Spruit and Mooi River, and associated ANOVA/Kruskal-Wallis tests.

Variables		Min	Max	Mean	SD	Test	p value ≤ 0.05		Min	Max	Mean	SD	Test	p value ≤ 0.05
pH	**W1**	7.3	8.9	8.1	0.56	ANOVA	Yes	**M1**	7.8	8.5	8.1	0.20	ANOVA	Yes
	W2	7.0	8.9	7.7	0.52			**M2**	7.3	8.2	7.7	0.24		
	W3	7.1	9.4	7.7	0.79			**M3**	7.0	7.9	7.5	0.23		
	W4	7.1	8.2	7.6	0.34			**M4**	6.8	7.9	7.4	0.27		
	W5	7.5	8.1	8.2	0.39									
Temperature	**W1**	6.4	28	18	7.7	ANOVA	No	**M1**	12	26	20	4.9	ANOVA	No
	W2	10	24	18	4.8			**M2**	8.7	22	17	1.7		
	W3	9.1	23	17	5.0			**M3**	9.1	23	18	4.0		
	W4	9.8	23	19	4.6			**M4**	9.1	24	18	5.1		
	W5	10	24	19	5.0									
Dissolved Oxygen	**W1**	2.3	9.8	5.8	2.4	Kruskal-Wallis	No	**M1**	4.1	20	6.9	4.3	Kruskal-Wallis	Yes
	W2	2.6	10	4.9	2.2			**M2**	2.3	26	7.2	7.8		
	W3	2.8	7.1	5.1	1.4			**M3**	2.2	6.2	3.9	1.2		
	W4	3.0	9.4	5.4	2.1			**M4**	1.6	17	4.0	4.4		
	W5	3.4	10	7.2	2.1									
Conductivity	**W1**	0.73	2.0	1.0	0.38	Kruskal-Wallis	No	**M1**	0.39	0.50	0.45	0.033	ANOVA	Yes
	W2	0.66	1.1	0.93	0.11			**M2**	0.40	0.49	0.45	0.031		
	W3	0.73	1.0	0.91	0.086			**M3**	0.35	0.50	0.44	0.052		
	W4	0.85	1.1	0.97	0.090			**M4**	0.30	0.38	0.34	0.028		
	W5	0.74	1.1	0.90	0.10									

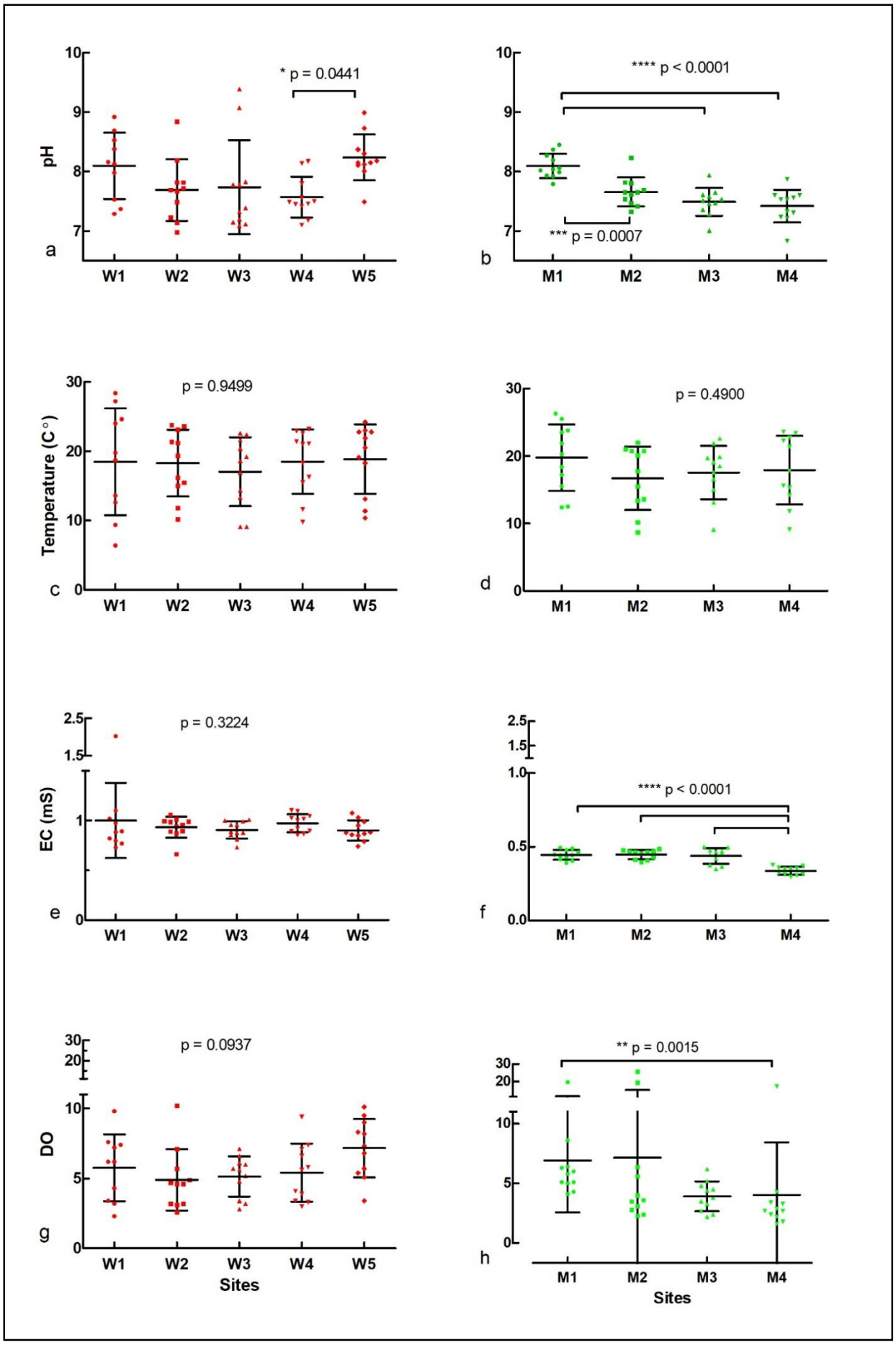

Figure 3.3: ANOVA/Kruskall-Wallis tests of water quality variables of the different sites of Wonderfontein Spruit and Mooi River (a and b - pH, c and d - temperature, e and f - conductivity, g and h - dissolved oxygen).

Table 3.3: Summary of dissolved inorganic nutrients of the different sites of the Wonderfontein Spruit and Mooi River, and associated ANOVA/Kruskal-Wallis tests.

Nutrients		Min	Max	Mean	SD	Test	p value ≤ 0.05		Min	Max	Mean	SD	Test	p value ≤ 0.05
Phosphorus	**W1**	0.17	5.4	2.1	1.96	Kruskal-Wallis	No	**M1**	0.09	114	17	36	Kruskal-Wallis	No
	W2	1.6	110	14	32			**M2**	0.10	103	17	36		
	W3	0.33	96	12	28			**M3**	0.12	122	13	36		
	W4	1.2	61	8.4	18			**M4**	0.13	131	21	41		
	W5	0.95	9.8	3.1	2.5									
Sulphate	**W1**	115	860	275	238	Kruskal-Wallis	No	**M1**	1.00	270	33	81	Kruskal-Wallis	No
	W2	100	420	217	118			**M2**	0.50	150	18	47		
	W3	104	620	246	167			**M3**	0.50	840	82	252		
	W4	116	300	196	78			**M4**	1.50	450	46	134		
	W5	103	305	180	78									
Nitrite	**W1**	0.001	0.052	0.009	0.016	Kruskal-Wallis	Yes	**M1**	0.001	0.017	0.0053	0.0046	Kruskal-Wallis	No
	W2	0.002	0.092	0.035	0.035			**M2**	0.0005	0.13	0.016	0.038		
	W3	0.0005	0.018	0.0053	0.0065			**M3**	0.0005	0.037	0.0068	0.011		
	W4	0.001	0.025	0.0054	0.0071			**M4**	0.002	0.018	0.0059	0.0049		
	W5	0.001	0.035	0.0095	0.0093									
Nitrate	**W1**	0.01	0.12	0.039	0.039	Kruskal-Wallis	No	**M1**	0.01	0.05	0.016	0.012	Kruskal-Wallis	No
	W2	0.01	0.22	0.094	0.071			**M2**	0.01	0.04	0.015	0.0093		
	W3	0.005	0.40	0.034	0.039			**M3**	0.005	0.06	0.027	0.019		
	W4	0.01	0.13	0.035	0.038			**M4**	0.005	0.03	0.015	0.0087		
	W5	0.005	0.29	0.080	0.10									
Ammonia	**W1**	0.005	1.4	0.20	0.43	Kruskal-Wallis	Yes	**M1**	0.01	0.25	0.044	0.069	Kruskal-Wallis	No
	W2	0.005	1.5	0.45	0.58			**M2**	0.005	0.05	0.014	0.013		
	W3	0.005	0.33	0.074	0.11			**M3**	0.005	0.05	0.018	0.013		
	W4	0.005	0.04	0.0094	0.010			**M4**	0.005	0.05	0.024	0.016		
	W5	0.005	0.07	0.032	0.027									

Dissolved Inorganic Nitrogen	**W1**	0.018	1.6	0.25	0.47	Kruskal-Wallis	Yes	**M1**	0.023	0.26	0.066	0.067	Kruskal-Wallis	No
	W2	0.019	1.8	0.58	0.65			**M2**	0.018	0.16	0.044	0.043		
	W3	0.021	0.35	0.11	0.11			**M3**	0.016	0.13	0.051	0.033		
	W4	0.017	0.15	0.049	0.038			**M4**	0.013	0.047	0.045	0.019		
	W5	0.022	0.33	0.12	0.11									

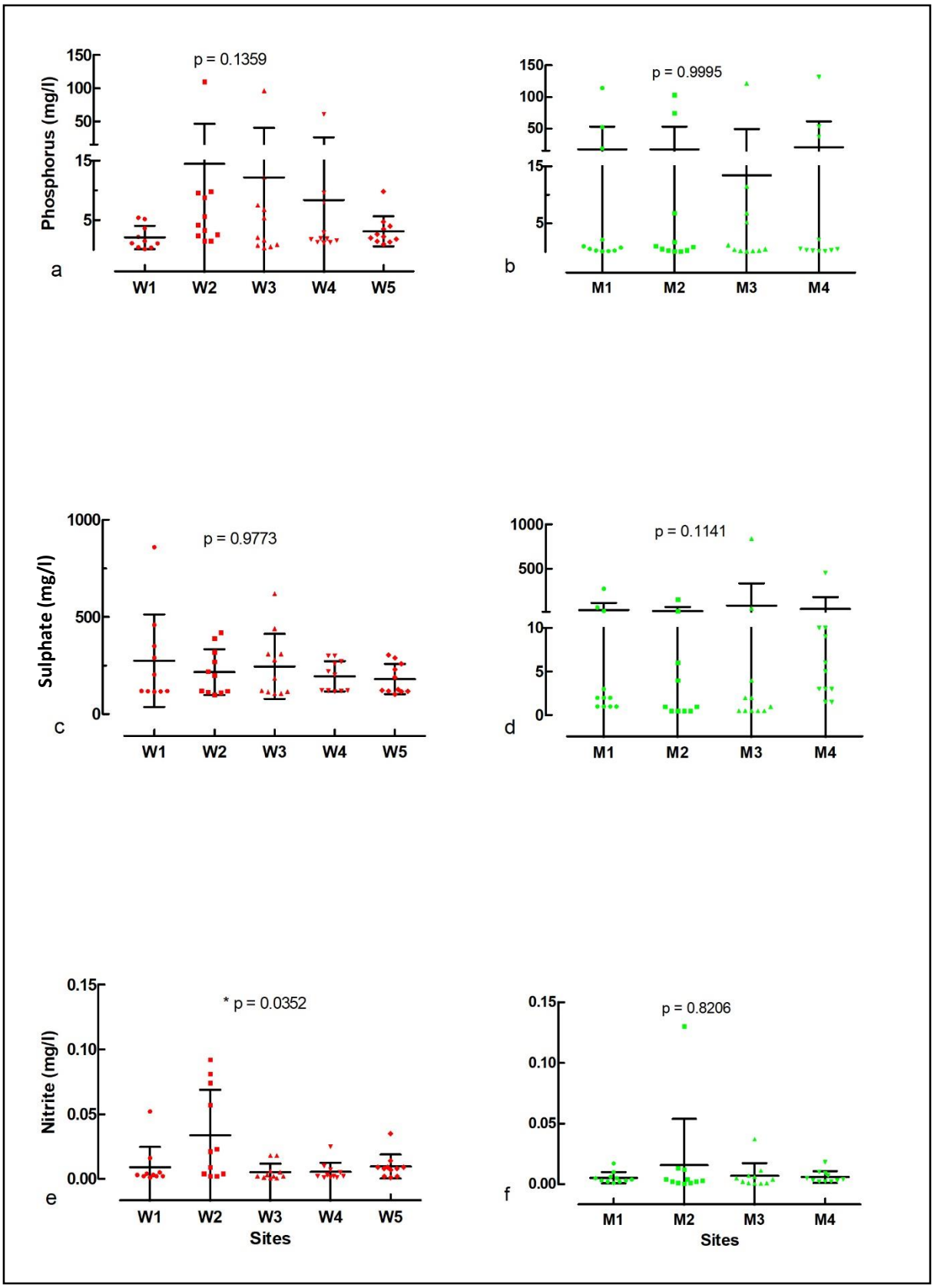

Figure 3.4: ANOVA/Kruskall-Wallis tests of dissolved inorganic nutrients of the different sites of the Wonderfontein Spruit and Mooi River (a and b - phosphorus, c and d - sulphate, e and f - nitrite).

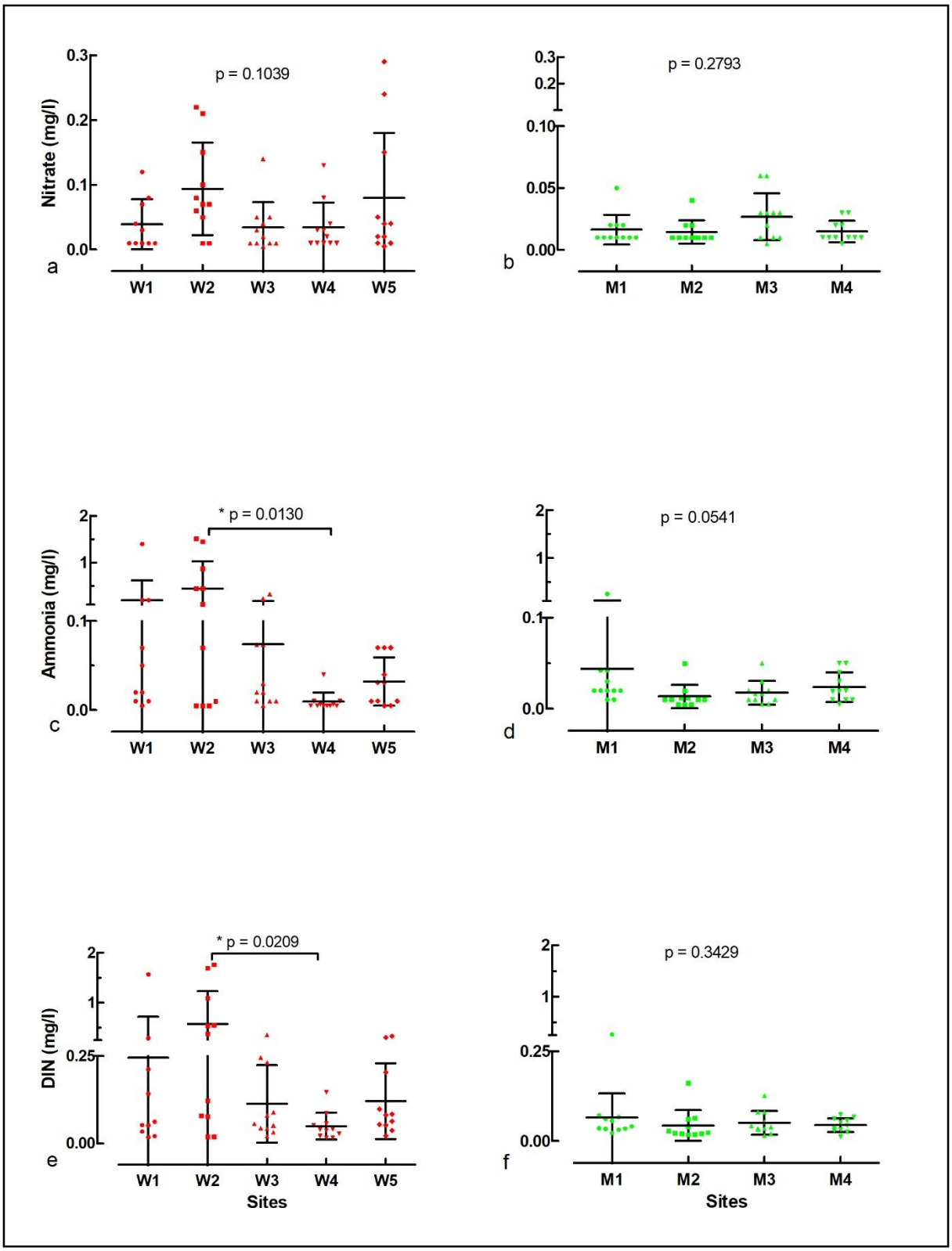

Figure 3.5: ANOVA/Kruskall-Wallis tests of dissolved inorganic nutrients of the different Wonderfontein Spruit and Mooi River sites (a and b - nitrate, c and d - ammonia, e and f - dissolved inorganic nitrogen).

3.1.3 Additional variables

Additional variables measured include surface area of the water of each site, edge (length of vegetation in contact with water), edge-surface area ratio, mean water depth, as well as the water volume of each site. T-tests and Mann-Whitney tests were performed to compare WFS and MR with regard to the abovementioned variables.

Surface area of water bodies of WFS sites varied between 6 245 m^2 - 65 364 m^2, with a mean of 25 985 m^2. Surface area of water bodies of MR sites varied between 2 396 m^2 - 12 554 m^2, with a mean of 7 898 m^2. A Mann-Whitney test showed no significant difference between medians ($p = 0.2857$) (Figure 3.6a).

Edge of WFS sites varied between 663 m - 1 500 m, with a mean of 1 043 m. Edge of MR sites varied between 302 m - 803 m, with a mean of 619 m. A Mann-Whitney test showed no significant difference between medians ($p = 0.0635$) (Figure 3.6b).

The edge to surface area ratio of WFS sites varied between 0.019 - 0.11, with a mean of 0.063. The edge to surface area ratio of MR varied between 0.065 - 0.13, with a mean of 0.09. A Mann-Whitney test showed no significant difference between medians ($p = 0.2857$) (Figure 3.6c).

Mean water depths of WFS sites varied between 11 cm - 207 cm, with a mean of 73 cm, while that of MR sites varied between 194 cm - 332 cm, with a mean of 258 cm. A Mann-Whitney test showed that the median of MR was significantly deeper than that of WFS ($p = 0.0317$) (Figure 3.6d).

Water volume of WFS sites varied between 687 m^3 - 135 303 m^3, with a mean of 33 656 m^3. Water volume of MR sites varied between 6 877 m^3 - 41 679 m^3, with a mean of 20 296 m^3. One value from WFS was excluded due to being an outlier. A Mann-Whitney test showed no significant difference between medians ($p = 0.2000$) (Figure 3.6e).

Table 2.4: Additional variables of the Wonderfontein Spruit and Mooi River sites.

	Additional variables measured										
	Area (m2)	**Edge (m)**	**E/A**	**Depth (cm)**	**Volume**		**Area (m2)**	**Edge (m)**	**E/A**	**Depth (cm)**	**Volume**
W1	6 245	663	0.11	11	687	**M1**	12 554	883	0.070	332	41 679
W2	30 351	1 500	0.049	74	22 460	**M2**	9 789	638	0.065	220	19 336
W3	19 015	1 145	0.060	31	5 895	**M3**	6 853	654	0.095	194	13 295
W4	65 364	1 217	0.019	207	135 303	**M4**	2 396	302	0.13	287	6 877
W5	8 948	691	0.077	44	3 937						

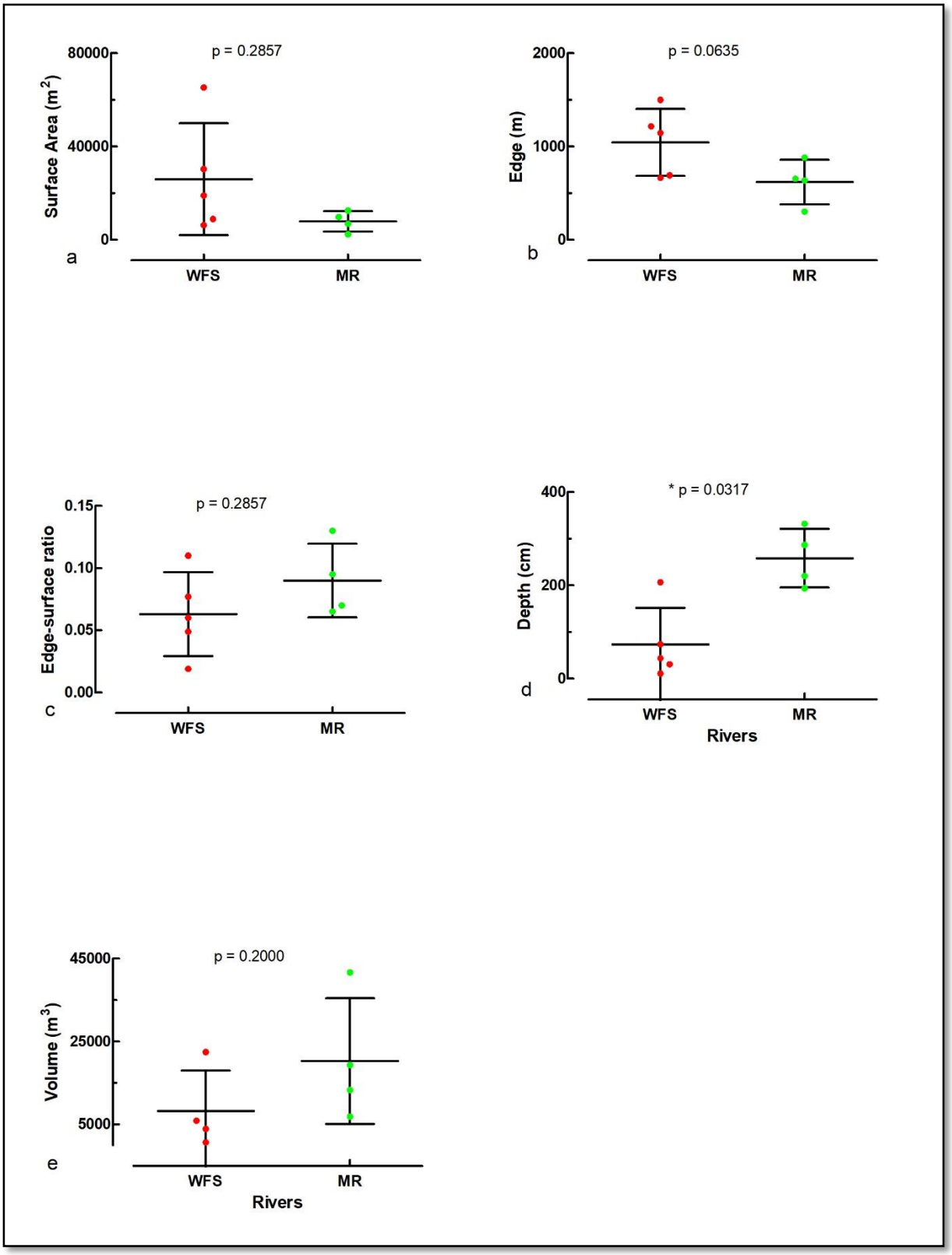

Figure 3.6: T-tests and Mann-Whitney tests of additional site variables of the Wonderfontein Spruit and Mooi River (a - surface area, b - edge, c - edge to surface ratio, d - water depth, e - water volume).

3.2 ALGAE

3.2.1 Species accumulation curve:

Species-area curves can be used to evaluate the adequacy of sample size in community data sets (McCune & Grace, 2002). The idea behind the use of a species-area curve, also called 'species-effort curve' or 'species-accumulation curve' is that the number of observed species increases with an increase in sample area, but only up to a certain point (Peck, 2010). The species-accumulation curve will flatten out as it approaches an asymptote, and additional surveys will yield relatively small increases in the number of species (McCune & Grace, 2002). The observed species richness is normally less than the true species richness of an area. Correction factors can then be applied to estimate the true species richness of an area. Two such correction factors include 'jackknife estimates' and 'Chao-2 estimator'. These nonparametric resampling procedures adjust the richness estimate based on different ratios of the number of species that occur only once and/or twice in the matrix relative to the sample size. These estimators are useful to improve accuracy in datasets with numerous rare species (Peck, 2010).

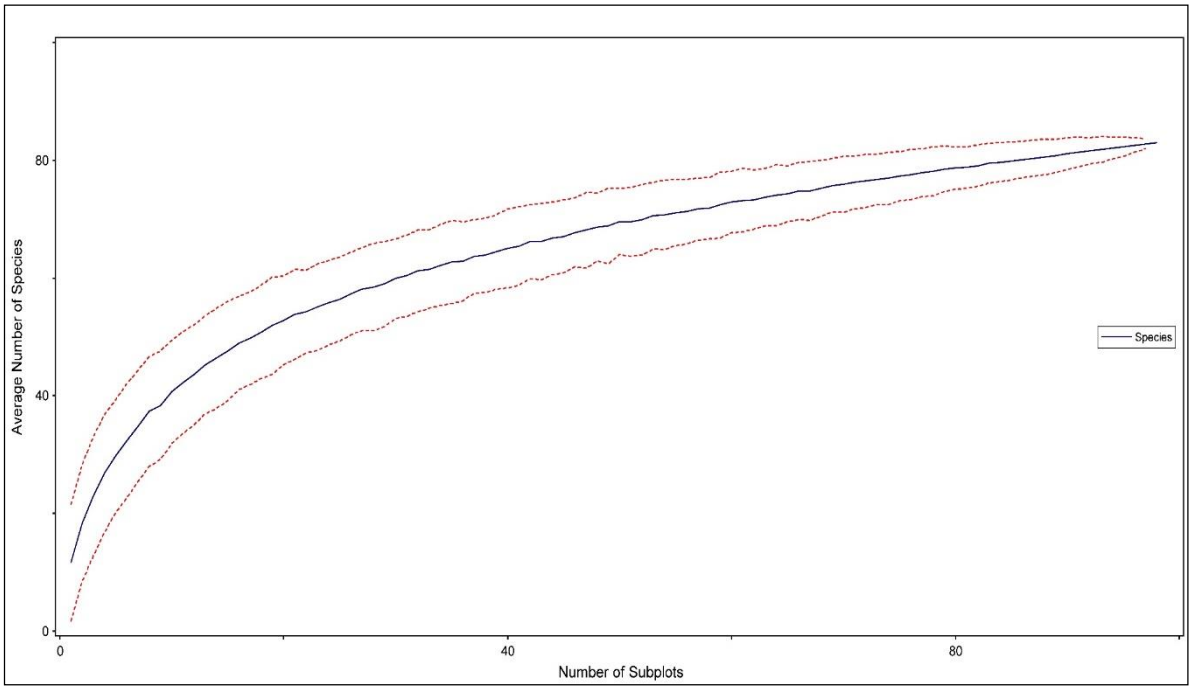

Figure 3.7: Species-accumulation curve of all algal genera recorded along the Wonderfontein Spruit and Mooi River in 98 samples (surveys). The dotted lines are confidence bands and represent 95% confidence intervals.

Although the species-accumulation curve for algae flattens considerably after 30 subplots (± 60 genera), it does not flatten out completely (Observed genera richness = 83; Number of subplots = 98). This however, is a consequence of the high number of genera with only one or two occurrences, rather than an inadequate sampling size (number of genera with only one occurrence = 22; number of genera with only two occurrences = 9).

3.2.2 Richness, abundance and diversity

I recorded 189 507 cells consisting of 83 genera from the Mooi River and Wonderfontein Spruit. The genus richness of MR sites varied between 30 (M4) - 39 (M1) with a mean of 34, while abundances varied between 4 586 cells/ml (M2) - 14 572 cells/ml (M1) with a mean of 9 135 cells/ml. The genus richness of WFS sites varied between 39 (W4) - 49 (W1) with a mean of 43, while abundances varied between 9 215 cells/ml (W2) - 44 212 cells/ml (W5) with a mean of 30 594 cells/ml. Shannon index values of MR sites varied between 1.4 (M3, M4) - 2.0 (M2) with a mean of 1.7, and that of WFS between 2.1 (W4) - 2.7 (W3) with a mean of 2.4 (Table 3.5).

T-tests and Mann-Whitney tests were performed to compare WFS and MR in terms of genus richness, abundance, and Shannon index value per survey, and showed significant differences between rivers for all of them.

Genus richness for WFS varied between 3 - 26 with a mean and SD of 13.5 ± 5.2, while that of MR varied between 3 - 17 with a mean and SD of 9.3 ± 3.6. An unpaired t-test showed that the mean of WFS was significantly higher than that of MR ($p < 0.0001$) (Figure 3.8a).

Abundance for WFS varied between 17 cells/ml - 12 504 cells/ml with a mean and SD of 2 833 ± 2 791, while that of MR varied between 14 cells/ml - 8 295 cells/ml with a mean and SD of 831 ± 1 442. A Mann-Whitney test showed that the median for WFS was significantly higher than that of MR ($p < 0.0001$) (Figure 3.8b).

Shannon index values of WFS varied between 0.14 - 2.5 with a mean and SD of 1.6 ± 0.54, while that of MR varied between 0.23 - 2.1 with a mean and SD of 1.3 ± 0.51. An unpaired t-test showed that the mean of WFS was significantly higher than that of MR ($p = 0.0271$) (Figure 3.8c).

Table 3.5: All algal genera and their accumulative abundance (cells/ml), including richness, Shannon index values, and their classification, per site.

Genus	Abbreviated name	Class	MR				WFS				
			1	2	3	4	1	2	3	4	5
Anabaena	Anab	Cyanobacteria	620	143	0	0	810	0	0	2 464	0
Aphanocapsa	Acaps	Cyanobacteria	7 376	0	0	0	0	0	0	0	0
Aphanothece	Atec	Cyanobacteria	0	0	0	29	0	0	0	0	0
Cylindrospermopsis	Cyli	Cyanobacteria	0	24	0	0	0	0	0	358	0
Gleocapsa	Gcaps	Cyanobacteria	0	0	0	19	0	0	0	0	0
Komvophoron	Komv	Cyanobacteria	0	0	48	0	191	0	262	0	0
Merismopedia	Meris	Cyanobacteria	133	19	153	0	19	133	1 392	0	0
Oscillatoria	Oscl	Cyanobacteria	1 335	0	334	2 812	1 096	1 096	2 145	13 149	2 383
Phormidium	Phorm	Cyanobacteria	1 954	2 383	6 078	4 791	7 817	2 836	8 413	5 603	15 063
Spirulina	Spirl	Cyanobacteria	33	0	0	0	0	67	0	0	0
Synechococcus	Synccs	Cyanobacteria	5	0	0	14	0	0	0	0	0
Achnanthes	Achns	Bacillariophyceae	0	0	0	5	83	14	10	0	48
Amphora	Amph	Bacillariophyceae	0	0	2	0	48	36	0	26	138
Amphipleura	Ampl	Bacillariophyceae	0	0	0	0	0	0	7	0	0
Achnanthidium	Achnd	Bacillariophyceae	0	0	0	0	0	0	0	0	10
Aulacoseira	Aulcs	Bacillariophyceae	0	0	0	0	1 132	5	5	229	131
Cocconeis	Ccneis	Bacillariophyceae	12	10	0	14	43	48	5	5	14
Craticula	Crat	Bacillariophyceae	0	0	0	0	83	24	21	24	250
Cyclotella	Cyclt	Bacillariophyceae	12	2	0	17	31	303	1 566	38	238
Cymatopleura	Cympl	Bacillariophyceae	0	0	0	0	0	0	0	0	36
Cymbella	Cymb	Bacillariophyceae	2	0	5	5	24	10	0	45	136
Diadesmis	Dides	Bacillariophyceae	269	19	0	0	0	0	0	262	358
Diatoma	Dtm	Bacillariophyceae	21	0	0	0	0	0	0	0	0
Diploneis	Dplneis	Bacillariophyceae	0	2	0	0	0	0	0	0	0
Epithemia	Epth	Bacillariophyceae	0	0	0	21	0	0	0	0	0

Eunotia	Eunt	Bacillariophyceae	0	0	19	0	0	0	0	10	0
Frustulia	Frust	Bacillariophyceae	0	0	0	0	0	0	0	0	19
Gomphonema	Gmph	Bacillariophyceae	0	0	14	72	2	12	21	0	188
Gyrosigma	Gyro	Bacillariophyceae	0	0	0	0	12	19	231	0	0
Hantzschia	Hantz	Bacillariophyceae	0	14	0	0	0	0	0	0	0
Melosira	Melo	Bacillariophyceae	0	0	0	0	60	12	0	0	1 680
Navicula	Nav	Bacillariophyceae	67	29	88	74	665	131	141	157	1 749
Nitzschia	Nitz	Bacillariophyceae	83	293	126	64	4 381	763	2 190	1 625	3 060
Pinnularia	Pinnu	Bacillariophyceae	0	5	0	2	12	0	0	0	48
Placoneis	Plneis	Bacillariophyceae	0	0	0	0	14	0	5	0	0
Pleurosigma	Plsig	Bacillariophyceae	0	0	0	0	2	0	0	0	0
Rhopalodia	Rhopa	Bacillariophyceae	0	2	0	26	0	0	0	0	0
Surirella	Suri	Bacillariophyceae	0	0	0	0	0	0	0	12	0
Synedra	Synd	Bacillariophyceae	12	41	14	64	72	10	52	207	398
Actinastrum	Actstrum	Chlorophyceae	0	0	0	0	19	114	419	38	76
Actinotaenium	Actnium	Chlorophyceae	0	0	0	2	0	0	0	0	0
Ankistrodesmus	Anks	Chlorophyceae	36	14	14	0	0	19	0	882	0
Characium	Chrcm	Chlorophyceae	0	0	0	0	38	0	0	0	0
Chlamydomonas	Chlamy	Chlorophyceae	107	529	126	72	3 754	472	553	3 582	977
Chlorella	Chlrla	Chlorophyceae	19	48	0	0	0	29	3 218	107	0
Chlorococcum	Chlccm	Chlorophyceae	5	12	19	17	107	52	331	31	12
Closterium	Clst	Chlorophyceae	2	0	26	5	21	24	114	38	12
Coelastrum	Coels	Chlorophyceae	0	76	410	0	629	305	858	343	95
Cosmarium	Cosm	Chlorophyceae	10	0	2	10	67	12	41	0	10
Crucigenia	Crgn	Chlorophyceae	0	0	0	0	0	0	124	0	0
Desmodesmus	Dsmd	Chlorophyceae	0	0	0	0	19	0	0	0	0
Dictyosphaerium	Dictyo	Chlorophyceae	591	91	95	0	162	105	1 420	191	191
Euastrum	Eustr	Chlorophyceae	2	0	0	0	0	0	0	0	0
Gonatozygon	Gzyg	Chlorophyceae	0	21	0	0	10	0	0	12	0
Kirchneriella	Kirch	Chlorophyceae	19	38	0	0	0	0	0	0	0

Koliella	Koli	Chlorophyceae	0	0	0	0	0	24	95	14	10
Mesotaenium	Meso	Chlorophyceae	0	0	0	0	0	2	0	0	0
Microspora	Micr	Chlorophyceae	0	0	0	0	36	7	0	0	0
Monoraphidium	Mrphd	Chlorophyceae	229	145	79	167	582	181	481	284	2 360
Mougeotia	Moug	Chlorophyceae	5	5	0	0	205	0	0	453	0
Oedogonium	Oedog	Chlorophyceae	0	5	0	0	76	0	0	334	0
Oocystis	Oocys	Chlorophyceae	43	57	98	31	319	133	937	41	21
Pandorina	Pand	Chlorophyceae	0	0	114	76	5 987	0	3 851	0	0
Pediastrum	Pedi	Chlorophyceae	0	10	76	76	534	153	38	191	191
Penium	Pen	Chlorophyceae	0	0	0	0	0	0	0	0	5
Pleurococcus	Plccus	Chlorophyceae	19	0	0	0	0	0	0	0	0
Scenedesmus	Scndsm	Chlorophyceae	825	224	124	76	1 425	758	1 363	267	410
Sphaerocystis	Sphaero	Chlorophyceae	38	0	0	0	0	0	0	0	0
Spirogyra	Spirg	Chlorophyceae	0	0	29	0	191	29	133	10	124
Staurastrum	Staurst	Chlorophyceae	0	0	2	0	5	0	7	0	0
Tetmemorus	Tmrus	Chlorophyceae	0	0	0	0	0	2	0	0	0
Tetrachlorella	Tchlor	Chlorophyceae	0	0	0	0	0	0	48	0	0
Tetraedron	Tedro	Chlorophyceae	0	0	0	0	7	5	10	0	0
Tetrastrum	Tastr	Chlorophyceae	543	0	5	0	0	0	0	0	0
Treubaria	Treub	Chlorophyceae	0	2	0	0	2	0	0	0	0
Ulothrix	Uthrix	Chlorophyceae	14	131	50	150	2 841	88	52	279	11 230
Cryptomonas	Crypt	Cryptophyceae	10	12	33	0	2	19	489	83	12
Dinobryon	Dbry	Chrysophyceae	17	0	0	0	0	0	0	0	0
Peridinium	Peri	Dinophyceae	2	10	0	0	0	33	136	551	48
Euglena	Eugl	Euglenophyceae	5	29	41	33	145	551	729	64	1 897
Phacus	Phcs	Euglenophyceae	21	5	52	38	29	150	617	81	155
Strombomonas	Stromb	Euglenophyceae	2	0	0	0	12	7	19	0	36
Trachelomonas	Trach	Euglenophyceae	74	136	174	148	276	422	665	141	393
		Abundance (cells/ml)	**14 572**	**4 586**	**8 450**	**8 930**	**34 097**	**9 215**	**33 214**	**32 231**	**44 212**
		Genus Richness	**39**	**35**	**31**	**30**	**49**	**43**	**42**	**39**	**40**

Shannon value	**1.8**	**2.0**	**1.4**	**1.4**	**2.5**	**2.6**	**2.7**	**2.1**	**2.2**

Table 3.6: Summary of genus richness, abundance, and Shannon index values of the two rivers, and associated tests.

	WFS				**MR**					
Algae	**Min**	**Max**	**Mean**	**SD**	**Min**	**Max**	**Mean**	**SD**	**Test**	**p value ≤ 0.05**
Richness	3	26	13.5	5.2	3	17	9.3	3.6	Unpaired t test (Two-tailed)	Yes
Abundance	17	12 504	2 833	2 791	14	8 295	831	1 442	Mann-Whitney test (Two-tailed)	Yes
Shannon	0.14	2.5	1.6	0.54	0.23	2.1	1.3	0.51	Unpaired t test (Two-tailed)	Yes

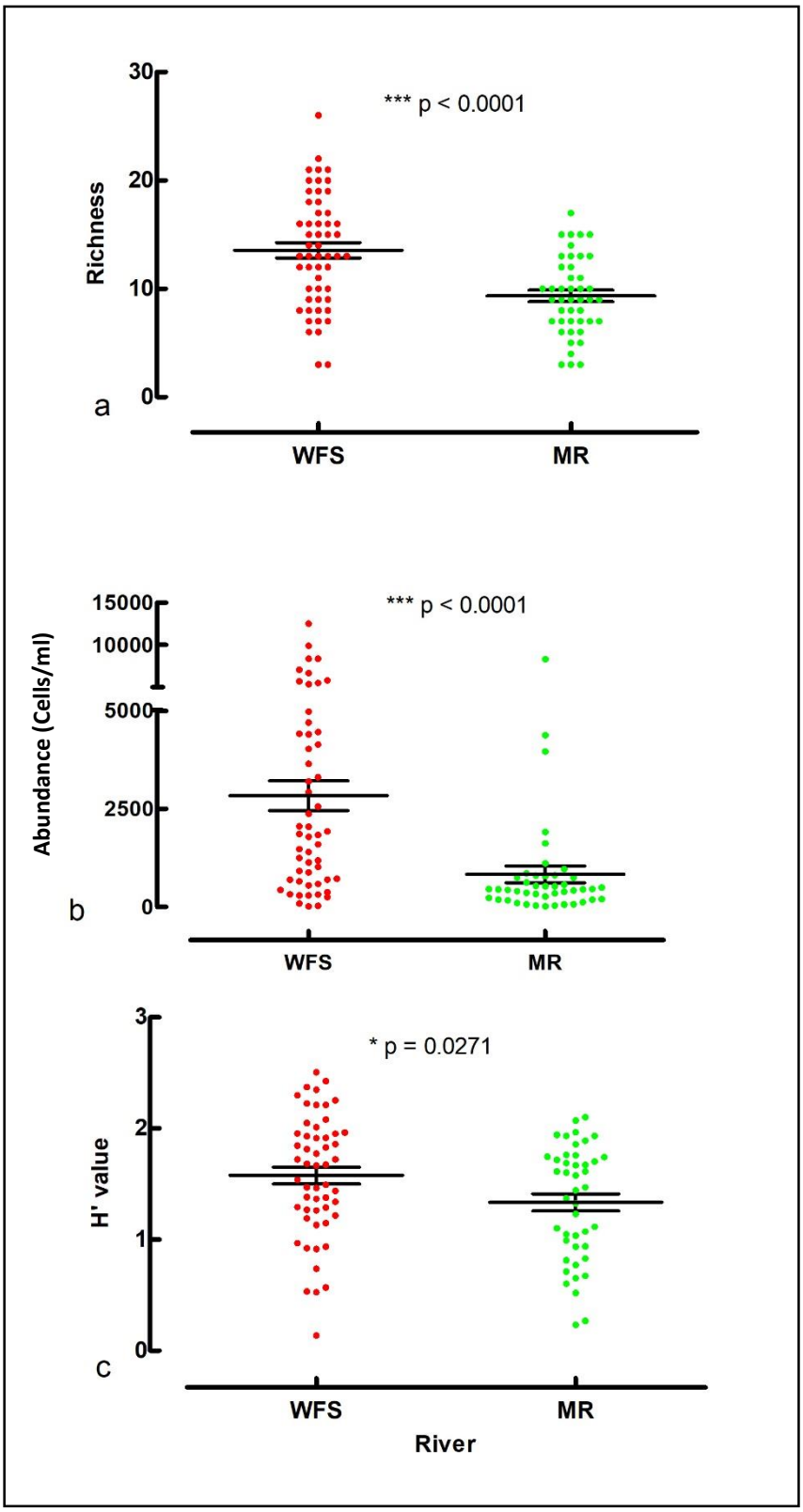

Figure 3.8: T-tests and Mann-Whitney tests of richness (a), abundance (b), and Shannon index value (c) of algae from Wonderfontein Spruit and Mooi River.

One-way Analysis of Variance (One-way ANOVA) tests were performed to determine the differences in genus richness, abundance and Shannon index values between rivers. Genus richness and abundance per survey were used to determine Shannon index values per survey. All survey values per site were then used to determine the mean and variance of each site and then compared to the means of other sites from the same river (Table 3.7)

Means of genus richness for WFS varied between 11 (W4) - 15 (W3), with SD between 3.4 (W2) - 6.4 (W1). A Kruskall-Wallis test showed no significant difference between medians ($p = 0.2108$) (Figure 3.9a). For MR, means varied between 8.7 (M2 - M4) - 11 (M1), with a SD between 2.6 (M4) - 4.3 (M3). A One-way ANOVA showed no significant differences between means ($p = 0.3095$) (Figure 3.9b). Bartlett's test for equal variance showed no significant differences ($p = 0.3780$).

Means of abundance for WFS varied between 383 cells/ml (W2) - 4 020 cells/ml (W5), with SD between 348 (W3) - 3 467 (W4). A Kruskall-Wallis test showed a significant difference between medians ($p = 0.0265$). Dunn's multiple comparison test showed a significant difference between the mean rank of W2 and W5 ($p < 0.05$) (Figure 3.9c). For MR, means varied between 417 cells/ml (M2) - 1 325 cells/ml (M1), with SD between 220 (M2) - 2 355 (M1). A Kruskall-Wallis test showed no significant difference between medians ($p = 0.5902$) (Figure 3.9d).

Means of Shannon index value for WFS varied between 1.2 (W4) - 1.9 (W2), with SD between 0.34 (W2) - 0.59 (W1). A One-way ANOVA showed a significant difference between means ($p = 0.0080$). Bartlett's test for equal variance showed no significant differences ($p = 0.4135$). Tukey's multiple comparison test showed a significant difference between the means of W2 and W4 ($p < 0.05$), and W3 and W4 ($p < 0.05$). The mean of W4 was significantly lower than that of W2 and W3 (Figure 3.9e). The means off Shannon index value for MR varied between 1.2 (M2) - 1.5 (M1), with SD between 0.46 (M4) - 0.58 (M3). A One-way ANOVA showed no significant differences between means ($p = 0.5168$). Bartlett's test for equal variance showed no significant differences ($p = 0.9001$) (Figure 3.9f).

Table 3.7: Summary of genus richness, abundance, and Shannon index values of algae of the different Wonderfontein Spruit and Mooi River sites, as well as associated ANOVA/Kruskal-Wallis tests.

Algae		Min	Max	Mean	SD	Test	p value ≤ 0.05		Min	Max	Mean	SD	Test	p value ≤ 0.05
Richness	**W1**	3	12	14	6.4	Kruskall-Wallis	No	**M1**	7	15	11	3.0	ANOVA	No
	W2	8	18	14	3.4			**M2**	3	17	8.7	4.0		
	W3	3	21	15	5.4			**M3**	3	15	8.7	4.3		
	W4	6	26	11	6.0			**M4**	3	14	8.7	2.6		
	W5	8	21	13	4.3									
Abundance	**W1**	296	5 804	3 410	1 977	Kruskall-Wallis	Yes	**M1**	38	8 295	1 325	2 355	Kruskall-Wallis	No
	W2	32	2 057	838	618			**M2**	193	968	417	220		
	W3	17	9 904	3 020	348			**M3**	14	4 375	769	1 233		
	W4	590	12 504	2 931	3 467			**M4**	63	3 961	812	1 171		
	W5	88	8 369	4 020	2 638									
Shannon	**W1**	0.14	2.3	1.4	0.59	ANOVA	Yes	**M1**	0.52	2.1	1.5	0.49	ANOVA	No
	W2	1.2	2.4	1.9	0.34			**M2**	0.23	2.1	1.2	0.53		
	W3	0.92	2.5	1.8	0.58			**M3**	0.27	1.9	1.3	0.58		
	W4	0.53	2.0	1.2	0.51			**M4**	0.60	2.0	1.3	0.46		
	W5	0.74	2.0	1.5	0.41									

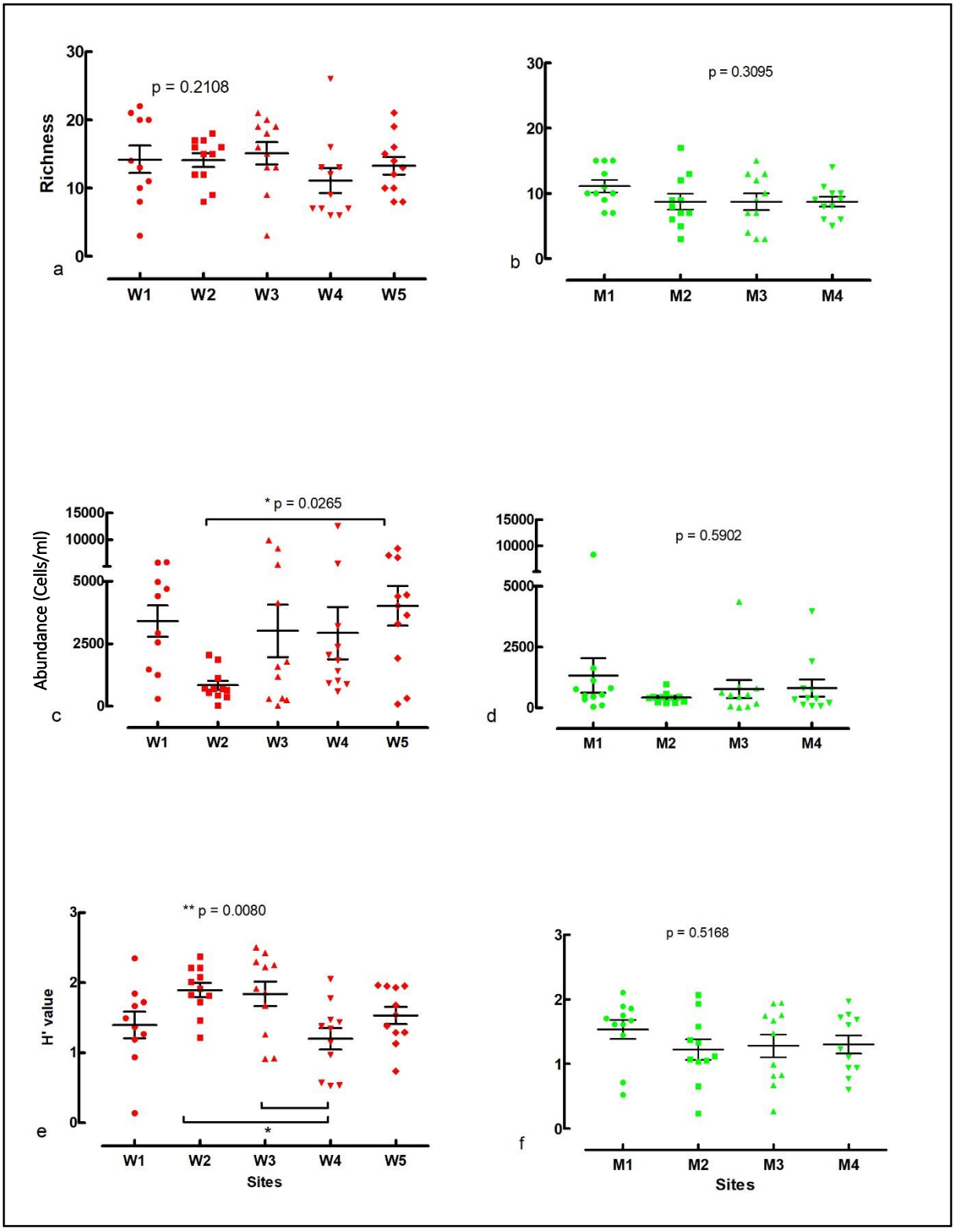

Figure 3.9: ANOVA/Kruskal-Wallis tests of genus richness (a and b), abundance (c and d), and Shannon index values (e and f) of the different sites of Wonderfontein Spruit and Mooi River.

All algal genera recorded from Wonderfontein Spruit and Mooi River belong to seven classes, namely Bacillariophyceae, Chlorophyceae, Chrysophyceae, Cryptophyceae, cyanobacteria, Dinophyceae, and Euglenophyceae. Abundances of each class for every site are shown in Table 3.8. The percentage composition that each class made up of the total was calculated for both rivers. The mean percentage of the two rivers was then determined. T-tests were performed for classes that contributed a mean of more than 5 percent of the total. Cyanobacteria (60%), Chlorophyceae (27%), and Bacillariophyceae (9.6%) met this criterion with a cumulative contribution of 96.6% of all algae recorded from Wonderfontein Spruit and Mooi River.

Abundance of Bacillariophyceae for WFS varied between 1 385 cells/ml - 8 501 cells/ml with a mean and SD of 4 689 ± 2 904, while that of MR varied between 269 cells/ml – 479 cells/ml, with a mean and SD of 383 ± 89. An unpaired t-test (unequal variances) showed that the mean of WFS was significantly higher than that of MR ($p = 0.0294$) (Figure 3.10a).

Abundance of Chlorophyceae for WFS varied between 2 514 cells/ml - 17 036 cells/ml with a mean and SD of 11 293 ± 6 228, while that of MR varied between 682 cells/ml - 2 507 cells/ml with a mean and SD of 1 467 ± 762. An unpaired t-test (unequal variances) showed that the mean of WFS was significantly higher than that of MR ($p = 0.0236$) (Figure 3.10b).

Abundance of cyanobacteria for WFS varied between 4 133 cells/ml - 21 574 cells/ml with a mean and SD of 13 060 ± 6 744, while that of MR varied between 2 569 cells/ml - 11 457 cells/ml with a mean and SD of 7 076 ± 3 655. An unpaired t-test (unequal variances) showed no significant difference between means ($p = 0.1380$) (Figure 3.10c).

Abundance of WFS had a significantly higher mean than that of MR ($p < 0.0001$) (Figure 3.8b). It is thus not surprising that the abundances of MR classes were not comparable to that of WFS ($p < 0.05$). The abundance of cyanobacteria for MR however, was comparable to that of WFS ($p = 0.1380$). Consequently, MR sites comprises of a much greater proportion of cyanobacteria than other classes (Figure 3.11). WFS sites had a much higher composition of Bacillariophyceae (8% - 20%) and Chlorophyceae (22% - 50%), compared to that of MR (3% - 9%) and (8% - 31%). MR sites however, had much higher cyanobacteria composition (56% - 86%) compared with WFS sites (29% - 67%).

Table 3.8: Algal abundance (expressed in cells/ml) in each class per site, and percentage composition of each class to the total abundance, for both Wonderfontein Spruit and Mooi River.

	Cyanobacteria	Bacillariophyceae	Chlorophyceae	Cryptophyceae	Chrysophyceae	Dinophyceae	Euglenophyceae
W1	9 934	6 664	17 036	2	0	0	462
W2	4 133	1 385	2 514	19	0	33	1 130
W3	12 212	4 254	14 095	489	0	136	2 031
W4	21 574	2 641	7 095	83	0	551	286
W5	17 446	8 501	15 723	12	0	48	2 481
%	42	15	37	0.4	0	0.50	4.2
M1	11 457	479	2 507	10	17	2	102
M2	2 569	417	1 409	12	0	10	169
M3	6 611	269	1 270	33	0	0	267
M4	7 665	365	682	0	0	0	219
%	77	4.2	16	0.15	0.05	0.03	2.1
Mean %	**60**	**9.6**	**27**	**0.28**	**0.025**	**0.27**	**3.2**

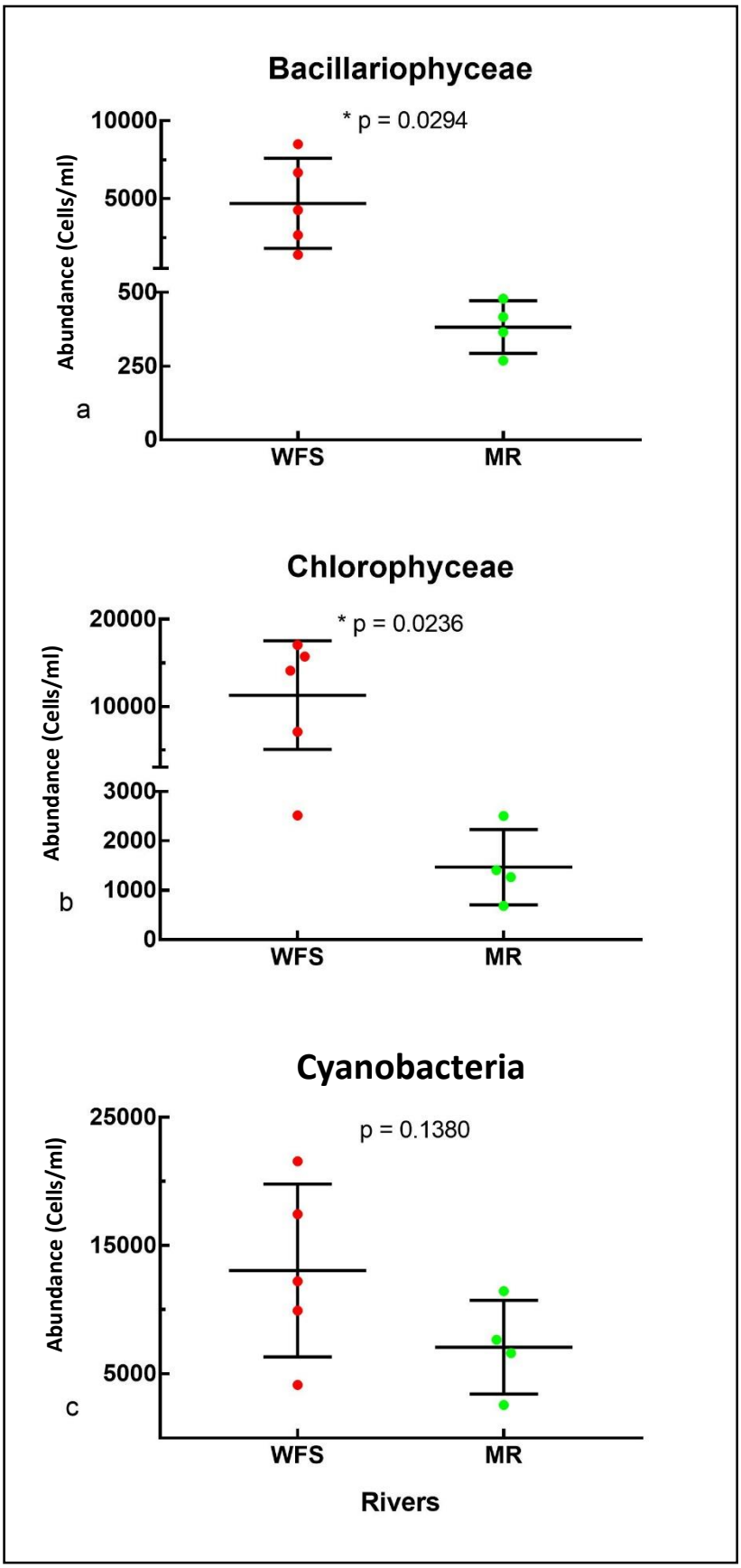

Figure 3.10: T-tests of abundances of three algal classes (a - Bacillariophyceae, b - Chlorophyceae and c - cyanobacteria) from Wonderfontein Spruit and Mooi River.

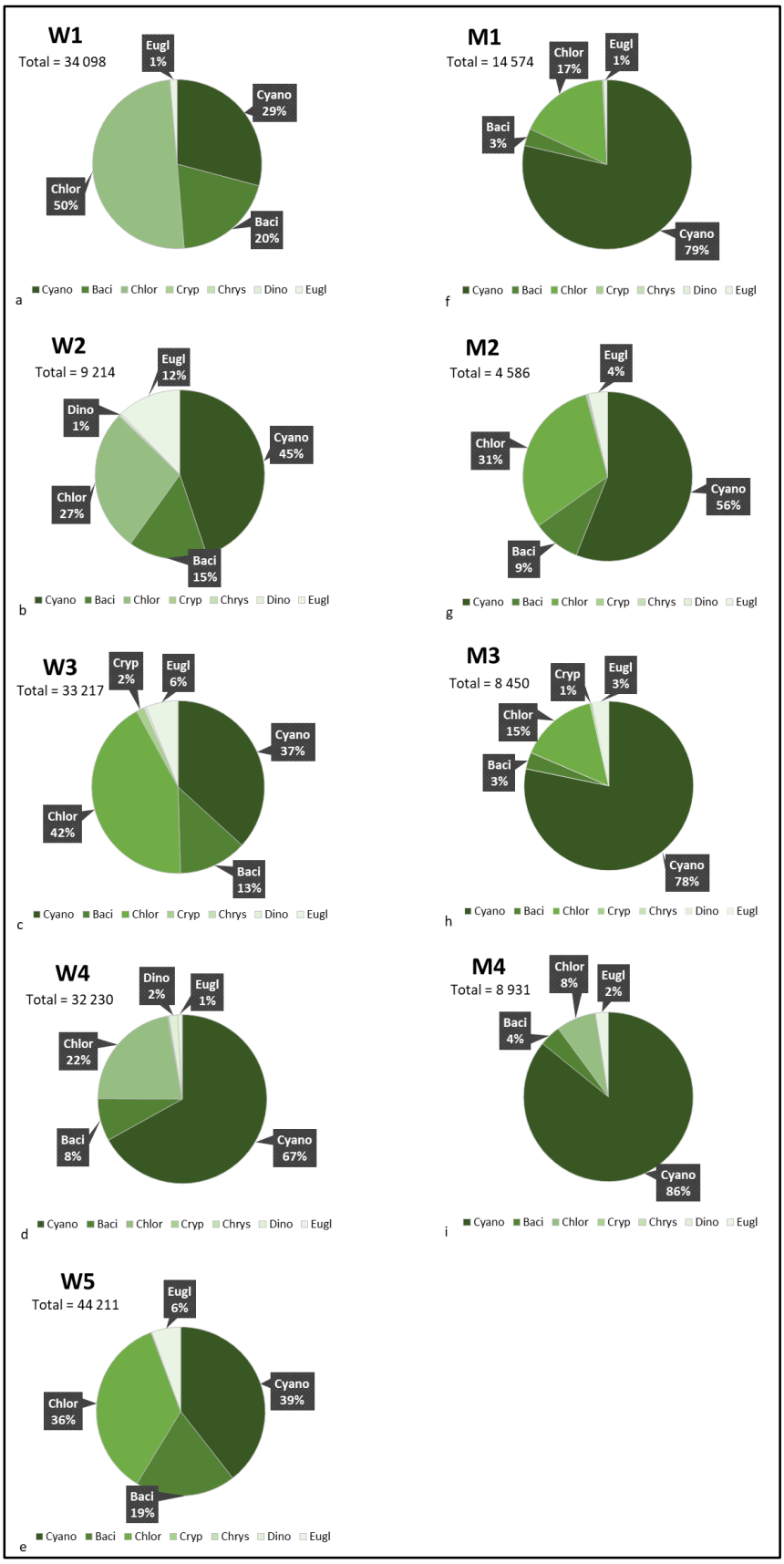

Figure 3.11: Percentage composition of each class for both Wonderfontein Spruit (a - e) and Mooi River (f - i) sites.

3.3 BIRDS

3.3.1 Species accumulation curve

The species accumulation curve started to flatten between 60 and 80 surveys. At subplot 80, - 115 species with a SD ± 1.8 were reached, while the remaining 18 subplots only yielded four additional species (119 ± 0.44). Similarly, 60 surveys will yield a Sørensen distance of less than 0.085 (< 8.5%), which means that after 60 surveys, the subsample is more than 90% representative of the whole sample. It is therefore safe to conclude that sample size is adequate and that additional surveys would yield very small increases in the number of species.

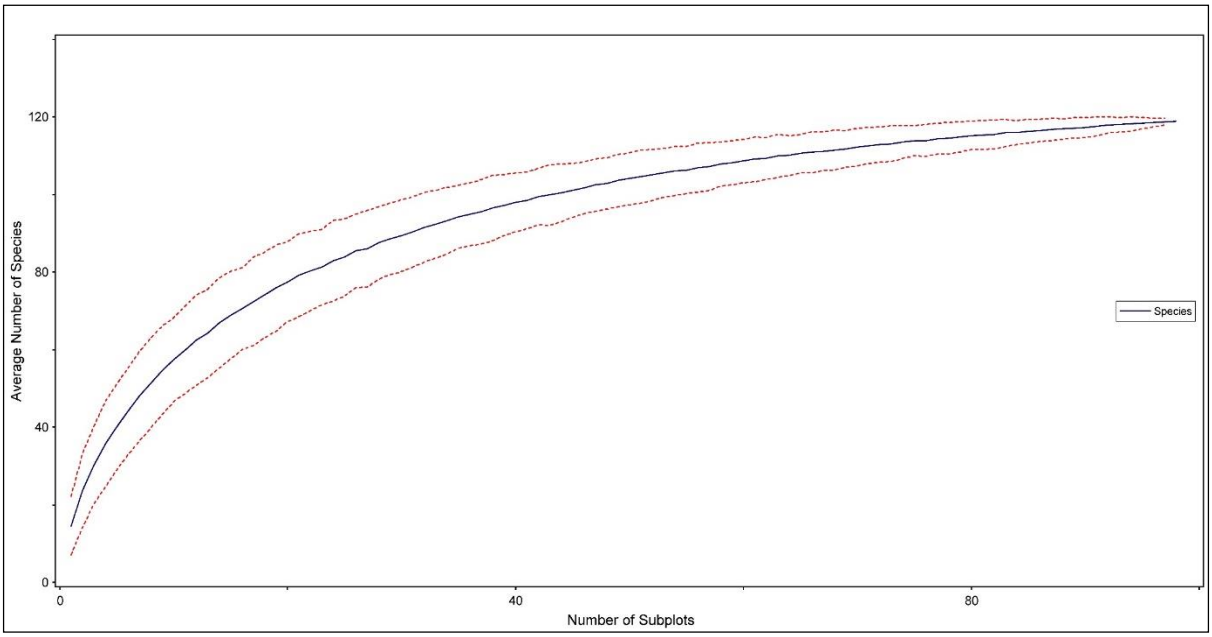

Figure 3.12: Species-accumulation curve of all bird species recorded along the Wonderfontein Spruit and Mooi River in 98 samples (surveys). The dotted lines are confidence bands and represent 95% confidence intervals.

3.3.2 Richness, Abundance and Diversity

I recorded 6 116 individuals consisting of 119 species along the Wonderfontein Spruit and Mooi River. The species richness of WFS varied between 40 (W4) - 65 (W1) with a mean of 55, while that of MR varied between 29 (M4) - 48 (M2) with a mean of 40. Abundance of WFS varied between 623 (W1) - 941 (W4) with a mean of 776, while that of MR varied between 490 (M1) - 629 (M4), with a mean of 560. The Shannon index values of WFS varied between 2.5 (W4) - 3.1 (W2, W3) with a mean of 2.9, while that of MR varied between 1.9 (M4) - 3.0 (M2) with a mean of 2.6. The total avian biomass (kg) for WFS varied between 156 kg (W1) -

667 kg (W5) with a mean of 361 kg, while that of MR varied between 23 kg (M4) - 93 kg (M3) with a mean of 68 kg (Table 3.9).

T-tests and Mann-Whitney tests were performed to compare WFS and MR in terms of species richness, abundance, Shannon index value, and total avian biomass, per survey (Table 3.10).

Species richness for WFS varied between 8 - 26 and a mean and SD of 16 ± 3.5, while that of MR varied between 7 - 23 with a mean and SD of 13 ± 3.5 (Figure 3.13a). An unpaired t-test showed that the mean of WFS was significantly higher than that of MR ($p < 0.0001$).

The abundances for WFS varied between 21 - 228 with a mean and SD of 72 ± 39, while that of MR varied between 15 - 150 with a mean and SD of 51 ± 26 (Figure 3.13b). A Mann-Whitney test showed that the median for WFS was significantly higher than that of MR ($p = 0.0004$).

Shannon index values of WFS varied between 0.97 - 2.9 with a mean and SD of 2.2 ± 0.41, while that of MR varied between 1.0 - 2.8 with a mean and SD of 2.0 ± 0.45 (Figure 3.13c). A Mann-Whitney test showed no significant difference between medians ($p = 0.1291$).

Total avian biomass for WFS varied between 0.86 kg - 120 kg with a mean and SD of 29 ± 30 kg, while that of MR varied between 0.63 kg - 23 kg with a mean and SD of 6.1 ± 46 kg (Figure 3.13d). One value from WFS was excluded due to being an outlier. A Mann-Whitney test showed that the median for WFS was significantly higher than that of MR ($p < 0.0001$).

Table 3.9: All bird species and numbers recorded including richness, Shannon index values, and total biomass, per site.

R No.	Common Name	Scientific Name	Abbrev. Name	MR				WFS				
				1	2	3	4	1	2	3	4	5
294	Avocet, Pied	*Recurvirostra avosetta*	PAvo	0	0	0	0	0	0	1	0	4
464	Barbet, Black-collared	*Lybius torquatus*	BCBarb	0	0	0	0	0	0	0	1	1
473	Barbet, Crested	*Trachyphonus vaillantii*	CBarb	0	0	1	0	0	0	0	0	2
440	Bee-eater, Blue-cheeked	*Merops persicus*	BCBee	0	0	0	0	19	0	0	0	0
824	Bishop, Southern Red	*Euplectes orix*	SRBish	58	112	67	110	38	99	69	113	37
826	Bishop, Yellow-crowned	*Euplectes afer*	YCBish	0	0	0	0	3	0	2	0	1
78	Bittern, Little	*Ixobrychus minutus*	LBitt	0	0	2	0	0	3	1	0	0
746	Bokmakierie	*Telophorus zeylonus*	Bokmk	0	0	0	0	0	1	0	0	0
736	Boubou, Southern	*Laniarius ferrugineus*	SBou	0	0	0	0	0	0	0	0	2
567	Bulbul, African Red-eyed	*Pycnonotus nigricans*	REBul	14	1	11	4	0	3	0	0	12
870	Canary, Black-throated	*Crithagra atrogularis*	BTCan	0	0	0	2	2	0	1	0	0
677	Cisticola, Levaillant's	*Cisticola tinniens*	LCist	10	19	0	14	10	11	7	2	15
228	Coot, Red-knobbed	*Fulica cristata*	RKCoot	0	28	25	0	18	112	113	178	202
58	Cormorant, Reed	*Phalacrocorax africanus*	RCorm	13	10	9	0	3	21	79	14	6
55	Cormorant, White-breasted	*Phalacrocorax lucidus*	WBCorm	0	0	0	0	0	2	1	1	0
391	Coucal, Burchell's	*Centropus burchellii*	BCouc	0	2	0	0	0	0	0	0	0
213	Crake, Black	*Amaurornis flavirostris*	BCrak	1	6	5	2	0	2	3	0	0
386	Cuckoo, Diederic	*Chrysococcus caprius*	DCuck	0	0	0	0	0	0	1	0	4
377	Cuckoo, Red-chested	*Cuculus solitarius*	RCCuck	0	0	1	0	0	0	0	0	0
60	Darter, African	*Anhinga rufa*	ADart	1	0	1	0	0	6	25	2	20
354	Dove, Cape Turtle	*Streptopelia capicola*	CTDve	1	4	0	2	1	3	4	7	8
355	Dove, Laughing	*Streptopelia senegalensis*	LDve	3	19	16	0	0	0	4	1	1
352	Dove, Red-eyed	*Streptopelia semitorquata*	REDve	10	29	35	9	6	14	86	25	77
105	Duck, African Black	*Anas sparsa*	ABDck	1	1	1	0	0	0	0	2	0
101	Duck, White-backed	*Thalassornis leuconotus*	WBDck	0	2	0	0	0	0	0	0	0

99	Duck, White-faced Whistling	*Dendrocygna viduata*	WFDck	0	0	0	0	15	1	3	0	0
104	Duck, Yellow-billed	*Anas undulata*	YBDck	2	5	24	3	17	8	20	1	10
139	Eagle, Long-crested	*Lophaetus occipitalis*	LCEagl	1	1	0	0	0	0	0	0	0
66	Egret, Great	*Egretta alba*	GEgr	0	0	0	0	1	0	1	0	0
67	Egret, Little	*Egretta garzetta*	LEgr	1	0	0	0	2	0	2	0	4
71	Egret, Western Cattle	*Bubulcus ibis*	WCEgr	0	0	0	0	8	1	93	0	0
732	Fiscal, Southern	*Lanius collaris*	SFisc	0	0	0	0	0	1	0	0	0
148	Fish-Eagle, African	*Haliaeetus vocifer*	AFEagl	0	0	0	0	1	0	1	0	0
96	Flamingo, Greater	*Phoenicopterus ruber*	GFlam	0	0	0	0	10	0	50	0	118
217	Flufftail, Red-chested	*Sarothrura rufa*	RCFluf	0	1	0	0	0	0	0	0	0
102	Goose, Egyptian	*Alopochen aegyptiacus*	EGse	18	2	4	0	4	4	14	0	6
116	Goose, Spur-winged	*Plectopterus gambensis*	SWGse	0	0	0	0	0	0	16	0	0
6	Grebe, Great Crested	*Podiceps cristatus*	GCGrb	0	0	1	0	0	0	0	45	1
8	Grebe, Little	*Tachybaptus ruficollis*	LGrb	1	54	14	4	0	5	17	33	13
270	Greenshank, Common	*Tringa nebularia*	Grnsh	0	0	1	0	0	0	0	0	0
203	Guineafowl, Helmeted	*Numida meleagris*	HGuin	0	0	0	0	1	0	0	0	5
69	Heron, Black	*Egretta ardesiaca*	BHer	0	0	0	0	2	0	6	0	3
63	Heron, Black-headed	*Ardea melanocephala*	BHHer	0	1	0	0	0	0	0	0	1
64	Heron, Goliath	*Ardea goliath*	GlHer	0	0	0	0	0	1	0	2	0
74	Heron, Green-backed	*Butorides striata*	GBHer	0	0	0	0	1	0	0	0	0
62	Heron, Grey	*Ardea cinerea*	GHer	0	0	0	0	1	0	0	0	0
65	Heron, Purple	*Ardea purpurea*	PHer	0	0	0	0	3	2	2	0	3
72	Heron, Squacco	*Ardeola ralloides*	SHer	0	0	1	0	1	0	5	4	4
91	Ibis, African Sacred	*Threskiornis aethiopicus*	SIbis	0	0	0	0	1	0	10	1	0
93	Ibis, Glossy	*Plegadis falcinellus*	GIbis	0	0	0	0	19	3	1	0	0
94	Ibis, Hadeda	*Bostrychia hagedash*	HIbis	2	4	0	0	0	0	1	0	0
431	Kingfisher, Malachite	*Alcedo cristata*	MKing	5	5	1	0	1	1	3	1	2
428	Kingfisher, Pied	*Ceryle rudis*	PKing	5	4	2	0	0	0	0	0	7
260	Lapwing, African Wattled	*Vanellus senegallus*	AWLapw	0	0	0	0	8	4	2	0	0
258	Lapwing, Blacksmith	*Vanellus armatus*	BLapw	15	14	0	0	29	13	0	5	5

727	Longclaw, Cape	*Macronyx capensis*	CLngc	1	2	0	1	0	1	0	0	0
165	Marsh-Harrier, African	*Circus ranivorus*	AMHar	0	0	0	0	0	0	2	0	1
534	Martin, Banded	*Riparia cincta*	BMart	0	0	0	1	0	3	0	0	1
533	Martin, Brown-throated	*Riparia paludicola*	BTMart	94	42	15	5	11	32	0	42	11
532	Martin, Sand	*Riparia riparia*	SMart	2	1	0	0	4	0	0	0	0
814	Masked-Weaver, Southern	*Ploceus velatus*	SMWeav	64	52	182	199	33	9	32	44	56
226	Moorhen, Common	*Gallinula chloropus*	CMoor	11	27	48	10	8	23	8	59	59
426	Mousebird, Red-faced	*Urocolius indicus*	RFMous	0	0	0	0	0	0	0	0	6
424	Mousebird, Speckled	*Colius striatus*	SMous	0	0	1	0	0	0	0	0	0
758	Myna, Common	*Acridotheres tristis*	CMyn	4	0	0	0	0	2	0	0	0
76	Night-heron, Black-crowned	*Nycticorax nycticorax*	BCNHer	0	0	0	0	0	0	1	0	0
349	Pigeon, Speckled	*Columba guinea*	SPig	0	0	0	0	9	0	3	0	0
716	Pipit, African	*Anthus cinnamomeus*	APip	0	1	0	0	3	0	0	0	0
249	Plover, Three-banded	*Charadrius tricollaris*	TBPlov	13	0	0	0	2	0	2	1	0
685	Prinia, Black-chested	*Prinia flavicans*	BCPrin	1	0	0	0	0	0	0	0	1
683	Prinia, Tawny-flanked	*Prinia subflava*	TFPrin	0	0	0	0	0	1	0	0	3
852	Quailfinch, African	*Ortygospiza artricollis*	AQfnch	0	4	0	0	2	10	0	0	0
821	Quelea, Red-billed	*Quelea quelea*	RBQuel	1	0	0	1	0	0	0	0	1
210	Rail, African	*Rallus caerulescens*	ARail	0	1	0	0	1	0	1	1	0
631	Reed-Warbler, African	*Acrocephalus baeticatus*	ARWarb	6	21	6	11	0	11	10	6	5
628	Reed-Warbler, Great	*Acrocephalus arundinaceus*	GRWarb	0	2	0	1	0	0	0	0	1
601	Robin-chat, Cape	*Cossypha caffra*	CRCht	0	1	3	0	0	0	0	1	0
284	Ruff	*Philomachus pugnax*	Ruff	2	0	0	0	10	0	0	0	0
638	Rush-Warbler, Little	*Bradypterus baboecala*	LRWarb	10	10	4	11	1	15	13	9	9
269	Sandpiper, Marsh	*Tringa stagnatilis*	MSndp	0	0	0	0	2	0	0	0	0
266	Sandpiper, Wood	*Tringa glareola*	WSndp	0	0	0	0	1	0	0	0	0
103	Shelduck, South African	*Tadorna cana*	SASDck	0	0	0	0	0	33	1	0	18
112	Shoveler, Cape	*Anas smithii*	CShov	0	0	0	0	5	0	1	0	0
286	Snipe, African	*Gallinago nigripennis*	ASnp	0	0	0	0	2	0	0	0	0
803	Sparrow, Cape	*Passer melanurus*	CSpar	0	0	0	0	1	2	3	0	0

804	Sparrow, Southern Grey-headed	*Passer diffusus*	GHSpar	0	0	0	0	0	0	1	0	0
156	Sparrowhawk, Ovambo	*Accipiter ovampensis*	OSphwk	0	0	0	0	1	0	0	0	0
95	Spoonbill, African	*Platalea alba*	ASpnb	0	0	0	0	2	2	9	0	2
760	Starling, Wattled	*Creatophora cinerea*	WStarl	0	0	0	0	15	0	0	0	0
295	Stilt, Black-winged	*Himantopus himantopus*	BWStlt	0	0	0	0	3	0	5	0	4
274	Stint, Little	*Calidris minuta*	LStnt	0	0	0	0	5	0	0	0	0
596	Stonechat, African	*Saxicola torquatus*	Stchat	12	4	1	8	5	2	0	1	0
90	Stork, Yellow-billed	*Mycteria ibis*	YBStrk	0	0	0	0	0	0	3	0	2
518	Swallow, Barn	*Hirundo rustica*	BSwal	44	32	5	187	209	61	0	233	26
526	Swallow, Greater Striped	*Hirundo cucullata*	GSSwal	5	3	6	2	1	0	0	4	8
528	Swallow, South-african Cliff	*Hirundo spilodera*	SACSwal	0	0	0	0	0	19	0	0	0
520	Swallow, White-throated	*Hirundo albigularis*	WTSwal	4	1	3	2	2	3	0	7	6
223	Swamphen, African Purple	*Porphyrio madagascariensis*	APSwmph	0	1	0	0	0	4	3	2	0
635	Swamp-Warbler, Lesser	*Acrocephalus gracilirostris*	LSWarb	20	23	12	26	1	32	28	29	24
421	Swift, African Palm	*Cypsiurus parvus*	APSwft	0	0	0	2	0	9	20	42	2
417	Swift, Little	*Apus affinis*	LSwft	2	0	0	0	0	1	6	6	0
415	Swift, White-rumped	*Apus caffer*	WRSwft	9	2	3	0	1	6	0	6	0
107	Teal, Hottentot	*Anas hottentota*	HTeal	0	0	0	0	2	4	9	0	3
108	Teal, Red-billed	*Anas erythroryncha*	RBTeal	0	0	0	0	29	1	4	0	21
338	Tern, Whiskered	*Chlidonias hybrida*	WTern	0	0	0	0	3	0	2	4	1
339	Tern, White-winged	*Chlidonias leucopterus*	WWTern	0	0	0	0	0	0	0	2	3
577	Thrush, Karoo	*Turdus smithi*	KThrsh	0	0	4	0	4	0	0	0	0
713	Wagtail, Cape	*Motacilla capensis*	CWag	18	2	2	0	5	4	4	1	0
643	Warbler, Willow	*Phylloscopus trochilus*	WWar	0	0	1	0	0	0	0	0	0
846	Waxbill, Common	*Estrilda astrild*	CWax	0	1	15	7	1	0	0	0	11
854	Waxbill, Orange-breasted	*Sporaeginthus subflavus*	OBWax	0	3	0	1	0	2	0	0	2
813	Weaver, Cape	*Ploceus capensis*	CWeav	1	0	0	0	0	0	0	0	0
807	Weaver, Thick-billed	*Amblyospiza albifrons*	TBWeav	0	0	19	1	5	12	3	0	0
796	White-eye, Cape	*Zosterops virens*	CWhteye	3	2	1	0	0	0	0	0	1
796	White-eye, Orange-river	*Zosterops pallidus*	ORWhteye	0	1	0	0	0	0	0	0	0

860	Whydah, Pin-tailed	*Vidua macroura*	PTWhy	0	0	0	0	3	0	0	0	0
832	Widowbird, Long-tailed	*Euplectes progne*	LTWid	1	1	0	1	4	0	0	0	0
831	Widowbird, Red-collared	*Euplectes ardens*	RCWid	0	0	0	2	0	1	0	0	1
829	Widowbird, White-winged	*Euplectes albonotatus*	WWWid	0	2	0	0	2	3	1	3	3
			Abundance	**490**	**566**	**553**	**629**	**623**	**629**	**819**	**941**	**866**
			Species Richness	**42**	**48**	**39**	**29**	**65**	**53**	**59**	**40**	**59**
			Shannon index value	**2.9**	**3.0**	**2.6**	**1.9**	**3.0**	**3.1**	**3.1**	**2.5**	**3.0**
			Biomass (kg)	**72**	**82**	**93**	**23**	**156**	**200**	**558**	**225**	**667**

Table 3.10: Summary of species richness, abundance, Shannon index values, and avian biomass of the two rivers, and associated tests.

	WFS				**MR**					
Birds	**Min**	**Max**	**Mean**	**SD**	**Min**	**Max**	**Mean**	**SD**	**Test**	**p value ≤ 0.05**
Richness	8	26	16	3.5	7	23	13	3.5	Unpaired t test (Two-tailed)	Yes
Abundance	21	228	72	39	15	150	51	26	Mann-Whitney test (Two-tailed)	Yes
Shannon	0.97	2.9	2.2	0.41	1.0	2.8	2.0	0.45	Mann-Whitney test (Two-tailed)	No
Biomass	0.86	120	29	30	0.63	23	6.1	4.6	Mann-Whitney test (Two-tailed)	Yes

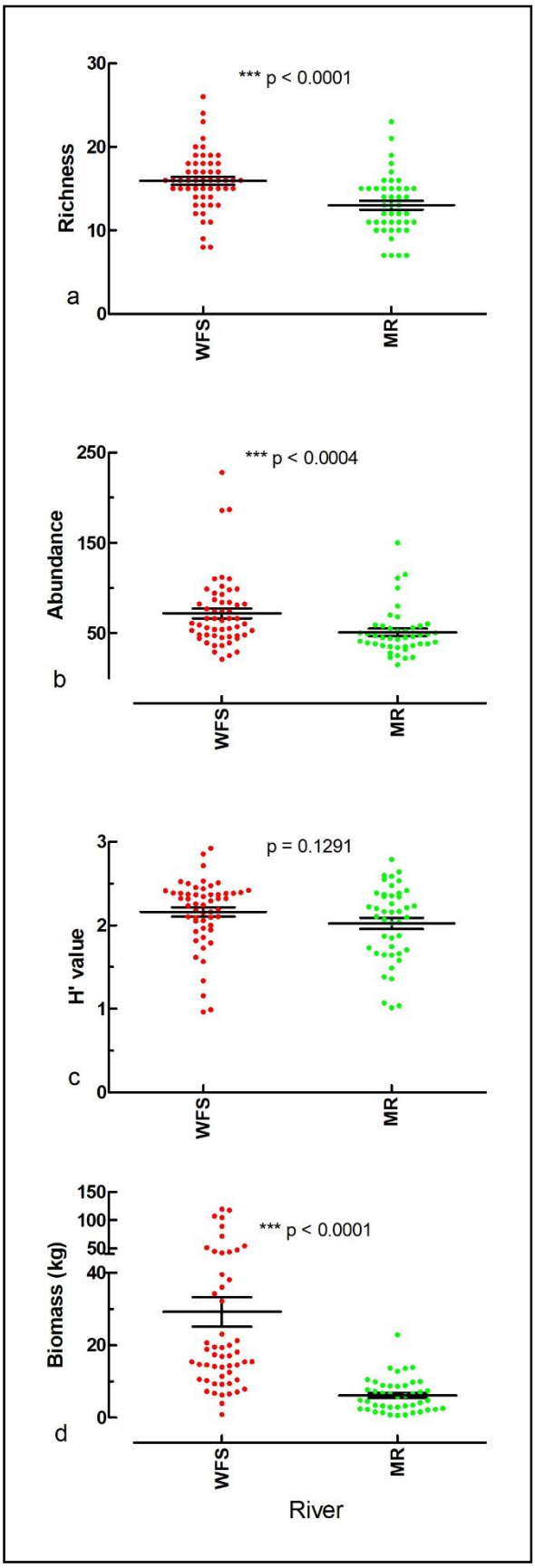

Figure 3.13: T-tests and Mann-Whitney tests of species richness (a), abundance (b), Shannon index values (c) and avian biomass (d) between Wonderfontein Spruit and Mooi River.

One-way Analysis of Variance (One-way ANOVA) tests were performed to determine the differences in species richness, abundance, Shannon index values, and total avian biomass between rivers. Species richness and abundance per survey were used to determine Shannon index values per survey. All survey values per site were then used to determine the mean and variance of each site and then compared to the means of other sites from the same river (Table 3.11).

Means of species richness for WFS varied between 14 (W4) - 17 (W3, W5), with SD between 2.7 (W4) - 4.8 (W5). A Kruskall-Wallis test showed no significant difference between medians ($p = 0.3389$) (Figure 3.14a). For MR, means varied between 9.7 (M4) - 15 (M2) with SD between 2.1 (M3) - 3.6 (M1). A Kruskall-Wallis test showed a significant difference between medians ($p = 0.0010$). Dunn's multiple comparison test showed a significant difference between the mean rank of M1 and M4 ($p < 0.05$), as well as M2 and M4 ($p <0.005$) (Figure 3.14b).

Means of abundance for WFS varied between 57 (W2) - 86 (W4) with SD between 18 (W3) - 55 (W5). A Kruskall-Wallis test showed no significant difference between medians ($p = 0.0700$) (Figure3.14c). For MR, means varied between 45 (M1) - 57 (M4) with SD between 12 (M3) - 37 (M1). A Kruskall-Wallis test showed no significant difference between medians ($p = 0.1219$) (Figure3.14d).

Means of Shannon index values for WFS varied between 1.9 (W4) - 2.3 (W2, W3, W5) with SD between 0.25 (W3) - 0.55 (W1). A Kruskall-Wallis test showed no significant difference between medians ($p = 0.0778$) (Figure 3.14e). For MR, means varied between 1.6 (M4) - 2.3 (M2) with SD between 0.25 (M1) - 0.45 (M4). A Kruskall-Wallis test showed a significant difference between medians ($p = 0.0009$). Dunn's multiple comparison test showed a significant difference between the mean rank of M1 and M4, as well as M2 and M4 (Figure 3.14f).

Means of biomass for WFS varied between 16 kg (W1) - 51 kg (W3) with SD between 13 kg (W2) - 45 kg (W5). One value from WFS was excluded due to being an outlier. A Kruskall-Wallis test showed a significant difference between medians ($p = 0.0046$) (Figure 3.14g). Dunn's multiple comparison test showed a significant difference between the mean rank of W1 and W3 as well as W2 and W3. For MR, means varied between 2.1 kg (M4) - 8.5 kg (M3) with SD between 1.0 kg (M4) - 6.7 kg (M1). A Kruskall-Wallis test showed a significant difference between medians ($p = 0.0002$). Dunn's multiple comparison test showed a significant difference between the mean rank of M2 and M4, as well as M3 and M4 (Figure 3.14h).

Table 3.11: Summary of species richness, abundance, Shannon index values, and biomass of birds of the Wonderfontein Spruit and Mooi River sites, as well as associated Kruskal-Wallis tests.

		Min	Max	Mean	SD	Test	p value ≤ 0.05		Min	Max	Mean	SD	Test	p value ≤ 0.05
Richness	**W1**	8	19	15	3.1	Kruskall-Wallis	No	**M1**	10	23	14	3.6	Kruskall-Wallis	Yes
	W2	11	24	16	3.3			**M2**	11	21	15	3.1		
	W3	11	21	17	3.0			**M3**	10	16	13	2.1		
	W4	8	17	14	2.7			**M4**	7	15	9.7	2.7		
	W5	9	26	17	4.8									
Abundance	**W1**	29	187	62	46	Kruskall-Wallis	No	**M1**	15	150	45	37	Kruskall-Wallis	No
	W2	21	110	57	24			**M2**	38	111	51	21		
	W3	48	102	74	18			**M3**	36	80	50	12		
	W4	29	186	86	42			**M4**	22	115	57	30		
	W5	25	228	79	55									
Shannon	**W1**	0.99	2.5	2.0	0.55	Kruskall-Wallis	No	**M1**	1.6	2.5	2.2	0.25	Kruskall-Wallis	Yes
	W2	1.8	2.9	2.3	0.34			**M2**	1.7	2.8	2.3	0.34		
	W3	1.6	2.5	2.3	0.25			**M3**	1.4	2.4	2.0	0.31		
	W4	0.97	2.4	1.9	0.44			**M4**	1.0	2.6	1.6	0.45		
	W5	1.7	2.9	2.3	0.32									
Biomass	**W1**	0.86	45	16	14	Kruskall-Wallis	Yes	**M1**	0.76	23	6.5	6.7	Kruskall-Wallis	Yes
	W2	6.6	42	18	13			**M2**	4.5	10	7.4	2.1		
	W3	19	107	51	34			**M3**	3.5	14	8.5	3.7		
	W4	9.4	54	20	15			**M4**	0.63	3.4	2.1	1.0		
	W5	9.3	120	41	45									

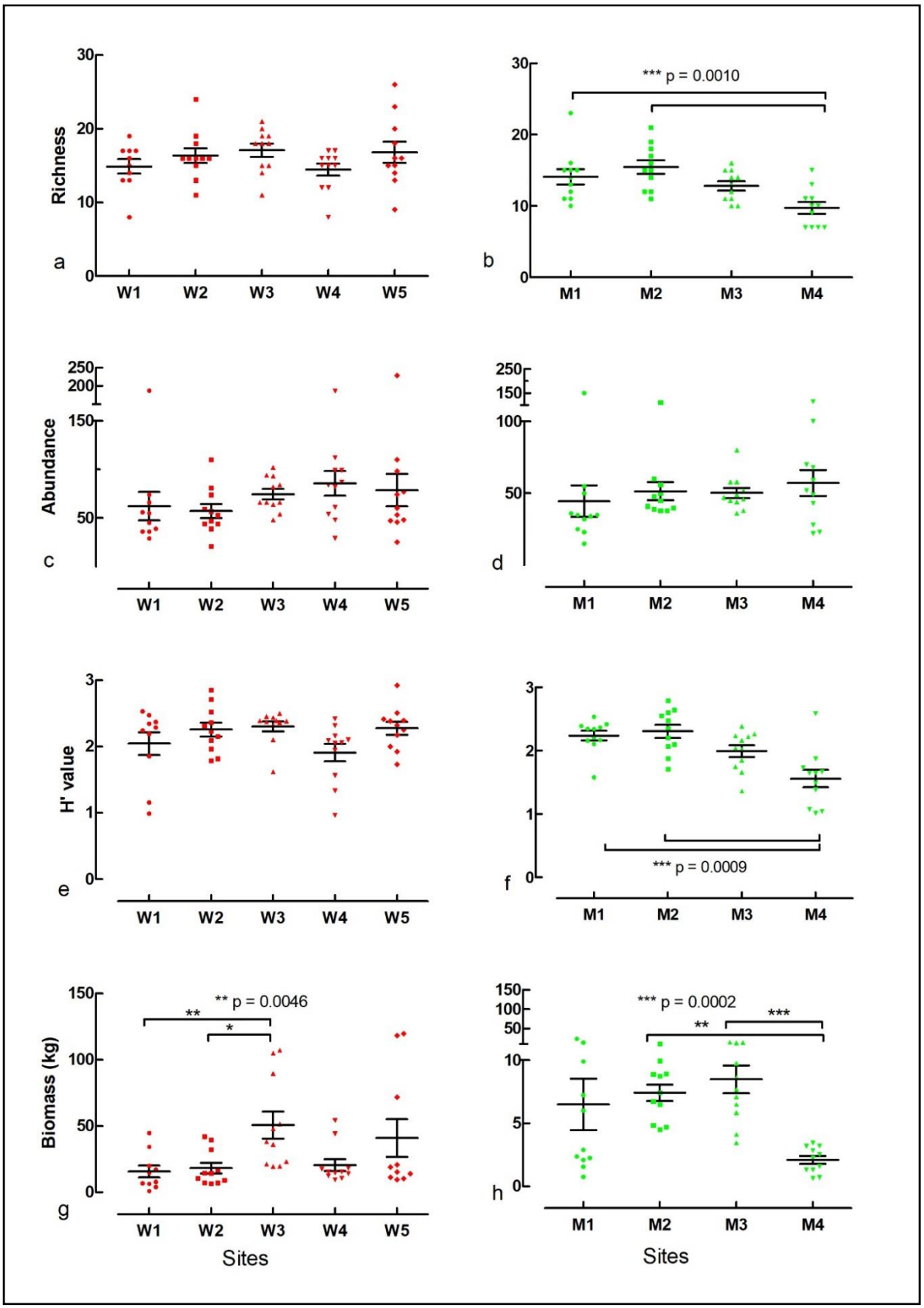

Figure 3.14: ANOVA/Kruskal-Wallis tests of species richness (a and b), abundance (c and d), Shannon index values (e and f) and avian biomass (g and h) of the different sites of Wonderfontein Spruit and Mooi River.

3.3.3 Linear regression of birds and algae

Regression involves the determination of the degree of relationships in the patterns of variation of two or more variables through the calculation of the coefficient of correlation (r), which rises to a maximum of 1 with a perfect fit. In regression, one variable is deemed dependent on the other (Van Emden, 2008). When r = 0, there is zero correlation between the two variables, meaning that the variation of one variable cannot be used to explain any of the variation in the other variable. The coefficient of determination (r^2) is a measure of how well the variation of variable explains the variation of the other, and corresponds to the percentage of the variation explained by a best-fit regression line which is calculated for the data (Pidwirny, 2006).

A linear regression was done to evaluate whether bird abundance is related to algal abundance (Figure 3.15a). This was done for abundances of all, aquatic, and terrestrial birds. Increases in abundance of all ($p = 0.0254$), and aquatic birds ($p = 0.0190$) were related to an increase of in algal abundance. Increase in algal abundance explained 59 % of variance of avian abundance ($r^2 = 0.5931$) and 63 % of variance of aquatic bird abundances ($r^2 = 0.6283$).

A linear regression was done to evaluate whether avian biomass is associated with algal abundance (Figure 3.15b). This was done for the biomass of all recorded, aquatic, and terrestrial birds. Increases in biomass of all birds ($p = 0.0115$) and biomass of aquatic birds ($p = 0.0012$) were related to an increase in algal abundance. Increase in algal abundance explained 62% of variance of both avian biomass ($r^2 = 0.6223$) and biomass of aquatic birds ($r^2 = 0.6247$).

The slope and intercepts of aquatic birds and all birds were compared for both bird abundances and biomass. The difference between the two slopes of bird abundances were not significant ($p = 0.9097$). The difference between intercepts, however, was extremely significant ($p < 0.0001$) (Figure 3.15a). The difference between the two slopes of avian biomass was not significant ($p = 0.9505$). The difference between intercepts was not significant ($p = 0.7560$) (Figure 3.15b). Since the difference between intercepts for biomass was not significant, while the intercepts of abundance was extremely significant, one can conclude that terrestrial birds contributed significantly to abundance but not biomass.

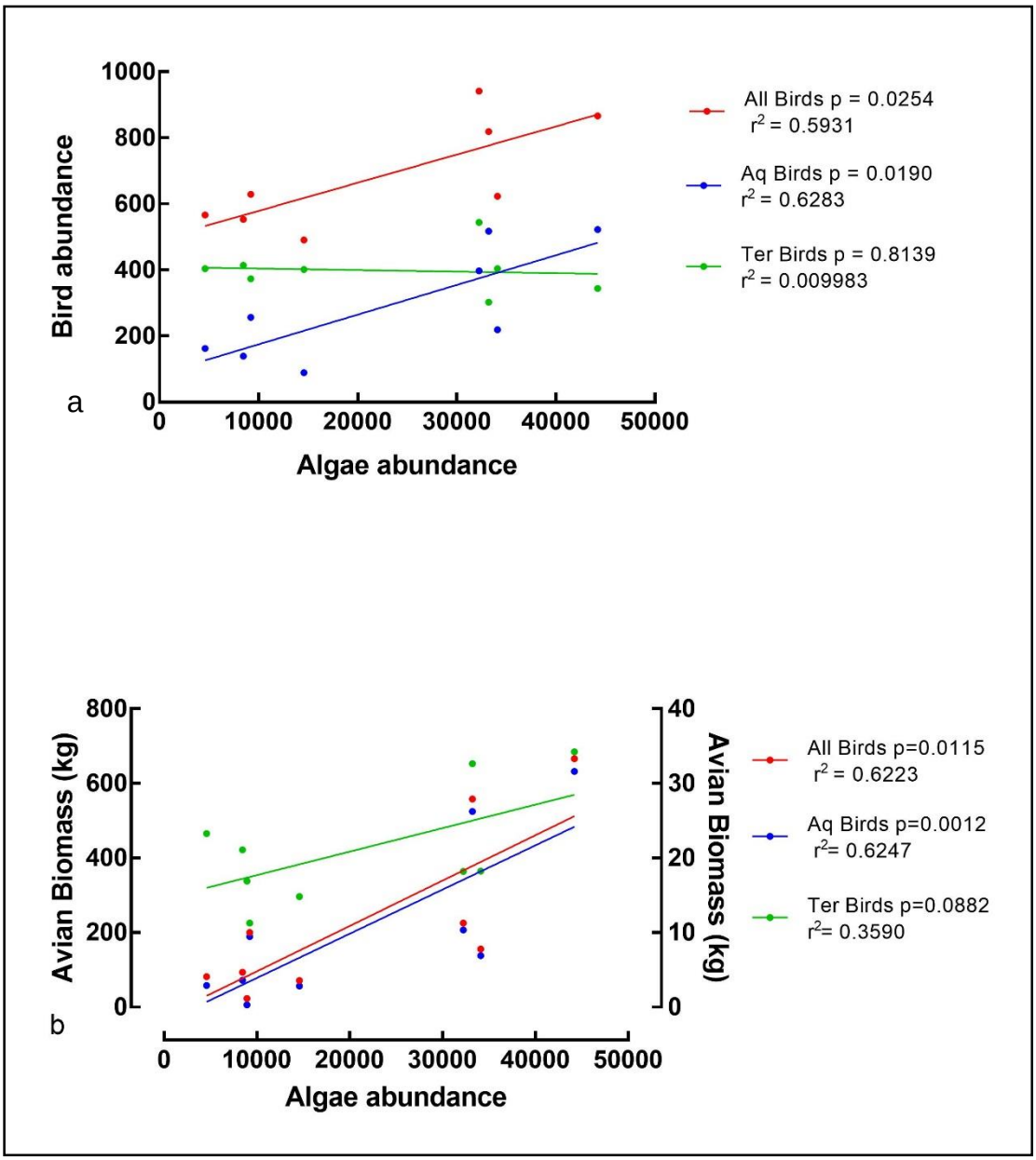

Figure 3.15: Linear regressions between birds and algae from Wonderfontein Spruit and Mooi River (a - bird abundances and algal abundances, b - avian biomass and algal abundances).

3.4. MULTIVARIATE ANALYSIS OF ALGAE

3.4.1. Cluster Analysis

A hierarchical cluster analysis was performed to group all sites according to their algal assemblages. Cluster analysis allows you to assign sample units to groups based on the similarity of the redundant patterns of their responses (Peck, 2010). The distance measure used was Sorensen, with Flexible Beta of -0.25 as linkage method. With the Flexible Beta method, the user controls the degree to which the results are space conserving by entering a beta value. A β value of -0.25 has been found to be space conserving (Peck, 2010). A cluster dendrogram (Figure 3.16) indicates that algal assemblages of the WFS sites (excluding W2) are closer related to the other WFS sites, than any other site belonging to MR. Algal assemblages of MR sites were more closely related to one another than those of WFS. W2 however, was grouped together with the MR sites.

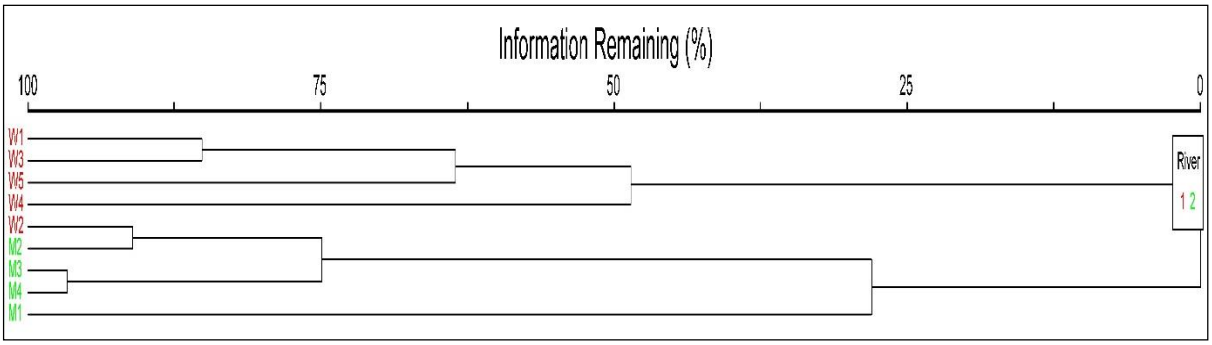

Figure 3.16: Cluster dendrogram of algal assemblages of all the different sites (Distance measure = Sørensen; Linkage method = flexible beta of -0.25; Percent chaining = 13.33).

3.4.2 Nonmetric multidimensional scaling (NMS)

Ordination provides views into a high-dimensional space by seeking and displaying the strongest structure (McCune and Grace, 2002). NMS has the advantage over other ordination methods in that it avoids the assumption of linear relationships among variables, it makes use of ranked distances, and it allows the use of any distance measure or relativisation. NMS is a most effective ordination method for ecological community data, and should be considered the method of choice (McCune & Grace, 2002).

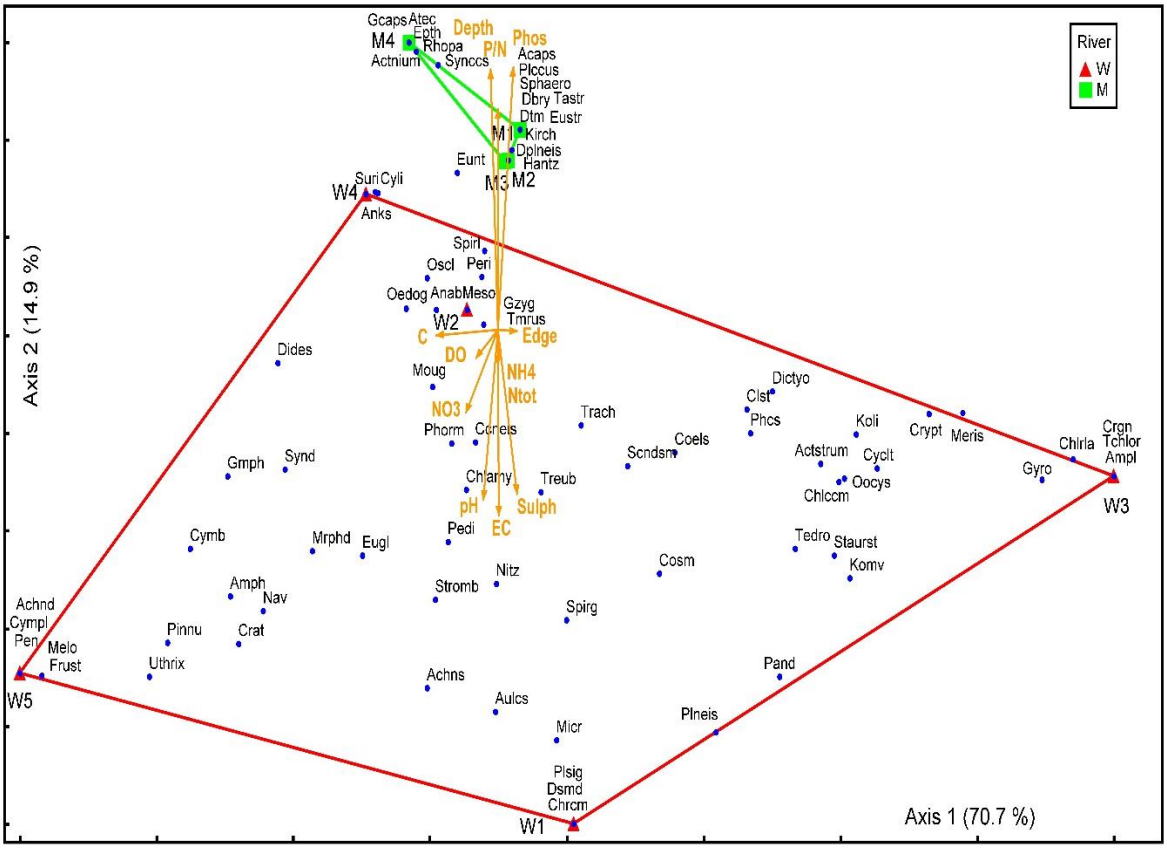

Figure 3.17: NMS joint plot of algae (83 genera and 9 sites) abundances and variables. (Distance measure = Gower Ignore 0; Number of dimensions in final solution = 3; Variance: Axis 1 = 70.7%, Axis 2 = 14.9%; Final stress = 0.43802; Final instability = 0.00000).

An NMS was carried out in PC-ORD. NMS was undertaken using Gower ignore 0 distance measure and random starting coordinates with four axes. Dimensionality was reduced by one at each cycle. Initial step length towards minimum stress was 0.20. The stability criterion was 0.000010, with 10 iterations to evaluate stability. A Monte Carlo test was carried out using 50 runs. Three dimensions were derived. Axis 1 explained 70.7% of variation and Axis 2 14.9% of variation, for a cumulative explanation of 85.6%. A Monte Carlo test was not significant for both Axes ($p = 0.0588$). A final stress of 0.43802 with a final instability of 0.00000 was reached after 122 iterations.

Guidelines have been developed to interpret stress values. Generally, stress values less than 10 are associated with interpretable and reliable ordination axes, and as stress increase thereafter, the associated ordinations are useful but increasingly become interpretable only at a broad scale. However, it should be noted that stress tends to increase with both sample size and the number of responses (Peck, 2010). McCune and Grace (2002) stated that most ecological community datasets will have solutions with stress between 10 and 20 and that values in the lower half of this range are quite satisfactory, while values approaching or exceeding 20 are cause for concern.

The ordination in Figure 3.17 is an NMS joint plot of the algal abundances from all sites, and associated variables. Final stress was very low (<1), which indicates an excellent representation with no prospect of misinterpretation. Axis 1 explained the majority of variation while axis 2 explained relatively little. Consequently, horisontal variation explained more than vertical variation. Convex hulls show much less variation (both axes) between MR sites than WFS sites. This indicates a much higher diversity for WFS than for MR, along with a much more homogenous composition of algae for MR, when compared with WFS. MR sites are strongly correlated with depth, phosphorus, and phosphorus-nitrogen ratio. W1 was strongly correlated with pH, sulphate, and conductivity.

Genera associated with M1, M2, and M3 were *Aphanocapsa*, *Diatoma*, *Diploneis*, *Eunotia*, *Hantzschia*, *Euastrum*, *Kirchneriella*, *Pleurococcus*, *Sphaerocystis*, *Tetrastrum*, and *Dinobryon*. Genera associated with M4 were *Aphanothece*, *Gleocapsa*, *Synechococcus*, *Epithemia*, *Rhopalodia*, and *Actinotaenium*. W1 was associated with *Achnanthes*, *Aulacoseira*, *Placoneis*, *Pleurosigma*, *Characium*, *Desmodesmus*, and *Microspora*. W2 was associated with *Anabaena*, *Oscillatoria*, *Spirulina*, *Gonatozygon*, *Mesotaenium*, *Oedogonium*, *Tetmemorus*, and *Peridinium*. W3 was associated with *Amphipleura*, *Gyrosigma*, *Chlorella*, *Crucigenia*, and *Tetrachlorella*. W4 was associated with *Surirella*, *Cylindrospermopsis* and *Ankistrodesmus*, while W5 was associated with *Achnanthidium*, *Cymatopleura*, *Frustulia*, *Melosira*, *Pinnularia*, *Penium*, and *Ulothrix*.

Genera associated with high phosphorus concentrations were *Aphanocapsa*, *Diatoma*, *Diploneis*, *Hantzschia*, *Euastrum*, *Kirchneriella*, *Pleurococcus*, *Sphaerocystis*, *Tetrastrum*, *Dinobryon*. Genera associated with high sulphate concentrations were *Microspora*, *Pleurosigma*, *Desmodesmus* and *Characium*. Genera associated with higher pH were *Achnanthidium*, *Cocconeis*, *Chlamydomonas*, *Pediastrum* and *Strombomonas*.

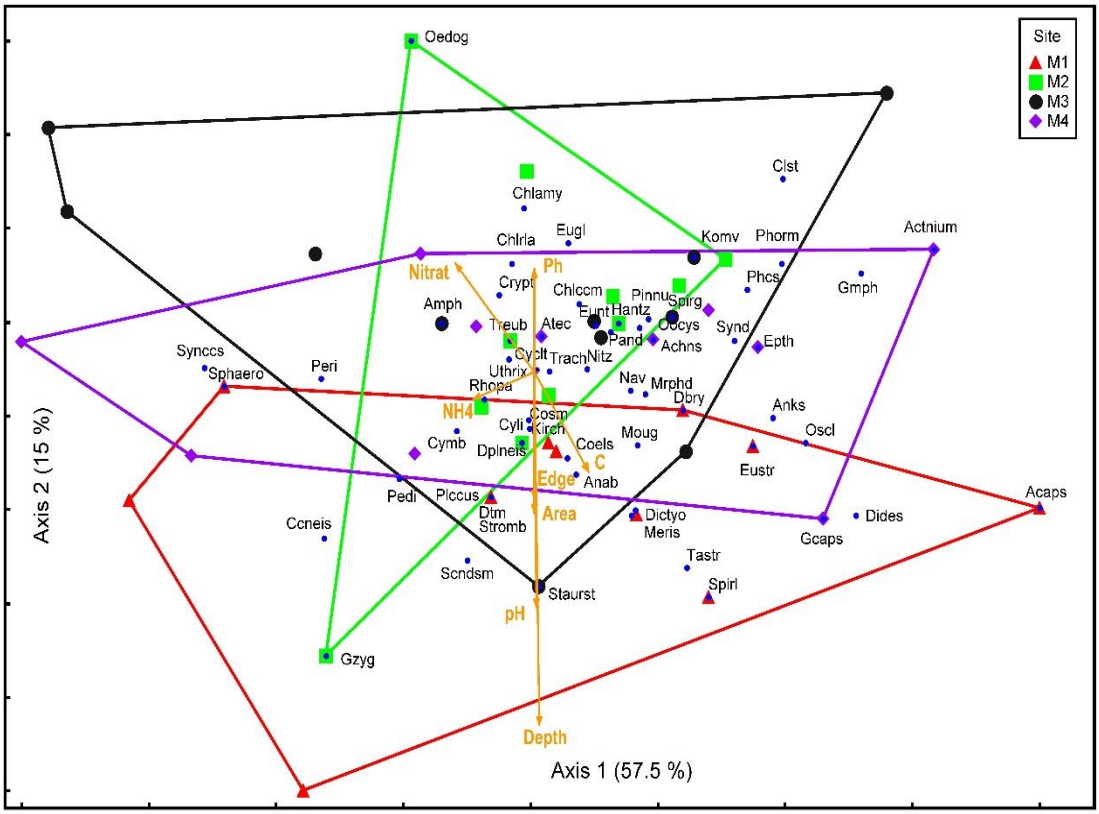

Figure 3.18: NMS joint plot of Algae (61 genera and 44 sites) abundances of all samples from MR and environmental variables. (Distance measure = Sørensen; Number of dimensions in final solution = 2; Variance: Axis 1 = 57.5%, Axis 2 = 15%; Final stress = 15.57997; Final instability = 0.00000).

An NMS was carried out in PC-ORD. NMS was undertaken using Sørensen distance measure and random starting coordinates with four axes. Dimensionality was reduced by one at each cycle. Initial step length towards minimum stress was 0.20. The stability criterion was 0.000010, with 10 iterations to evaluate stability. A Monte Carlo test was carried out using 50 runs. Two dimensions were derived. Axis 1 explained 57.5% of variation and Axis 2 15% of variation, for a cumulative explanation of 72.5%. A Monte Carlo test was significant for both Axes ($p = 0.0196$). A final stress of 15.57997 with a final instability of 0.00000 was reached after 89 iterations.

The ordination in Figure 3.18 is an NMS joint plot of the algal abundances from all MR samples, and associated variables. Final stress was moderate (±15). This ordination can still correspond to a usable picture, and given the complexity of most ecological community data sets, the stress value is satisfactory. Figure 3.18 shows that the algal composition of the MR sites was rather homogenous when comparing the different sites with one another.

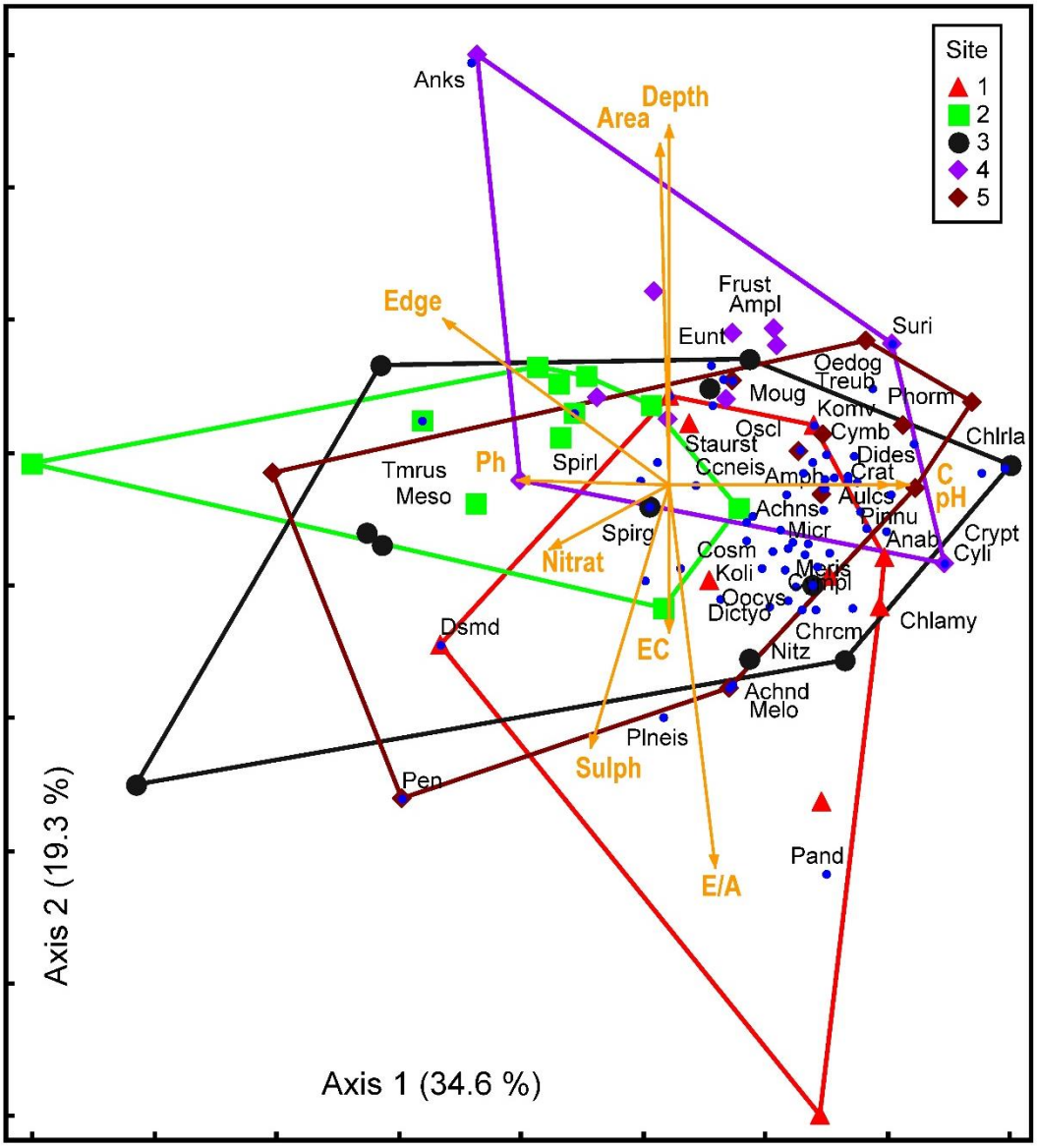

Figure 3.19: NMS joint plot of Algae (67 genera and 54 sites) abundances of all samples from WFS and environmental variables. (Distance measure = Sørensen; Number of dimensions in final solution = 3; Variance: Axis 1 = 34.6%, Axis 2 = 19.3%; Final stress = 14.10570; Final instability = 0.00000).

An NMS was carried out in PC-ORD. NMS was undertaken using Sørensen distance measure and random starting coordinates with four axes. Dimensionality was reduced by one at each cycle. Initial step length towards minimum stress was 0.20. The stability criterion was 0.000010, with 10 iterations to evaluate stability. A Monte Carlo test was carried out using 50 runs. Three dimensions were derived. Axis 1 explained 34.6% of variation and Axis 2 19.3% of variation, for a cumulative explanation of 53.9%. A Monte Carlo test was significant for both Axes (p = 0.0196). A final stress of 14.10570 with a final instability of 0.00000 was reached after 108 iterations.

The ordination in Figure 3.19 is an NMS joint plot of the algal abundances from all WFS samples, and associated variables. Final stress was moderate (<15) and the ordination can still correspond to a usable picture. Figure 3.19 shows that the algal composition of WFS was rather homogenous when comparing the different sites with one another.

NMS ordinations of algal assemblages show a clear distinction between rivers (Figure 3.17), but a relatively homogenous distribution in ordination space of the sites within each river (Figure 3.18 and Figure 3.19).

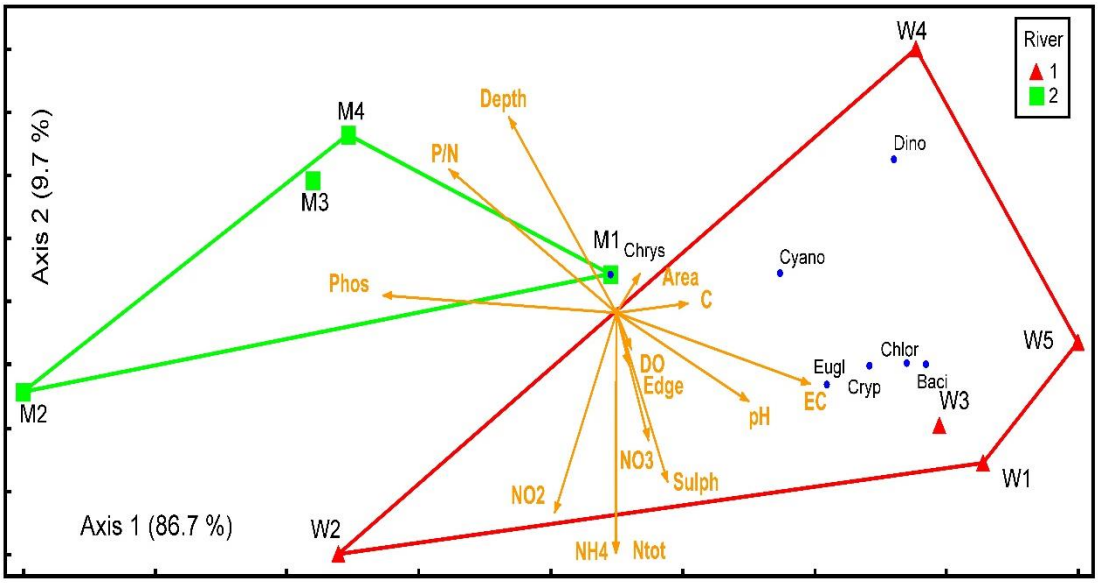

Figure 3.20: NMS joint plot of algal classes and environmental variables. (Distance measure = Sørensen; Number of dimensions in final solution = 2; Variance: Axis 1 = 86.7%, Axis 2 = 9.7%; Final stress = 1.94960; Final instability = 0.00000).

An NMS was carried out in PC-ORD. NMS was undertaken using Sørensen distance measure and random starting coordinates with four axes. Dimensionality was reduced by one at each cycle. Initial step length towards minimum stress was 0.20. The stability criterion was 0.000010, with 10 iterations to evaluate stability. A Monte Carlo test was carried out using 50 runs. Two dimensions were derived. Axis 1 explained 86.7% of variation and Axis 2 9.7% of variation, for a cumulative explanation of 96.4%. A Monte Carlo test was significant for both Axes (Axis 1 p = 0.0196; Axis 2 p = 0.0392). A final stress of 1.94960 with a final instability of 0.00000 was reached after 65 iterations.

The ordination in Figure 3.20 is an NMS joint plot of abundances of algal classes for all sites and associated variables. Final stress was very low (<2) which indicates an excellent representation with no prospect of misinterpretation. Axis 1 explained the majority of variation (86.7%) with axis 2 explaining relatively little (9.7%). Bacillariophyceae, Chlorophyceae, Cryptophyceae, and Euglenophyceae were ordinated towards W1, W3 and W5.

Cyanobacteria were ordinated closer toward WFS sites and Dinophyceae was ordinated close to W4. None of the algal classes were closely correlated with MR sites. Phosphorus, depth and phosphorus-nitrogen ratio were strongly correlated with MR. pH and conductivity were strongly correlated with WFS.

3.4.3 Two-way cluster analysis

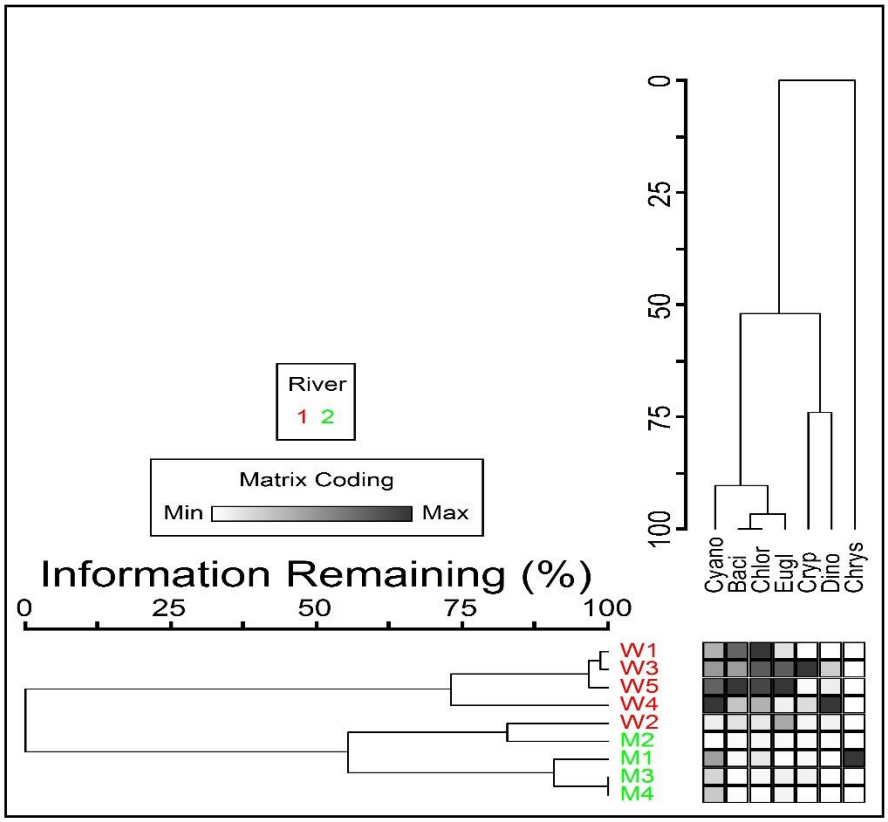

Figure 3.21: Two-way cluster dendrogram of algal classes of all the different sites (Distance measure = Sørensen; Linkage method = flexible beta of -0.25; Percent chaining on first cluster = 6.67; Percent chaining on transpose cluster = 100).

Two-way cluster analysis allows one to assign simultaneously sample units and species to groups by performing two separate cluster analysis: one on the normal matrix, looking for groups within your rows, and one on a transposed matrix, looking for groups within columns (Peck, 2010). The cluster analysis of abundances of algal classes looks similar to the cluster analysis of algal abundances (Figure 3.16). This is because the data sets are in essence the same data with the same abundances, but each genus is now assigned to a class. A two-way cluster analysis allows one to identify which class or combination of classes, and abundance per class were responsible for grouping certain sites closer to one another. W1, W3 and W5 were grouped very close together and the transposed cluster shows that this was because of similarities of cyanobacteria, Bacillariophyceae and Chlorophyceae abundances. W4 were clustered with the abovementioned sites, differing from them in higher

cyanobacteria and Dinophyceae abundances. There is a division between the two rivers, with W2 being clustered together with MR sites. This is due to dissimilar abundances of cyanobacteria, Bacillariophyceae, Chlorophyceae, and Euglenophyceae.

3.4.4 Principle component analysis (PCA)

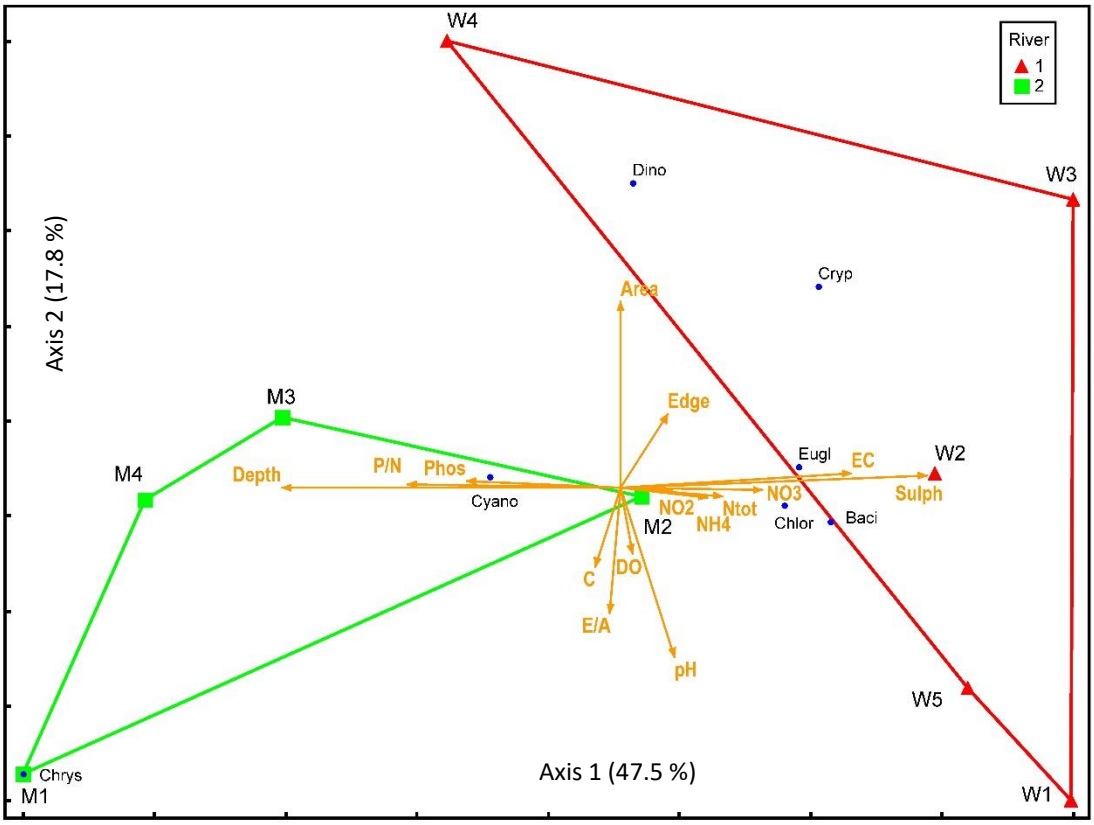

Figure 3.22: PCA joint plot of algal classes relativised by sites and environmental variables.

The ordination in Figure 3.22 is a PCA joint plot of abundances of algal classes and associated variables. Abundances were relativised by site to indicate which classes form the main components of all sites. Two axes were derived. Axis 1 explained 47.5% of variance and axis 2 explained 17.8% of variance, for a cumulative explanation of 65.3%. MR sites were ordinated to the left and WFS sites were ordinated to the right, and the two rivers are clearly separated in terms of algal class composition.

PCA is an ideal technique to use for data with approximately linear relationships among variables. Ecological community data, however, is often not compatible with this method because it does not deal well with zeros. This occurs because PCA interprets shared zeros as an indication of a positive relationship (McCune & Grace, 2002). PCA was used here because an NMS ordination could not be reached. Abundances were relativised by site to show the contribution of each class to the site total. Relativisation eliminates extremities in the

data matrix and results in a much more homogenous dataset. With relatively homogenous community data sets, PCA can be an effective tool for ordinating community data (McCune & Grace, 2002). PCA was used to identify components in the data set that maximises variance and which variables are correlated with those components. Cyanobacteria were strongly correlated with water depth, phosphorus, and phosphorus-nitrogen ratio. Dinophyceae was correlated with surface area, while Euglenophyceae, Bacillariophyceae, and Chlorophyceae were strongly correlated with sulphate, conductivity, and all dissolved inorganic nitrogen forms.

3.4.5 Indicator species analysis (ISA)

Dufrêne and Legendre's (1997) method of indicator species analysis allows one to assess the degree to which a species (in this case genus) indicates a group based on its constancy and distribution of abundance (Peck, 2010). A perfect indicator of a particular group should be faithful (always present) and exclusive to that group, never occurring in other groups. This method produces indicator values (IV) for each species, based on the standards of a perfect indicator. These indicator values range from 0 (no indication) to 100 (perfect indication) and can be tested for statistical significance using a randomisation (Monte Carlo) technique (McCune & Grace, 2002; Peck, 2010).

Table 3.12: Observed indicator values (OIV) of algae genera between rivers and for sites within each river.

Genus	Abbr	Observed Indicator Value										
		River						Sites				
		MR	WFS	M1	M2	M3	M4	W1	W2	W3	W4	W5
Oscillatoria	Oscl		43.5**								53.8**	
Merismopedia	Meris									32.7*		
Aulacoseira	Aulcs		24.1***					15.4				
Craticula	Crat		31.5***									44.3**
Nitzschia	Nitz		77***					34.8				
Amphora	Amph		18.3**									19.9
Cyclotella	Cyclt		38.3**							32.7		
Gyrosigma	Gyro		18.5**							39.9**		
Navicula	Nav		63.3**									60.1**
Cymbella	Cymb		19.1*									28.5*
Rhopalodia	Rhopa	9.1*					25.0					
Diadesmis	Dides			50.9**								
Gomphonema	Gmph											30.5*
Ulothrix	Uthrix		37.8***									76***
Tetrastrum	Tastr	15.9**		54.1***								
Actinastrum	Actstrum		14.8*							17.1		
Chlamydomonas	Chlamy		61.4*					34.0				
Chlorococcum	Chlccm		23.1*							22.1		
Closterium	Clst		25*			30.7*				19.6		
Monoraphidium	Mrphd		66.6*									43.5
Scenedesmus	Scndsm		46.2*	54**				28.7				
Dictyosphaerium	Dictyo			34.6*								
Characium	Chrcm							20*				
Euglena	Eugl		49.9**									35.5
Phacus	Phcs		43.9**							43.4*		

Trachelomonas	Trach	63.4**	31.4
Strombomonas	Stromb	12.5*	8.7

* $p < 0.05$ ** $p < 0.01$ ***$p < 0.001$

All algae genera with a significant IV ($p < 0.05$) are listed in Table 3.12. Three ISAs were done for algae, one to assess indicators of each river (WFS vs MR), and one each per river. Indicator values of genera identified in the first ISA (WFS vs MR) are given for the following ISA, even if values were not significant.

Indicator species analysis between rivers showed that MR had very few indicator genera (2) compared with WFS (20). This is because MR had few genera that was exclusive (not occurring in WFS) and those that were exclusive were not faithful (ever present) to MR. WFS on the other hand had a large number of genera that was exclusive (only occurring in WFS) and faithful. The two indicator genera of MR were *Rhopalodia* and *Tetrastrum*. Indicator genera of WFS were from four classes:

1) Cyanobacteria:
   - *Oscillatoria*;
2) Bacillariophyceae*:*
   - *Amphora*,
   - *Aulacoseira*,
   - *Craticula*,
   - *Cyclotella*,
   - *Cymbella*,
   - *Gyrosigma*,
   - *Navicula*, and
   - *Nitzschia*;
3) Chlorophyceae:
   - *Actinastrum*,
   - *Chlamydomonas*,
   - *Chlorococcum*,
   - *Closterium*,
   - *Monoraphidium*,
   - *Scenedesmus*, and
   - *Ulothrix*;
4) Euglenophyceae:
   - *Euglena*,
   - *Phacus*,
   - *Strombomonas*, and
   - *Trachelomonas*.

The genera listed for rivers in Table 3.12 are those with a significant indicator value; however, some of these indicator values were quite low, and it may therefore not be that

useful. For rivers, genera with an OIV above 30, I regard as moderate indicators, above 60 as good indicators, and above 75 as very good indicators. Both indicators for MR have very low indicator values. Genera regarded as moderate indicators of WFS were *Oscillatoria*, *Cyclotella*, *Ulothrix*, *Scenedesmus*, *Euglena*, and *Phacus*. Genera regarded as good indicators of WFS were *Nitzschia*, *Navicula*, *Chlamydomonas*, *Monoraphidium*, and *Trachelomonas*.

Indicator species analysis between sites showed that MR sites had relatively few significant indicator genera. M1 had four (*Diadesmis*, *Dictyosphaerium*, *Scenedesmus*, and *Tetrastrum*) and M3 one (*Closterium*), while M2 and M4 had none, of which all were moderate indicators (30 <IV<60). Indicator species analysis between sites showed that WFS sites had twice as many significant indicator genera. W1 (*Characium*) and W4 (*Oscillatoria*) had one each, W3 had three (*Merismopedia*, *Gyrosigma*, and *Phacus*), and W5 had five (*Craticula*, *Navicula*, *Cymbella*, *Gomphonema*, and *Ulothrix*) indicator genera. Genera that were moderate indicators included *Merismopedia*, *Oscillatoria*, *Craticula*, *Gyrosigma*, *Gomphonema*, and *Phacus* (30 <IV<60), while *Navicula* and *Ulothrix* were good indicators (IV>60).

3.4.6 Analysis of similarity (ANOSIM) and similarity percentage (SIMPER)

ANOSIM is a non-parametric test of significant difference between two or more groups, based on any distance measure. The distances were converted to ranks (Hammer *et al*., 2001). ANOSIM gives a p-value (significance level) and an R-value (strength of factors on samples). The R-value vary between 0 and 1, with a value close to one indicating high separation between levels of your factor, while an R-value close to zero indicates no separation. The R-value in ANOSIM is a ratio between within-group and between-group dissimilarities. ANOSIM calculates a matrix of dissimilarity scores for every pair of sites, and converts the dissimilarities to ranks. These ranks are then used to calculate the R-value as the ratio between dissimilarities between sites within a group, and the dissimilarities between sites of different groups. The significance of the R-value is then determined by permuting the memberships of sites in groups.

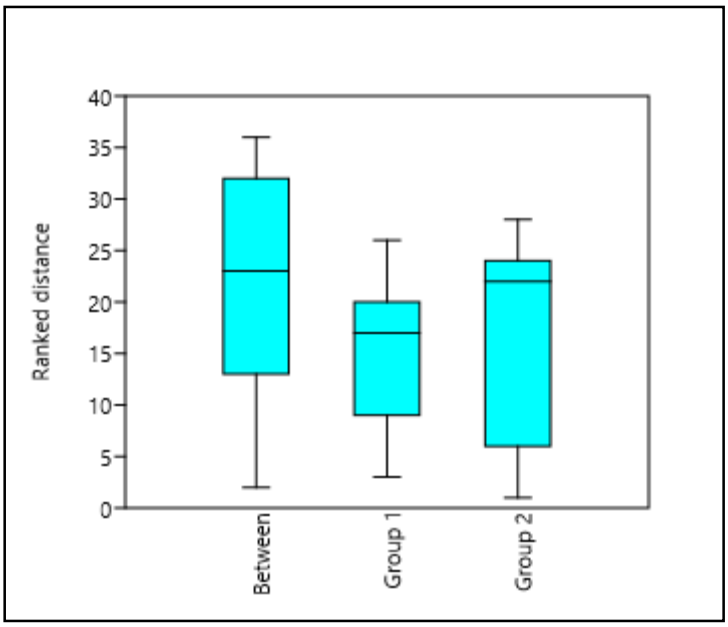

Figure 3.23: Box plot indicating the mean rank within groups and mean rank between groups (Distance measure = Sørensen; Mean rank within 14.56; Mean rank between = 21.65; Number of permutations = 9 999; R = 0.3937).

Figure 3.23 displays the differences between groups and the differences within each group (Group 1 = MR; Group 2 = WFS) as a box plot of ranked distances. Analysis of similarities yielded an R-value of 0.3937, indicating that WFS and MR are different, with some overlap. A one-tailed significance was computed by permutation of group membership, with 9 999 replicates. The mean rank between groups was greater than the mean rank within groups (p = 0.0439).

Similarity Percentage (SIMPER) is a simple method for assessing which taxa are primarily responsible for an observed difference between groups of samples (Hammer *et al*., 2001). The Sørensen similarity measure was used. The overall average dissimilarity was 66.55. Table 3.13 shows the genera that had the greatest influence on dissimilarity between WFS and MR. *Phormidium*, *Oscillatoria*, *Ulothrix*, *Nitzschia*, *Pandorina*, *Aphanocapsa*, and *Chlamydomonas* contributed 66% of the observed differences between groups (Rivers). From the 83 genera recorded on both rivers, 21 genera contributed over 90% of the observed difference between WFS and MR (see Table 3.13). Table 3.14 shows that Chlorophyceae and cyanobacteria had the greatest influence on dissimilarity and accounted for 75% of the observed difference between rivers.

Table 3.13: SIMPER results showing genera that had the greatest influence on dissimilarity between WFS and MR.

Genus	Average dissimilarity	Contribution percentage (%)	Cumulative percentage (%)
Phormidium	11.07	16.63	16.63
Oscillatoria	8.703	13.08	29.71
Ulothrix	5.654	8.496	38.2
Nitzschia	5.446	8.183	46.39
Pandorina	4.669	7.016	53.4
Aphanocapsa	4.495	6.755	60.16
Chlamydomonas	4.032	6.059	66.21
Scenedesmus	1.829	2.748	68.96
Anabaena	1.743	2.619	71.58
Euglena	1.701	2.555	74.14
Chlorella	1.605	2.412	76.55
Monoraphidium	1.308	1.965	78.51
Cyclotella	1.189	1.786	80.3
Navicula	1.075	1.616	81.92
Coelastrum	1.016	1.527	83.44
Dictyosphaerium	0.9716	1.46	84.9
Merismopedia	0.8038	1.208	86.11
Trachelomonas	0.7503	1.127	87.24
Aulacoseira	0.6961	1.046	88.28
Melosira	0.6741	1.013	89.3
Oocystis	0.6487	0.9747	90.27

Table 3.14: SIMPER results showing algal classes that had the greatest contribution on dissimilarity between WFS and MR.

Class	Average dissimilarity	Contribution percentage (%)	Cumulative percentage (%)
Chlorophyceae	22.68	40.74	40.74
Cyanobacteria	19.28	34.64	75.38
Bacillariophyceae	10.07	18.08	93.46
Euglenophyceae	2.969	5.332	98.79
Dinophyceae	0.3816	0.6854	99.47
Cryptophyceae	0.2825	0.5075	99.98
Chrysophyceae	0.01036	0.01861	100

3.5 MULTIVARIATE ANALYSIS OF BIRDS

3.5.1 Cluster analysis

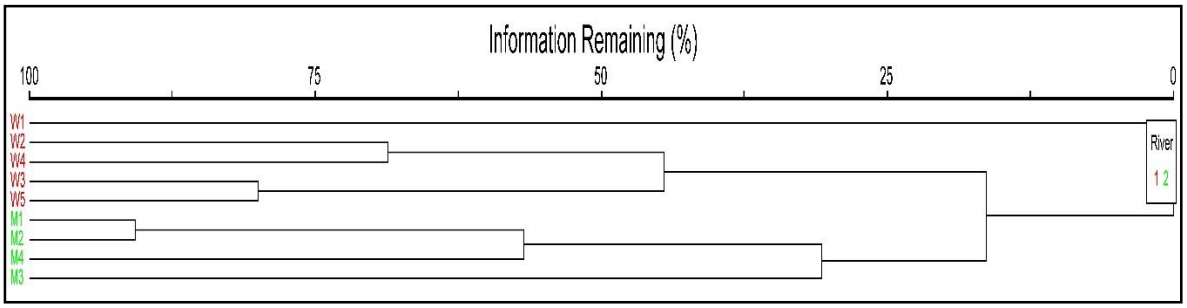

Figure 3.24: Cluster dendrogram of bird assemblages of all the different sites (Distance measure = Sørensen; Linkage method = group average; Percent chaining = 33.33).

A hierarchical cluster analysis was performed to group all sites according to their avian composition. The distance measure selected was Sørensen, with group average as linkage method. This linkage method is space conserving, not dependent on sample size, and not known to combine groups out of order (Peck, 2010). WFS and MR sites are completely split at around 30% of information remaining. This shows that there is a clear distinction between the bird composition of WFS and MR sites. From WFS sites, one can see that W2 and W4 are similar, W3 and W5 are similar, and that W1 is dissimilar to the other WFS sites. MR sites are separated from WFS sites, with M1 and M2 being very similar (combining at 90% of information remaining).

3.5.2 Nonmetric multidimensional scaling (NMS)

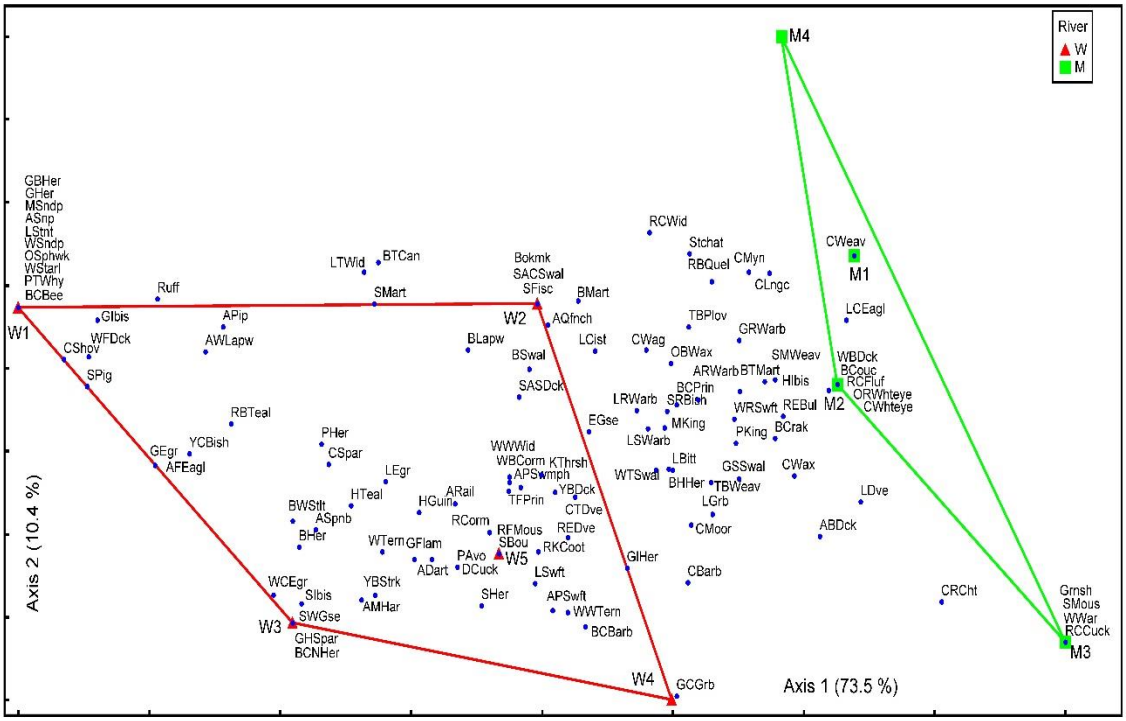

Figure 3.25: NMS of bird (119 species and 9 sites) abundances per site. (Distance measure = Sørensen; Number of dimensions in final solution = 2; Variance: Axis 1 = 73.5%, Axis 2 = 10.4%; Final stress = 8.77393; Final instability = 0.00000).

An NMS was carried out in PC-ORD. NMS was undertaken using Sørensen distance measure and random starting coordinates with four axes. Dimensionality was reduced by one at each cycle. Initial step length towards minimum stress was 0.20. The stability criterion was 0.000010, with 10 iterations to evaluate stability. A Monte Carlo test was carried out using 50 runs. Two dimensions were derived. Axis 1 explained 73.5% of variation and Axis 2 10.4% of variation, for a cumulative explanation of 83.9%. A Monte Carlo test was significant for both Axes ($p = 0.0196$). A final stress of 8.77393 with a final instability of 0.00000 was reached after 42 iterations.

Final stress was fair (<10) which indicates a good ordination with no real risk of drawing false inferences. Axis 1 explained majority of variance (73.5%) with Axis 2 explaining relatively little (10.4%). Because an open radius were used when conducting point counts, units are not necessarily on the same scale as water masses differed in surface area. Abundances were therefore relativised by species to make units comparable. Convex hulls were used to indicate the boundaries of the different sites of each river in ordination space. There was no overlap of convex hulls signifying that there was a distinction between rivers with regard to bird assemblages. MR sites are ordinated closer toward each other in comparison to WFS sites, indicating that WFS had a greater diversity than MR.

Species outside the convex hulls for WFS and MR, and ordinated between the two rivers indicate species that occurred on both rivers at more or less equal ratios. These include 37 species that can be placed in six broad artificial groups:

1) Waxbill-widow-weavers:
   - Common Waxbill,
   - Orange-breasted Waxbill,
   - Red-collared Widowbird,
   - Red-billed Quelea,
   - Southern Red Bishop,
   - Southern Masked Weaver, and
   - Thick-billed Weaver;
2) Small insectivores:
   - African Stonechat,
   - Levaillant's Cisticola,
   - Black-chested Prinia,
   - Cape Wagtail,
   - Cape Longclaw, and
   - Cape Robin-Chat;
3) Warblers:
   - Great Reed Warbler,
   - African Reed Warbler,
   - Little Rush Warbler, and
   - Lesser Swamp Warbler;
4) Swallows-martins-swifts:
   - Banded Martin,
   - Brown-throated Martin,
   - White-throated Swallow,
   - Greater Striped Swallow, and
   - White-rumped Swift;
5) Water birds:
   - Malachite Kingfisher,
   - Pied Kingfisher,
   - Black Crake,
   - Common Moorhen,
   - Little Grebe,
   - Little Bittern,

- Three-banded Plover,
- African Black Duck, and
- Egyptian Goose;

6) Other:

- Black-headed Heron,
- Hadeda Ibis,
- Laughing Dove,
- Common Myna,
- Crested Barbet, and
- African Red-eyed Bulbul.

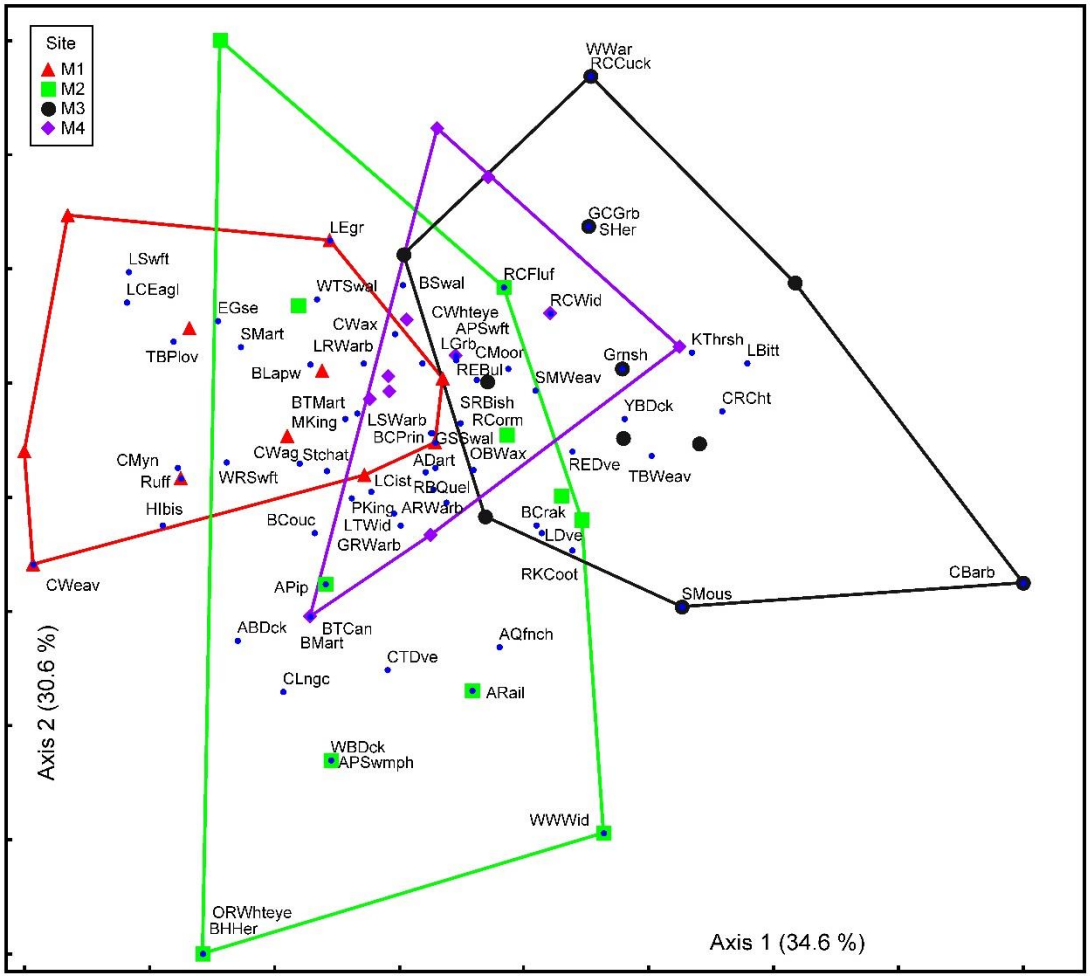

Figure 3.26: NMS of bird abundances (71 species and 44 sites) using all surveys from MR. (Distance measure = Gower Ignore 0; Number of dimensions in final solution = 2; Variance: Axis 1 = 34.6%, Axis 2 = 30.6%; Final stress = 25.86177; Final instability = 0.00000)

An NMS was carried out with PC-ORD. NMS was undertaken using Gower ignore 0 distance measure and starting coordinates from file with two axes. Dimensionality was reduced by two at each cycle. Initial step length towards minimum stress was 0.20. The

stability criterion was 0.000010, with 10 iterations to evaluate stability. A Monte Carlo test was carried out using 50 runs. Two dimensions were derived. Axis 1 explained 34.6% of variation and Axis 2 30.6% of variation, for a cumulative explanation of 65.2%. A Monte Carlo test was significant for both Axes (Axis 1 p = 0.0392; Axis 2 p = 0.0196). A final stress of 25.86177 with a final instability of 0.00000 was reached after 107 iterations.

Final stress was poor (>25) which indicates an ordination that should be interpreted with care. It is however, sufficient to conclude that the avian compositions of MR sites are rather homogenous as the convex hulls of all sites overlapped to a large degree.

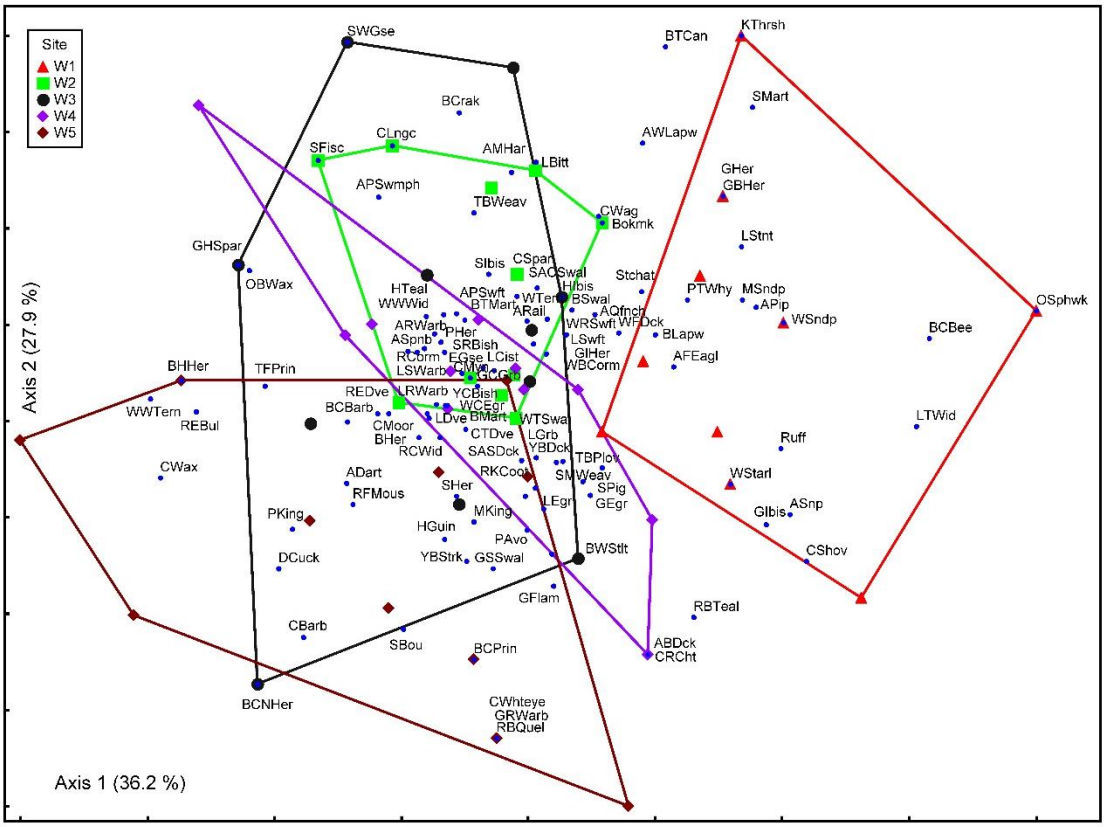

Figure 3.27: NMS of bird abundances (109 species and 54 sites) of all samples from WFS. (Distance measure = Gower Ignore 0; Number of dimensions in final solution = 2; Variance: Axis 1 = 36.2%, Axis 2 = 27.9%; Final stress = 27.39688; Final instability = 0.00000)

An NMS was carried out in PC-ORD. NMS was undertaken using Gower ignore 0 distance measure and random starting coordinates with four axes. Dimensionality was reduced by one at each cycle. Initial step length towards minimum stress was 0.20. The stability criterion was 0.000010, with 10 iterations to evaluate stability. A Monte Carlo test was carried out using 50 runs. Two dimensions were derived. Axis 1 explained 36.2% of variation and Axis 2 27.9% of variation, for a cumulative explanation of 64.1%. A Monte Carlo test was significant for only one Axis (Axis 1 p = 0.0784; Axis 2 p = 0.0392). A final stress of 27.39688 with a final instability of 0.00000 was reached after 79 iterations.

Final stress was poor (>25) which indicates an ordination that should be interpreted with care. It is however, sufficient to conclude that the avian compositions of W2 - W5 are rather homogenous as the convex hulls of each site overlapped to a large degree. The convex hull of W1 did not overlap with the rest of the WFS sites, which indicates that its avian composition could be considered different when compared with the other WFS sites.

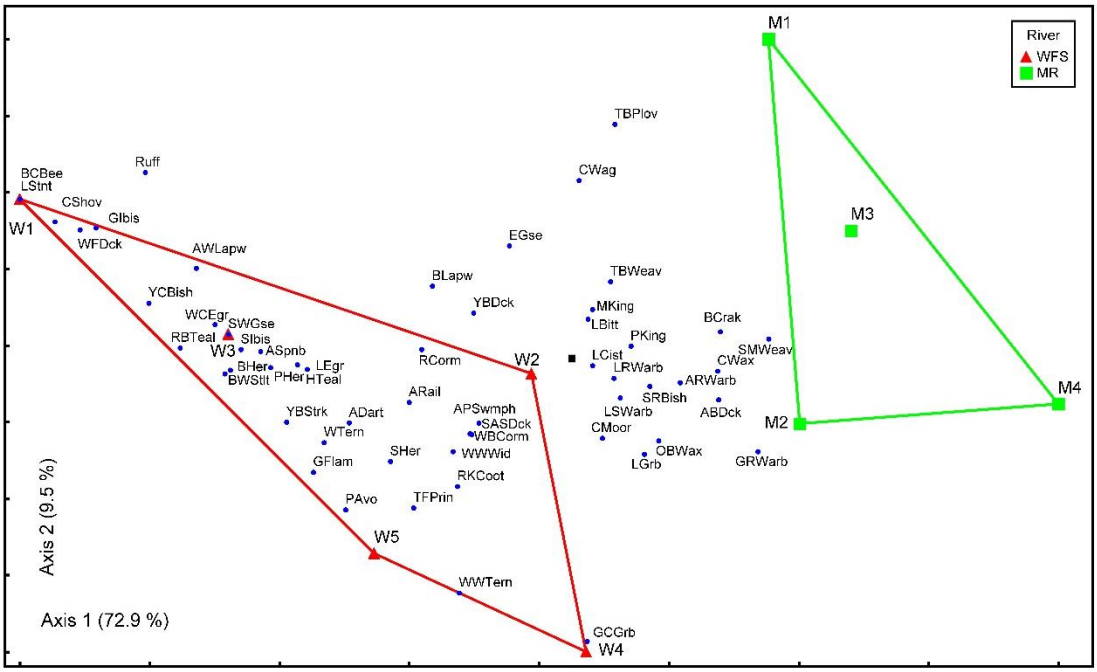

Figure 3.28: NMS of water associated bird (56 species and 9 sites) abundances per site. (Distance measure = Sørensen; Number of dimensions in final solution = 2; Variance: Axis 1 = 72.9%, Axis 2 = 9.5%; Final stress = 7.89073; Final instability = 0.00000)

The data set was split into two data sets, aquatic (water associated) species and terrestrial (non-water associated) species. Species with abundances of three and less were excluded for both data sets. The swallows, swifts, and martins were also excluded, as direct interaction with water is difficult to confirm while flying, or merely resting in the vegetation. An NMS was carried out in PC-ORD. NMS was undertaken using Sørensen distance measure and random starting coordinates with four axes allowed. Dimensionality was reduced by one at each cycle. Initial step length towards minimum stress was 0.20. The stability criterion was 0.000010, with 10 iterations to evaluate stability. A Monte Carlo test was carried out using 50 runs. Two dimensions were derived. Axis 1 explained 72.9% of variation and Axis 2 9.5% of variation, for a cumulative explanation of 82.4%. A Monte Carlo test was significant for both Axes (p = 0.0196). A final stress of 7.89073 with a final instability of 0.00000 was reached after 43 iterations.

Figure 3.28 is an NMS of aquatic bird abundances. Final stress was fair (<10) indicating an ordination with no real risk of drawing false inferences. Convex hulls were used to indicate the boundaries of the different sites of each river in ordination space. There was

no overlap of convex hulls indicating a distinction between rivers with regard to water-associated bird assemblages. MR sites ordinated to the right of the origin, while WFS sites ordinated to the left, which indicates that the aquatic bird assemblages of the two rivers are completely different. W1 is ordinated furthest from the origin. This indicates that W1 had a unique water bird assemblage, when compared with all other sites.

Species ordinated between WFS and MR can be placed in four groups representing the species responsible for similarities between rivers. This include 1) weavers-waxbills-bishops - Thick-billed Weaver, Southern Masked Weaver. Southern Red Bishop, Common Waxbill, and Orange-breasted Waxbill; 2) Warblers - Little Rush Warbler, Lesser Swamp Warbler, African Reed Warbler, and Great Reed Warbler; 3) small piscivores - Malachite Kingfisher, Pied Kingfisher, and Little Bittern; 4) swimming/floating water birds - Common Moorhen, African Black Duck, and Little Grebe. Species ordinated towards WFS can be placed into seven functional groups, namely:

1) bishop-widows:
    - White-winged Widowbird, and
    - Yellow-crowned Bishop;
2) ducks-geese-teals (order Anseriformes):
    - South African Shelduck,
    - Spur-winged Goose,
    - Hottentot Teal,
    - Red-billed Teal,
    - Cape Shoveler, and
    - White-faced Whistling Duck;
3) diving-swimming piscivores:
    - Reed Cormorant,
    - White-breasted Cormorant,
    - Great Crested Grebe, and
    - African Darter;
4) herons-egrets:
    - Squacco Heron,
    - Purple Heron,
    - Black Heron,
    - Little Egret, and
    - Western Cattle Egret;
5) probing-waders:
    - African Rail,
    - Pied Avocet,

- Black-winged Stilt,
- African Sacred Ibis,
- African Spoonbill,
- Glossy Ibis,
- Little Stint, and
- African Wattled Lapwing;

6) other piscivores:
   - White-winged Tern,
   - Whiskered Tern, and
   - Yellow-billed Stork;
7) herbivores:
   - African Purple Swamphen, and
   - Red-knobbed Coot.

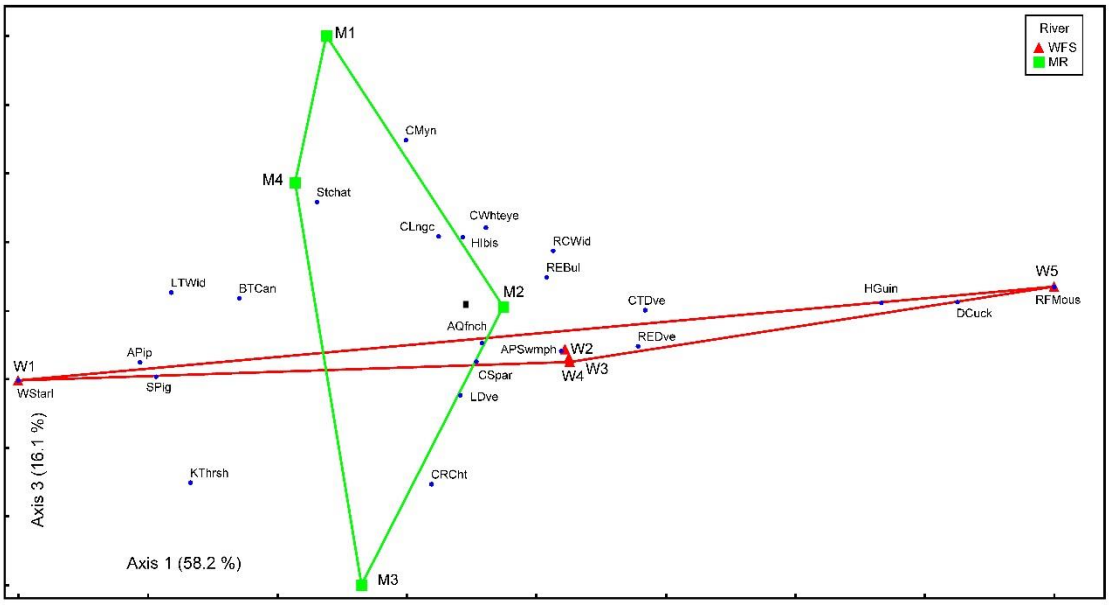

Figure 3.29: NMS of terrestrial bird abundances per site (23 species and 9 sites). (Distance measure = Gower ignore 0; Number of dimensions in final solution = 3; Variance: Axis 1 = 58.2%, Axis 2 = 16.1%; Final stress = 0.16069; Final instability = 0.00000)

An NMS was carried out in PC-ORD for terrestrial birds. NMS was undertaken using Gower ignore 0 distance measure and random starting coordinates with four axes. Dimensionality was reduced by one at each cycle. Initial step length towards minimum stress was 0.20. The stability criterion was 0.000010, with 10 iterations to evaluate stability. A Monte Carlo test was carried out using 50 runs. Two dimensions were derived. Axis 1 explained 58.2% of variation and Axis 2 16.1% of variation, for a cumulative explanation of 74.3%. A

Monte Carlo test was not significant for both Axes (Axis 1 p = 0.1176; Axis 2 p = 0.1765). A final stress of 0.16069 with a final instability of 0.00000 was reached after 39 iterations.

Figure 3.29 is an NMS of non-water associated bird abundances. Final stress was excellent (<1) indicating an ordination with no risk of drawing false inferences. After excluding water associated bird species, the two rivers were much more comparable with regard to terrestrial bird assemblages. Axis 1 explained the majority of variation. This indicates that the terrestrial bird communities of W2, W3, and W4, were quite similar to that of MR. Terrestrial bird communities of W1 and W5, however, differed considerably from the rest of WFS sites. Terrestrial bird composition of W5 was most dissimilar from MR sites.

3.5.3 Indicator Species Analysis (ISA)

Table 3.15: Observed indicator values (OIV) of bird species between rivers and for sites within each river.

Species	Abbr	Observed Indicator Value										
		River						Sites				
		MR	WFS	M1	M2	M3	M4	W1	W2	W3	W4	W5
Bee-eater, Blue-cheeked	BCBee							30**				
Bulbul, African Red-eyed	REBul	25.8*		33.9*								29.1*
Coot, Red-knobbed	RKCoot		80.5***		43.2**							26.5
Cormorant, Reed	RCorm		39.3*	18.5						46.6**		
Crake, Black	BCrak	15.8*				13				10.9		
Darter, African	ADart		24.8**							21.4		
Dove, Cape Turtle	CTDve		25.6*		20.8						16.5	
Dove, Laughing	LDve	32.2***			31.8					18.2		
Dove, Red-eyed	REDve		48.5*			38.3*				41.2**		
Duck, White-faced	WFDck		13*					32.2*				
Duck, Yellow-billed	YBDck					57.8***		16.2				
Egret, Western Cattle	WCEgr		18.5**							49.3**		
Flamingo, Greater	GFlam		16.7**									24.0
Goose, Egyptian	EGse			20.5						31.4**		
Grebe, Great Crested	GCGrb		19.8**			9.1					88.9***	
Grebe, Little	LGrb				40.3*						39.7**	
Heron, Black	BHer		11.1*							14.6		
Heron, Purple	PHer		13*					9.6				
Heron, Squacco	SHer		17*			9.1				12.9		
Ibis, African Sacred	SIbis		11.1*							30.1*		
Ibis, Glossy	GIbis		11.1*					33.6**				
Kingfisher, Pied	PKing				9.9							36.4**
Lapwing, Blacksmith	BLapw			37.6*				52.3***				

Martin, Sand	SMart			12.1				20*				
Masked-Weaver, Southern	SMWeav	77.8***					40.0					25.8
Moorhen, Common	CMoor					45.5**					37.4**	
Pipit, African	APip							20*				
Plover, Three-banded	TBPlov			54.5***								
Reed-Warbler, African	ARWarb	34.2*			39*				18.8			
Ruff	Ruff			9.1				30**				
Sandpiper, Marsh	MSand							20*				
Shelduck, South African	SASDck		24.1**						46.2**			
Snipe, African	ASnp							20*				
Spoonbill, African	ASpnb		14.8*							16.1		
Stilt, Black-winged	BWStlt		13*							11.1		
Stint, Little	LStnt							30*				
Stonechat, African	Stchat	28.8***		30.5				12.9				
Swallow, South-african Cliff	SACSwal								45.5***			
Swamphen, African Purple	APSwmph		14.7*		9.1				16.2			
Swift, African Palm	APSwft		21.5**				9.1				36.6**	
Swift, White-rumped	WRSwft			29.2*							12.5	
Teal, Hottentot	HTeal		16.7**							13.5		
Teal, Red-billed	RBTeal		16.7**					16.5				
Tern, Whiskered	WTern		11.1*								7.1	
Thrush, Karoo	KThrsh					36.4**						
Wagtail, Cape	CWag			52.1**								
Waxbill, Common	CWax					11.9						24.8*
Weaver, Thick-billed	TBWeav					51.8**						
Whydah, Pin-tailed	PTWhy							30*				
Widowbird, Long-tailed	LTWid							30*				
Widowbird, White-winged	WWWid		13.8*		9.1							

* $p < 0.05$ ** $p < 0.01$ ***$p < 0.001$

All bird species with a significant IV ($p < 0.05$) were listed in Table 3.15. Three ISAs were done, one to assess indicators of each river (WFS vs MR), and one each per river. Indicator values of genera identified in the first ISA (WFS vs MR) are given for the following ISA, even IF values were not significant.

Birds are much more mobile when compared with algae and can easily cover the relatively small distance between the two rivers even if not directly connected by water flow. Therefore, the same criteria as algae for indicator values cannot be used as majority of bird species will not be exclusive to one river. Consequently, indicator values will be lower for bird species than for algal genera. Indicator values above 20 were considered moderate, above 45 as good and above 75 as excellent. Indicator species analysis between rivers showed that MR had very few significant indicator species (6) compared to WFS (23). This is because most species that were recorded along the MR were also present on WFS and in similar or greater numbers.

Indicator species that were significant for MR included African Red-eyed Bulbul, Black Crake, Laughing Dove, Southern Masked Weaver, African Reed Warbler, and African Stonechat. From these, African Red-eyed Bulbul, Laughing Dove, African Reed Warbler, and African Stonechat were moderate indicators, with Southern Masked Weaver being an excellent indicator for MR.

Indicator species significant for WFS were Red-knobbed Coot, Reed Cormorant, African Darter, Cape Turtle Dove, Red-eyed Dove, White-faced Whistling Duck, Western Cattle Egret, Greater Flamingo, Great-crested Grebe, Black Heron, Purple Heron, Squacco Heron, African Sacred Ibis, Glossy Ibis, South African Shelduck, African Spoonbill, Black-winged Stilt, African Purple Swamphen, African Palm Swift, Hottentot Teal, Red-billed Teal, Whiskered Tern, and White-winged Widowbird. Moderate indicators for WFS were Reed Cormorant, African Darter, Cape Turtle Dove, South African Shelduck, and African Palm Swift. Red-eyed Dove was a good and Red-knobbed Coot an excellent indicator for WFS.

Indicator species analysis between MR sites showed that M1 and M3 had the most significant indicator species (5 and 6 respectively), with M2 having three and M4 none. Indicator species significant for M1 were African Red-eyed Bulbul, Blacksmith Lapwing, White-rumped Swift (moderate), Three-banded Plover, and Cape Wagtail (good). Significant indicators for M2 were Red-knobbed Coot, Little Grebe, and African Reed Warbler (moderate), while Red-eyed Dove, Karoo Thrush (moderate), Yellow-billed Duck, Common Moorhen, and Thick-billed Weaver (good) were significant indicators for M3.

Indicator species analysis between WFS sites showed that W1 had much more significant indicator species (12) when compared to the rest of the sites. Blue-cheeked Bee-eater, White-faced Whistling Duck, Glossy Ibis, Sand Martin, African Pipit, Ruff, Marsh

Sandpiper, Little Stint, African Snipe, Pin-tailed Whydah, and Long-tailed Widowbird were all moderate indicators, with Blacksmith Lapwing being the only good indicator species for W1. South African Shelduck and South African Cliff-swallow were good indicators for W2, while Red-eyed Dove, Egyptian Goose, African Sacred Ibis (moderate), Reed Cormorant, and Western Cattle Egret (Good) were indicators for W3. Little Grebe, Common Moorhen, and African Palm Swift were moderate, and Great Crested Grebe good indicators of W4. African Red-eyed Bulbul, Pied Kingfisher, and Common Waxbill were moderate indicators of W5.

3.5.4 Analysis of similarity (ANOSIM) and similarity percentage (SIMPER)

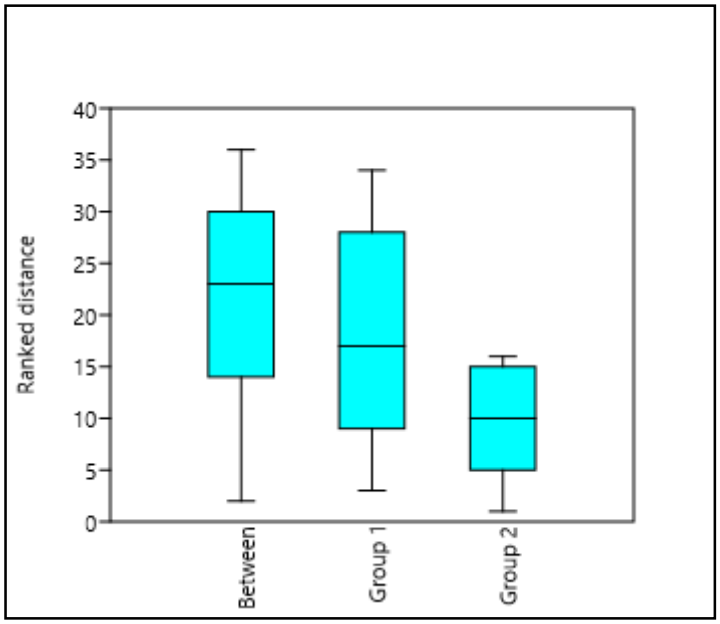

Figure 3.30: Box plot indicating the mean rank within groups and mean rank between groups (Distance measure = Sørensen; Mean rank within 14.19; Mean rank between = 21.95; Number of permutations = 9 999; R = 0.4312).

Figure 3.30 displays the differences between groups and the differences within each group (Group 1 = WFS; Group 2 = MR) as a box plot of ranked distances. Analysis of similarities yielded an R-value of 0.4312, which indicates that WFS and MR are different, with little overlap. A one-tailed significance was computed by permutation of group membership, with 9 999 replicates. The mean rank between groups was greater than the mean rank within groups (p = 0.0231).

Table 3.16: SIMPER results showing species that had the greatest influence on dissimilarity between WFS and MR.

Species	Average dissimilarity	Contribution percentage (%)	Cumulative percentage (%)
RKCoot	8.189	13.810	13.810
BSwal	7.260	12.240	26.050
SMWeav	6.764	11.410	37.460
SRBish	2.623	4.423	41.880
GFlam	2.553	4.306	46.190
BTMart	2.463	4.154	50.340
REDve	2.327	3.925	54.270
CMoor	1.690	2.850	57.120
RCorm	1.505	2.539	59.660
WCEgr	1.503	2.535	62.190
LGrb	1.381	2.329	64.520
APSwft	1.011	1.705	66.230
RBTeal	0.861	1.453	67.680
SASDck	0.824	1.389	69.070
LSWarb	0.823	1.388	70.460
BLapw	0.793	1.337	71.790
ADart	0.751	1.266	73.060
YBDck	0.746	1.259	74.320
LDve	0.684	1.154	75.470
GCGrb	0.620	1.045	76.520
TBWeav	0.521	0.878	77.390
LCist	0.515	0.869	78.260
REBul	0.514	0.867	79.130
ARWarb	0.492	0.830	79.960
EGse	0.486	0.819	80.780
CWax	0.445	0.750	81.530
CWag	0.431	0.726	82.250
Stchat	0.397	0.669	82.920
GIbis	0.387	0.653	83.580
LRWarb	0.360	0.607	84.180
BCBee	0.322	0.543	84.730
SACSwal	0.320	0.540	85.270
WFDck	0.315	0.531	85.800
TBPlov	0.296	0.498	86.290
WRSwft	0.276	0.465	86.760
HTeal	0.274	0.462	87.220
WStarl	0.254	0.429	87.650
GSSwal	0.254	0.429	88.080
CTDve	0.242	0.408	88.490
PKing	0.233	0.392	88.880
SWGse	0.232	0.392	89.270
AWLapw	0.232	0.391	89.660
AQfnch	0.227	0.384	90.050

Similarity Percentage (SIMPER) was used to assess which species were primarily responsible for an observed difference between the bird composition of WFS and MR. Sørensen similarity measure was used. The overall average dissimilarity was 59.3. Table 3.16 shows the species that had the largest influence on dissimilarity between WFS and MR. Red-knobbed Coot, Barn Swallow, Southern Masked Weaver, Southern Red Bishop, Greater Flamingo, and Brown-throated Martin were the main contributors to the observed difference between rivers, with a cumulative contribution of 50%. From the 119 species recorded on both rivers, 43 species contributed over 90 % of the observed difference between WFS and MR (Table 3.16).

CHAPTER 4: DISCUSSION, CONCLUSIONS, AND RECOMMENDATIONS

4.1 INFLUENCE OF WATER QUALITY PARAMETERS ON ALGAL COMPOSITION

4.1.1 pH

pH plays a major role in the biology of algae (Section 1.5.2.1). Moss (1973) investigated the effects of pH-CO_2-bicarbonate system on algal growth. He found that not only did different species show optimum growth at different pH values, but they also varied in their range of tolerance. pH values for WFS had a greater variance than that of MR, and a significantly higher mean. Therefore, algal genera that characterise WFS should be expected to have an optimum growth at higher pH, or have a greater tolerance range. There are several ways in which high pH might influence algae: 1) an intrinsic effect of pH on enzymes, in the cell wall or membrane, responsible for of one or more essential nutrients; 2) toxic effect of relatively high total dissolved ion content associated with high pH, 3) co-precipitation of phosphate with calcium, magnesium and carbonate at high carbonate levels, and 4) differential availability of different inorganic carbon compounds for photosynthesis (Moss, 1973). Genera strongly correlated with an increase in pH (Figure 3.17) include *Chlamydomonas*, *Pediastrum*, *Strombomonas*, and *Achnanthes*. This is consistent with the findings of Moss (1973), which showed a very high tolerance range for *Chlamydomonas* and an optimal growth at high pH for *Pediastrum*.

4.1.2 Conductivity

A higher conductivity is a consequence of a larger number of ions in solution (Section 1.5.2.1). Various experiments showed that the ratio of monovalent to divalent cations does not affect algal growth, but that growth might be affected by different quantities of various major ions (Moss, 1972). Although the concentrations of these major ions were not measured in this study, conductivity was significantly higher for WFS when compared to MR (Figure 3.1d). In addition, conductivity of M4 was significantly lower than the rest of MR sites (Figure 3.3f). Genera strongly correlated with EC were the diatoms *Nitzschia* and *Aulacoseira* (Figure 3.17). Algal classes strongly correlated with EC included Euglenophyceae, and to a lesser extent Chlorophyceae and Bacillariophyceae (Figure 3.22).

4.1.3 Temperature and dissolved oxygen

All organisms have a range of temperatures at which optimal growth, reproduction, and general fitness occur. Elevated temperatures increase metabolic rate, including

respiration and thus oxygen demand, of aquatic organisms, while higher temperatures reduce the solubility of dissolved oxygen in water, decreasing its concentration and availability to aquatic organisms (Dallas & Day, 2004). Cassidy (2011) found the optimum temperature for growth of different Chlorophyceae species to be 30°C, while Sheldon & Boylen (1975) found that the optimum temperature for photosynthesis of a diatom-populated epiphytic community was also at 30°C. However, the maximum temperature for WFS and MR was lower than this with a much lower mean temperature for both rivers (Table 3.1). There was no significant difference in temperature between rivers (Figure 3.1b).

The maintenance of adequate concentrations of dissolved oxygen is critical for survival and functioning of aquatic biotas. Generally, it is a depletion of DO that is observed in aquatic systems, although, super-saturation may occur in eutrophic waters. Dissolved oxygen concentrations fluctuate diurnally, and are lowest near dawn, increasing to a maximum in the afternoon, and decreasing during the night. Typical saturation concentrations at sea level, for TDS values less than 3 000 mg/l are: 9.09 mg/l at 20°C (Dallas & Day, 2004). This is greatly influenced by atmospheric pressure, which will decrease with an increase in altitude. Dissolved oxygen concentrations were measured early mornings, following bird surveys, and therefore, concentrations noted would be expected to be close to minimum. Dissolved oxygen concentrations of WFS were significantly higher than that of MR (Figure 3.1c). This may be ascribed to differences in water flow rate and turbulence between rivers, or differences in photosynthetic activity of the two rivers.

4.1.4 Dissolved inorganic nutrients

Phosphorus is recognised as the fundamental cause of eutrophication. Nitrogen plays a secondary role, but may become important at a high level of eutrophication (Paerl *et al*., 2001; Smith, 2003; Walmsley, 2000) (Section 1.5.2.1).

Phosphorus concentrations were higher than nitrogen concentrations for both WFS and MR. Nitrogen can thus be regarded as the nutrient limiting algal growth in these two river systems, especially since algae need nitrogen to phosphorus in a ratio of 7:1 (known as the Redfield ratio) (Dodds & Whiles, 2010). Phosphorus concentrations of MR were significantly higher than that of WFS; however, nitrogen concentrations (DIN) for MR were significantly lower than that of WFS (Figure 3.2a, Figure 3.2f). The Organisation for Economic Cooperation and Development (OECD) published guidelines that relate phosphorus and chlorophyll α concentrations to trophic condition and these values are considered universal for temperate zone systems (Walmsley, 2000). Based on the guidelines published by the OECD, both WFS and MR are considered in a eutrophic state, based on total phosphorus concentrations, although the productivity of MR might be lower than that of WFS due to lower concentrations of nitrogen, limiting algal growth.

The high phosphorus concentrations in MR may be attributed mainly to agricultural activities surrounding the Mooi River area between Klerkskraal Dam and Boskop Dam. The rapid intensification of agriculture is a primary cause of altered nutrient concentrations in aquatic systems. A small, but ecologically very significant portion of agriculturally applied phosphorus enters aquatic environments through leaching (Smith, 2003). High phosphorus concentrations in WFS are likely due to non-agricultural rural runoff and sewage. The most common effect of increased nitrogen and phosphorus supplies to aquatic systems is an increase in the productivity and biomass of phytoplankton and suspended algae, but excessive nutrient enrichment has several other adverse effects. This includes shifts in phytoplankton composition to bloom-forming species, of which many may be toxic, or may not be consumed effectively by aquatic grazers (Smith, 2003).

Total phosphorus and total nitrogen concentrations below 0.005 mg/l and 0.5 mg/l respectively are considered sufficiently low to limit eutrophication and reduce the likelihood of nuisance algae growth (Dallas & Day, 2004). However, only inorganic phosphorus and inorganic nitrogen were measured in this study. Inorganic phosphorus concentrations > 0.25 mg/l are indicative of hypertrophic conditions, and concentrations for both rivers were significantly higher (Dallas & Day, 2004). Inorganic nitrogen concentrations < 0.5 mg/l is indicative of oligotrophic conditions, and concentrations for both rivers were lower (Dallas & Day, 2004). Dissolved inorganic nitrogen for MR, however, was significantly lower than that of WFS. Consequently, the high concentrations of phosphorus are limited by much lower concentrations of nitrogen, preventing hypertrophic symptoms. It is important to note, that in the presence of sufficient available phosphorus, nitrogen-fixing organisms will be able to fix atmospheric nitrogen to make up for any deficit caused by low inorganic nitrogen concentrations (Dallas & Day, 2004). Therefore, phosphorus-driven eutrophication has been strongly implicated in the development of both nitrogen-fixing and non-nitrogen-fixing cyanobacteria (Paerl *et al*., 2001). Based on the phosphorus and nitrogen concentrations, WFS are expected to be more productive regarding algae abundance, compared with MR.

4.1.5 Depth and volume

Major differences in physical and chemical conditions are seen through the depth of the water column (Dallas & Day, 2004). Structural characteristics of a water mass, such as water volume and depth, affect the amount of solar radiation and heating of water, and thus its thermal regime. The high specific heat of water results in a high capacity for heat absorption, as well as slow release of heat, which therefore contributes to thermal stability (Dallas & Day, 2004). There was a significant difference in depth between MR and WFS. Despite MR being significantly deeper than WFS (Figure 3.6d) there was no significant difference in the mean temperature between rivers. This is due to the volume of WFS being

comparable to that of MR. There was however, a difference in the temperature range, which can be attributed to depth, as shallow water will have lower minimums and higher maximums, compared to deeper water.

Although turbidity was not measured, light penetration will decrease with an increase in depth. As light penetration is reduced, primary production decreases, and food availability to organisms higher in the food chain is diminished (Dallas & Day, 2004). Although there was no significant difference in volumes between rivers, the significant deeper water depth of MR may have reduced the portion of the water column was deprived of sunlight, possibly decreasing the rate of photosynthesis and therefore primary productivity.

Sriyasak *et al*. (2015) showed that surface and bottom water temperatures in ponds between 0.8 - 2 m deep differed between 1.3 - 4.0 °C. This is because shallower ponds undergo diel cycles of thermal vertical stratification. Stratification of water arises due to differences in water density, as the absorption of solar radiation decreases with increasing depth. Warm surface waters also have higher dissolved oxygen concentrations from photosynthesis, while cooler bottom waters have lower dissolved oxygen concentrations. De-stratification of water occur as air temperature drops and the surface layer cools down, becoming denser than the water in the bottom layer. Surface water then sinks, forcing water at the bottom to rise, thus, turning over the layers (Sriyasak *et al*., 2015). Water depth of WFS was significantly lower than that of MR. WFS had a mean water depth of 0.73 m, while that of MR was 2.6 m (Figure 3.6d). This resulted in daily cycles of thermal stratification for MR, but not for WFS. Consequently, dissolved oxygen concentrations were significantly lower in MR (Figure 3.1c), probably influencing the survival and functioning of aquatic biota.

4.2 ALGAL COMPOSITION, ABUNDANCE, AND DIVERSITY

4.2.1 Species accumulation curve

Species-accumulation curves are used to evaluate the adequacy of sample size in community data sets to give reliable results. Figure 3.7 shows that the species accumulation curve has flattened significantly, however, it still has not reached an asymptote. This was strongly influenced by a significant number of rare species, occurring only once or twice. The number of individuals that must be sampled is often prohibitively large especially when species diversity is large and most species are rare (Gotelli *et al*., 2011). This was illustrated by Longino *et al*. (2002) where sampling of a tropical rainforest ant assemblage in Costa Rica still has not reached an asymptote after almost 30 consecutive years of sampling. Most phytoplankton is subject to a great deal of temporal variation, occurring as a defined seasonal succession of species (Bellinger & Sigee, 2010). This temporal sequence depends on lake trophic status, and results in certain genera only occurring over a short period in favourable

conditions. Therefore, monthly sampling over a one-year period is likely to yield a large number of species with only one or two occurrences. In the current study, despite not reaching an asymptote, additional sampling would yield very small increases in the number of species and therefore sample size was adequate to give reliable results.

4.2.2 Cluster analysis

Cluster analyses were performed to determine spatial variation in algal composition. Cluster analysis allows one to assign sample units to groups based on the similarity of the redundant patterns of their responses (Peck, 2010).

Figure 3.16 shows a clear distinction in algal assemblages between rivers. The algal composition of W2, however, was more similar to that of MR sites than associated WFS sites. Contributing factors include phosphorus concentrations, algal abundance, and water volume. The mean phosphorus concentration of W2 (14 mg/l) was more similar to the mean of MR (17 mg/l) than that of WFS (8.2 mg/l). Various studies have shown phosphorus to be the dominant factor influencing eutrophication, leading to shifts in phytoplankton composition with an increasing dominance by blue-green bacteria (Smith, 2003; Walmsley, 2000). An NMS of algal abundances (Figure 3.17) shows that W2 was strongly correlated with four genera of blue-green bacteria (*Anabaena*, *Oscillatoria*, *Spirulina*, and *Phormidium*) which are consistent with the effects of increased phosphorus loadings. Algal abundance of W2 (9 215 cells/ml) was also closer to the mean of MR (9 135 cells/ml) than that of WFS (30 594 cells/ml). Lastly, the water volume of W2 (22 460 m^3) was more similar to the mean water volume of MR (20 296 m^3) than that of WFS (33 656 m^3). This could explain the similarity in algal composition of W2 and MR sites.

4.2.3 Differences between rivers

4.2.3.1 Richness and diversity indices

Species diversity is a key indicator of water quality as it is closely related to the trophic state of the water body, and several studies have shown that a high diversity index indicates that an ecosystem is in a healthy and stable state, while a lower index value suggests a degraded ecosystem (Zhao *et al.*, 2017). In the past two decades, many experiments have manipulated richness of various taxa to assess how this aspect of diversity affects the efficiency by which communities capture limiting resources and convert them into biomass (Weiss *et al*., 2008). Results have shown, when averaged across all species used in an experiment that increasing species richness tends to increase resource capture and production of biomass in any given trophic group. This is because diverse communities should exploit resources in a complementary way, using available resources to produce more biomass (Weiss *et al*., 2008). Both species richness and Shannon-index of WFS were

significantly higher than that of MR (Figure 3.8). The higher Shannon-index is a consequence of a lower evenness index of the MR sites compared to WFS, which indicates that a large portion of abundance of MR algae is contributed by a relatively small number of species. In this case, MR was dominated by several blue-green bacteria genera where five genera (*Anabaena*, *Aphanocapsa*, *Merismopedia*, *Oscillatoria*, and *Phormidium*) contributed 77 % of the total abundance. WFS on the other hand, were co-dominated by blue-green bacteria (cyanobacteria) and green (Chlorophyceae) algae. Many studies have thoroughly documented that cyanobacteria blooms cause decreases in both diversity and evenness (Zhao *et al.*, 2017). This suggests that WFS is a more productive system, compared with MR.

4.2.3.2 Algal classes

Table 3.14 shows that the Chlorophyceae, cyanobacteria, and Bacillariophyceae, with a cumulative contribution of 93%, were primarily responsible for the observed difference between rivers. MR was dominated by cyanobacteria, while WFS was dominated by cyanobacteria and Chlorophyceae. The role phytoplankton in aquatic ecology is described in Section 1.5.1.

Phytoplankton composition in MR is dominated by cyanobacteria. Five cyanobacteria genera comprise 77% of the total abundance, while 15 Chlorophyceae genera only contribute an additional 14.2%. Causative factors include significant difference in depth, and extremely high phosphorus concentrations coupled with low nitrogen concentrations. Smith *et al*. (2003) found that variations in depth can modify algal growth and that deep lakes produce a lower algal biomass per unit total phosphorus than shallow lakes.

The five cyanobacteria genera include *Anabaena*, *Aphanocapsa*, *Merismopedia*, *Oscillatoria*, and *Phormidium,* which have all been found to be able to fix atmospheric nitrogen, whether aerobically or anaerobically (Bergman *et al*., 1997; Hasan, 2012; Issa *et al*., 2014). In addition, from the abovementioned genera, only *Merismopedia* have not been found to produce cyanotoxins, although genera may vary in toxicity and toxins produced (McAllistar *et al*., 2016; Paerl *et al*., 2001). While cyanotoxins may mediate microbial interactions, they may simultaneously inhibit potential competitors and consumers. There has been substantial study of interactions between cyanobacteria and herbivorous zooplankton, showing considerable evidence of detrimental effects of cyanobacteria on zooplankton (Paerl *et al*., 2001). However, very little work has been done on the direct impact on birds. Kihwele *et al*. (2014) studied temporal changes in Lesser Flamingo (*Phoenicopterus minor*) populations in relation to phytoplankton abundance in Lake Manyara, Tanzania. Lesser Flamingo feed primarily on cyanobacteria, with *Arthrospira fusiformis* being their preferred food source. Kihwele *et al*. (2014) found a significant correlation between the abundance of *Arthrospira fusiformis* and

Lesser Flamingo numbers, and a significant negative correlation between other toxic cyanobacteria genera (such as Anabaena) and Lesser Flamingo numbers.

Inhibitory effects of cyanobacteria on zooplankton grazing may be attributed to morphological factors (mechanical interference with feeding due to size or shape of colonies and filaments), chemical factors (toxicity and poor nutritional value), or high densities during blooms (displacing more nutritious algae, or limit availability of herbivores to utilise coexisting algae) (Paerl *et al*., 2001; Paerl & Otten, 2012; Smith, 2003). Recent studies suggest that the inhibitory effect of cyanobacteria on grazers is a result of chemical factors rather than mechanical interference (Paerl *et al*., 2001; Paerl & Otten, 2012).

In addition to cyanobacteria, Chlorophyceae was the second most abundant algal class in the MR. Chlorophyceae is an ecologically important group as major producers of biomass in freshwater ecosystems (Bellinger & Sigee, 2010). Unlike cyanobacteria, other algae do not have the ability to regulate buoyancy and have to find other ways to maintain their position the euphotic zone of deep waters. One way to achieve this is by maintaining a high reproductive rate to compensate for a loss of cells that settles. Consequently, energy is used for reproduction, rather than cell growth, resulting in small-sized algae with a lower biomass. Advantages of being small-sized include an increased surface area to volume ratio, lower sinking rate, and lower zooplankton predation susceptibility (Silvoso *et al*., 2011).

In contrast to MR, the phytoplankton composition of WFS was co-dominated by both cyanobacteria and Chlorophyceae, with Bacillariophyceae also contributing to a lesser extent. Six cyanobacteria and 19 Chlorophyceae genera comprised 43% and 37% respectively, while 14 Bacillariophyceae genera made up an additional 15% of the total composition.

The decrease in cyanobacteria dominance, in comparison to MR, is caused by a decrease in water depth, and significantly higher nitrogen concentrations. When both phosphorus and nitrogen are supplied at close to non-limiting rates, factors other than nutrient limitation may dictate algal community composition. In such conditions, algae capable of nitrogen fixation have little advantage, and non-nitrogen-fixing taxa will dominate (Paerl *et al*., 2001). In mesotrophic and eutrophic lakes, green algae do not normally produce the dense blooms seen with diatoms and especially cyanobacteria, but may become dominant or co-dominant under excessive nutrient conditions (Bellinger & Sigee, 2010). Phytoplankton in shallow waters have the advantage of sufficient light for photosynthesis, even at the bottom (depending on turbidity). Light availability plays a fundamental role in lakes, directly affecting the competition outcome between primary producers (Silvoso *et al*., 2011). Allende *et al*. (2009) found that shallow lakes with high dissolved inorganic nutrients and high phytoplankton abundances are among the most productive and efficient aquatic systems. Phytoplankton is not required to spend energy to keep them suspended in shallow lakes where light penetrates to the bottom. Consequently, energy can be used to optimise growth and biomass

accumulation. Many algae genera have a wide range of size and individuals from the same genus may vary considerably in size, according to the environmental conditions it is exposed to. Therefore, algae in the shallower WFS may well be to the larger side of the spectrum, compared to smaller individuals in the deeper MR. This may alter the primary production of the two different systems dramatically.

4.2.3.3 Algal genera

Primary production in the MR is limited by low nitrogen concentrations, despite having very high phosphorus levels. This, together with deep waters gives cyanobacteria the competitive edge over Chlorophyceae and Bacillariophyceae. Cyanobacteria in the MR are represented by 11 genera. This includes *Anabaena*, *Aphanocapsa*, *Merismopedia*, *Oscillatoria*, and *Phormidium*, which dominates in the MR, while *Aphanothece*, *Cylindrospermopsis*, *Gleocapsa*, *Komvophoron*, *Spirulina*, and *Synechococcus* were present in low concentrations. Most of the genera (some heterocystous, other non-heterocystous) are able to fix atmospheric nitrogen and the majority have been found to produce toxins, having adverse effects on higher trophic levels (Bergman *et al*., 1997; Bláha *et al*., 2009; Hasan, 2012; McAllistar *et al*., 2016). Indicator species analysis identified only two genera (*Rhopalodia* and *Tetrastrum*) that are indicators of MR. *Rhopalodia* is a diatom known to contain nitrogen-fixing prokaryotes endosimbiotically (Taylor & Cocquyt, 2016). Indicator genera of WFS could be grouped in three classes: Bacillariophyceae, Chlorophyceae, and Euglenophyceae. Genera with significant indicator values within Bacillariophyceae include *Aulacoseira*, *Amphora*, *Craticula*, *Cyclotella*, *Cymbella*, *Gyrosigma*, *Navicula,* and *Nitzschia*. Genera with significant indicator values within Chlorophyceae include *Actinastrum*, *Chlamydomonas*, *Chlorococcum*, *Closterium*, *Monoraphidium*, *Scenedesmus*, and *Ulothrix*. Genera with significant indicator values within Euglenophyceae include *Euglena*, *Phacus*, *Trachelomonas*, and *Strombomonas*. The total dominance of cyanobacteria, accompanied with lower biomass of more nutritious genera means that the MR is a system with low productivity.

Algal composition of WFS is typical that of a shallow eutrophic system with excess nutrients where Chlorophyceae is dominant or co-dominant, typically with non-nitrogen-fixing cyanobacteria and Bacillariophyceae (Allende *et al.*, 2008; Paerl *et al*., 2001). Although nitrogen concentrations were moderate, it was not supplied at close to non-limiting rates, which resulted in nitrogen-fixing cyanobacteria being present in moderate quantities. Abundances of Chlorophyceae and Bacillariophyceae in WFS were significantly higher than MR, which contributed to a system with a higher primary productivity.

4.2.4 Importance of algal composition

Phytoplankton are the primary source of organic matter supporting food webs in freshwater ecosystems, and are regulated by nutrient supply (Paerl *et al*., 2001). The productivity of these aquatic systems is primarily determined by the amount of carbon being fixed by phytoplankton, but also by the efficiency of consumption of phytoplankton, that results in energy transfer to higher trophic levels. The concept of cascading trophic interactions, explains differences in productivity among lakes with similar nutrient supplies, but contrasting food webs (Carpenter *et al*., 1985).The trophic cascade theory encompasses the relative roles of nutrients and grazers in controlling algal biomass and species composition (Levine *et al*., 1999).

One important paradigm in phytoplankton ecology is the existence of low grazing pressures on cyanobacteria, which can be attributed to toxicity, low nutrient content, or size (Arnold, 1971). Levine *et al*. (1999) found that grazing mortality of cyanobacteria was consistently minimal, compared to other algae. Additionally, the highly diverse Chlorophyceae appeared to consist of both edible and inedible genera, but overall was one of the most heavily grazed groups (Levine *et al*., 1999). Several studies confirmed that species from Cryptophyceae, Chrysophyceae and small non-colonial Bacillariophyceae were among the most edible phytoplankton (Levine *et al*., 1999; Porter, 1977; Sommer *et al*., 1986). Phytoplankton dimensions also have a great influence on zooplankton community structure. The size of the dominant algae will determine whether micro- or macro-grazers will dominate, which will ultimately shape the food web (Carpenter *et al*., 1985; Levine *et al*., 1999).

Abundance of algae is also affected by the presence or absence of submerged macrophytes. Phytoplankton are less abundant when macrophytes are present. Macrophytes outcompete phytoplankton for nutrients and provide shading and shelter for grazers, who primarily feed at night and avoid feeding at high light intensity. The low abundance of MR algae may be a result of rooted macrophyte domination (Allende *et al*., 2009).

From the knowledge of selective grazing, one can conclude that species from Bacillariophyceae, Chlorophyceae, Chrysophyceae, and Cryptophyceae are among the most edible by herbivorous zooplankton. This indicates that MR is a system with very low phytoplankton productivity. In contrast, WFS contained a substantial portion of edible phytoplankton, resulting in a system with significantly higher phytoplankton productivity.

4.3 BIRD COMPOSITION, ABUNDANCE AND DIVERSITY

4.3.1 Species accumulation curve

As mentioned, species-accumulation curves are used to evaluate whether the sample size in community data sets are adequate as to give reliable results. Figure 3.12 shows that very few species were added after 80 surveys, indicating that 98 surveys were sufficient to compare the avian diversity of the two rivers.

4.3.2 Cluster analysis

Cluster analysis of bird assemblages of the different sites showed a clear distinction between rivers. This is not surprising as species richness, abundance, Shannon-index, and biomass of the two rivers were significantly different. Bird assemblages of MR were very similar. Bird assemblages of WFS were similar, although W1 was not grouped with the other WFS sites. W1 however, was still closer related to the remaining WFS sites than MR sites. This difference can possibly be attributed to water depth and water volume, which was quite dissimilar to the rest of WFS sites. This is implicated by the presence of several probing wader species that characterise W1 (Figure 3.25) as is shown by the ISA of WFS (Table 3.15).

4.3.3 Differences between rivers

4.3.3.1 Richness, abundance, and diversity

Natural riparian ecosystems, as interfaces between terrestrial and aquatic systems, are an unusually diverse mosaic of landforms, communities, and environments on the terrestrial portion of the Earth (Section 1.1). As such, they serve as a framework for understanding the organisation, diversity, and dynamics of communities associated with fluvial ecosystems (Naiman *et al.*, 1993). The most basic patterns of communities have to do with the number of species they contain (Wiens, 1989a). An important aspect of community structure is ignored when the composition of a community is described simply in terms of the number of species present, as it misses the information on commonness and rarity (Begon *et al.*, 2008; Wiens, 1989a). Community diversity, therefore, are dependent on both species richness and equitability. However, knowing the numbers of individuals of each species may not provide a full answer either. Such measures of diversity might ignore the enormous disparity in size, or interactions between species (Begon *et al.*, 2008; Swingland, 2001). In this study, 6 116 individual birds were observed, consisting of 119 species. This confirms the diverse nature of riparian ecosystems, certainly concerning birds. However, there was great contrast between the avian composition of WFS and MR. Species richness, and abundance of WFS were significantly higher than that of MR, however, there was no significant difference between the Shannon-indexes of the two rivers (Figure 3.13a-c). This indicates that bird

abundance was much more evenly distributed among species for MR when compared with WFS.

4.3.3.2 Biomass

Bio-energetic approaches may be applied to community analysis at several levels, although, the expression of patterns in terms of biomass is perhaps the simplest (Wiens, 1989a) (Section 1.3.2). Avian biomass is therefore a good indication of the productivity of aquatic ecosystems.

The total avian biomass of WFS was significantly higher than that of MR (Figure 3.13d). Total avian biomass would presumably be directly proportional to abundance, with an increase in total biomass dependent on an increase in abundance. This, however, was not entirely so. The fact that total avian biomass of WFS was significantly higher than MR was to be expected as the abundance of WFS was significantly higher than that of MR. The total avian biomass relative to abundance showed a mean mass of 0.121 kg/individual for MR, compared to 0.466 kg/individual for WFS.

Because riparian ecosystems are transitional zones of both aquatic and terrestrial habitats, aquatic and terrestrial food webs are not discrete, but rather tightly linked by an energy flux between contiguous habitats. A study showed that productivity in riparian systems fluctuates seasonally, and that productivity of terrestrial and aquatic systems tends to be asynchronous (Nakano & Murakami, 2000). Terrestrial species thus benefits from the productivity of aquatic systems in times of low terrestrial productivity, and vice versa. This is evident from the number of individuals of terrestrial species that make use of aquatic systems for foraging (534 on MR and 1 003 on WFS).

To investigate the effect of aquatic productivity on avian biomass in this study, birds were divided into two groups: a) aquatic or water associated, and b) terrestrial or non-water associated. MR and WFS were comparable in terms of terrestrial bird composition (Figure 3.29). However, MR and WFS differed considerably when compared in terms of water associated species (Figure 13). This indicates that the productivity of riparian ecosystems is strongly related to the productivity of the aquatic component and energy transfer between contiguous habitats.

Based on this knowledge, linear regressions were done to test for correlation between algal – and avian abundance, as well as algal abundance and avian biomass. Linear regression based on bird abundance was significant for all birds and water-associated birds, but not for terrestrial birds (Figure 3.15a). Algal abundance explained 59% of variation in bird abundances, and 63% of variation in water-associated bird abundances. Linear regression based on biomass was significant for all birds and water-associated birds, but not for terrestrial birds (Figure 3.15b). Algal abundance explained 62% of both total biomass and biomass of

water-associated species. This finding suggests a strong and causal interaction between algae and water-associated birds.

4.3.3.3 Community patterns

Community patterns are accompanied by niche theory and the guild concept where communities can be divided into ecologically similar groups with emphasis on resource dimensions and competitive interactions between species and individuals (Begon *et al.*, 2008; Wiens, 1989a). Although this study does not elaborate on guild partitioning, particularly with regard to foraging and resource use, its relevance must be stated.

The avian composition of MR was much more homogenous in comparison to WFS. MR had relatively few species that were present in high numbers. These species could be broadly grouped into four feeding guilds. This includes granivores (Southern Red Bishop, Laughing Dove, Red-eyed Dove, Southern Masked Weaver, and Common Waxbill), aerial insectivores (Brown-throated Martin, Barn Swallow, Greater-striped Swallow, and White-rumped Swift), reed-dwelling insectivores (Levaillant's Cisticola, African Reed Warbler, Little Rush Warbler, Lesser Swamp Warbler, and African Stonechat), and water-associated birds (Reed Cormorant, Black Crake, Yellow-billed Duck, Egyptian Goose, Little Grebe, and Common Moorhen).

WFS had a much more heterogeneous composition and noticeably more species that were present in relatively high numbers. These species could also be broadly grouped into the same four feeding guilds. These include:

1. Granivores:
    - Southern Red Bishop,
    - Red-eyed Dove, and
    - Southern Masked Weaver;
2. aerial insectivores:
    - Brown-throated Martin,
    - Barn Swallow, and
    - African Palm Swift;
3. reed-dwelling insectivores:
    - Levaillant's Cisticola,
    - African Reed Warbler,
    - Little Rush Warbler, and
    - Lesser Swamp Warbler;
4. water birds:
    - Red-knobbed Coot,

- Reed Cormorant,
- African Darter,
- Yellow-billed Duck,
- Greater Flamingo,
- Egyptian Goose,
- Little Grebe,
- Great Crested Grebe,
- Glossy Ibis,
- Blacksmith Lapwing,
- Common Moorhen,
- South African Shelduck,
- Hottentot Teal,
- Red-billed Teal, and
- African Spoonbill.

It is apparent that WFS has many more water birds (2875), compared to MR (1704) (Table 3.9).

Indicator species analysis for MR identified only five species that had significant indicator values (Table 3.15). They were African Red-eyed Bulbul, Black Crake, Southern Masked Weaver, African Reed Warbler, and African Stonechat. Indicator species analysis for WFS on the other hand identified 23 species that had significant indicator values of which 17 were water birds (Table 3.15). These include seven piscivorous species (Reed Cormorant, African Darter, Great Crested Grebe, Black Heron, Purple Heron, Squacco Heron, and Whiskered Tern), and five species which are at least partially filter feeders (White-faced Whistling Duck, Greater Flamingo, South African Shelduck, Hottentot Teal, and Red-billed Teal (Hockey *et al*., 2009).

Table 3.16 shows the results of SIMPER analyses. Taking into account the differences in community composition between WFS and MR, it is not surprising that from the 20 species that were responsible for the greatest observed difference between rivers (cumulative > 75%), 15 were water associated – and 10 water birds.

Wetlands are naturally patchy within the terrestrial landscape. Species often select resources and microhabitats in different ways, depending on their behavioural and morphological adaptations (Weller, 1999). Because of their dynamic nature, changes in wetland size may alter the avian composition according to alterations in the availability of suitable habitats or resources. Paracuellos (2006) argued that species which are specialist feeders, will use resources in short supply, and that these specialists will easier reach thresholds that threaten their survival in smaller ponds. Consequently, they will occupy larger

water masses with sufficient food resources. The significant difference in composition of aquatic birds between WFS and MR cannot be ascribed to the differences in surface area. This is inconsistent with the findings of Paracuellos (2006) of a hierarchical loss of species as pond size diminishes, strongly suggesting factors overriding surface area, such as algae composition as indicated from Section 3.4.

Wetland birds may discriminate the suitability of the habitat in accordance with bird morphology and diet. Bird foraging behaviour also limits whether an individual will be able to use a habitat for foraging. Limitations of locomotory technique, often results that access to food, in itself abundant, is difficult (Hildén, 1965). Hildén (1965) stated that the total abundance of birds is directly proportional to the quantity of food in the environment. Thus, we can safely assume that WFS had significantly higher food availability; compared to MR. Higher food availability is reflected by the algal composition and its function as primary producers in the food web.

4.3.4 Species preferences

As mentioned (section 1.3 & 1.4), there is a wide range of adaptations of living with water in wetland-associated birds. Differences between avian compositions of the two rivers will be discussed based on adaptations which allows it to be successful, and which factors influenced them to choose one river above the other.

Two species of grebe were recorded. Little Grebe were omnipresent, while Great Crested Grebe was strongly associated with W4. Great Crested Grebes prefer large inland lakes, usually fringed with emergent vegetation, and eats almost exclusively small fish (Hockey *et al*., 2009). The surface area of W4 was double that of the second largest site (Table 3.4), likely explaining its presence here.

African Darter and Reed Cormorant forage in similar places. Both tend to fish at a depth of 2 m, but African Darter takes a wider variety of rather larger prey. In this way, the two species appear to reduce competition (Maclean, 1990). Two species of cormorant were recorded. Reed Cormorant was present at all sites, except for M4. White-breasted Cormorant was present only on WFS and in low numbers. Cormorants are skilled aquatic divers and feed predominantly on fish (Weller, 1999). Both species of cormorant as well as African Darter was were strongly associated with WFS sites.

Ten species from the order Anseriformes were recorded. This includes African Black Duck, White-backed Duck, White-faced Whistling Duck, Yellow-billed Duck, Egyptian Goose, Spur-winged Goose, South African Shelduck, Cape Shoveler, Hottentot Teal, and Red-billed Teal. Species with more than three occurrences were included in the ordination. African Black Duck was the only species ordinated toward MR. Egyptian Goose, Yellow-billed Duck, South African Shelduck, Hottentot Teal, Red-billed Teal, Spur-winged Goose, White-faced Whistling

Duck and Cape Shoveler was associated with WFS. White-faced Whistling Duck and Cape Shoveler were ordinated toward W1 (Figure 3.28). Both species prefer extensive shallows. Cape Shoveler prefers shallow plankton-rich waters where it feeds by filtering. Its numbers have been found to increase when macrophytes are absent, a phenomenon usually associated with high plankton density (Hockey *et al*., 2009). This is consistent with the results from ISA, indicating that the combination of shallow water and high phytoplankton abundance explains the presence of these filter feeders at shallow plankton-rich waters.

Flamingos are specialised waders that feed by filtering water through lamellae along the side of their bills (Maclean, 1990). Greater Flamingo feed mainly on brine shrimps and brine flies, but also molluscs and diatoms (Hockey *et al*., 2009). Only Greater Flamingo was recorded, although Lesser Flamingo has been known to occur along the WFS (CWAC, 2018). Greater Flamingo was only recorded along WFS, and was only present at W1, W3, and W5. They seem to prefer shallow water and were not present at the two WFS sites with a mean water depth > 50 cm. However, abundances decreased dramatically with decreasing water depth.

Twelve species from the family Ardeidae were recorded. This includes Herons, Bitterns, and Egrets. Only four species were present on MR, while all twelve were recorded along the WFS. MR species were Little Bittern, Little Egret, Black-headed Heron, and Squacco Heron. Six species occurred more than three times and were included in the NMS ordination (Figure 3.28). Little Bittern was ordinated between MR and WFS, while Purple Heron, Black Heron, Squacco Heron, Little Egret, and Western Cattle Egret were ordinated rather centrally between WFS sites. All of them except Western Cattle Egret feeds mainly on fish and prefer shallow slow-moving waters (Hockey *et al*., 2009).

The family Threskiornithidae contain the Ibises and Spoonbills. Four species were recorded along WFS, which includes African Sacred Ibis, Glossy Ibis, Hadeda Ibis, and African Spoonbill. Only Hadeda Ibis was present along MR. These birds are waders that feed by probing through moist substrate in shallow waters, and rely on touch for locating their food (Hockey *et al*., 2009; Maclean, 1990). African Sacred Ibis and African Spoonbill, and Glossy ibis were ordinated close to W3 and W1, respectively, indicating that they prefer relatively shallow water for foraging.

Six species from the family Rallidae were recorded. They can be grouped into two groups based on abundance. The first group contains two ubiquitous species namely Red-knobbed Coot and Common Moorhen, while the second group contained Black Crake, Red-chested Flufftail, African Rail, and African Purple Swamphen, which were present in much lower numbers. Common Moorhen was ordinated between the two rivers, while African Rail, African Purple Swamphen, and Red-knobbed Coot were ordinated between W2 - W5 (Figure

3.28). Those present in higher numbers can be described as generalist feeders, while those present in lower numbers are more specialist feeders (Hockey *et al*., 2009).

Thirteen species from the order Charadriformes were observed. This order consists of small waders that forage by probing through soft substratum. MR contained four species, although only Three-banded Plover were regularly encountered. WFS contained 11 species, of which nine were present at W1. This strong affinity can be ascribed to the very shallow water level at this site.

4.4 INTERPRETATION AND SYNTHESIS

Sampling sites were all within a 15 km radius (Figure 2.1); this distance is easily covered for organisms as mobile as birds. Differences in avian composition between rivers can therefore not be attributed to distance between sites. This aspect of the study design should therefore be considered as a strong point.

There were significant differences in algal richness, abundance, Shannon-index, and algal composition between rivers. Differences in algal composition were attributed to differences in physiochemical parameters between rivers. WFS had significantly higher pH (although both are located in the Carletonville dolomite grassland; Section 2.1.2), dissolved oxygen, conductivity, sulphate, and dissolved inorganic nitrogen compared with MR. MR had significantly higher phosphorus concentrations, and coupled with lower nitrogen concentrations and therefore significantly higher phosphorus-nitrogen ratios. These differences I ascribe to different water quality profiles (most likely due to different pollution sources) between two otherwise largely comparable rivers.

MR was dominated by cyanobacteria, while cyanobacteria and green algae (Chlorophyceae) were co-dominant in WFS. Based on the work of (Bellinger & Sigee, 2010), the dominance of blue-green bacteria in MR can be attributed to:

1) An increase in water depth compared with WFS - depth regulation by buoyancy, avoiding photo-inhibition during the early phase of population increase, and allowing them to obtain inorganic nutrients from the hypolimnion when the epilimnion becomes depleted in mid to late summer.
2) A tolerance to low nitrogen/phosphorus ratios - allowing continued growth when nitrogen becomes limiting as blue-green bacteria are able to fix atmospheric nitrogen.
3) A low light tolerance that is an important attribute enabling blue-green bacteria to survive lower in the water column during dense algal blooms.

The two rivers differed in bird species richness, abundance, and biomass, which was significantly higher for WFS when compared with MR. Although more polluted, the higher

species richness and abundance of WFS can possibly be attributed to a 'higher quality' habitat for birds regarding:

- food abundance,
- food availability,
- suitable nesting sites, and
- presence of other species (Maronne *et al*., 1997).

According to habitat selection theory, individuals make the best settlement decisions, selecting the highest-quality habitats available in a heterogeneous landscape, thus maximising their fitness (Hollander *et al.*, 2011). Following the habitat selection theory, two density dependence models have evolved (Jones, 2001):

1) The ideal-free distribution model - where an individual is free to settle in the habitat with the highest resource quality and availability.
2) The ideal-despotic distribution model - where territory and dominance limit the density within a habitat, as individuals that are more dominant will deny less dominant ones access to resources.

Wetlands are among the richest of ecosystems in terms of annual productivity, measured in primary production based on the amount of energy fixed per year (Weller, 1999). Measuring productivity in terms of biomass is perhaps the simplest (Wiens, 1989a). Avian biomass of WFS were significantly higher compared with MR ($p < 0.0001$), indicating that the WFS system is much more productive in terms of primary production. Linear regression analyses showed that algal abundance explained 62% of variance of avian biomass (Figure 3.15b).

The difference in avian biomass between rivers may be attributed to differences in primary production between rivers. A reduction in primary productivity of MR can almost certainly be ascribed to the presence of high numbers of blue-green bacteria when compared with WFS. One important paradigm of phytoplankton ecology is the existence of low grazing pressures on blue-green bacteria, which are toxic, of low nutrient content, or too large for easy consumption (Levine *et al*., 1999). Because of the high proportion of blue-green bacteria in MR, energy transfer to higher trophic levels is most likely reduced, supporting the finding of the differences in bird biomass between the two rivers.

Ecosystems are considered as being controlled by either top-down (consumer-driven) or bottom-up (resource-driven) mechanisms. If an ecosystem is productive enough to sustain the existence of vertebrate predators, the exploitation ecosystem hypothesis (EEH) predicts that the predators keep the population size of herbivores low, enabling phytoplankton to grow and reproduce. Ecosystems controlled by bottom-up mechanisms, on the other hand, are

shaped by inorganic resources, rather than by predation (Mäntylä *et al*., 2011). The number of trophic levels in an ecosystem is therefore determined by the primary productivity of the system. This determines the extent to which top-down and bottom up regulation influence the biomass ratios of the various trophic levels (Choquenot & Forsyth, 2013).

WFS contained great numbers of piscivorous birds, while MR had practically none, strongly suggesting that WFS is a highly productive ecosystem (compared with MR), which is controlled by top-down mechanisms. In contrast, MR appears to be a system with low primary productivity, resulting in the absence of organisms from higher trophic levels. Consequently, MR could be considered as controlled by bottom-up mechanisms.

Additionally, WFS contained a greater array of specialist feeders (most noticeably Greater Flamingo, Great Crested Grebe, Black Heron, Red-billed Teal, and Cape Shoveler), which were practically absent from MR. This is consistent with the Optimal Foraging Theory (OFT) stating that the proportion of individuals in a population that forages in ways that enhance their fitness will increase over time. The OFT assumes that the most economically advantageous foraging pattern will be selected for a species through natural selection (Pyke, 1984), which is further supported by the short distances (for birds) between the sites.

All water bird species recorded along MR were present in lower abundances compared with WFS, and consequently no aquatic bird species ordinated within the convex hulls of MR (Figure 3.28). This would be consistent with the ideal-despotic distribution model, and one may well assume that the individuals found along the MR are denied access to the more productive WFS by individuals that are more dominant. However, the previous explanations I consider as being more likely in this case.

One might also consider the relevancy of the “Intermediate Disturbance Hypothesis” which states that diversity will be highest when disturbances are intermediate in terms of frequency and intensity (Connell, 1978). The intensity of disturbance in the WFS was higher relative to MR (according to water quality parameters), and it had higher bird and algal parameters.

4.5 CONCLUSIONS

My hypothesis was that “Freshwater quality and environmental parameters affect algal community parameters, which, in turn, affect bird community parameters” (Section 1.6.2).

My results showed that:

- algal diversity was associated with water quality and environmental parameters, and
- that avian diversity was associated with the primary productivity of the two systems, largely represented by their respective phytoplankton characteristics.

The hypothesis of the study can therefore not be rejected, based on the interpretation of the data of my study. The causality of the associations however, is more complex and cannot be explained by a single variable, but rather by considering all the variables holistically.

4.6 RECOMMENDATIONS

Several aspects fell outside the scope of the study, but became apparent during the course of the study. In future, it might be useful to include:

- Turbidity and suspended solids
- Water movement/discharge
- Rainfall
- Intensity and frequency of disturbances (intermediate disturbance hypothesis)
- Riparian vegetation structure
- Habitat occupancy (foraging-, resting-, or nesting site)
- Macrophyte presence/abundance
- Determination of phytoplankton biomass and dynamics rather than abundance (This is important since it provides more accurate information on the primary productivity of the aquatic system)
    - total biomass, as well as
    - species and group biomass.

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