Compendium of Plant Genomes
Series Editor: Chittaranjan Kole

Karam B. Singh
Lars G. Kamphuis
Matthew N. Nelson *Editors*

The Lupin Genome

Springer

Compendium of Plant Genomes

Series Editor

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Whole-genome sequencing is at the cutting edge of life sciences in the new millennium. Since the first genome sequencing of the model plant Arabidopsis thaliana in 2000, whole genomes of about 100 plant species have been sequenced and genome sequences of several other plants are in the pipeline. Research publications on these genome initiatives are scattered on dedicated web sites and in journals with all too brief descriptions. The individual volumes elucidate the background history of the national and international genome initiatives; public and private partners involved; strategies and genomic resources and tools utilized; enumeration on the sequences and their assembly; repetitive sequences; gene annotation and genome duplication. In addition, synteny with other sequences, comparison of gene families and most importantly potential of the genome sequence information for gene pool characterization and genetic improvement of crop plants are described.

Interested in editing a volume on a crop or model plant? Please contact Prof. C. Kole, Series Editor, at ckoleorg@gmail.com

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This book series is dedicated to my wife Phullara, and our children Sourav, and Devleena
Chittaranjan Kole

Preface to the Series

Genome sequencing has emerged as the leading discipline in the plant sciences coinciding with the start of the new century. For much of the twentieth century, plant geneticists were only successful in delineating putative chromosomal location, function, and changes in genes indirectly through the use of a number of "markers" physically linked to them. These included visible or morphological, cytological, protein, and molecular or DNA markers. Among them, the first DNA marker, the RFLPs, introduced a revolutionary change in plant genetics and breeding in the mid-1980s, mainly because of their infinite number and thus potential to cover maximum chromosomal regions, phenotypic neutrality, absence of epistasis, and codominant nature. An array of other hybridization-based markers, PCR-based markers, and markers based on both facilitated construction of genetic linkage maps, mapping of genes controlling simply inherited traits, and even gene clusters (QTLs) controlling polygenic traits in a large number of model and crop plants. During this period, a number of new mapping populations beyond F_2 were utilized and a number of computer programs were developed for map construction, mapping of genes, and for mapping of polygenic clusters or QTLs. Molecular markers were also used in the studies of evolution and phylogenetic relationship, genetic diversity, DNA fingerprinting, and map-based cloning. Markers tightly linked to the genes were used in crop improvement employing the so-called marker-assisted selection. These strategies of molecular genetic mapping and molecular breeding made a spectacular impact during the last one and a half decades of the twentieth century. But still they remained "indirect" approaches for elucidation and utilization of plant genomes since much of the chromosomes remained unknown and the complete chemical depiction of them was yet to be unraveled.

Physical mapping of genomes was the obvious consequence that facilitated the development of the "genomic resources" including BAC and YAC libraries to develop physical maps in some plant genomes. Subsequently, integrated genetic–physical maps were also developed in many plants. This led to the concept of structural genomics. Later on, emphasis was laid on EST and transcriptome analysis to decipher the function of the active gene sequences leading to another concept defined as functional genomics. The advent of techniques of bacteriophage gene and DNA sequencing in the 1970s was extended to facilitate sequencing of these genomic resources in the last decade of the twentieth century.

As expected, sequencing of chromosomal regions would have led to too much data to store, characterize, and utilize with the-then available computer software could handle. But the development of information technology made the life of biologists easier by leading to a swift and sweet marriage of biology and informatics, and a new subject was born—bioinformatics.

Thus, the evolution of the concepts, strategies, and tools of sequencing and bioinformatics reinforced the subject of genomics—structural and functional. Today, genome sequencing has traveled much beyond biology and involves biophysics, biochemistry, and bioinformatics!

Thanks to the efforts of both public and private agencies, genome sequencing strategies are evolving very fast, leading to cheaper, quicker, and automated techniques right from clone-by-clone and whole-genome shotgun approaches to a succession of second-generation sequencing methods. The development of software of different generations facilitated this genome sequencing. At the same time, newer concepts and strategies were emerging to handle sequencing of the complex genomes, particularly the polyploids.

It became a reality to chemically—and so directly—define plant genomes, popularly called whole-genome sequencing or simply genome sequencing.

The history of plant genome sequencing will always cite the sequencing of the genome of the model plant Arabidopsis thaliana in 2000 that was followed by sequencing the genome of the crop and model plant rice in 2002. Since then, the number of sequenced genomes of higher plants has been increasing exponentially, mainly due to the development of cheaper and quicker genomic techniques and, most importantly, the development of collaborative platforms such as national and international consortia involving partners from public and/or private agencies.

As I write this preface for the first volume of the new series "Compendium of Plant Genomes," a net search tells me that complete or nearly complete whole-genome sequencing of 45 crop plants, eight crop and model plants, eight model plants, 15 crop progenitors and relatives, and 3 basal plants is accomplished, the majority of which are in the public domain. This means that we nowadays know many of our model and crop plants chemically, i.e., directly, and we may depict them and utilize them precisely better than ever. Genome sequencing has covered all groups of crop plants. Hence, information on the precise depiction of plant genomes and the scope of their utilization are growing rapidly every day. However, the information is scattered in research articles and review papers in journals and dedicated Web pages of the consortia and databases. There is no compilation of plant genomes and the opportunity of using the information in sequence-assisted breeding or further genomic studies. This is the underlying rationale for starting this book series, with each volume dedicated to a particular plant.

Plant genome science has emerged as an important subject in academia, and the present compendium of plant genomes will be highly useful both to students and teaching faculties. Most importantly, research scientists involved in genomics research will have access to systematic deliberations on the plant genomes of their interest. Elucidation of plant genomes is of interest not only for the geneticists and breeders, but also for practitioners of an array of plant science disciplines, such as taxonomy, evolution, cytology, physiology, pathology, entomology, nematology, crop production, biochemistry, and obviously bioinformatics. It must be mentioned that information regarding each plant genome is ever-growing. The contents of the volumes of this compendium are, therefore, focusing on the basic aspects of the genomes and their utility. They include information on the academic and/or economic importance of the plants, description of their genomes from a molecular genetic and cytogenetic point of view, and the genomic resources developed. Detailed deliberations focus on the background history of the national and international genome initiatives, public and private partners involved, strategies and genomic resources and tools utilized, enumeration on the sequences and their assembly, repetitive sequences, gene annotation, and genome duplication. In addition, synteny with other sequences, comparison of gene families, and, most importantly, the potential of the genome sequence information for gene pool characterization through genotyping by sequencing (GBS) and genetic improvement of crop plants have been described. As expected, there is a lot of variation of these topics in the volumes based on the information available on the crop, model, or reference plants.

I must confess that as the series editor, it has been a daunting task for me to work on such a huge and broad knowledge base that spans so many diverse plant species. However, pioneering scientists with lifetime experience and expertise on the particular crops did excellent jobs editing the respective volumes. I myself have been a small science worker on plant genomes since the mid-1980s and that provided me the opportunity to personally know several stalwarts of plant genomics from all over the globe. Most, if not all, of the volume editors are my longtime friends and colleagues. It has been highly comfortable and enriching for me to work with them on this book series. To be honest, while working on this series I have been and will remain a student first, a science worker second, and a series editor last. And I must express my gratitude to the volume editors and the chapter authors for providing me the opportunity to work with them on this compendium.

I also wish to mention here my thanks and gratitude to the Springer staff particularly, Dr. Christina Eckey and Dr. Jutta Lindenborn for the earlier set of volumes and presently Ing. Zuzana Bernhart for all their timely help and support.

I always had to set aside additional hours to edit books beside my professional and personal commitments—hours I could and should have given to my wife, Phullara, and our kids, Sourav, and Devleena. I must mention that they not only allowed me the freedom to take away those hours from them but also offered their support in the editing job itself. I am really not sure whether my dedication of this compendium to them will suffice to do justice to their sacrifices for the interest of science and the science community.

New Delhi, India Chittaranjan Kole

Preface to the Volume

Introduction to the Lupin Genome

A major development over the last couple of decades has been the development and influence of genomic approaches to help advance our understanding of many crop species; knowledge that in turn can greatly benefit efforts to improve these crops. This book belongs to a book series by Springer called the 'Compendium of Plant Genomes' that describes genomic and related resources in many different crops. It focuses on lupins which are grain legume crops. Legumes, which belong to the Fabaceae (or Leguminosae) family, are widely distributed and form the third-largest land plant family in terms of number of species. From an agricultural point of view, they can occur as both grain crops, also known as pulses, and as fodder crops. Lupins are important ecological 'engineers', able to colonise extremely impoverished soils as well as thrive on low nutrient soils due to their ability to fix atmospheric nitrogen in symbiosis with bacteria and take up phosphorus efficiently from soils.

Lupins belong to the genus *Lupinus* in the Genistoid clade of legumes, which diverged early in Papillionoid legume evolution (Lavin et al. 2005). Lupins are receiving considerable interest recently not only for their value for sustainable farming as a break crop but also as a potential 'superfood' for fighting major health issues around diabetes and obesity. The genus *Lupinus* encompasses around 275 species that are widely distributed geographically, primarily in the Mediterranean region and North and South America, and can be found in a wide range of habitats (Drummond et al. 2012). Only a few lupin species have been domesticated and today the most widely cultivated species are *L. angustifolius* and *L. albus*, while *L. luteus* and *L. mutabilis* are niche crops. Although production has fluctuated over the last 20 years, over a million tonnes are produced every year. In 2017, the largest producers were Australia (1,031,425 t), Poland (168,678 t) and the Russian Federation (161,680 tonnes) (FAO 2017).

This volume on lupin genomics focuses primarily on narrow-leafed lupin (*L. angustifolius* or NLL), which is the main lupin crop primarily grown in Australia. Its genome has been recently sequenced with a focus on the gene-rich space and this has helped lead to the development of new breeding tools for the improvement of this and related lupin crops. This book describes these developments and also has chapters that detail the genomic and related genetic and cytogenetic resources that have been developed for NLL and how they are being used to help advance both fundamental and applied research on NLL in areas ranging from its domestication to syntenic relationships between NLL and other legume crops. Additional chapters report on genomic efforts being undertaken in other lupin crops. A brief outline of the book follows:

Chapter 1 by Dr. Wallace Cowling entitled 'Genetic diversity in narrow-leafed lupin breeding after the domestication bottleneck', and helps set the scene well for the following chapters. Narrow-leafed lupin was not fully domesticated until the 1950s in Australia and Dr. Cowling describes in detail the breeding efforts that led to this achievement and the following efforts to improve the crop. However, the breeding efforts to date have resulted in genome diversity being much lower in domesticated accessions compared with wild relatives, representing a severe domestication bottleneck. Dr. Cowling suggests methods for improving genetic diversity and the potential for long-term genetic gain, including the use of genomic information now available for this crop.

In Chap. 2, entitled 'Ecophysiology and phenology: genetic resources for genetic/genomic improvement of narrow-leafed lupin', Dr. Candy Taylor and colleagues describe the extensive genetic resources available in lupins with a focus on narrow-leafed lupin phenology. They describe how there are around 33,000 accessions of various lupin species that have been accumulated by more than 20 substantially sized and independent gene banks across the globe. They demonstrate how valuable these collections are as resources to breeding programmes to introduce new variation for traits, by focusing on examples related to phenology and in particular flowering time, and how these have benefited crop adaptation in narrow-leafed lupin.

In Chap. 3, entitled 'Overview of genomic resources available for lupins with a focus on narrow-leafed lupin (*Lupinus angustifolius*)', Dr. Karam B. Singh and colleagues provide an overview of the genomic resources available for narrow-leafed lupin with a focus on the current reference genome which underpins many of the other resources. They also describe how the narrow-leafed lupin reference genome has provided valuable insight into narrow-leafed lupin evolution and important information on some of its key plant-microbe interactions. The chapter also touches on some of the genomic resources that are in the pipeline in narrow-leafed and some other lupin species and describes the lupin genome portal, a web-based resource that houses genomic and related information for narrow-leafed lupin.

In Chap. 4, entitled 'Cytomolecular insight into lupin genomes' Dr. Karolina Susek and Dr. Barbara Naganowska summarise a large body of work that has been conducted using cytogenetic approaches in lupins, where again the focus has been on narrow-leafed lupin, which has served as a model for other lupin species. They describe cytogenetic efforts to estimate genome size, identify the number of chromosomes and integrative genetic and cytogenetic mapping in narrow-leafed lupin and discuss how insight into chromosome rearrangements has led to a hypothetical model of lupin karyotype evolution.

Chapter 5, by Dr. Lars G. Kamphuis and colleagues entitled 'Transcriptome resources paving the way for lupin crop improvement' describes the transcriptomic datasets that have been generated for lupin species from expressed sequence tags (EST) libraries through to more recent next generation RNA sequencing libraries. These datasets have been used to generate gene-based molecular markers in lupins, assist with the annotation of the narrow-leafed lupin genome and looked into specific global gene expression studies in different tissue types to address specific research questions around, for example, alkaloid biosynthesis, cluster root formation and organ abscission.

Chapter 6 by Dr. Michał Książkiewicz and Dr. Huaan Yang is entitled 'Molecular marker resources supporting the Australian lupin breeding programme' and provides a detailed overview of the different types of molecular markers that have been used in the Australian and European narrow-leafed lupin breeding programmes. It describes the implementation and accuracy of current molecular markers for domestication traits such as flowering time, seed permeability, pod shattering, alkaloid content, flower colour and disease resistance such as anthracnose caused by *Colletotrichum lupini* and phomopsis stem blight caused by *Diaporthe toxica* and concludes with the opportunities that next generation sequencing has to offer to provide additional molecular markers linked to important traits for lupin crop improvement.

Chapter 7 by Dr. Steven Cannon is entitled 'Chromosomal structure, history, and genomic synteny relationships in *Lupinus*' and capitalises on the genome sequence of narrow-leafed lupin and utilises it to infer the evolutionary history of narrow-leafed lupin relative to other legume species. Using synteny analyses the chapter demonstrates that the ancestor of all lupin species underwent a whole-genome triplication and that chromosome breakages, fusions and independent duplications subsequently led to various chromosome counts in lupin species. It also presents a detailed overview of the online resources generated to view the NLL genome and compare and contrast these to other legumes in various synteny viewers.

The next chapter (Chap. 8) by Dr. Matthew N. Nelson and colleagues entitled 'How have narrow-leafed lupin genomic resources enhanced our understanding of lupin domestication?' focuses on the domestication of lupin species pre- and post- the genomic revolution. It highlights how advances in genetic and genomic technologies have increased our understanding of lupin domestication and how it has led to the identification of key genes that control particular domestication traits such as flowering time and alkaloid content. It also highlights that the domestication process of lupins has led to a significant reduction in genetic diversity in both the Australian and European breeding programs.

Dr. Candy Taylor and colleagues explore the molecular control of time to flowering in narrow-leafed lupin in Chap. 9, which is entitled 'Genomic applications and resources to dissect flowering time control in narrow-leafed lupin'. They describe how modification of phenology was fundamental to the successful adaptation of narrow-leafed lupin to its key growing environments in southern Australia and northern Europe. They go on to recount recent advances in our understanding of the molecular mechanisms underlying these phenology changes, most notably the central role of a *Flowering Locus T* homologue in narrow-leafed lupin.

Chapter 10 by Dr. Paolo Annicchiaricho and colleagues is entitled 'Genetic and genomic resources in white lupin and the application of genomic selection'. Genotyping-by-sequencing technology has enabled cost-effective, accurate and high-density genotyping of white lupin. Two genomic selection approaches were compared and both were able to predict yield, architecture and phenology traits at moderate to high accuracy. The authors then discuss how genomic technology can be applied more broadly to other lupin crops.

In Chap. 11, Dr. Muhammad Munir Iqbal and colleagues review recent advances in 'Genomics of yellow lupin (*Lupinus luteus* L.)'. As a niche crop, yellow lupin has attracted little breeding effort or investment in genomic resources. Recently, the first genetic map for this species was released as well as transcriptomic resources. A genome sequencing project is underway for yellow lupin. The authors discuss how these rapidly developing tools can be used to help plant breeders overcome restraints holding back yellow lupin as a more widely adapted crop.

Finally, in Chap. 12, Dr. Abdelkader Aïnouche and colleagues conducted a detailed analysis of the 'The repetitive content in lupin genomes'. Focusing on four closely related species with striking differences in chromosome number and genome size, they found transposable elements accounted for most of the genome size variation, while many tandem repeats were unique to each species. The authors argue for a centralised resource to house the growing information on the repeat compartment of lupin genomes.

Our hope is that this book will provide a valuable resource to lupin/legume researchers and breeders to understand lupin genomes and a guide on how best to use rapidly developing genomic resources to understand and improve these fascinating legume species.

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Contents

1 Genetic Diversity in Narrow-Leafed Lupin Breeding After the Domestication Bottleneck

Wallace A. Cowling

Abstract

Narrow-leafed lupins (*Lupinus angustifolius* L.) were fully domesticated as a valuable grain legume crop in Australia during the mid-twentieth century. Pedigree records are available for 31 released varieties and 93 common ancestors from 1967 to 2016, which provides a rare opportunity to study genetic diversity and population inbreeding in a crop following a domestication bottleneck. From the 1930s–1960s, partially domesticated germplasm was exchanged among lupin breeders in eastern and western Europe, Australia, and USA. Mutants of two founder parents contributed to the first fully domesticated narrow-leafed lupin variety "Uniwhite" in 1967. Four Phases of breeding are proposed after domestication in the Australian lupin breeding program: Foundation (1967–1987), First Diversification (1987–1998), Exploitation (1998–2007), and Second Diversification (2007–2016) Phases. Foundation Phase varieties had only two or three founder parents following the domestication bottleneck and high average coefficient of coancestry ($f = 0.45$). The First Diversification Phase varieties were derived from crosses with wild lupin ecotypes, and varieties in this Phase had lower average coefficient of coancestry ($f = 0.27$). Population coancestry increased in varieties of the Exploitation Phase ($f = 0.39$). The rate of inbreeding (ΔF) between the First Diversification and Exploitation Phase (10 years) was 0.09 per cycle, which equates to 9% loss of alleles per cycle due to random drift and low-effective population size ($N_e = 5.4$), assuming two 5-year cycles. New genetic diversity was introduced in the Second Diversification Phase varieties ($f = 0.24$) following more crossing with wild lupins. Genetic progress in Australian lupin breeding so far has been substantial with improvements in grain yield and disease resistance, but narrow genetic diversity will limit future genetic progress. The pedigree of the latest varieties includes 39.1% from three founder varieties in the domestication bottleneck and 48.3% from 9 wild ecotypes that survived 50 years of selection. In terms of conservation genetics, the Australian lupin breeding program is a critically endangered population, and subject to excessive random drift. Migration of genetic diversity from wild lupins or exchange with international breeding programs will improve long-term genetic gain and effectiveness of genomic selection.

The original version of this chapter was revised: Figure 1.1 has been updated with part figure. The correction to this chapter is available at https://doi.org/10.1007/978-3-030-21270-4_13

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1.1 Introduction

Narrow-leafed lupins (*Lupinus angustifolius* L.) provide a rare opportunity to study the impact of a recent domestication bottleneck on reducing genetic diversity and its subsequent recovery in a self-pollinating crop. Sweet narrow-leafed lupins were fully domesticated in the mid-twentieth century, following the discovery of domestication genes in different parts of the world and the exchange of germplasm among breeders in eastern and western Europe, USA, and Australia (Gladstones 1970). Pedigree records are available for 31 varieties released in Australia from 1967 to 2016 (Cowling 1999; IP Australia 2019), and 93 common ancestors. For more information on the history and attributes of narrow-leafed lupin breeding globally, readers are directed to several extensive reviews on the subject (Clements et al. 2005; Cowling and Gladstones 2000; Cowling et al. 1998b; Gladstones 1970, 1998; Święcicki et al. 2015).

Genome diversity is much lower in domesticated narrow-leafed lupins compared with their wild relatives, and wild and landrace *L. angustifolius* ecotypes provide a wealth of genetic and phenological diversity for potential use by lupin breeders (Berger et al. 2012; Mousavi Derazmahalleh et al. 2018; Cowling et al. 1998a). Wild narrow-leafed lupins have contributed to improved grain yield and disease resistance in sweet domesticated varieties (Cowling and Gladstones 2000; Stefanova and Buirchell 2010). The progeny of several wild × domesticated lupin crosses were fully fertile and released as improved varieties in the Australian lupin breeding program in the 1980s (Cowling 1999). The best lines from this round of crossing were recombined to produce high-performing varieties released in the 2000s (Stefanova and Buirchell 2010).

This chapter investigates genetic diversity and population inbreeding in the Australian lupin breeding program over 50 years from 1967 to 2016 based on pedigrees, and suggests methods for improving genetic diversity and the potential for long-term genetic gain, including the use of genomic and pedigree information and optimal contributions selection to achieve these goals.

1.2 Analysis of Genetic Diversity and Population Inbreeding

Pedigree records exist for 31 varieties released from 1967 to 2016 including 93 common ancestors in the pedigree (Cowling 1999; IP Australia 2019, Dr. Bevan Buirchell *pers. comm.*). This information was used to develop a pedigree including founder lines, varieties, and presumed or known common ancestors (Table 1.1). The number of generations of selfing in each line ("fgen") was used to calculate the level of inbreeding in each line. The value of fgen was assumed to be "0" for F_1 progeny, "5" for released varieties, and "10" for landraces or wild ecotypes (Table 1.1).

These records were used to construct a numerator relationship matrix (A-matrix) using ASREML software (VSN International, UK), and pedigrees were plotted in a pedigree chart (Fig. 1.1). The most significant feature of the lupin pedigree is the relatively small number of individuals which contribute to variety development over 50 years (total 124), compared with animal breeding where thousands of animals in the pedigree typically contribute to future performance (Goddard and Hayes 2009).

1.2.1 Coefficient of Coancestry and Inbreeding Coefficient

From pedigree records (Table 1.1), the coefficient of coancestry or kinship coefficient (*f*) between each pair of lines was calculated as ½ the numerator relationship value (*a*-value), which is the proportion of additive genetic variance that two individuals have in common. The coancestry of two individuals is "the probability that two gametes taken at random, one from each, carry alleles that are identical by descent" (Falconer and Mackay 1996), or put another way, the chance that a randomly chosen allele in two potential crossing parents is the same allele as in the common ancestor. In *L. angustifolius*, commercial varieties are homozygous at most loci, and therefore identity by descent represents the

Table 1.1 Pedigrees of Australian narrow-leafed lupin varieties during four Phases of variety release: Phase 1 (Foundation Phase, 1967–1987), Phase 2 (First Diversification Phase, 1987–1998), Phase 3 (Exploitation Phase, 1998–2007), and Phase 4 (Second Diversification Phase, 2007–2016). Key contributing ancestors are shown together with released varieties, indicated by date of release. Where parents are not known, the symbol "0" appears. "fgen" is the number of generations of selfing in the line or variety. "Var. no." is the number of the line or variety in temporal order of the pedigree. Wild ecotypes from the Australian Lupin Collection are indicated by the suffix "w", e.g. P22750w. Where numbers were not located in the records, these are replaced with "xx", e.g. 62Axx1 is a line derived from a cross made in 1962.

Name of line or variety	Female parent	Male parent	fgen	Var. no	Phase of release
New Zealand Blue	0	0	10	V1	
Germany-iuc	0	0	10	V2	
Landrace-moll	0	0	10	V3	
Borre 1947	Germany-iuc	Landrace-moll	10	V4	
New Zealand Blue-le	New Zealand Blue	New Zealand Blue	5	V5	
New Zealand Blue-ta	New Zealand Blue	New Zealand Blue	5	V6	
New Zealand Blue-leuc	New Zealand Blue	New Zealand Blue	5	V7	
Borre-Ku	Borre 1947	Borre 1947	5	V8	
Borre-efl	Borre 1947	Borre 1947	5	V9	
62Axx1	New Zealand Blue-leuc	Borre 1947	2	V10	
62Axx2	New Zealand Blue-le	New Zealand Blue-ta	2	V11	
64Axx2	62Axx1	New Zealand Blue-ta	0	V12	
64Axx1	64Axx2	62Axx2	0	V13	
Rancher	0	0	5	V14	
66A001	64Axx1	Rancher	0	V15	
66Axx2	64Axx1	Borre-Ku	0	V16	
Uniwhite 1967	64Axx2	64Axx2	5	V17	Phase1
P20722w	0	0	10	V18	
P20723w	0	0	10	V19	
AB12	66Axx2	66Axx2	2	V20	
Borre-efl/Uw	Borre-efl	Uniwhite 1967	0	V21	
Borre-efl/Uh	Borre-efl	64Axx1	0	V22	
65G-251	0	0	5	V23	
70A61	P20722w	AB12	0	V24	
70A62	P20723w	AB12	0	V25	
71Axx1	Borre-efl/Uw	64Axx1	0	V26	
65G-251/Uh	65G-251	64Axx1	5	V27	
Pxxxx1w	0	0	10	V28	
P20639w	0	0	10	V29	
P22661w	0	0	10	V30	
72Axx1	65G-251/Uh	66A001	5	V31	
Uniharvest 1972	64Axx1	64Axx1	5	V32	Phase1
72A014	66A001	66Axx2	0	V33	
72A015	71Axx1	66A001	0	V34	
Unicrop 1973	66Axx2	66Axx2	5	V35	Phase1
Fest 1973	62Axx2	62Axx2	5	V36	Phase1

(continued)

Table 1.1 (continued)

Name of line or variety	Female parent	Male parent	fgen	Var. no	Phase of release
64A02	Uniwhite 1967	P20639w	5	V37	
73Axx1	Borre-efl/Uh	Uniharvest 1972	5	V38	
P22750w	0	0	10	V39	
P22872w	0	0	10	V40	
P22748w	0	0	10	V41	
P22721w	0	0	10	V42	
72A014-1	72A014	72A014	2	V43	
72A014-2	72A014	72A014	2	V44	
72A015-2	72A015	72A015	2	V45	
74Axx1	72Axx1	Unicrop 1973	0	V46	
74A003	74Axx1	Unicrop 1973	0	V47	
75A045	P22872w	72A014-1	0	V48	
75A054	P22721w	72A014-1	0	V49	
75A060	P22748w	72A014-1	0	V50	
75A061	P22750w	72A014-1	0	V51	
Unicrop-E	Unicrop 1973	Unicrop 1973	5	V52	
Marri 1976	66A001	66A001	5	V53	Phase1
CE2-1-1	Pxxxx1w	72A014-1	5	V54	
76A106-31	Unicrop 1973	P22661w	5	V55	
76A106-32	Unicrop 1973	P22661w	5	V56	
76A6-11-3-1-2	Marri 1976	Unicrop-E	5	V57	
79A078	70A62	70A61	0	V58	
Illyarrie 1979	72A014-1	72A014-1	3	V59	Phase1
Yandee 1980	72A014-2	72A014-2	3	V60	Phase1
Chittick 1982	72A015-2	72A015-2	3	V61	Phase1
75A061-3	75A061	75A061	2	V62	
75A054-5	75A054	75A054	2	V63	
79A078-14-10	79A078	79A078	5	V64	
84A086	75A061	CE2-1-1	0	V65	
84L528-18	CE2-1-1	76A106-31	2	V66	
84L551-13	76A106-32	76A6-11-3-1-2	2	V67	
75A054-5-8	75A054-5	75A054-5	2	V68	
75A061-3-1	75A061-3	75A061-3	2	V69	
84S019-96-2	79A078-14-10	84A086	4	V70	
P26672w	0	0	10	V71	
P22764w	0	0	10	V72	
84A086-12-17	84A086	84A086	4	V73	
84A086-73-10	84A086	84A086	4	V74	
Danja 1986	74A003	74A003	5	V75	Phase1
Wandoo 1986	73Axx1	64A02	5	V76	Phase1

(continued)

Table 1.1 (continued)

Name of line or variety	Female parent	Male parent	fgen	Var. no	Phase of release
83A025	75A061-3-1	75A054-5-8	0	V77	
Geebung 1987	73Axx1	64A02	5	V78	Phase1
Gungurru 1988	75A061	75A061	2	V79	Phase2
88L152-29	Gungurru 1988	P26672w	5	V80	
Yorrel 1989	75A045	75A045	5	V81	Phase2
Warrah 1989	75A060	75A060	5	V82	Phase2
75A045-10-8	Yorrel 1989	Yorrel 1989	1	V83	
Merrit 1991	Gungurru 1988	Gungurru 1988	2	V84	Phase2
84S019-96-2-11	84S019-96-2	84S019-96-2	1	V85	
84A086-73-10-37	84A086-73-10	84A086-73-10	0	V86	
84A041	Yorrel 1989	83A025	2	V87	
83A008-71-41(sel)	75A061-3-1	75A045-10-8	5	V88	
84S035-48-2	Yorrel 1989	84A086	3	V89	
84S035-48-4	Yorrel 1989	84A086	3	V90	
90A050	Merrit 1991	84S035-48-2	0	V91	
95L335-17-15	88L152-29	84S019-96-2-11	5	V92	
84S017	79A078-14-10	84A041	0	V93	
Myallie 1995	CE2-1-1	76A106-31	5	V94	Phase2
84S035-48-4-24	84S035-48-4	84S035-48-4	0	V95	
Wonga 1996	83A025	83A025	4	V96	Phase2
Kalya 1996	Warrah 1989	79A078-14-10	4	V97	Phase2
Tallerack 1997	84L528-18	84L551-13	5	V98	Phase2
84S017-50S-62	84S017	84S017	5	V99	
Tanjil 1998	Wonga 1996	Wonga 1996	2	V100	Phase2
Belara 1997	84S035-48-2	84S035-48-2	1	V101	Phase3
Moonah 1998	84S017	84S017	1	V102	Phase3
Quilinock 1999	84S019-96-2	84S019-96-2	1	V103	Phase3
90S085-107-33	Tanjil 1998	90A050	5	V104	
90S085-107-39	Tanjil 1998	90A050	5	V105	
91A047-58	Tanjil 1998	84A086-12-17	3	V106	
97L122-1	91A047-58	Kalya 1996	3	V107	
01LF1 bulk	90S085-107-39	0	0	V108	
01L576-108	P22764w	83A008-71-41(sel)	5	V109	
95L256-17	84A086-73-10-37	Quilinock 1999	0	V110	
97L182-5-7	84S017-50S-62	0	5	V111	
03A013R	95L335-17-15	0	0	V112	
04A010	97L182-5-7	03A013R	0	V113	
03LF1 bulk	0	95L335-17-15	0	V114	
Mandelup 2004	84A086-12-17	84S035-48-2	4	V115	Phase3

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