

Systematics in the *Bulbine glauca* complex (Asphodelaceae or Xanthorrhoeaceae subfam. Asphodeloideae)

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Declaration

I certify that the substance of this thesis has not already been submitted for any degree and is not currently being submitted for any other degree or qualification.

I certify that any help received in preparing this thesis and all sources used have been acknowledged in this thesis.



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Abstract

Bulbine glauca (Raf.) E.M.Watson, as currently applied, is a perennial herb disjunctly distributed in south-eastern Australia. The scale of these disjunctions together with apparently covarying morphological variation present among populations within *B. glauca* suggested a complex in need of testing.

Putative species limits within the complex were tested by phenetic analysis, using UPGMA clustering and semi-strong hybrid MDS ordination of 75 living samples, 11 herbarium samples and 72 characters. According to morphology, six species were recognised.

Cytological analysis undertaken for a wide sample of *B. glauca s. lat.* populations indicated a chromosome count for *B. glauca* of $2n = 46$. The species showed a variable asymmetric karyotype across its distribution, indicating karyotypic evolution involving structural rearrangements. There appeared to be distinctive groups within the complex based on karyomorphology, with variations in chromosome morphology suggesting the possibility of more than one species.

Phylogenetic analysis (maximum parsimony and maximum likelihood) using *matK*, *rbcLa*, *trnH-psbA* and ITS regions from specimens across 25 sites indicated a number of monophyletic clades within the complex with low support. Analysis of combined DNA and morphological data resolved six well supported clades within *Bulbine glauca s. lat.*, providing support for the recognition of the same six species as from the phenetic analysis.

Four additional species are described as new: *B. kaputarensis* I.S.F.Moore, J.J.Bruhl and I.Telford, *B. watsoniae* I.S.F.Moore, J.J.Bruhl and I.Telford, *B. petraea* I.S.F.Moore, J.J.Bruhl and I.Telford, *B. ardua* I.S.F.Moore, J.J.Bruhl and I.Telford. A new combination under *Bulbine* is provided for *Bulbinopsis terrae-victoriae* Poelln. as *Bulbine terrae-victoriae* (Poelln.) I.S.F.Moore, J.J.Bruhl and I.Telford. The circumscription of *Bulbine glauca* is also emended to account for removal of these extraneous elements, leaving only Tasmanian populations.

Prologue

Format

The format of this thesis follows that of *Australian Systematic Botany*, except for the numbering of the headings, figures and tables.

The bibliographic style was formatted using Endnote Version X3 Software and with few exceptions, follows the protocol of *Australian Systematic Botany*. The exceptions to the protocol are that:

- figures, plates and tables are located throughout the text
- section headings are numbered
- spaces have been placed between paragraphs

Thesis layout

The Table of Contents identifies six chapters which comprise the body of this thesis but does not include a List of Figures or List of Tables. Figures and tables are provided as soon as possible after being referenced in the text. A general introduction is presented in Chapter 1 introducing the *Bulbine glauca* complex. The aims of the thesis are also covered in Chapter 1. Chapter 2 is the phenetic analysis of the morphological data matrix. Chapter 3 presents a cytological analysis of the complex. Chapter 4 presents a cladistic analysis of the *matK*, *rbcLa*, *trnH-psbA* and ITS regions in examining entities within the *Bulbine glauca* complex. This chapter also analyses the effect of a combined molecular and morphological dataset. Chapter 5 presents the taxonomy of the *Bulbine glauca* complex that results from the analyses presented in chapters 2–4. Finally, chapter 6 provides the general discussion and conclusions for the thesis.

Data availability

The phenetic matrix and the DELTA dataset, due to their large size are held by ISFM and Prof. J.J. Bruhl at Botany, UNE and will be available on request following the publication of relevant sections. Gene sequences will be lodged with GenBank and phylogenetic trees with TreeBASE prior to publication of Chapter 4.

Scope of and approach to project

The present study was completed on a part-time basis, 2009–2014. Field work was undertaken—30,000 km were travelled by car on nine major collecting trips—to collect fresh plant material from 25 sites from eastern NSW, the ACT, eastern Victoria and eastern and central Tasmania. Collections occurred in the summer months of 2008–2009, 2009–2010, 2010–2011, 2011–2012 and 2012–2013, and were based on herbarium records and knowledge of known populations. I had available specimens lodged with herbaria throughout Australia, plus the specimens I collected in the field. I was also able to survey and collect living material over five breeding seasons. These living collections enabled detailed morphological, cytological and molecular work to be undertaken.

Nevertheless, time limits prevented any detailed breeding experiments and /or the assessment of edaphic factors affecting possible distributions. My approach to the research presented here has been to use methods of comparative morphology, microscopy, DNA sequencing and cytogenetics. All these approaches have been considered in evaluating and circumscribing taxa.

Acknowledgements

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I thank the directors and staff of BM, BRI, CANB, HO, K, MEL, and WRSL for providing access to specimens and facilities, and especially of NE, NSW for access to collections, libraries and laboratories, where this project was based.

I provide a special thankyou to my late supervisor, Dr Elizabeth Brown, who tragically passed away just weeks prior to completion of my work. Elizabeth's guidance and expertise ensured I maintained an objective and balanced approach to my research. Elizabeth also provided me with great encouragement, and without her help would likely have given up the project early on.

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Table of Contents

Declaration	i
Abstract	ii
Prologue	iii
Format	iii
Thesis layout	iii
Data availability	iii
Scope of and approach to project	iv
Acknowledgements	v
Chapter 1: General introduction and aims	1
<i>Bulbine</i> Wolf	1
Australian <i>Bulbine</i>	1
<i>Bulbine glauca</i> complex	5
Aims and relevance of the project	7
References	8
Chapter 2: Morphometric analysis of the <i>Bulbine glauca</i> complex (Asphodelaceae or Xanthorrhoeaceae subfam. Asphodeloideae) indicates six not one species from south-eastern Australia.	11
Abstract	11
Introduction	11
Materials and Methods	12
Results	24
Discussion	28
Conclusion	34
Acknowledgements	37
References	37
Chapter 3: Cytological studies in <i>Bulbine glauca</i> and <i>B. crassa</i> (Asphodelaceae or Xanthorrhoeaceae subfam. Asphodeloideae)	42
Abstract	42
Introduction	42
Materials and Methods	44
Results	52
Discussion	60
Conclusion	63
Acknowledgments	63
References	64

Chapter 4: Phylogenetic relationships in the <i>Bulbine glauca</i> complex (Asphodelaceae or Xanthorrhoeaceae s. lat.) inferred from phenetic data and plastid and nuclear DNA sequence data supports six rather than one species from South-eastern Australia.	70
Abstract	70
Introduction	70
Materials and Methods	72
Results	81
Discussion.....	93
Conclusions	97
Acknowledgements.....	98
References	98
Chapter 5: Four new species, a new combination and an emended circumscription in <i>Bulbine</i> (Asphodelaceae or Xanthorrhoeaceae s. lat.) from South-eastern Australia.....	105
Abstract	105
Introduction	105
Materials and Methods.....	106
Taxonomy.....	106
Nomina dubia.....	125
Key to the species of <i>Bulbine glauca</i> found in Australia.....	126
Acknowledgements.....	128
References	128
Chapter 6: Conclusion.....	131
Introduction	131
Overall contribution of this project to taxonomic knowledge.....	131
Summary of findings against the aim of the project	131
Taxonomic utility of data sources used.....	132
Approaches to future collection and studies in <i>Bulbine</i>	132
Limitations of the current study.....	133
Recommendations for further work.....	134
Conservation of Australian species of <i>Bulbine</i> of the study group.....	134
References	135