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Nuclear DNA Amounts in Angiosperms: Progress, Problems and Prospects

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CONTENTS

• *Background* The nuclear DNA amount in an unreplicated haploid chromosome complement (1C-value) is a key diversity character with many uses. Angiosperm C-values have been listed for reference purposes since 1976, and pooled in an electronic database since 1997 (http://www.kew.org/cval/homepage). Such lists are cited frequently and provide data for many comparative studies. The last compilation was published in 2000, so a further supplementary list is timely to monitor progress against targets set at the first plant genome size workshop in 1997 and to facilitate new goal setting.

• *Scope* The present work lists DNA C-values for 804 species including first values for 628 species from 88 original sources, not included in any previous compilation, plus additional values for 176 species included in a previous compilation.

• *Conclusions* 1998–2002 saw striking progress in our knowledge of angiosperm C-values. At least 1700 first values for species were measured (the most in any five-year period) and familial representation rose from 30 % to 50 %. The loss of many densitometers used to measure DNA C-values proved less serious than feared, owing to the development of relatively inexpensive flow cytometers and computer-based image analysis systems. New uses of the term genome (e.g. in 'complete' genome sequencing) can cause confusion. The *Arabidopsis* Genome Initiative C-value for *Arabidopsis thaliana* (125 Mb) was a gross underestimate, and an exact C-value based on genome sequencing alone is unlikely to be obtained soon for any angiosperm. Lack of this expected benchmark poses a quandary as to what to use as the basal calibration standard for angiosperms. The next decade offers exciting prospects for angiosperm genome size research. The database (http://www.kew.org/cval/homepage) should become sufficiently representative of the global flora to answer most questions without needing new estimations. DNA amount variation will remain a key interest as an integrated strand of holistic genomics.

Key words: Angiosperm DNA amounts, DNA C-values, nuclear genome size, plant DNA C-values database.

INTRODUCTION

It has been possible to estimate the amount of DNA in plant nuclei for over 50 years, and since the key role of DNA in biology was discovered in 1953, such research has increased in each successive decade. Work on plants has played a leading part in research to describe and understand the origin, extent and effects of variation in the DNA amount in the unreplicated haploid nuclear chromosome complement (defined by Swift, 1950, as the 1C-value) of different taxa. Indeed, angiosperms are probably the most intensively

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studied major taxonomic 'group' of organisms, with published C-values for over 4100 species.

Early research to address questions such as possible relationships between DNA C-value and the rate of cell development (e.g. Van't Hof, 1965) usually required work to estimate C-values for most of the taxa concerned, as these were unavailable. Later, as taxa with 'known' C-values increased, it was possible to use such data in new comparisons (supplemented by further first estimates made for sample taxa). However, it was often difficult to know whether a C-value existed for a particular taxon, and if so, where to find it. Such estimates were widely scattered in the literature or even unpublished. Small lists of nuclear DNA amounts were published in reviews and research papers, but the first large list of DNA amounts for angiosperms, compiled primarily as a reference source was published in 1976. This contained data for over 750 species from 54 original sources (Bennett and Smith, 1976), and noted an intention to publish supplementary lists for reference purposes at intervals. Five such lists, together giving pooled data for over 2900 species from 323 original sources, have followed (Bennett *et al*., 1982, 2000; Bennett and Smith, 1991; Bennett and Leitch, 1995, 1997). Data from the first five publications were pooled in an electronic form – the Angiosperm DNA C-values database, which went live in April 1997. This was updated as release 3.1 and incorporated, with databases for gymnosperms, pteridophytes and bryophytes, into the Plant DNA C-values database (release 1.0) in 2001.

These data are clearly much used, as the published lists have been cited over 1400 times, including over 700 times since 1997, whilst the electronic database has received over 50 000 hits. Recently they have provided the large samples of data needed for many diverse comparative studies, such as testing for possible relationships between nuclear DNA amount and risk of extinction (Vinogradov, 2003), ecological factors in California (Knight and Ackerly, 2002), lead pollution in Slovenia (B. Vilhar, University of Ljubljana, Slovenia, pers. comm.); ploidy level (Leitch and Bennett, 2004), and land plant evolution (Leitch *et al*., 2005).

Given their ongoing use as reference sources, publication of a sixth supplementary list of angiosperm C-values is timely, if not overdue. The present work lists DNA C-values for 804 species from 88 original sources, including first estimates for 628 species not included in any previous compilation, plus additional estimates for 176 species already included in one or more previous compilation. Data in the Appendix table were prepared for analysis at the second Plant Genome Size Discussion Meeting in September 2003, so it is fitting that they are included in this special supplement. Whilst they represent most of the new C-value data published or estimated in 2000–2002, we are already aware of a further large sample estimated but unpublished either by late 2002, or subsequently. Thus, despite its large size, the present list will soon be followed by a seventh supplement.

PROGRESS

Research on DNA C-values in angiosperms is unique in having been subject to detailed analyses of its quantity and quality over a long period (Bennett and Leitch, 1995). The importance of identifying gaps in our knowledge concerning this key biodiversity character, of recommending targets for new work to fill them by collaboration of international partners, and of monitoring progress to ensure that any shortfall is recognized, was confirmed by the first plant genome size workshop in 1997 (http://www.kew.org/cval/conference.html#outline, Bennett *et al*., 2000) and reviewed by participants at the second plant genome size workshop in 2003. Thus, what follows is mainly a summary of the overall progress for angiosperms against key targets set in 1997 for the following quinquennium (1998–2002). However, it also notes meaningful statistics for the data included in the Appendix table, or known to us from personal communications made after the Appendix table was closed.

In 1997 C-values for 2802 species (approximately 1 %) of angiosperm species had been estimated in the previous 40 years. The 1997 workshop concluded that the ideal of a C-value for all taxa was unrealistic, but long-term, estimates for 10–20 % of angiosperms seemed both ultimately achievable and adequate for all conceivable uses provided they were carefully targeted to be representative of the various taxonomic groups, geographical regions, and life forms in the global flora. So the first recommended target was to estimate first C-values for the next 1 % of angiosperm species (i.e. another 2500 species) by 2003. Many saw this goal as aspirational, as achieving it would mean estimating as many C-values in five years as in the past 40. Others thought that new technology (e.g. flow cytometry) would make it easy to achieve.

Improved systematic representation (species and families)

(i) First estimates for species. In September 1997 the Angiosperm DNA C-values database contained data for 2802 species. By September 2003 C-values were listed for 4119 species, including 689 first values for species listed in Bennett *et al*. (2000) and 628 such values for species in the Appendix table. Progress toward the first target in the five year period (1998–2002) considerably exceeded the average of ~110 first values for species per annum in the early 1990s. Clearly, the 1997 workshop stimulated an increase in the total output of first C-values for species to its highest level for any five-year period (almost 200 per annum; Fig. 1A). Moreover, the proportion of newly published C-values that were also first estimates for species, which had previously fallen (Bennett *et al*., 2000), rose as a result of recent targeting and averaged 72·5 % for values published since 1997 (Fig. 1B). Nevertheless, the total number of published first C-values for species (1032) listed since 1997 was only 41 % of the 1997 target of approx. 2500.

The real total of first C-values for angiosperms estimated after 1996 but unpublished by 2003 was much higher, but is difficult to determine exactly. For example, several hundred values were measured by Ben Zonneveld (pers. comm.) using flow cytometry but not published. Listing

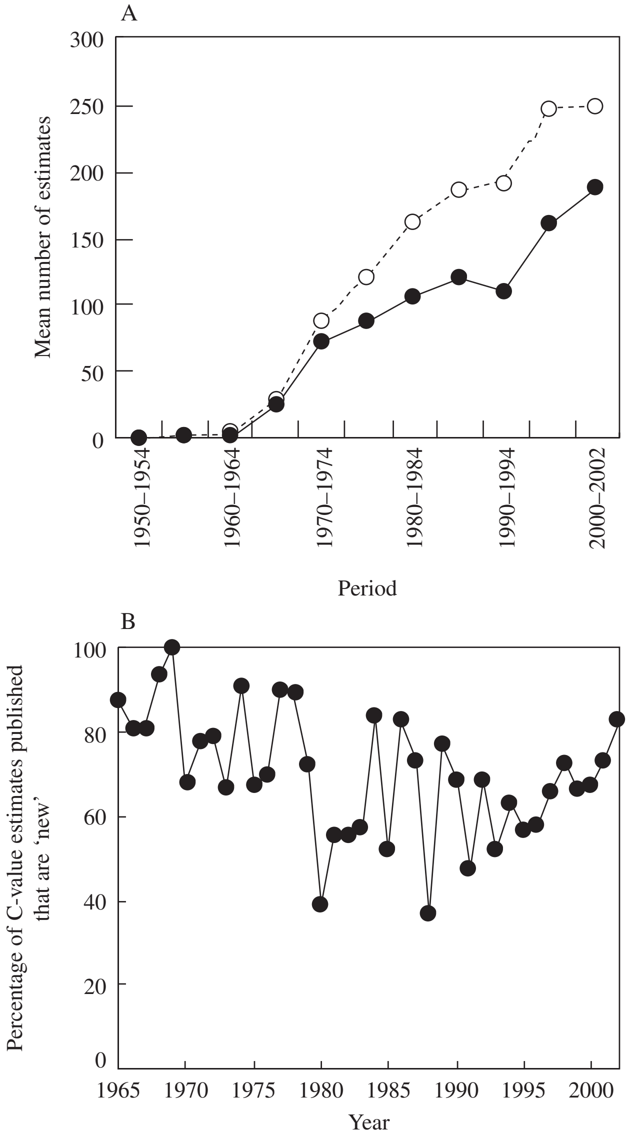

FIG. 1. (A) Mean number per year of total (open symbols) and 'first' (closed symbols) DNA C-value estimates communicated in ten successive 5-year periods and the 3-year period 2000–2002, between 1950 and 2002. Based on analysis of data listed in the present Appendix table, and the Angiosperm DNA C-values database (release 4.0, January 2003). (B) Percentage of C-value estimates published or communicated during 1965–2002 that are first values for species listed in the present Appendix table and the Angiosperm DNA C-values database (release 4.0, January 2003).

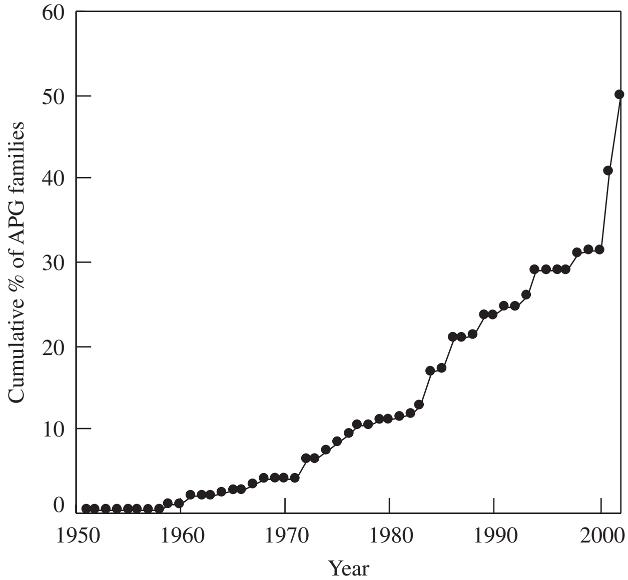

FIG. 2. Cumulative percentage of angiosperm families recognized by the Angiosperm Phylogeny Group (APG) (APGII, 2003) with a first C-value represented in the present Appendix table, the Angiosperm DNA C-values database (release 4.0, January 2003), plus eleven known to the present authors in September 2003.

for the Appendix table closed in August 2002, ready for the workshop; however, we saw 158 first C-values published by other authors later in 2002, and 22 such values were estimated at RBG, Kew. Adding these data to those listed in our compilations suggests that the total number of first C-values for species estimated in 1997–2002 was probably at least 1700 and hence not less than approx. 66 % of the target set in 1997. Analysis shows that this was achieved by international collaboration involving at least 18 research groups in ten countries. Whilst a target of 2500 was aspirational, it seems attainable as a future five-year goal. However, at the present rate achieving 20 % species representation would take 100 years, so an ultimate goal of 10 % (approx. 25 000 angiosperm species) is more sensible.

(ii) First estimates for families. The 1997 workshop noted that a first C-value was available for only 30 % of angiosperm families recognized at that time. Thus, a second recommended target was 'To obtain at least one C-value estimate for a species in all angiosperm families'. Monitoring first C-values for species listed in Bennett *et al.* (2000) showed that progress towards this goal was initially very slow. Indeed, 'since 1997 first C-values had been listed for 691 angiosperm species, but only 12 (1·7 %) were also first estimates for families'. Work to correct this began at RBG, Kew in 1999. In 2001 two papers reported first C-values for 50 families (Hanson *et al.*, 2001*a*, *b*), and 30 more followed, including five basal angiosperm families (Leitch and Hanson, 2002; Hanson *et al.*, 2003), all included in the present Appendix table.

Analysis of listed data for 4119 species shows that a first published value is available for at least 217 of the 457 angiosperm families currently recognized by the Angiosperm Phylogeny Group (APG) (APG II, 2003). Together with first estimates for 11 unlisted families (Hanson, RBG, Kew, pers. comm.; Koce *et al.*, 2003) measured or seen after listing for the Appendix table was closed, the total is 228. Thus, since 1997 (after losses owing to new familial circumscriptions—APG II, 2003; Hanson *et al.*, 2003) first values for at least 85 such families have been measured, so good progress has been made. However, the proportion of families represented rose only from 30 % to 49·9 % (Fig. 2), which is less than one third of the target (100 %) set in 1997. Major factors limiting progress were

TABLE 1. *The number and percentage (in brackets) of original references with first authors from various geographical areas among the total of 465 sources contributing to the present Appendix table and the six lists of angiosperm DNA amounts previously compiled for reference purposes that were pooled in the Angiosperm DNA C-values database (release 4.0, January 2003)*

	DNA C-value compilation							
Area	1976[1]	1982[2]	1991[3]	1995[4]	1997[5]	2000[6]	Present Appendix	Total
Europe	34 (63·0)	38 (71·7)	30 (53·6)	43 (40·6)	18 (48·6)	38 (51·4)	54 (61·4)	255 (54·8)
UK	28 (51·9)	13 (24·5)	22 (39·3)	23 (21·7)	5 (13·5)	8 (10·8)	10 (11·4)	109 (23·4)
North America	14 (25·9)	11 (20·8)	16 (28·6)	19 (17·9)	5 (13·5)	11 (14·9)	13 (14·8)	89 (19·1)
South and Meso America	0 (0·0)	0 (0·0)	3 (5·4)	9 (8·5)	1 (2·7)	6 (8·1)	2 (2·3)	21 (4·5)
Africa	1 (1·9)	0 (0·0)	0 (0·0)	1 (0·9)	2 (5·4)	1 (1·4)	2 (2·3)	7 (1·5)
Asia	1 (1·9)	3 (5·7)	4 (7·1)	30 (28·3)	11 (29·7)	8 (10·8)	17 (19·3)	74 (15·9)
India	1 (1·9)	1 (1·9)	2 (3·6)	28 (26·4)	11 (29·7)	4 (5·4)	11 (12·5)	58 (12·5)
China	0 (0·0)	0 (0·0)	0 (0·0)	0 (0·0)	0 (0·0)	0 (0·0)	2 (2·3)	2 (0·4)
Australasia	4 (7·4)	1 (1·9)	3 (5·4)	4 (3·8)	0 (0·0)	7 (9·5)	0 (0·0)	19 (4·1)
Australia	4 (7·4)	1 (1·9)	3 (5·4)	1 (0·9)	0 (0·0)	1 (1·4)	0 (0·0)	10 (2·2)
Total	54	53	56	106	37	71	88	465 (100)

[1] Bennett and Smith (1976); [2] Bennett *et al*. (1982); [3] Bennett and Smith (1991); [4] Bennett and Leitch (1995); [5] Bennett and Leitch (1997); [6] Bennett *et al*. (2000).

discussed previously (Hanson *et al*., 2003). Unlike progress towards the species target, which involved many research groups, movement towards the goal for families since 1997 has depended mainly on work by one institution, as RBG Kew estimated 65 of the 74 (87 %) first values for families listed in the Appendix table.

The Plant Genome Size Workshop in 2003 confirmed that global capacity for estimating DNA C-values (determined by available equipment, funding and trained operators) remains very limited. Consequently, any increased focus on targets for other plant groups (e.g. bryophytes, pteridophytes, gymnosperms—reviewed in Leitch and Bennett, 2002*b*) inevitably reduces progress to improve representation for angiosperm targets, a problem discussed below. However, it should not detract from the highly successful progress to make C-values more representative of the global flora described above.

PROBLEMS

Geographical representation and distribution

We first noted the need to improve geographical representation for angiosperm C-values in Bennett and Leitch (1995). This was confirmed by the 1997 plant genome size workshop, although no specific regional targets were recommended. Perhaps, in consequence, progress in this area has never been monitored in detail, although we have been at pains to advertise the problem in a general way and to provoke action to rectify it in particular regions, such as southern Africa (Leitch and Bennett, 2002*a*).

There are two critical concerns regarding the geographical distribution of angiosperm C-value work. (i) The first concerns the small number of publications with original C-values by first authors in many regions (Table 1). This reflects a serious imbalance between the geographical distribution of research scientists working on genome size and of taxa whose C-values are unknown. Bennett *et al*. (2000) noted that 'Africa remains an unexplored continent' and that 'Whereas six out of 377 original sources have first authors with addresses in Africa, still none has an angiosperm C-value estimated in Africa, as all six reported work done in Europe or the USA.' Analysis of the 88 original sources in the present work shows no improvement, as the number of original sources from Africa (2), China (2), and South America (2) remains low (Table 1). (ii) The second concerns the small number of first C-values by any authors for species endemic to several large geographical regions. With some exceptions, the sample is still dominated by crops and their wild relatives, model species grown for experimental use, and other species growing near laboratories in temperate regions, mainly in Western Europe and North America. Analysis of data in the Appendix table shows that none presented data for other taxa endemic to China, Japan, Brazil, Mexico or Central Africa. Similarly, although island floras are known to be rich in endemics, no original source has reported C-values for any large islands such as Borneo, New Guinea or Madagascar, where 80 % of the 12 000 described plant species are endemic (Robinson, 2004).

Plant life form

There is also a need for the overall sample to represent better the full range of plant types and life forms. We previously identified several associations and life forms as being poorly represented in the database (Bennett and Leitch, 1995), yet taxa from bog, fen, tundra, alpine and desert environments, and halophytic, insectivorous, parasitic, saprophytic and epiphytic species and their associated taxa are all still under-represented.

Solving this problem needs a proactive approach, as recent experience with first C-values for angiosperm families shows. First, a target must be set for each gap. Second, monitoring newly published data against targets must begin. Third, if work on poorly-represented floras or life forms does not increase, then established research groups must re-focus on target material available in existing collections. Unless global capability for estimating plant DNA C-values is significantly increased by new technology, funds or skilled operators, then this change in strategy will reduce progress towards achieving other targets. However, the prime objective remains: to generate a sample representative of the global flora that is able to support most comparative studies. Managers of the limited global capacity for estimating genome size should keep this firmly in mind when targeting taxa for new work.

Obsolescence time bomb

Several methods have been used to measure plant DNA C-values, but most values have been estimated by Feulgen microdensitometry (Fe), both overall and since 1997. In 1997 we identified an imminent problem, likely to limit future estimations. This was the failure and non-replacement of densitometers long used by many groups to estimate DNA C-values. Manufacturers were ending their support for such equipment, and users faced difficulty in funding new equipment for this purpose. Moreover, this problem was likely to be most acute in regions where some of the greatest gaps in our knowledge lay. Reviewing the position at the second Plant Genome Size Workshop confirmed that, as predicted, the 'obsolescence time bomb' had exploded. By 2003 several laboratories that had long published C-values listed in the Angiosperm DNA C-values database were now unable to estimate C-values by this (e.g. in Mexico, the USA), or any method (e.g. in Argentina). Vickers Instruments no longer supports their M85 microdensitometer, and spare parts for it are unobtainable. A few laboratories, including ours, can still use such machines, but now without servicing and only until they fail catastrophically.

As expected, one response to this problem was the increased use of flow cytometry (FC) to replace Fe. Analysis of data in the Appendix table shows a higher proportion of C-values obtained by FC (58·4 %), mostly since 1997, than noted previously (48·6 %) for data listed in Bennett and Leitch (2000), whilst in Bennett and Leitch (1995, 1997) FC averaged 26·7 %. Several groups have undertaken careful studies to compare DNA estimates made by FC and Fe, to define best practice for FC, or to show that FC can be applied widely to most plants across the full range of known DNA C-values (e.g. see review by Doležel and Bartos, 2005, this volume). Fortunately, the cost of a basic flow cytometer for such work has fallen, and suitable models (e.g. Partec PAII) have recently been set up for this use for approx. £20K (US$30K). If this technology continues to improve, and its costs continue to fall, FC should be more easily available. However, FC easily yields poor data in unskilled hands and by itself does not provide the cytological view of test material(s) that is essential to count chromosome number(s). Its use in some less-developed countries (where the greatest gaps in our knowledge still remain) will depend on training local operators, but such capacity-building may be thwarted by a lack of in-country support by the suppliers of flow cytometers.

A second solution to the problem is a new availability of relatively inexpensive computer-based image analysis (CIA) systems, which can estimate DNA amounts using Feulgen-stained cytological preparations in place of a microdensitometer. Although proprietary hard-wired CIA systems have been available since the 1970s (e.g. Zeiss Quantimet system), they cost much more than microdensitometers, and analysis of the literature shows they have not been used to estimate plant C-values. However, in the 1990s, with advances in computer technology, less expensive systems were developed (e.g. CIRES system) primarily for medical use, and these have also been used to good effect for plant C-value estimations (e.g. Temsch *et al*., 1998; Greilhuber *et al*., 2000).

Sadly, the CIRES system that adapted well for this purpose is no longer available, as the software is incompatible with the operating system used on modern PCs. However, computer-literate groups can assemble the kit needed to estimate C-values using CIA, and several software packages written specifically for this purpose are available (Vilhar *et al*., 2001; Hardie *et al*., 2002). Hardie *et al*. (2002) give an excellent review of this technique and practical issues concerned with its use for animal materials, and Vilhar *et al*. (2001) have compared CIA, Fe and FC, to help define best practice for CIA, demonstrating that CIA can be applied to plants with an approx. 100-fold range of C-values. Vilhar *et al*. (2001) concluded that 'DNA image photometry gives accurate and reproducible results, and may be used as an alternative to photometric cytometry in plant nuclear DNA measurements'. CIA can use an existing microscope, costs less than FC to set up, and is easier to service in countries that lack FC manufacturers' support. The field would benefit from development of a standard inexpensive CIA 'kit', an agreed best practice CIA technique, and easy access to leading laboratories for training and technology transfer. Given this, CIA could soon become the method of choice for estimating C-values in angiosperms, replacing Fe as a method of choice along with FC, but with the advantage that, unlike FC, it uses microscope slide preparations, allowing users to make cytological observations.

Errors and inexactitudes

Swift (1950) defined the DNA content of an unreplicated haploid complement as its 1C-value (C standing for 'constant'). Thus, replicated diplophase nuclei have a 4C DNA amount and produce two unreplicated 2C nuclei by mitotic division, and four 1C gametic nuclei after meiosis, irrespective of the organism's ploidy level. This convention applies well to polyploid taxa with diploidized meiotic chromosome pairing such as hexaploid breadwheat, which produce mainly functional, balanced polyhaploid gametes with 1C DNA amounts at meiosis (Rees and Walters, 1965). Consequently, for several previous reference lists, 4C DNA estimates for all taxa were divided by 2 and 4 to generate 2C- and 1C-values respectively (e.g. Bennett *et al*., 2000). However, a problem with this practice was identified for the few taxa with odd ploidy levels in release 3.1 of the Angiosperm DNA C-values database (namely 45 out of 3493 listed taxa, ~1·3 %), as the resulting 1C-values are not biologically meaningful. For example, triploids with a 4C amount in their fully replicated metaphase nuclei do regularly produce two 2C nuclei at mitosis, but do not regularly produce four 1C products at meiosis. The authors are grateful to several colleagues who noted this problem and suggested solutions.

This problem has several practical consequences. (i) Regrettably, researchers who use 1C data from the literature or downloaded from the Angiosperm DNA C-values database may have included this error in the samples that they used for comparative analyses. However, this is unlikely to have influenced their conclusions significantly, since the magnitude of the error is relatively small (ranging between −0·25C for a triploid, to +0·25C for a pentaploid—which tend to cancel out), and affects only 1·3 % of all taxa listed. Overall, errors in mean DNA amounts for samples are probably less than 0·5 %. Studies that used data from the 2C or 4C columns for samples of odd-ploid taxa are unaffected by the error. (ii) To ensure that researchers are aware of the problem and do not generate 1C data for taxa with odd ploidy levels in the future, release 4.0 of the Angiosperm DNA C-values database gives 2C- and 4C-values for the 45 out of 3493 entries with odd ploidy levels, plus a warning note in response to any queries for 1C-values. This approach is also followed in the present Appendix table (see footnote t). (iii) This problem also highlights a general need to re-assess definitions of 'C-value' and 'genome size' in light of recent usage and new theoretical understanding, a topic explored by Greilhuber *et al.* (2005). Indeed, the above problem shows the need for care when handling data, and the danger of using computer-generated numbers uncritically. It is clearly perilous to ignore basic biology or the literature, as the recent history of genome size, 'complete' genome sequencing, and interest in the smallest angiosperm genome clearly shows.

Genome size, 'complete' genome sequencing, and, the euchromatic genome

A growing semantic problem concerns different uses of the term 'genome' (Greilhuber *et al.*, 2005). As originally defined by Winkler (1920), genome referred to a monoploid chromosome complement. Since a monoploid is defined as 'having one chromosome set with the basic (x) number of chromosomes' (Rieger *et al.*, 1991), it followed by definition that any polyploid taxon had three or more genomes. However, an alternative meaning, now in common usage, uses genome as an interchangeable alternative for the 1C-value to refer to the DNA content of an unreplicated gametic nuclear complement, irrespective of ploidy level. Unless the meaning intended is clearly defined on each occasion, this can be confusing, especially when authors use both meanings for a polyploid taxon in the same paper. For example, Devos and Gale (1997) used the term 'genome' to refer to both the entire complement of nuclear DNA in a hexaploid wheat nucleus and to the individual A, B and D 'genomes'.

Further potential for confusion comes from new uses of the term 'genome' recently spawned by genome sequencers. These concern the counter-intuitive meaning of a 'wholly', 'completely' or 'entirely' sequenced genome, or of equating 'genome' with 'euchromatic genome'—a confusing concept in which 'genome' equals the parts which could be cloned and sequenced, but not the rest (see below). None of these qualitative new uses of genome equates to its quantitative use to mean either a 1C-value, or one monoploid parental genome in a polyploid.

The completely sequenced genome

Since 2000 the scientific and popular press has reported and celebrated the 'complete' sequencing of the first insect (*Drosophila melanogaster*) and plant genome (*Arabidopsis thaliana*) and the human genome (in 2001). For example, a title in *Nature* reported: 'The sequencing of an entire plant genome is now complete.' Readers could be forgiven for assuming this meant the entire linear sequence of the nuclear DNA had been sequenced and assembled, so that the total size of the nuclear genome in these organisms was now known with certainty, and hence much more accurately than any previous estimate based on other methods subject to various experimental errors. The popular and scientific literature easily gives that impression, and unfortunately that is what many, incorrectly, understood. The truth is otherwise, as a 'completely sequenced' genome is a very relative concept. In the same issue of *Science* where Brenner (2000) wrote 'We have the complete sequence of the 125-megabase genome of the fruit-fly *Drosophila*', Pennisi (2000) noted that 'the fly sequence still has c. 1000 small gaps'—referring only to the sequenced euchromatin part. But what of the rest? Speaking of heterochromatin, Adams *et al.* (2000) explained that the 'genomes of eukaryotes generally contain heterochromatic regions surrounding the centromeres that are intractable to all current sequencing methods' and that 'Because of the unclonable repetitive DNA surrounding the centromeres it is highly unlikely that the genomic sequence of chromosomes from eukaryotes such as *Drosophila* or human will ever be 'complete'. Moreover, Adams *et al.* (2000) stated that the unsequenced centric heterochromatin regions comprised 'one third' of the approx.180 Mb genome of *Drosophila*. But how was its size determined? Careful reading revealed that the Mb size of these unsequenced centromeric heterochromatic segments was measured not by any modern molecular method, but by using a ruler on one cell of a plate in a paper by Yamamoto *et al.* (1990). This important detail is not stated in the main text, but in the legend to fig. 1 in Adams *et al.* (2000). As Bork and Copley (2001) clearly explain, 'There are regions, often highly repetitive, that are difficult or impossible to clone (one of the initial steps in a sequencing project) or sequence with current technology. . . . The extent of these regions varies widely in different species. So, rather than applying a universal gold standard, each sequencing project has made pragmatic decisions as to what constitutes a sufficient level of coverage for a particular genome. For example, as much as one-third of the sequence of the fruitfly *Drosophila melanogaster* was not stable in the cloning systems used, and so was not sequenced.'

Thus, workers interested in C-values should clearly understand that a 'completely', 'entirely' or 'wholly' sequenced genome is not what those words might imply if taken at face value, and the size given for such a genome may indicate either the amount of DNA sequenced, or the size of that euchromatic genome sequenced plus a best-guess estimate of a lot of unsequenced heterochromatin. Further, it can mean that every type of sequence in an organism has been sequenced, but it need not mean that all copies of all types have been sequenced, or that their copy numbers are known. Without this information total genome size (the DNA C-value) cannot be determined based on genome sequencing (Bennett *et al*., 2003).

Swift (1953) stated that, 'in general estimates of the nucleic acids in cells are at present accurate to 10 or 20 %'. Later, Bennett and Smith (1976) concluded that 'While a few estimates are not accurate even to within 20 %, careful measurements of 4C DNA amounts in species with 0·5–2·0 times that of a standard species are probably accurate to within 5–10 %'. Greilhuber (1998) noted 'much suspect or demonstrably wrong data have accumulated and continue to be accumulated in the literature'. Sadly, the 'complete' genome sequencing of *Arabidopsis* (*Arabidopsis* Genome Initiative, 2000), which was expected to provide a new baseline, only added to this phenomenon.

Plant genome size researchers have long recognized the need for an exact calibration standard, whose C-value is not subject to technical errors. Thus, the publication of a precise C-value for the first plant to have its genome completely sequenced was eagerly awaited, as it was expected to provide a baseline, gold-standard reference point, against which all other plants could be compared and expressed. *Arabidopsis thaliana* ecotype 'Columbia' was chosen for complete genome sequencing, partly because its tiny genome should be less costly to sequence than larger genomes in other species.

In 2000 the *Arabidopsis* Genome Initiative (AGI) published the genome size of *Arabidopsis thaliana* as 125 Mb, comprising 115·4 Mb in the sequenced regions plus a rough estimate of 10 Mb in unsequenced centromere and ribosomal DNA regions. The accuracy of this estimate was set not by the precision of sequencing and assembling contigs, but by the total inaccuracy in the sizes assumed for the unsequenced gaps (Bennett *et al*., 2003) and hence was no more accurate than many estimates in the range 150–180 Mb made by other methods. Further analysis showed that the AGI's rough estimate of 10 Mb in the unsequenced gaps was highly inaccurate. Thus, new comparisons using flow cytometry, which co-ran *A. thaliana* ecotype 'Columbia' with three animal species including *Caenorhabditis elegans* Bristol N2 (whose genome size is accurately established by genome sequencing as just over 100 Mb), gave C-value estimates for *A. thaliana* in the range 154–162 Mb (with 157 Mb when *C. elegans* was used as the standard) (Bennett *et al*., 2003). This value is about 25 % larger than the AGI estimate of 125 Mb which was clearly a gross underestimate, and hence is not the long-awaited first benchmark C-value for a completely sequenced plant genome—giving those words their natural meaning. Other molecular work has confirmed this conclusion (e.g. Hosouchi *et al*., 2002).

More recently, the draft DNA sequence of the rice (*Oryza sativa*) genome was published (*O. sativa* ssp. *japonica*, Goff *et al*., 2002; *O. sativa* ssp. *indica*, Yu *et al*., 2002). However, while the estimated genome sizes based on DNA sequencing did not suffer from the serious shortcomings of the *Arabidopsis* estimate, neither did they fulfil the criteria essential for a new benchmark calibration standard. Yu *et al*. (2002) gave a new C-value of 466 Mb for *O. sativa* ssp. *indica* calculated by adding up the DNA sequencing data for 362 Mb of sequenced scaffolds and 104 Mb of 'unassembled data'. In contrast Goff *et al*. (2002) reported the sequencing of DNA which covered a total of 389 809 244 bp of the *O. sativa* ssp. *japonica* genome. They stated that this represented 93 % of the 420 Mb rice genome but did not give a reference to the source of 420 Mb. It is therefore unclear whether the C-value of 420 Mb given by Goff *et al*. (2002) represents a new C-value based on genome sequencing alone. The 1C-value for rice may yet prove to be slightly higher than the values assumed by Goff *et al*. (2002) and Yu *et al*. (2002), and approach 490 Mb, equivalent to the 0·5 pg estimated by Bennett and Smith (1991).

Exact C-values based on complete genome sequences would be invaluable (Bennett *et al*., 2003). The need to complete sequencing gaps in *Arabidopsis* remains technically difficult, and it is unclear how, when, or if it will be achieved. Genome sequencing becomes more difficult as genome size increases, and experience with *Arabidopsis* implies that exact C-values are unlikely to be obtained in this way soon for any larger plant genomes, including the established plant C-value standard *Oryza sativa*.

The current situation poses a quandary for the plant genome size community, who have long paid serious attention to trying to maximize the accuracy and comparability of plant DNA C-values by using agreed calibration standards (both materials and assumed values; e.g. see http://www.rbgkew.org.uk/cval/conference.html#outline, Bennett *et al*., 2000), while eagerly awaiting the first absolute measurement for a plant obtained by really complete DNA sequencing. Current options include: (i) continue to use the existing small group of plant calibration standards until a plant C-value which meets the required criteria becomes available; (ii) adopt an animal C-value which meets these criteria as the baseline reference for expressing all other plant species values, e.g. *Caenorhabditis elegans* Bristol N2, whose C-value is known with confidence to within 1 % from genome sequencing to be just above 100 Mb (or roughly 0·1 pg); (iii) adopt a plant value based on direct comparisons with *C. elegans*, as the base calibration standard for plants, and create a ladder of secondary calibration standards all measured against it in a study replicated between several groups able to use best practice. The C-value for *Arabidopsis thaliana* (1C = 157 Mb or 0·16 pg), recently measured against *C. elegans* (Bennett *et al*., 2003), could be adopted as the basal plant calibration standard. Seed is readily available from stock centres and gives small, easily grown plants. Moreover, the ladder of values for its many endopolyploid nuclei would also provide convenient calibration reference points for higher values up to approx. 2500 Mb or 2·5 pg (i.e. 0·64 – 4C, 1·28 – 8C, and 2·56 – 16C).

Weeding out erroneous data

The value of the database is determined by the accuracy of the data it contains. Ideally, values should be exact, but in reality they are all subject to various technical and other errors, as noted above. This raises questions as to how accurate data are, and what level of error is acceptable in practice, or makes a datum valueless for a particular use or study.

The existence of a database itself is a valuable means of identifying real or potential errors, and hence of improving the accuracy and quality of the whole body of data. For example, where estimates for the same taxon (with the same chromosome number) disagree greatly this suggests an error. Further, where a body of data for a taxon shows close agreement except for one major departure, this identifies the outlier as almost certainly incorrect. For example, in the Appendix table, the 2C-value for diploid *Acacia dealbata* (1·7 pg) reported by Blakesley *et al*. (2002) is similar to that reported by Bukhari (1997) of 2C = 1·6 pg (listed in Bennett *et al*., 2000), but both values differ considerably from the 2C-value of 2·9 pg reported by Mukerjee and Sharma (1993*b*) (see Notes to the Appendix bb). Another example concerns *Brachypodium distachyon*. In 1991, the PhD thesis of Shi reported a 1C-value of 0·15 pg, but later Shi *et al*. (1993) gave its 1C-value as 0·3 pg. To resolve this discrepancy, RBG, Kew obtained some original material studied by Shi and estimated its 1C-value to be 0·36 pg, confirming the larger C-value for this species (see also footnote br). Thus, real errors can be identified with certainty, and potential errors flagged up for users in cautionary footnotes following Appendix tables.

DNA C-values in angiosperms vary approx. 1000-fold (over three orders of magnitude) from approx. 0·1 pg to over 100 pg. It is, therefore, often useful to know whether a species' 1C DNA amount has approximately 0·1, 1, 10 or 100 pg, even if there is still uncertainty regarding whether a species with approximately 1 pg is really closer to 0·8 pg than to 1·2 pg (an error ±20 %). In terms of its predictive value in nucleotypic correlations, such an error still permits useful conclusions to be drawn. The *Arabidopsis* community laboured long under the misapprehension that its 1C DNA amount was approx. 70 Mb (Leutwiler *et al*., 1984), and later approx. 100 Mb (Meyerowitz, 1994), when in reality it is much higher (about 157 Mb, Bennett *et al*., 2003). The level of inaccuracy involved (approx. 50–100 %) was considerable, yet it did not prevent the selection of *Arabidopsis* as the model plant for first complete genome sequencing, in no small part on the basis of its 'small genome size' (NSF, 1990; Somerville and Somerville, 1999). The Convention on Biological Diversity (United Nations Environment Programme, 1992) noted the need to make biodiversity data available, despite imperfections; a view which merits support (Bennett, 1998). Thus, it is better to list available C-value data subject to errors, until improved data with fewer errors become available. The body of data is needed by the scientific community and can clearly already be used to draw important conclusions, to make valuable predictions, and as a basis for necessary planning.

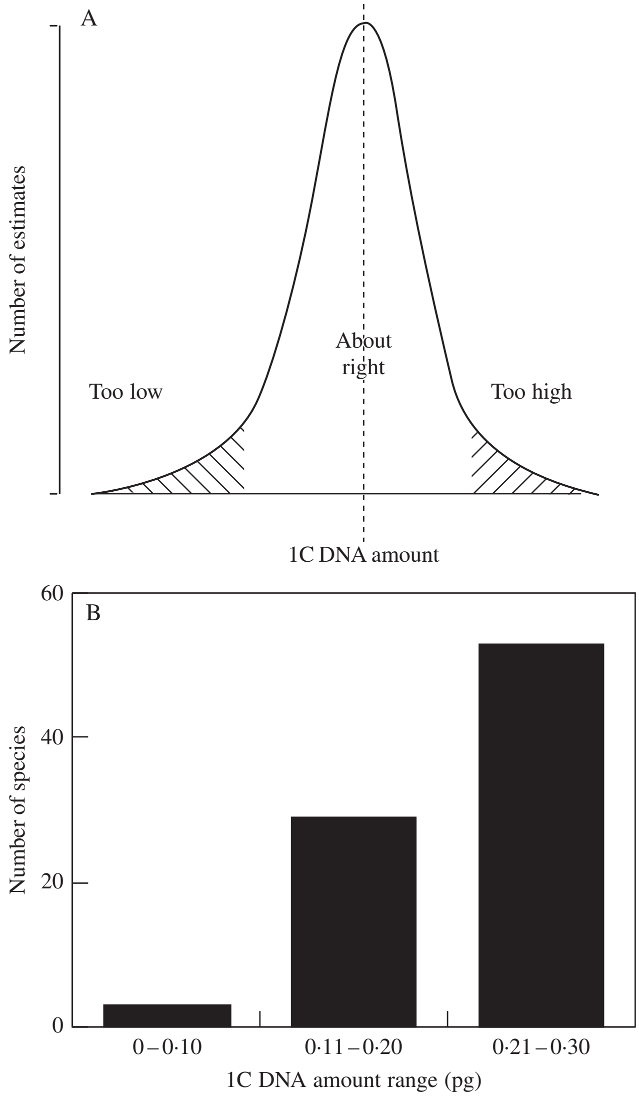

FIG. 3. (A) Expected error variation in a large population of DNA C-value estimates for one genotype as underestimates (in the lower tail) and overestimates (in the upper tail) surround more accurate, intermediate, genome size estimates. (B) Histogram showing frequency of C-values for the 85 smallest species in the database or Appendix.

What is the smallest reliable C-value for an angiosperm?

The above examples show how seeing data in the comparative context of the database can help to identify real or potential errors in particular species. It can also facilitate broader enquiries such as 'what is the smallest reliable C-value for an angiosperm?'. Again, the comparative approach has enabled researchers to be active in identifying potential errors in species with the smallest reported C-values, and to be transparent in correcting mistakes.

Because of error variation, a population of 1C-value estimates for one taxon should vary according to a normal curve, so those in the lower tail are all too low (Fig. 3A).

TABLE 2. *The 24 lowest angiosperm 1C DNA estimates among data listed in the present Appendix table and the Angiosperm DNA C-values database (release 4.0, January 2003)*

Taxon	1C (pg)	Original reference
Arabidopsis thaliana	0·051	Francis *et al.* (1990)
Cardamine amara	0·055	Band SR (pers. comm. 1984)
Arabidopsis thaliana	0·073	Leutwiler *et al.* (1984)
Fragaria viridis	0·108	Antonius and Ahokas (1996)
Rosa wichuriana	0·125	Bennett and Smith (1991)
Aesculus hippocastanum	0·125	Bennett *et al.* (1982)
Arabidopsis thaliana	0·128	Arabidopsis Genome Initiative (2000)
Sedum album	0·145	Hart (1991)
Arabidopsis thaliana	0·150	Arumaganathan and Earle (1991)
Carex nubigera	0·150	Nishikawa *et al.* (1984)
Carex paxii	0·150	Nishikawa *et al.* (1984)
Epilobium palustre	0·150	Band SR (pers. comm. 1984)
Hypericum hirsutum	0·150	Hanson, Leitch and Bennett (pers. comm. 2002)
Thlaspi alpestre	0·150	Band SR (pers. comm. 1984)
Arabidopsis thaliana	0·153	Bennett *et al.* (2003)
Arabidopsis thaliana	0·160	Bennett *et al.* (2003)
Arabidopsis thaliana	0·160	Galbraith *et al.* (1991)
Arabidopsis thaliana	0·165	Galbraith *et al.* (1991)
Arabidopsis thaliana	0·167	Krisai and Greilhuber (1997)
Arabidopsis thaliana	0·167	Bennett *et al.* (2003)
Amoreuxia wrightii	0·168	Hanson *et al.* (2001a)
Arabidopsis thaliana	0·170	Galbraith *et al.* (1991)
Arabidopsis thaliana	0·175	Bennett and Smith (1991)
Arabidopsis thaliana	0·175	Marie and Brown (1993)

Such values are lost in the frequency histogram for all angiosperm C-value estimates except at its lowest tail where some of the lowest C-values claimed are expected to be too low. This expectation is strongly supported in practice, as shown below. There are 53 1C estimates in the Angiosperm DNA C-values database or the present Appendix with 0·21–0·30 pg, 29 with 0·11–0·20 pg, but only three with 0·10 pg or below (Fig. 3B). Table 2 lists the 24 lowest estimates listed with 0·175 pg or less, but how robust are they?

Thirteen of the 24 estimates in Table 2 are for *Arabidopsis thaliana.* A comparative approach suggests that some, which featured among the lowest C-values reported for angiosperms, are too low. Thus several C-value estimates made by molecular means in the range 0·05–0·125 pg (Leutwiler *et al.*, 1984; Francis *et al.*, 1990; *Arabidopsis* Genome Initiative, 2000) are now seen as gross underestimates, while many others in the range 0·15–0·18 pg are shown to span the true value of about 0·16 pg (Bennett *et al.*, 2003).

After discounting the 1C estimate for *Arabidopsis thaliana* of 0·051 pg by Francis *et al.* (1990), the next smallest estimate listed is 0·055 pg for *Cardamine amara* (communicated from S. R. Band in 1984). With only a third the DNA amount of its related crucifer *A. thaliana* (0·16 pg), it seemed suspiciously low. *Cardamine amara* seed cannot survive drying, so it is unavailable from seed banks. However, we recently used flow cytometry to compare diploid *C. amara* collected near Sheffield with several calibration standards including *A. thaliana* ecotype 'Columbia'. The 1C-value we obtained was around 0·24 pg (almost five-fold the earlier report). This is in close agreement with independent estimates made elsewhere (e.g. see Bennett and Leitch, 2005; Johnston *et al.*, 2005).

Once the underestimates for *Arabidopsis thaliana* and *Cardamine amara* are discounted, few 1C-values of 0·125 pg or below remain for other species. One is the 1C estimate of 0·125 pg for *Rosa wichuriana*, estimated using callus material from Dr Andy Roberts (Bennett and Smith 1991). This value seemed questionably low in the context of the database, especially as it became clear that culturing may induce stain inhibitors. This concern led to a new collaboration with RBG, Kew using non-callous material, and our doubts were confirmed when it was re-estimated as 1C = 0·575 pg (Yokoya *et al.*, 2000).

Perhaps all estimates below 0·125 pg should be doubted until confirmed. Another candidate was *Aesculus hippocastanum* whose 1C-value was listed as 0·125 pg (Bennett *et al.*, 1982). This material is rich in tannins and a likely candidate for underestimating its DNA amount (Noirot *et al.*, 2000, 2005). Recent work using flow cytometry at RBG, Kew, showed that the 1C-value of 0·125 pg was clearly an underestimate, as the true value is approx. 0·60 pg (L. Hanson, RBG, Kew, pers. comm.). With 0·125 pg for *A. hippocastanum* rejected, only one estimate below 0·14 pg remains, namely 0·11 pg for the Green strawberry, *Fragaria viridis*. Since there is considerable interest in knowing the smallest possible angiosperm genome, checks to establish whether this estimate is robust are now urgently required.

What is the minimum C-value for a free-living angiosperm and other free-living organisms?

Such comparative approaches can also facilitate broader questions such as: 'what is the minimum genome size in angiosperms and other free-living organisms?'. There is a minimum compendium of nuclear genes essential for the life of any organism. This concept was behind Craig Venter's declared intension to synthesize from scratch a minimal bacterial genome (Check, 2002), and a project for a minimal eukaryote genome may eventually follow. Meanwhile we can only speculate on how small the minimum genome is for an angiosperm, and how closely extant species approach the minimum. It is, of course, below the lowest robust C-value for the group, i.e. less than 0·16 pg established for *Arabidopsis thaliana.* The presence of six other species with C-values of 0·15–0·169 pg in Table 2 strongly supports this conclusion. The estimate(s) of approx. 0·108 pg for *Fragaria viridis* may indicate a minimum C-value for extant angiosperms of about 100 Mb, but if so, is it a diploid, or a polyploid with three or more even smaller ancestral genomes?

Whilst the robust 1C-value for *A. thaliana* is 0·16 pg, this includes >25 % of repeated DNA (Bennett *et al.*, 2003) and analysis of sequenced regions shows that >70 % of coding genes are duplicated (Bowers *et al.*, 2003). Thus, in theory, a minimal genome without duplicated coding genes or repetitive DNA should not exceed approx. 50 Mb. Currently, there is no robust 1C estimate below 0·1 pg for an angiosperm, but if any of the seven species with C-values

TABLE 3. *Robust minimum 1C-value estimates for several widely different groups of free-living, multicellular, higher organisms obtained by genome sequencing (*), other best practice techniques, or static cytometry using the fluorochrome DAPI for algae*[1]

Group	Species	Mb	Original reference
ANIMALS			
Nematode	*Caenorhabditis elegans*	100*	*C. elegans* sequencing Consortium (1998)
Platyhelminthes (flatworms)	*Stenostomum brevipharyngium*	59	Gregory *et al.* (2000)
Crustacea	*Scapholeberis kingii* (water flea)	157	Beaton (1988)
Annelid	*Dinophilus gyrociliatus* (polychaete worm)	59	Soldi *et al.* (1994)
Tardigrades (water bears)	*Isohypsibius lunulatus*	78	Redi and Garagna (1987)
Insect	*Peristenus stygicus*	98	TR Gregory (pers. comm.)
Arachnid	*Tetranychus urticae* (spider mite)	78	TR Gregory (pers. comm.)
Urochordates (*tunicates*)	*Oikopleura dioica*	72	Seo *et al.* (2001)
PLANTS			
Chlorophyta (*green alga*)	*Caulerpa paspaloides*	88	Kapraun (2005)
Rhodophyta *(red algae)*	*Heydrichia wolkerlingii*	69	Kapraun (2005)
Phaeophyta *(brown algae)*	*Stilophora rhizodes*	98	Kapraun (2005)
Bryophyte	*Holomitrium arboreum*	167	Voglmayr (2000)
Lycophyte	*Selaginella kraussiana*	157	Obermayer *et al.* (2002)
Angiosperm	*Arabidopsis thaliana*	157	Bennett *et al.* (2003)

[1]The use of the base-specific fluorochrome DAPI for estimating DNA amounts may be less reliable than using intercalating fluorochromes such as propidium iodide (e.g. Doležel *et al.*, 1992).

between 0·14–0·15 pg is a tetraploid, this would indicate a minimum genome size in extant taxa of approx. 75 Mb, or approx. 50 Mb if it is a hexaploid.

The comparative approach is usefully extended to include other groups of organisms. Table 3 shows minimum C-value estimates for multicellular organisms in several widely differing groups obtained by genome sequencing or other methods. Such minima for groups as diverse as nematodes, insects, algae and angiosperms range from 59 to 160 Mb. Thus, the minimum C-value known in extant free-living multicellular higher organisms is around 60 Mb. All may be diploidized paleopolyploids (Wendel, 2000), but except for one early and unconfirmed report of a 1C-value of approx. 39 Mb in a most simple multicellular placozoan animal (Ruthmann and Wenderoth, 1975) there is no evidence for extant diploid multicellular eukaryotic life forms with only 40–50 Mb. This tantalizing possibility will be an interesting driver for new work to find a first angiosperm whose 1C-value is <100 Mb, or a first free-living multicellular plant or animal with a robust 1C-value <50 Mb.

PROSPECTS FOR THE NEXT TEN YEARS

Apart from better defining the limits of genome size variation, what key developments are targeted, or likely, to occur in angiosperm genome size research in the next decade?

The first concerns the expected progress to increase the total number and representation of angiosperms in the C-values database. As noted above, estimating first values for species reached a historic high during recent years (Fig. 1). At least 1700 such values were added in 1997–2002, and the total number of species' C-value estimates probably reached around 4300. In 2003 the second Plant Genome Size Workshop set a goal of estimating a further 1 % (i.e. approx. 2500 species) in the next five years, and a similar target is likely for the following quinquennium. If so, there is a reasonable prospect that the number of species with a C-value estimate will reach, or significantly exceed 7500 by 2014.

More important than the expected increase in total numbers is the predicted improvement in the spread of new values across taxa, geographical regions and life forms, making the sample more representative of the global angiosperm flora, based on careful targeting to identify and fill knowledge gaps. The next decade should see almost complete representation for families, and a greatly increased representation for genera (especially in monocots), as work focuses increasingly at this taxonomic level. Representation at the generic level is currently approx. 1042 out of an estimated 14 000 genera (7·4 %) and is targeted to rise to 10 % by 2009, and might reasonably be expected to approach 15 % within a decade. Moreover, this may approach 100 % for monocots, as they are targeted for holistic genomic studies (including C-values) for the global Monocot Checklist Project (Govaerts, 2004).

Recent experience shows that identifying a gap and setting a target may still not provoke the work needed to fill it. Positive monitoring of trends in published C-value data may also be required to achieve a significant change in research activity (e.g. as with the level of family representation in angiosperms; Hanson *et al.*, 2003). Thus it will be important to monitor by 2009 whether the gaping chasms in the representation of African, South American and Chinese floras noted previously have yet resulted in a significant rise in first estimates for taxa from those regions. If not, then a major effort will be needed to correct this. The same applies to other groups of plants that have been identified as poorly represented in the Angiosperm DNA C-values database (e.g. halophytes, parasitic species and their hosts and tundra species). Whilst less certain, there is a good prospect that this vital process will occur in the next decade, driven by the Genome Size Initiative (GESI: see Bennett and Leitch, 2005).

Hitherto, when a question regarding C-value was framed (e.g. is genome size related to weediness?), it was often necessary to estimate C-values for many species before it could be addressed (Bennett *et al*., 1998). Clearly, the prime aim is to create a sample of C-values that is sufficiently representative for systematic, regional and life form variation as to allow most questions to be answered with confidence using the available dataset, without recourse to further C-value estimations. This goal is likely to be achieved in the next ten years. Thus, the next decade may be the last to see major efforts devoted to estimating first DNA C-values for taxa. Thereafter, new C-value research will probably concentrate on using and understanding such data, rather than acquiring them.

What important questions regarding genome size in angiosperms are likely to be answered in the next decade? Three closely interrelated issues concerning the possible significance of genome size for extinction, conservation and pollution are worth mentioning here.

The possibility that a large C-value might correlate with an increased risk and rate of extinction was suggested by Rejmanek (1996) and by Bennett *et al*. (2000). To test this, Vinogradov (2003) identified 3036 diploid species from the Plant DNA C-values database and compared each one against the United Nations Environmental Programme World Conservation Monitoring Centre (UNEP-WCMC) species database to determine its conservation status (i.e. global concern, local concern or no concern). He noted a striking relationship between genome size and conservation status; species with large genomes appeared to be at greater risk of extinction that those with smaller genomes.

Clearly, this was an important finding that now requires independent confirmation, drawn from further independent samples of species in different local regions and environments. Obtaining data for meaningfully large samples of species for such studies will probably be one main driver determining which taxa are targeted for C-value estimates in the future. If so, the next decade offers the prospect of a more definite and detailed understanding of any relationships between C-value and/or genome size and the risk of extinction. This, in turn, may have important practical and theoretical implications for conservation models and strategies. A key question is whether a large nuclear DNA amount gives an increased risk of extinction equally in diploid or polyploid taxa? Vinogradov (2003) tested whether ploidy played a role in increasing a species' risk of extinction, concluding that C-value *per se* was most important. Polyploidy is supposed to confer many advantages based on increased gene dosage and diversity, but do such advantages overcome the possible risks of a high C-value? If so, the proportion of polyploids should be higher for species with very high C-values than for those with lower C-values. In a test different from that of Vinogradov (2003), we compared the percentage of polyploids in 3400 extant species with known DNA amount and ploidy level in the Angiosperm DNA C-values database, ranked in order of increasing DNA amount and divided into five groups each containing 680 species. We found the percentage of polyploids for species in group 5 with the highest C-values (29·9 %) was actually lower than for species in group 4 (32·1 %) (Fig. 4). This confirms Vinogradov's finding that the prime factor determining increased risk of extinction is high C-value, and that polyploidy does not reduce this risk.

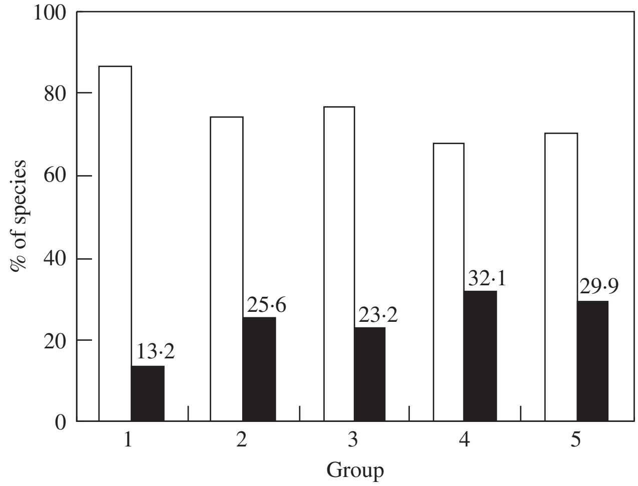

FIG. 4. The percentage of diploids (open bars) and polyploids (closed bars) among 3400 species of known DNA amount and ploidy level ranked in order of increasing DNA amount and divided into five groups with 680 species per group. Data taken from the Angiosperm DNA C-values database (release 4.0, January 2003) and the present Appendix.

Other enquiries should test whether the risk of extinction in relation to high C-value or genome size varies for different threats and environments. This should compare variation in internal factors affecting the structure and ecology of the genome (e.g. increased ploidy level, and heterochromatin distribution), and in external factors (e.g. pollution and increased competition for space, minerals, light, and pollinators). Vilhar (pers. comm., and Vidic *et al*., 2003) investigated the effect of genome size on plant survival in lead-polluted soils. With increasing lead concentration in the soil the percentage of species with large genomes decreased significantly, suggesting that species with large genomes were at a selective disadvantage. Similar work on local floras in different areas with various threats is now needed to test whether their results are typical for other pollutants and environments. Understanding which species survive locally is always important, but especially as local loss equals global extinction if a species range is restricted to just that one locality. Such work will increasingly inform local environmental action plans and conservation strategies.

Holistic genomics

Early interest in plant genome size variation (c. 1950s and 1960s) ranged broadly across many fields including its genetic, developmental, ecological and evolutionary implications. However, after the molecular revolution the field fragmented somewhat as interest in DNA sequences was largely separated from more macro interests in C-values. However, given 'complete sequences' for genomes and homoeologous segments, and greater computing power, this post-genomic age is seeing a strong convergence of these interests. Thus, leading scientists who work at comparative sequence levels can also work on questions of genome size and evolution (e.g. Zhang and Wessler, 2004; Bennetzen *et al.*, 2005). This is the age of holistic genomics in which knowledge of variation in genome size and C-value can be seamlessly joined up with information at all other levels to embrace information from sequences to ecology and from evolution to the environment. This powerful approach should permit or provoke quantum leaps in understanding the significance of extant variation in C-value and genome size, the processes that produce it, the rate at which it occurs, the factors that limit its extent and the advantages and disadvantages that it confers. Together, such understanding will link across biological fields to explain patterns of genome size variation in development, floras, ecological niches and evolution. The next ten years offer many exciting prospects for angiosperm genome size research. Work on DNA amount will remain a key core interest in biological research, but will increasingly become one integrated strand in holistic genomic studies and understanding, covering its origin(s), mechanisms of change, phenotypic and phenological effects, and its significance for ecological, developmental and environmental issues.

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APPENDIX

Notes to the Appendix

The Appendix appears on pp. 59–88.

Named references in the following notes are given above in 'Literature Cited', while numbered references are given in 'Original references for DNA values' below.

(a) The original references for species DNA amounts in the Appendix are given in a numbered list following the Appendix table. Reference numbers follow on sequentially from those given in 'Notes to Table 8' by Bennett and Smith (1976, references 1–54) 'Notes to Table 1' by Bennett *et al*. (1982, references 55–107), Bennett and Smith (1991, references 108–163), 'Notes to the Appendix' by Bennett and Leitch (1995, references 164–269), 'Notes to the Appendix' by Bennett and Leitch (1997, references 270–306), and 'Notes to the Appendix' by Bennett *et al*. (2000, references 307–377).

TABLE 4. *The eleven angiosperm species recommended for use as calibration standards (see Notes to the Appendix, b1)*

Key	Standard species	4C DNA amount (pg)
A	*Triticum aestivum* 'Chinese Spring'	69·27
B	*Allium cepa* 'Ailsa Craig'	67·00
C	*Vicia faba* PBI, inbred line 6	53·31
D	*Anemone virginiana* line AV 200	35·67
E	*Secale cereale* 'Petkus Spring'	33·14
F	*Hordeum vulgare* 'Sultan'	22·24
G	*Pisum sativum* 'Minerva Maple'	19·46
H	*Zea mays* 'W64A'	10·93
I	*Senecio vulgaris* (PBI population)	6·33
J	*Vigna radiata* 'Berken'	2·12
K	*Oryza sativa* 'IR36'	2·02

(b1) Bennett and Smith (1991) gave absolute 4C DNA values for 11 angiosperm species recommended for use as calibration standards to estimate DNA amounts in other species. These species and their 4C DNA amounts are given in Table 4. If a species was calibrated in direct comparison with any one or more of the 11 standard species then the standard species used is identified in column 15 of the Appendix by the appropriate Key letter given above (e.g. F is *Hordeum vulgare*, etc.). If a species was first calibrated using a standard species listed above, then the original standard species is identified first and the intermediate standard species used to calibrate those species listed with it is also denoted by its number in column 1 of the Appendix. For instance, standard G (*P. sativum*) was used to calibrate *Capsicum annuum* 'Doux Long des Landes' (species 212 h in the Appendix), which was then used as an intermediate standard to estimate other *Capsicum* species given by Belletti *et al*. (1998, Ref. 434). The calibration standard for such *Capsicum* species is therefore given as G-212h.

(b2) In Refs 444 (Wendel *et al*., 2002) and 447 (Lin *et al*., 2001) *Pisum sativum* 'Minerva Maple' was used as the calibration standard but they assumed a 4C DNA value of 19·12 pg (Johnston *et al*., 1999) instead of 19·46 pg, which is the value given in Bennett and Smith (1976) and listed in Table 4. The 4C-value of *P. sativum* 'Minerva Maple' used in Refs 444 and 447 was estimated using *Hordeum vulgare* 'Sultan' as the calibration standard with an assumed 4C DNA content of 22·24 pg (Johnston *et al*., 1999).

(c) In several references listed in 'Original references for DNA values' the authors used a cultivar of a standard species different from that listed in Table 4, these are listed in Table 5. In some cases the C-value of the cultivar used was assumed to be the same as that of the cultivar given in Table 4. Evidence of intraspecific variation in a number of species suggests that such assumptions may sometimes be incorrect. In other cases the C-value of the cultivar was determined by the authors and was different from that of the standard species listed in Table 4. For example Refs 386,

TABLE 5. *Cultivars of standard species used that differ from those listed in Table 4*

Original reference number	Plant calibration standard used	Assumed 4C DNA amount and reference (pg)
	Allium cepa	
413	'Frühstamm'	67·0 (reference not given)
409	'Kantar topu'	67·0 (Van't Hof, 1965; Bennett and Smith, 1976)
435, 443, 449, 454, 455	'Nasik Red'	67·0 (Van't Hof, 1965)
427	'Stuttgarter Reisen'	67·0 (Bennett and Smith, 1976)
388, 411, 420, 422	var. *aggregata*	– (amount and reference not given)
	Hordeum vulgare	
417	'Stark'	21·36 (reference not given)
423	strain NE 86954	20·48 (Lee *et al*., 1997)
	Oryza sativa	
424	type *japonica*	2·20 (Bennett and Smith, 1991)
	Pisum sativum	
386, 397, 453,	'Express Long'	16·74 (Marie and Brown, 1993)
393, 394, 395, 396, 429, 458	'Kleine Rheinländerin'	17·68 (Greilhuber and Ebert, 1994)
434	'Lincoln'	18·14 (Doležel *et al*., 1992)
418	ssp. *sativum* convar. *sativum* var. *ponderosum* 'Viktoria'	18·18 (Doležel *et al*., 1998)
	Secale cereale	
418	ssp. *cereale*	32·38 (Doležel *et al*., 1998)
394	'Dankovske'	31·16 (Doležel *et al*., 1998)
	Vicia faba	
418	ssp. *minor* var. *minor* subvar. *rigida* 'Tinova'	54·00 (Doležel *et al*., 1998)
405	'Aquadulce'	53·31 (pers. comm. 2002)
430	'Superguadulce'	53·30 (Bennett and Smith, 1976)
	Zea mays	
391	'CE-777'	10·86 (Lysák and Doležel, 1998)
437	'C-777'	10·86 (Lysák and Doležel, 1998)
382	Va35	10·93 (Bennett and Leitch, 1995)

397, and 453 used the cultivar 'Express Long' of *Pisum sativum* with a 4C DNA value of 16·74 pg. This value is lower than the 4C DNA amount of the cultivar 'Minerva Maple' of 19·46 pg given in Table 4.

(d) In References 407, 408 and 457 the cultivar of the calibration standard was not given. Refs 407 and 408 used *Vicia faba* as a calibration standard, whereas Ref. 457 used *Allium cepa*. In Ref. 408 Cremonini *et al*. (1992) assumed the same 4C-value for *Vicia faba* as for PBI line 6 (i.e. 53·3 pg) given in Table 4. If this species exhibits intraspecific variation then such assumptions may be incorrect.

(e) In a number of original references the authors used a plant species not listed in Table 4 as a calibration standard. These are listed in Table 6.

(f) Several papers listed in 'Original references for DNA values' used animal cells as the calibration standards. Thus Refs 387, 417, 426, 442, 456, 463 used chicken erythrocytes with an assumed 4C DNA value of 4·66 pg (Galbraith *et al*., 1983). The calibration standard is abbreviated to *Gallus* in column 15 of the Appendix. In Ref. 438 blood cells from the catfish *Ictalurus punctatus* were used as a standard with an assumed 4C-value of 4·00 pg (Tiersch *et al*., 1989), this is abbreviated to *Ictal*. in the Appendix. In Ref. 438 domestic swine (*Sus scrofa*) erythrocytes were used as a standard with an assumed 4C-value of 11·34 pg (Taliaferro *et al*., 1997), and is abbreviated to *Sus* in the Appendix. Human cells with an assumed 4C DNA amount of 14·00 pg (Tiersch *et al*., 1989) were used as calibration standards in Refs 384, 428 and 419 (leucocytes, Ref. 384, 428; lymphocytes, Ref. 419) and the abbreviation of *Homo* is used in the Appendix. Finally, *Drosophila melanogaster* with an assumed 1C DNA amount of 180 Mb (Adams *et al*., 2000) and *Caenorhabditis elegans* with a 1C DNA amount of 100·25 Mb, based on complete genome sequencing (see *C. elegans* Sequencing Consortium, 1998 and http://wormbase.org), were used as calibration standards for Ref. 461, and the abbreviation of *Dros*. and *Caeno*. respectively are used.

If a plant species was calibrated using an animal species and then subsequently used as the calibration species for other plants, then the animal species is identified first, and the intermediate plant species is identified by its entry number given in column 1 of the Appendix. Thus Mishiba *et al*. (2000, Ref. 387) used *Gallus* with an assumed 4C DNA amount of 4·66 pg (Galbraith *et al*., 1983) to calibrate *Hordeum vulgare* 'New Golden' (species 398p in Appendix), this was then used as the calibration standard to estimate DNA C-values of *Petunia* and *Calibrachoa* species given by Mishiba *et al*. (2000). The calibration standard for these *Petunia* and *Calibrachoa* species is given as *Gallus*-398p.

(g) When a new estimate (or estimates) is given for a species or subspecies already listed by Bennett and Smith (1976, 1991), Bennett *et al*. (1982, 2000) or Bennett and Leitch (1995, 1997), the estimate is given a number and a lower case letter in column 1 of the Appendix. An 'a' implies that the value is preferred to any estimate for that species listed previously by the first author. Where several estimates are available for the same species, the 'a' value would automatically be chosen in any arithmetical or statistical calculations. In this context, single estimates for species and 'a' values are referred to as 'prime entries'.

(h) Intraspecific variation in nuclear DNA amount is claimed to occur in this species. Consequently the values given in the Appendix should not be assumed to be correct for all accessions of the species. Where several C-values are listed for a single species with the same ploidy level or chromosome number within a taxon, then only the minimum and maximum values reported from a single reference are listed in the Appendix.

(i) A range of DNA amounts was reported for this species in the reference cited in column 13 of the Appendix. Intraspecific variation was not claimed to occur, so the nature of this variation is unclear. Where estimates differed by more than 10 % the minimum and maximum values are given for the same ploidy level or chromosome number in the Appendix, otherwise only the highest value is given.

(j) According to the International Code of Botanical Nomenclature (Greuter *et al*., 1994), the names of plant families must end in *-aceae*. However, eight plant families are exceptions in that each has two alternative names, both of

TABLE 6. *Plant species used as calibration standards but not listed in Table 4*

Original reference number	Plant calibration standard used	Assumed 4C DNA amount and reference (pg)	Abbreviation used in column 15 of Appendix
383	*Agave americana*	31·80 (Zonneveld and Van Iren, 2001)	*Agave*
	Arabidopsis thaliana		
389	'Columbia'	– (amount and reference not given)	*Arab.*
414	'Columbia'	0·53 (Kaneko *et al.*, 1998)	"
427	*Cerastium eriophorum*	5·20 (Boscaiu *et al.*, 1999)	*Cerastium*
	Glycine max		
393	'Ceresia'	4·54 (Greilhuber and Obermayer, 1997)	*Glycine*
429	'Ceresia'	4·51 (Obermayer and Greilhuber, 1999)	"
421	var. Palmetto	5·00 (Doležel *et al.*, 1994)	"
432	'Burlison'	5·56 (Graham *et al.*, 1994)	"
402	'Polanka'	5·00 (Doležel *et al.*, 1994)	"
	Lycopersicon esculentum		
380, 382, 465	'Gardener's Delight'	4·00 (Obermayer *et al.*, 2002)	*Lycopers.*
437	'Stukické'	3·92 (Doležel *et al.*, 1992)	"
385	'Montfavet'	4·02 (Marie and Brown, 1993)	"
	Nicotiana tabacum		
427	'Petit Havana SR1'	18·00 (Bennett and Leitch, 1995)	*Nicot.*
417	'Samsun'	18·15 (reference not given)	"
	Petunia hybrida		
390, 410, 433, 452	'PxPC6'	5·70 (Godelle *et al.*, 1993; Marie and Brown, 1993)	*Petunia*
390	'Hit Parade Blau' R	5·70 (Marie and Brown, 1993)	"
401	No cultivar given	5·70 (Marie and Brown, 1993)	"
	Rhaphanus stativus		
404	'Saxa'	2·20 (Doležel *et al.*, 1992)	*Rhaphanus*
	Sorghum bicolor		
439	Line TX623	3·52 Price and Levin (pers. comm.)	*Sorghum*
462	No cultivar given	3·20 (Bennett and Smith, 1991)	"
406	*Vicia narbonensis*	29·10 (Frediani *et al.*, 1992)	*Vicia narb.*

which are correct under the Botanical Code. One is a standard name, ending in *-aceae*, the other is an exception, sanctioned by long usage. These and their alternatives are the following: Palmae (Arecaceae), Gramineae (Poaceae), Cruciferae (Brassicaceae), Leguminosae (Fabaceae), Guttiferae (Clusiaceae), Umbelliferae (Apiaceae), Labiatae (Lamiaceae) and Compositae (Asteraceae). To be consistent with previous DNA lists (Bennett and Smith, 1976, 1991; Bennett *et al.*, 1982, 2000; Bennett and Leitch, 1995, 1997) the 'non-standard' plant names are retained in the present work.

(k) Recent cladistic analysis using both molecular and non-molecular phylogenetic data has resulted in a revised classification of families by the Angiosperm Phylogeny Group (APG) (APG II, 2003). Familial names used in the APG classification are followed in the Appendix. Thus, although Zonneveld (2002, Ref. 440) placed *Aloe* in Aloeaceae, recent molecular and non-molecular phylogenetic data recognizes that this family is embedded within the newly circumscribed Xanthorrhoeaceae (APG II, 2003) so Xanthorrhoeaceae is given in the Appendix. Similarly, the APG II (2003) now recognizes that Hostaceae is embedded within the Asparagaceae, so *Hosta*, which was placed in Hostaceae in Ref. 384 (Zonneveld and Van Iren, 2000), is listed under Asparagaceae in the Appendix.

(l) The authority for this species is either unknown or unclear to the present authors.

(m) Whether or not voucher specimens exist for this species is unknown to the present authors.

(n) The chromosome number of this species is either unknown or unclear to the present authors.

(o) The chromosome count for this species was taken from the literature and not determined by the authors of the reference cited.

(p) The ploidy level of this species is either uncertain or unclear to the present authors.

(q) The life cycle type of this species is either unknown or unclear to the present authors.

(r) The method used to measure the DNA amount is unclear.

(s) The factor of 1 pg = 980 Mbp was used to convert picograms to Mbp (Cavalier-Smith, 1985; Bennett *et al.*, 2000).

(t) As a rule, replicated diplophase nuclei contain a 4C DNA amount producing two unreplicated 2C nuclei by mitotic division and four 1C gametic nuclei after meiosis (irrespective of ploidy level). This convention applies well to polyploid taxa with diploidized meiotic chromosome pairing which produce functional balanced polyhaploid gametes with 1C DNA amounts at meiosis. Thus 4C estimates were automatically divided by 4 to generate 1C-values given for all taxa of even ploidy level listed in the Appendix. However the resulting '1C' data are not biologically meaningful for taxa with odd ploidies. Consequently the Appendix gives only 2C- and 4C-values for such taxa.

(u) There is no obvious basic number for the genus *Luzula* due to the presence of holocentric chromosomes. It is therefore impossible to allocate *Luzula* species with high chromosome numbers to any ploidy level with certainty.

(v) Unal and Callow (1995, Ref. 412) obtained a regression of the nuclear fluorescence of *Allium cepa* (4C = 67·0 pg), *Crepis capillaris* (4C = 9·6 pg), *Hordeum vulgare* (4C = 22·2 pg), *Pisum sativum* (4C = 20·2 pg), *Secale cereale* (4C = 33·2 pg) and *Vicia faba* (4C = 47·9 pg) versus nuclear DNA content, and used this to estimate the DNA C-values of 13 *Lathryus* species. However, it is noted that the 4C-values for *P. sativum*, and *Vicia faba* are non-standard values compared with those given for these species in footnote (b1) above.

(w) The standard species used to convert arbitrary units into absolute DNA amounts is unclear to the present authors.

(x) The DNA value given for this species in the original reference differs considerably (i.e. >100 %) from that given in other original references cited in previous compiled lists of DNA amounts (i.e. Bennett and Smith, 1976, 1991; Bennett *et al*., 1982, 2000; Bennett and Leitch, 1995, 1997). The reason(s) for this is unknown. This C-value should therefore be used with caution until the question is resolved.

(y) The specific status of the material available for study is unclear. The data are included since information on DNA amounts for this genus is relatively sparse, so an indication of genome size in the genus may be useful.

(z) Zonneveld (2001, Ref. 383) gave C-values for 16 hybrid cultivars which fall within the range that he reported for *Helleborus* species listed in the Appendix. Our compiled lists have usually been restricted to C-values for species. Following this practice, C-values for *Helleborus* hybrids were not included in the present Appendix.

(aa) Zonneveld and Van Iren (2000, Ref. 384) gave DNA amounts for 94 accessions of *Hosta* which were recognised as 23 different species. Their table 1 gives a DNA amount for each accession together with a mean value for each recognised species. Only the later value is given in the present Appendix. They also included C-values for 16 *Hosta* cultivars (in their table 3). These were once recognized as species, but following pollen viability tests Zonneveld and Van Iren (2000) concluded they were hybrids. Our compiled lists have usually been restricted to C-values for species. Accordingly, C-values for *Hosta* hybrids were not included in the present Appendix.

(ab) Zonneveld and Van Iren (2000, Ref. 384) and Zonneveld (2002, Ref. 440) used male human leucocytes (2C = 7·0 pg; Tiersch *et al*., 1989) as their primary standard to estimate the DNA amount of three *Agave* species, namely: (i) *Agave stricta* (ii) *A. americana* and (iii) *A. sisalana*. *A. americana* was then used as internal calibration standard for most *Hosta* (Ref. 384) and *Aloe* (Ref. 440) taxa. However, in a few cases where the DNA content of *Hosta* or *Aloe* coincided with that of *A. americana*, one of the other two *Agave* species was used as the internal standard. As neither reference identified which *Agave* species was used, the calibration standard in column 15 of the present Appendix is given as *Agave* sp.

(ac) Thibault (1998, Ref. 385) claimed intraspecific variation ranging from 6 to 11 % in the *Salix* species he studied, but only a mean DNA C-value for each species was given in his table 3. It is these values that are listed in the present Appendix. Thibault (loc. cit.) also included C-values for five hybrids. Our compiled lists have usually been restricted to C-values for species, thus C-values for *Salix* hybrids are not included in the Appendix. In addition, Thibault (1998, Ref. 385) listed a C-value for '*S. triandra*?' but concluded its identity was 'hard to specify'. Consequently, this taxon was not included in the Appendix.

(ad) Thibault (1998, Ref. 385) used DNA C-values to predict the ploidy level of each *Salix* species given in his table 3, assuming direct proportionality. Moreover, their chromosome numbers were not counted by him, but derived by him assuming a constant basic chromosome number of $n = 19$ for the genus. These predictions are entered in columns 6 and 7 of the Appendix.

(ae) Some taxa once included in *Petunia* are now included in *Calibrachoa*. The taxonomy for most *Petunia* species listed in Mishiba *et al*. (2000, Ref. 387) follows that of Wijsman (1990) who split the genus *Petunia sensu* Jussieu (1803) into two; *Petunia sensu* Wijsman and *Calibrachoa*. However, five species listed in Mishiba *et al*. (2000) were not reclassified by Wijsman and so they were listed under the generic name of *Petunia sensu* Jussieu in Mishiba *et al*. (2000) although they 'were regarded as *Calibrachoa*' (see their table 3). By following the taxonomy of *Petunia sensu* Wijsman, several species originally listed under the genus *Petunia*, now belong to *Calibrachoa* (e.g. *parviflora* was listed in the genus *Petunia* by White and Rees, 1985, 1987) and this generic name was used in the list of Bennett and Leitch (1995). Yet Mishiba *et al*. (2000) assigned this species to *Calibrachoa*. To avoid confusion readers looking under *Petunia* are referred to *Calibrachoa* in the Appendix.

(af) Joachimiak *et al*. (2001, Ref. 391) reported chromosome numbers and C-values for six *Bromus* species. Chromosome numbers varied considerably in roots of three species, but variation in C-values was 'virtually absent within leaf mesophyll cells'. The C-values given by Joachimiak *et al*. (2001) were obtained using leaf mesophyll cells and are listed in the Appendix.

(ag) The study by Rosato *et al*. (1998, Ref. 392) was primarily concerned with polymorphism in *Zea mays* ssp. *mays* races with B-chromosomes, but gave C-values only for plants lacking B-chromosomes. Thus, they listed DNA amounts for 17 populations which differed by 36 % (2C = 5·008–6·757 pg) in plants with $2n = 20$. Similar intraspecific variation in this species was reported previously (Laurie and Bennett, 1985; Rayburn *et al*., 1985). Mean DNA amounts for only the populations with the largest and smallest C-values for A-chromosomes, are listed in the Appendix.

(ah) Dimitrova and Greilhuber (2000, Ref. 394) reported significant intraspecific variation in *Crepis biennis* ($P < 0·05$) and *C. sancta* ($P < 0·01$), some of which had variable numbers of B-chromosomes. As only means were given for material with 0–2 B-chromosomes, it was impossible to give values (presumably the largest) for the 2B complement. Consequently, the Appendix just lists the smallest and largest C-values for accessions without B-chromosomes.

(ai) Dimitrova and Greilhuber (2000, Ref. 394) reported significant ($P < 0{\cdot}001$) intraspecific variation of 11 % for *Crepis pulchra*. They suggested that the two accessions with the higher C-values may belong to subspecies *turkestanica*. This is not recognized in the Bulgarian flora (where these accessions were collected), but was described by Babcock (1947). In the Appendix the higher C-values listed for this species (entry numbers 305c and e) may thus correspond to *C. pulchra* ssp. *turkestanica*.

(aj) Temsch and Greilhuber (2000, Ref. 395) estimated C-values in 11 accessions of *Arachis hypogaea* using both Feulgen microdensitometry and flow cytometry. C-values for different accessions showed great stability, so they calculated a mean C-value for each method in the 'Results and Discussion' of their paper. Only these mean values are listed in the Appendix.

(ak) Previous estimates for *Vicia melanops* ($2n = 10$) (e.g. Chooi, 1971; Raina and Rees, 1983; Raina and Bisht, 1988) all report a 4C-value of approx. 40 pg, which is much higher than the value of 27·6 pg given in Cremonini *et al*. (1992, Ref. 408, entry number 780d). Thus, this estimate should be viewed with caution until confirmed independently.

(al) Akpinar and Bilaloglu (1997, Ref. 409) gave a 2C-value of 13·1 pg for *Vicia cracca* ssp. *cracca* (with $2n = 2x = 14$; their original count). However, six previous reports for *V. cracca* listed in the database (Bennett and Leitch, 2003) gave similar 2C-values (from 10 to 13 pg), but for $2n = 4x = 28$. The cause of this discrepancy is unknown, thus the estimate by Akpinar and Bilaloglu (loc. cit.) should be viewed with caution until confirmed independently.

(am) Sakamoto *et al*. (1998, Ref. 414) estimated the C-value of *Cannabis sativa* using *Arabidopsis thaliana* 'Columbia' (1C = 130 Mb, Kaneko *et al*., 1998) as the calibration standard. However, the 1C-value assumed for *A. thaliana* was low compared with its recently confirmed estimate of 157 Mb (Bennett *et al*., 2003). If 157 Mb is assumed for *A. thaliana*, then the 1C-value for *C. sativa* would be 988 Mb = 1·01 pg (female) and 1016 Mb = 1·04 pg (male).

(an) Gammar *et al*. (1999, Ref. 416) gave DNA amounts for eight *Lupinus* species in arbitrary units (a.u.) listed as Mn(x) values in their Figs. 1–4. Bennett and Smith (1976) gave the 4C DNA amount of *L. luteus* as 4·0 pg (allowing for recalibration of *Senecio vulgaris* from 5·88 pg to 6·33 pg, see Bennett and Smith, 1991). Gammar *et al*. (loc. cit.) gave Mn(x) values for three *L. luteus* populations as 60·4, 58·4, and 63·8 in figure 1A, noting they were not statistically different. The mean of these three values was calculated to be 60·86 a.u. To convert the Mn(x) values for each *Lupinus* species into absolute DNA amounts, they were multiplied by a conversion factor of 0·07 (i.e. 4·0 pg ÷ 60·86 a.u.).

In some *Lupinus* species more than one population was studied, and several Mn(x) values were listed. If these did not differ significantly, the average Mn(x) value was calculated and converted into absolute DNA amounts. However, chromosome counts of $2n = 38$, 42 and 44 were reported in *L. angustifolius*, so variation in Mn(x) may correspond to different cytotypes.

Some absolute DNA amounts calculated for Gammar *et al*. (loc. cit) do differ greatly from those previously reported for the same species (e.g. *L. pilosus*, 4C = 4·9 pg, is almost double the value of 2·5 pg given by Obermayer *et al*., 1999). Similarly, the 4C-value of 3·1 pg calculated for *L. angustifolius* with $2n = 38$, 42, or 44 is similar to the estimate (4C = 3·7 pg) by Barlow (pers. comm., listed in Bennett *et al*., 1982), yet the latter was for material with $2n = 26$. Data from Gammer *et al*. give a useful approximation of C-values in the five species not previously listed, but should be treated with caution unless confirmed independently.

(ao) Brandizzi and Grilli Caiola (1996, Ref. 419) gave $2n = 18$ for *Crocus biflorus* in their table 1, but $2n = 8$ in the first paragraph of their text. They also stated in their final paragraph: 'However, *C. biflorus* and *C. etruscus*, having half the chromosome number with respect to *C. thomasii* and *C. cartwrightianus* . . . ..' As *C. thomasii* and *C. cartwrightianus* were both recorded with $2n = 16$ by Brandizzi and Grilli Ciola (1996), we conclude that *C. biflorus* had $2n = 8$, and so this number is entered in the Appendix.

(ap) The 4C DNA amounts reported by Mukerjee and Sharma (1993*a*, Ref. 420) for *Luzula nivea* and *L. luzuloides* are over 50 % larger than those reported by Barlow (pers. comm. 1976; reference 36 in Bennett and Smith, 1976). The chromosome numbers for each species were the same, so the cause of the discrepancy is unknown. However, Mukerjee and Sharma (1993*a*) used a single wavelength method, which may suffer from distributional error (Greilhuber, 2005, this volume). Thus, estimates for *Luzula* in Mukerjee and Sharma (1993*a*) should be viewed with caution until confirmed independently for these species.

(aq) Asif *et al*. (2001, Ref. 421) estimated DNA amounts in 14 genotypes of *Musa acuminata.* Genotype BC3 (belonging to the separate subspecies *truncata*) had the highest DNA amount and its C-value was shown to be significantly different ($P < 0{\cdot}01$) from the other thirteen genotypes. Only the DNA amount of genotype BC3, corresponding to *M. acuminata* ssp. *truncata*, and the highest DNA amount out of the 13 other genotypes of *M. acuminata* are entered in the Appendix.

(ar) Chaudhuri and Sen (2001, Ref. 422) examined two *Scilla indica* cytotypes (entry numbers 710b and c) which differed considerably in both DNA amount and karyotype structure, although both had $2n = 30$. The differences may reflect problems with taxonomy. Studies by Greilhuber and colleagues (Greilhuber, 1979; Greilhuber and Speta, 1985) have shown that large intraspecific differences in C-values in other *Scilla* species (e.g. *S. bifolia*) reduce to a level hardly more than methodological error following taxonomic splitting.

(as) Chung *et al*. (1998, Ref. 423) estimated C-values in 12 soybean (*Glycine max*) strains varying in seed size. They reported statistically significant differences of 4·6 % in the 2C-values between strains. Only the smallest and largest C-values are entered in the Appendix.

(at) Hartman *et al.* (2000, Ref. 425) estimated C-values in 22 *Leucaena* species using flow cytometry. Three species (*Pisum sativum* 4C = 17·6 pg, *Oryza sativa* 4C = 1·8 pg and *Vicia faba* 4C = 53·0 pg) were used as calibration standards at various times, but unfortunately the authors did not state which standard(s) was compared with which *Leucaena* species.

(au) Boscaiu *et al.* (1999, Ref. 427) referred to plants of *Cerastium* with 2*n* = 36 as diploids in contrast with various other authors who consider them as tetraploids. The assumption was based on Boscaiu *et al.*'s observations that, while the base chromosome number in *Cerastium* may be *x* = 9, no *Cerastium* species is known with 2*n* = 18.

(av) The C-values reported for *Hedera helix* by Obermayer and Greilhuber (1999, Ref. 429) agree well with previous reports by König *et al.* (1987) of 2C = 3·0 pg, but are only about one third the value reported by Marie and Brown (1993) of 2C = 8·2 pg, which is unsupported.

(aw) Blanco *et al.* (1996, Ref. 431) gave DNA amounts for *Dasypyrum hordaceum* and *D. villosum* in arbitrary units (a.u.), listed as mean values in their fig. 3. The value for *D. hordaceum* was converted into an absolute DNA amount by multiplying the mean value of 381·7 a.u. by a conversion factor of 0·11. This conversion factor was obtained as the ratio of the 4C estimate for *Dasypyrum villosum* (listed as the synonym *Haynaldia villosa*) reported by Bennett (1972) as 21·4 pg, and the estimate of 193·7 a.u. reported by Blanco *et al.* (1996).

(ax) Rayburn *et al.* (1997, Ref. 432) estimated C-values in 90 accessions of *Glycine max*. Accessions showed a 12 % variation in DNA amount and these differences were statistically significant. Only the smallest and largest C-values are listed in the Appendix.

(ay) Comparing C-values given by Belletti *et al.* (1998, Ref. 434) with those previously published showed DNA amounts for *Capsicum baccatum*, *C. chinese*, *C. eximium*, *C. frutescens* and *C. pubescens* were around one third greater than those of Owens (pers. comm.) listed in Bennett and Smith (1976). Belletti *et al.* (1998) suggested that the cause of the discrepancy could be that Owens used *Allium cepa* as the calibration standard, whose 2C-value of 33·5 pg differs considerably from those reported in *Capsicum* species studied.

(az) Široký *et al.* (2001, Ref. 437) investigated C-values in four *Silene* species, including *S. latifolia*, which has previously been listed by Bennett and Leitch (1995) under its synonym *Melandrium album*.

(ba) Taliaferro *et al.* (1997, Ref. 438) gave DNA C-values for 18 accessions of *Cynodon* corresponding to two species: *C. transvaalensis* (2*n* = 2*x* = 18), and *C. dactylon* var. *dactylon* (2*n* = 4*x* = 36 and 2*n* = 6*x* = 54). Only small differences in DNA amounts were noted between five diploid and five tetraploid accessions, and a mean 2C-value for each ploidy level was also given in table 2 of their paper. This mean value is listed in the Appendix. However, the three hexaploid accessions examined comprised one accession of *C. dactylon* var. *dactylon* and two hybrids. Thus, only the C-value estimate for hexaploid *C. dactylon* var. *dactylon* is entered in the Appendix, rather than the mean for the three hexaploid accessions given in table 2 of Taliaferro *et al.* (1997).

(bb) Blakesley *et al.* (2002, Ref. 441) examined seven populations of *Acacia dealbata* and four of *A. mangium* to determine ploidy and DNA amount. In *A. dealbata*, they identified naturally occurring diploid, triploid and tetraploid genotypes. Chromosome numbers were counted in only one diploid and one tetraploid genotype, and C-values for only these populations are given in the Appendix. In naturally occurring *A. mangium* only diploid populations were found, and the C-value for the only population whose chromosome number was determined is given in the Appendix. C-values for colchicine-induced tetraploid genotypes of *A. mangium* are not included.

The 2C-value for diploid *A. dealbata* (1·7 pg) is similar to that reported by Bukhari (1997) as 2C = 1·6 pg. In contrast the 2C-value (2·9 pg) reported by Mukherjee and Sharma (1993*b*) is nearly twice that of Blakesley *et al.* (2002). Perhaps this discrepancy reflects the use of *Allium cepa* (2C = 33·5 pg), whose genome size is over an order of magnitude greater than that of *Acacia*, as a calibration standard by Mukherjee and Sharma (1993*b*). Similar discrepancies were noted between DNA estimates for *A. mangium* reported by Blakesley *et al.* (loc. cit.) of 2C = 1·3 pg, and those by Mukherjee and Sharma (1995) of 2C = 2·3 pg.

(bc) Ohri and Singh (2002, Ref. 443) listed C-values for 20 wild relatives of cultivated pigeon pea (*Cajanus cajan*). However, C-values for 14 of these species had already been communicated to MD Bennett in 1996 and listed in the Appendix of Bennett and Leitch (1997) under Original reference number 303. To avoid duplication of data in the database, only C-values for six species not listed previously are included in the Appendix.

(bd) Wendel *et al.* (2002, Ref. 444) listed DNA amounts for 13 species in the tribe Gossypieae. However, C-values for three of these species had already been communicated to MD Bennett in 1999 and listed in the Appendix of Bennett *et al.* (2000) under Original reference number 349. To avoid duplication of data in the database, only C-values for ten species not listed previously are included in the Appendix.

(be) The C-value of *Arabidopsis thaliana* given by the Arabidopsis Genome Initiative (2000, Ref. 448) was based on DNA sequencing data for 115·4 Mb of the genome, plus a guestimate of 10 Mb for several unsequenced gaps in the genome. Recent work places its 1C-value around 157 Mb (Bennett *et al.*, 2003).

(bf) Ohri (2002, Ref. 449) listed DNA amounts for 36 tropical hardwood species belonging to 13 families. However, C-values of 35 of these had already been communicated to MD Bennett in 1996 and listed in the Appendix of Bennett and Leitch (1997) under Original reference number 301. To avoid duplication of data in the database, a C-value for the only species not included in a previous compilation (*Drypetes roxburghii*) is listed in the present Appendix. A new C-value for *Melaleuca leucadendra*, double that given in Bennett and Leitch (1997), is also listed in the Appendix, to correct an error in communication which confused the 2C- and 4C-values for this species.

(bg) The C-value of 466 Mb for *Oryza sativa* ssp. *indica* given in Yu *et al*. (2002, Ref. 450) was based on DNA sequencing data for 362 Mb of sequenced scaffolds, and 104 Mb of 'unassembled data' subject to numerous assumptions (see Yu *et al*., loc. cit. – page 80).

(bh) The C-value of 420 Mb for *Oryza sativa* ssp. *japonica* given in Goff *et al*. (2002, Ref. 451) was derived from DNA sequencing data for 389·9 Mb, and their assumption that this equals 93 % of the genome, perhaps using some previously published 1C-value. The source of this assumption, as of any such DNA estimate, and the method by which it was obtained, was not clearly cited by Goff *et al*. (2002).

(bi) Redondo *et al*. (1996, Ref. 453) estimated C-values in four populations of *Saxifraga granulata*. In one population chromosome numbers ranged from $2n$ = 44 to 56, but $2n$ = 44 was predominant. They noted that the DNA amount was also variable but gave only one C-value, which is listed in the Appendix. However, intraspecific variation in DNA amount may occur in this species, so the C-value listed may not apply to all members of the population.

(bj) Redondo *et al*. (1996, Ref. 453) estimated DNA amounts in four populations of *Saxifraga granulata*. They reported DNA amounts for a population in which they could not obtain a chromosome count (entry number 706), but based on the DNA amount, they suggested this population may have $2n$ = 30.

(bk) Emshwiller (2002, Ref. 456) estimated C-values in 10 accessions of cultivated oca ($2n = 8x = 64$; *Oxalis tuberosa*), two tetraploid wild species, and 78 diploid accessions which were provisionally identified as 35 species. As variation in 2C DNA amounts was usually no more than 0·1 pg, and considered to be technical in nature, only the highest C-value was reported in table 3 of Emshwiller (2002) for most species and is entered in the Appendix. Variation in DNA amounts greater than 0·1 pg was considered real for *O. spiralis* (2C = 1·062–1·339 pg) and *O. peduncularis* (2C = 0·927–1·163 pg), so both the lowest and highest values are entered in the Appendix for these species. Emshwiller (2002) noted that this variation may reflect problems of taxonomy and species boundaries.

(bl) Emshwiller (2002, Ref. 456) estimated the DNA amounts in ten accessions of cultivated oca ($2n = 8x = 64$; *Oxalis tuberosa*). Variation was noted, even in measurements made for all accessions estimated on one day (see table 3 of Emshwiller, 2002), but she did not consider it to represent intraspecific variation and a mean 2C estimate calculated from all measurements made was given in her 'Results' section as 2C = 3·514 pg. It is this value that is entered in the Appendix.

(bm) Nagl *et al*. (1983, Ref. 457) included DNA amounts for 49 species. However, C-values for 20 of these had been published elsewhere, and already included in previous compilations by Bennett and colleagues (listed under original reference numbers 34, 36, 60, 61, 81, 82, 84, 85, 86). To avoid duplication only C-values for 29 species that had not been listed previously are included in the Appendix.

(bn) Values for *Phaseolus coccineus* and *P. vulgaris* given in Nagl *et al*. (1983, Ref. 457) are around twice those given in another paper by Nagl and Treviranus (1995, Ref. 390), listed in the present Appendix. 2C-values for both species given in Nagl *et al*. (loc. cit.) agree with those reported by Ayonoadu (1974), but are around twice that reported in Ingle *et al*. (1975) and Arumuganathan and Earle (1991). The basis of this discrepancy is unclear, so C-values for these *Phaseolus* taxa should be viewed with caution until confirmed independently.

(bo) The value for *Sambucus nigra* (2C = 30·5 pg) given by Nagl *et al*. (1983, Ref. 457) is similar to the value of 2C = 21·8 pg for a related species, *S. racemosa*, reported by Nagl *et al*. (1979) and listed under Ref. 86 in Bennett *et al*. (1982). However, it is very different from 2C = 3·1 pg reported for *S. nigra* by Mowforth (1986) and listed under Ref. 158 in Bennett and Smith (1991). The cause for the discrepancy remains unclear, so C-values for *S. nigra* should be used with caution until confirmed independently.

(bp) Baranyi *et al*. (1996, Ref. 458) investigated C-values in 75 accessions of four wild *Pisum* species. Results were given as percentages relative to *P. sativum* 'Kleine Rheinländerin' (= 100 %) which was used as the calibration standard. To convert these into absolute DNA amounts the 4C-values were multiplied by the value of *Pisum sativum* 'Kleine Rheinländerin' of 17·68 pg (Greilhuber and Ebert, 1994) and then divided by 100.

Pisum fulvum was homogeneous in DNA amount size (4C = approx. 19·3 pg), but wide variation was seen between accessions of the other species studied (*P. abyssinicum*, *P. humile* and *P. elatius*). This variation was interpreted to show that these taxa with variable genome sizes were genetically heterogeneous, suggesting that the current species delimitations did not reflect the true biological species groups adequately. Only the smallest and largest C-values for each of these species are listed in the Appendix.

(bq) Punina and Alexandrova (1992, Ref. 459) estimated DNA amounts in 11 *Paeonia* species but gave the results as percentage values relative to *P. caucasica*. Since Mulry and Hanson (pers. comm. 1999) had estimated the 4C DNA value of this species as 65·2 pg (see entry number 602 in Bennett *et al*., 2000), the relative percentage values given in Punina and Alexandrova (loc. cit.) were converted into absolute DNA amounts by multiplying by 0·652.

(br) A PhD thesis by Shi (1991) gave a 1C-value of 0·15 pg for two accessions of diploid *Brachypodium distachyon* ($2n$ = 10), plus values for four other *Brachypodium* species. Later, Shi *et al*. (1993, Ref. 460) gave the 1C-value for diploid *B. distachyon* as 1C = 0·3 pg, but cited the PhD thesis (Shi, 1991) as the source for this figure. In order to confirm which was correct, Clive Stace kindly supplied seed of one original accession (B306) and RBG, Kew estimated its DNA amount as 0·36 pg using *Oryza sativa* 'IR36' (4C = 2·02 pg) as a calibration standard (see entry number 161a in the present Appendix). This was much closer to the value in Shi *et al*. (1993). As C-values for four other *Brachypodium* species in Shi (1991) may also be underestimates, they are therefore not included in the present Appendix, and should be viewed with caution until confirmed independently.

APPENDIX. *Chromosome number, ploidy level, life-cycle type, and nuclear DNA content in 804 angiosperm species (the superscript letters refer to notes preceding this table)*

Entry number[g]	Species	Voucher	Family	Higher group[#]	2n‡	Ploidy level (*x*)	Life cycle type[§]	DNA amount 1C (Mbp[s])	1C (pg)	2C (pg)	4C (pg)	Original ref.[a]	Present amount[†]	Standard species[*b1]	Method[††]
1a	*Acacia dealbata* Link.	No	Leguminosae	E	26	2	P	853	0·9	1·7	3·5	441[bb]	O	J	FC:PI
2	*Acacia dealbata* Link.	No	Leguminosae	E	39°	3	P	—[t]	—[t]	2·5	5·1	441[bb]	O	J	FC:PI
3	*Acacia dealbata* Link.	No	Leguminosae	E	52	4	P	1,671	1·7	3·4	6·8	441[bb]	O	J	FC:PI
4a	*Acacia mangium* Willd.	No	Leguminosae	E	26	2	P	637	0·7	1·3	2·6	441[bb]	O	J	FC:PI
5	*Acridocarpus natalitius* A. Juss.	No	Malpighiaceae	E	c. 216	24	P	1,490	1·5	3·0	6·1	379	O	J	Fe
6	*Adenanthera microsperma* Teijsm & Binn.	No	Leguminosae	E	—[n]	—[p]	P	681	0·7	1·4	2·8	454	O	B[c]	Fe
7	*Adenanthera pavonina* L.	No	Leguminosae	E	26°	—[p]	P	666	0·7	1·4	2·7	454	O	B[c]	Fe
8	*Adina cordifolia* (Roxb.) Hook. f.	No	Rubiaceae	E	22°	2	P	816	0·8	1·7	3·3	454	O	B[c]	Fe
9	*Aeonium haworthii* Webb & Berth.	No	Crassulaceae	E	72°	4 or 8	P	760	0·8	1·6	3·1	378	O	J	Fe
10a	*Aesculus hippocastanum* L.	No	Sapindaceae	E	40	2	P	588	0·6	1·2	2·4	465	O	*Lycopers.*[c]	FC:PI
11b	*Agave americana* L.	—[m]	Asparagaceae	M	120	4	P	7,791	8·0	15·9	31·8	384[aa]	O	*Homo*[f]	FC:PI
12d	*Agave sisalana* Perr.	—[m]	Asparagaceae	M	150	5	P	—[t]	—[t]	20·0	40·0	384[aa]	O	*Homo*[f]	FC:PI
13	*Agave stricta* Salm.	—[m]	Asparagaceae	M	60	2	P	3,822	3·9	7·8	15·6	384[aa]	O	*Homo*[f]	FC:PI
14	*Agrostis palustris* Huds.	No	Gramineae	M	28	4	P	2,769	2·8	5·7	11·3	417	O	*Gallus*[f]	FC:PI
15	*Ailanthus grandis* Prain	No	Simaroubaceae	E	64°	—[p]	P	2,134	2·2	4·4	8·7	454	O	B[c]	Fe
16a	*Albuca pendula* B.Mathew	No	Asparagaceae	M	16	2	P	2,967	3·0	6·1	12·1	465	O	G	Fe
16b	*Albuca pendula* B.Mathew	No	Asparagaceae	M	14	2	P	3,033	3·1	6·2	12·4	465	O	G	Fe
17k	*Allium cepa* L.	No	Alliaceae[k]	M	16°	2	P	16,415	16·8	33·5	67·0	457[bm]	O	B[d]	Fe
18	*Allocasuarina verticillata* (Lam.) L.Johnson	No	Casuarinaceae	E	20-28°	2	P	931	1·0	1·9	3·8	452	O	*Petunia*[e]	FC:PI
19	*Alocasia cucullata* (Lour) Schott	No	Araceae	M	98	—[p]	AP	8,200	8·4	16·7	33·5	411	O	B[c]	Fe
20	*Alocasia hilobeauty* Host.	No	Araceae	M	32	—[p]	A	3,680	3·8	7·5	15·0	411	O	B[c]	Fe
21	*Aloe albiflora* Guillaumin	No	Xanthorrhoeaceae[k]	M	14°	2	P	15,337	15·7	31·3	62·6	440	O	*Agave* sp.[ab]	FC:PI
22	*Aloe alooides* (Bolus) Druten	No	Xanthorrhoeaceae[k]	M	14°	2	P	13,083	13·4	26·7	53·4	440	O	*Agave* sp.[ab]	FC:PI
23	*Aloe antandroi* (Decary) H.Perrier	No	Xanthorrhoeaceae[k]	M	14°	2	P	17,199	17·6	35·1	70·2	440	O	*Agave* sp.[ab]	FC:PI
24	*Aloe arborescens* (yellow flowers) Mill.[i]	No	Xanthorrhoeaceae[k]	M	14°	2	P	13,671	14·0	27·9	55·8	440	O	*Agave* sp.[ab]	FC:PI
25a	*Aloe aristata* Haw.	No	Xanthorrhoeaceae[k]	M	14°	2	P	15,729	16·1	32·1	64·2	440	O	*Agave* sp.[ab]	FC:PI
25b	*Aloe aristata* var. *parvifolia* Baker Haw.	No	Xanthorrhoeaceae[k]	M	14°	2	P	16,023	16·4	32·7	65·4	440	O	*Agave* sp.[ab]	FC:PI
26	*Aloe bakeri* Scott-Elliot	No	Xanthorrhoeaceae[k]	M	14°	2	P	15,925	16·3	32·5	65·0	440	O	*Agave* sp.[ab]	FC:PI
27	*Aloe barberae* Dyer	No	Xanthorrhoeaceae[k]	M	14°	2	P	15,043	15·4	30·7	61·4	440	O	*Agave* sp.[ab]	FC:PI
28	*Aloe bellatula* Reynolds	No	Xanthorrhoeaceae[k]	M	14°	2	P	16,268	16·6	33·2	66·4	440	O	*Agave* sp.[ab]	FC:PI
29	*Aloe boiteaui* Guillaumin	No	Xanthorrhoeaceae[k]	M	14°	2	P	16,023	16·4	32·7	65·4	440	O	*Agave* sp.[ab]	FC:PI
30	*Aloe bowiea* Schult. & Schult.f.	No	Xanthorrhoeaceae[k]	M	14°	2	P	16,268	16·6	33·2	66·4	440	O	*Agave* sp.[ab]	FC:PI
31	*Aloe brevifolia* Mill.	No	Xanthorrhoeaceae[k]	M	14°	2	P	14,553	14·9	29·7	59·4	440	O	*Agave* sp.[ab]	FC:PI
32b	*Aloe cameronii* Hemsl.	No	Xanthorrhoeaceae[k]	M	14°	2	P	17,052	17·4	34·8	69·6	440	O	*Agave* sp.[ab]	FC:PI
33	*Aloe capitata* Baker	No	Xanthorrhoeaceae[k]	M	14°	2	P	15,386	15·7	31·4	62·8	440	O	*Agave* sp.[ab]	FC:PI
34	*Aloe chabaudii* Schonland	No	Xanthorrhoeaceae[k]	M	14°	2	P	17,934	18·3	36·6	73·2	440	O	*Agave* sp.[ab]	FC:PI
35	*Aloe ciliaris* var. *tidmarshii* Schonland Haw.	No	Xanthorrhoeaceae[k]	M	14°	2	P	10,535	10·8	21·5	43·0	440	O	*Agave* sp.[ab]	FC:PI
36	*Aloe ciliaris* Haw.	No	Xanthorrhoeaceae[k]	M	35°	5	P	—[t]	—[t]	53·3	106·6	440	O	*Agave* sp.[ab]	FC:PI
37	*Aloe ciliaris* Haw.	No	Xanthorrhoeaceae[k]	M	42°	6	P	30,723	31·4	62·7	125·4	440	O	*Agave* sp.[ab]	FC:PI
38	*Aloe comptonii* Reynolds	No	Xanthorrhoeaceae[k]	M	14°	2	P	13,426	13·7	27·4	54·8	440	O	*Agave* sp.[ab]	FC:PI
39a	*Aloe cryptopoda* Baker	No	Xanthorrhoeaceae[k]	M	14°	2	P	14,161	14·5	28·9	57·8	440	O	*Agave* sp.[ab]	FC:PI
39b	*Aloe cryptopoda* ''Wickensii'' Baker	No	Xanthorrhoeaceae[k]	M	14°	2	P	14,357	14·7	29·3	58·6	440	O	*Agave* sp.[ab]	FC:PI
40	*Aloe dawei* Berger	No	Xanthorrhoeaceae[k]	M	28°	4	P	35,231	36·0	71·9	143·8	440	O	*Agave* sp.[ab]	FC:PI
41a	*Aloe descoingsii* Reynolds	No	Xanthorrhoeaceae[k]	M	14°	2	P	15,974	16·3	32·6	65·2	440	O	*Agave* sp.[ab]	FC:PI

41b	*Aloe descoingsii* Reynolds ssp. *augustina* Lavranos	No	Xanthorrhoeaceae[k]	M	14°	2	P	16,219	16·6	33·1	66·2	440	O	*Agave* sp.[ab]	FC:PI
42a	*Aloe dichotoma* Masson var. *ramosissima* (Pillans) Glen & D.S.Hardy	No	Xanthorrhoeaceae[k]	M	14°	2	P	12,005	12·3	24·5	49·0	440	O	*Agave* sp.[ab]	FC:PI
42b	*Aloe dichotoma* Masson	No	Xanthorrhoeaceae[k]	M	14°	2	P	12,103	12·4	24·7	49·4	440	O	*Agave* sp.[ab]	FC:PI
43	*Aloe dinteri* A.Berger	No	Xanthorrhoeaceae[k]	M	14°	2	P	16,366	16·7	33·4	66·8	440	O	*Agave* sp.[ab]	FC:PI
44b	*Aloe distans* Haw.	No	Xanthorrhoeaceae[k]	M	14°	2	P	13,622	13·9	27·8	55·6	440	O	*Agave* sp.[ab]	FC:PI
45	*Aloe dorotheae* A.Berger	No	Xanthorrhoeaceae[k]	M	14°	2	P	15,288	15·6	31·2	62·4	440	O	*Agave* sp.[ab]	FC:PI
46	*Aloe elegans* Tod.	No	Xanthorrhoeaceae[k]	M	14°	2	P	17,346	17·7	35·4	70·8	440	O	*Agave* sp.[ab]	FC:PI
47	*Aloe erinacea* D.S.Hardy	No	Xanthorrhoeaceae[k]	M	14°	2	P	12,103	12·4	24·7	49·4	440	O	*Agave* sp.[ab]	FC:PI
48	*Aloe ferox* Mill.	No	Xanthorrhoeaceae[k]	M	14°	2	P	14,896	15·2	30·4	60·8	440	O	*Agave* sp.[ab]	FC:PI
49	*Aloe fleurentiniorum* Lavranos & L.E.Newton	No	Xanthorrhoeaceae[k]	M	14°	2	P	18,179	18·6	37·1	74·2	440	O	*Agave* sp.[ab]	FC:PI
50	*Aloe gariepensis* (?) Pillans	No	Xanthorrhoeaceae[k]	M	14°	2	P	15,729	16·1	32·1	64·2	440	O	*Agave* sp.[ab]	FC:PI
51	*Aloe glauca* Mill.	No	Xanthorrhoeaceae[k]	M	14°	2	P	15,680	16·0	32·0	64·0	440	O	*Agave* sp.[ab]	FC:PI
52	*Aloe globuligemma* Pole-Evans	No	Xanthorrhoeaceae[k]	M	14°	2	P	16,611	17·0	33·9	67·8	440	O	*Agave* sp.[ab]	FC:PI
53	*Aloe haemanthifolia* A.Berger & Marloth	No	Xanthorrhoeaceae[k]	M	14°	2	P	7,938	8·1	16·2	32·4	440	O	*Agave* sp.[ab]	FC:PI

‡ Chromosome number.
§ E, ephemeral; A, annual; B, biennial; P, perennial.
† O, original value; C, calibrated value
* The standard species used to calibrate the present amount.
†† Fe, Feulgen microdensitometry; FC, flow cytometry using one of the following fluorochromes: PI, propidium iodide; DAPI, 4′, 6-diamidinophenylindole; EB, ethidium bromide; MI, mithramycin; HO, Hoechst 33258; GS, genome sequencing; CIA, computer image analysis; RK, reassociation kinetics.
\# E, eudicot; M, monocot; BA, basal angiosperm.

APPENDIX. *(continued, the superscript letters refer to notes preceding this table)*

Entry number[g]	Species	Voucher	Family	Higher group[#]	2n‡	Ploidy level (*x*)	Life cycle type[§]	DNA amount 1C (Mbp[s])	1C (pg)	2C (pg)	4C (pg)	Original ref.[a]	Present amount[†]	Standard species[*b1]	Method[††]
54	*Aloe haworthioides* Baker	No	Xanthorrhoeaceae[k]	M	14°	2	P	14,749	15·1	30·1	60·2	440	O	*Agave* sp.[ab]	FC:PI
55	*Aloe hereroensis* Engl.	No	Xanthorrhoeaceae[k]	M	14°	2	P	18,130	18·5	37·0	74·0	440	O	*Agave* sp.[ab]	FC:PI
56	*Aloe humilis* (small form) (L.) Mill.[i]	No	Xanthorrhoeaceae[k]	M	14°	2	P	16,562	16·9	33·8	67·6	440	O	*Agave* sp.[ab]	FC:PI
57	*Aloe jacksonii* Reynolds	No	Xanthorrhoeaceae[k]	M	28°	4	P	32,487	33·2	66·3	132·6	440	O	*Agave* sp.[ab]	FC:PI
58	*Aloe jucunda* Reynolds	No	Xanthorrhoeaceae[k]	M	14°	2	P	17,591	18·0	35·9	71·8	440	O	*Agave* sp.[ab]	FC:PI
59b	*Aloe juvenna* Brandham & Carter	No	Xanthorrhoeaceae[k]	M	28°	4	P	34,790	35·5	71·0	142·0	440	O	*Agave* sp.[ab]	FC:PI
60	*Aloe krapohliana* var. *dumoulinii* Lavranos	No	Xanthorrhoeaceae[k]	M	14°	2	P	17,346	17·7	35·4	70·8	440	O	*Agave* sp.[ab]	FC:PI
61	*Aloe linearifolia* A.Berger	No	Xanthorrhoeaceae[k]	M	14°	2	P	12,936	13·2	26·4	52·8	440	O	*Agave* sp.[ab]	FC:PI
62	*Aloe lomatophylloides* Balf.f.	No	Xanthorrhoeaceae[k]	M	14°	2	P	17,248	17·6	35·2	70·4	440	O	*Agave* sp.[ab]	FC:PI
63	*Aloe longistyla* Baker	No	Xanthorrhoeaceae[k]	M	14°	2	P	15,582	15·9	31·8	63·6	440	O	*Agave* sp.[ab]	FC:PI
64	*Aloe macrosiphon* Bak.	No	Xanthorrhoeaceae[k]	M	14°	2	P	17,934	18·3	36·6	73·2	440	O	*Agave* sp.[ab]	FC:PI
65	*Aloe maculata* Allionii	No	Xanthorrhoeaceae[k]	M	14°	2	P	18,620	19·0	38·0	76·0	440	O	*Agave* sp.[ab]	FC:PI
66a	*Aloe marlothii* A.Berger "Spectabilis"	No	Xanthorrhoeaceae[k]	M	14°	2	P	15,435	15·8	31·5	63·0	440	O	*Agave* sp.[ab]	FC:PI
66b	*Aloe marlothii* A.Berger var. *bicolor* Reynolds	No	Xanthorrhoeaceae[k]	M	14°	2	P	15,631	16·0	31·9	63·8	440	O	*Agave* sp.[ab]	FC:PI
67b	*Aloe mcloughlinii* Christian	No	Xanthorrhoeaceae[k]	M	14°	2	P	16,219	16·6	33·1	66·2	440	O	*Agave* sp.[ab]	FC:PI
68	*Aloe melanacantha* A.Berger	No	Xanthorrhoeaceae[k]	M	14°	2	P	12,299	12·6	25·1	50·2	440	O	*Agave* sp.[ab]	FC:PI
69	*Aloe microstigma* Salm-Dyck	No	Xanthorrhoeaceae[k]	M	14°	2	P	15,092	15·4	30·8	61·6	440	O	*Agave* sp.[ab]	FC:PI
70	*Aloe mitriformis* Mill.	No	Xanthorrhoeaceae[k]	M	14°	2	P	13,475	13·8	27·5	55·0	440	O	*Agave* sp.[ab]	FC:PI
71b	*Aloe ngobitensis* Reynolds	No	Xanthorrhoeaceae[k]	M	28°	4	P	28,420	29·0	58·0	116·0	440	O	*Agave* sp.[ab]	FC:PI
72	*Aloe occidentalis* (H.Perrier) L.E.Newton & G.D.Rowley	No	Xanthorrhoeaceae[k]	M	14°	2	P	20,286	20·7	41·4	82·8	440	O	*Agave* sp.[ab]	FC:PI
73	*Aloe parvula* A.Berger	No	Xanthorrhoeaceae[k]	M	14°	2	P	16,562	16·9	33·8	67·6	440	O	*Agave* sp.[ab]	FC:PI
74	*Aloe pearsonii* Schonland	No	Xanthorrhoeaceae[k]	M	14°	2	P	12,348	12·6	25·2	50·4	440	O	*Agave* sp.[ab]	FC:PI
75b	*Aloe peckii* Bally & Verdoorn	No	Xanthorrhoeaceae[k]	M	14°	2	P	17,444	17·8	35·6	71·2	440	O	*Agave* sp.[ab]	FC:PI
76	*Aloe peglerae* Schonland	No	Xanthorrhoeaceae[k]	M	14°	2	P	15,729	16·1	32·1	64·2	440	O	*Agave* sp.[ab]	FC:PI
77	*Aloe petricola* Pole-Evans	No	Xanthorrhoeaceae[k]	M	14°	2	P	15,092	15·4	30·8	61·6	440	O	*Agave* sp.[ab]	FC:PI
78	*Aloe pillansii* L.Guthrie	No	Xanthorrhoeaceae[k]	M	14°	2	P	12,593	12·9	25·7	51·4	440	O	*Agave* sp.[ab]	FC:PI
79	*Aloe plicatilis* (L.) Mill.	No	Xanthorrhoeaceae[k]	M	14°	2	P	8,624	8·8	17·6	35·2	440	O	*Agave* sp.[ab]	FC:PI
80	*Aloe pluridens* Haworth	No	Xanthorrhoeaceae[k]	M	14°	2	P	14,161	14·5	28·9	57·8	440	O	*Agave* sp.[ab]	FC:PI
81	*Aloe polyphylla* Schonland	No	Xanthorrhoeaceae[k]	M	14°	2	P	13,377	13·7	27·3	54·6	440	O	*Agave* sp.[ab]	FC:PI
82	*Aloe prinslooi* Verdoorn & Hardy	No	Xanthorrhoeaceae[k]	M	14°	2	P	17,444	17·8	35·6	71·2	440	O	*Agave* sp.[ab]	FC:PI
83	*Aloe prostrata* (H.Perrier) L.E.Newton & G.D.Rowley	No	Xanthorrhoeaceae[k]	M	14°	2	P	20,139	20·6	41·1	82·2	440	O	*Agave* sp.[ab]	FC:PI
84	*Aloe rauhii* Reynolds	No	Xanthorrhoeaceae[k]	M	14°	2	P	15,337	15·7	31·3	62·6	440	O	*Agave* sp.[ab]	FC:PI
85	*Aloe richardsiae* Reynolds	No	Xanthorrhoeaceae[k]	M	14°	2	P	21,756	22·2	44·4	88·8	440	O	*Agave* sp.[ab]	FC:PI
86	*Aloe rivierei* Lavranos & L.E. Newton	No	Xanthorrhoeaceae[k]	M	14°	2	P	16,562	16·9	33·8	67·6	440	O	*Agave* sp.[ab]	FC:PI
87	*Aloe secundiflora* Engl.	No	Xanthorrhoeaceae[k]	M	14°	2	P	17,591	18·0	35·9	71·8	440	O	*Agave* sp.[ab]	FC:PI
88	*Aloe sinkatana* Reynolds (red flowers)[i]	No	Xanthorrhoeaceae[k]	M	14°	2	P	17,542	17·9	35·8	71·6	440	O	*Agave* sp.[ab]	FC:PI
89	*Aloe sladeniana* Pole-Evans	No	Xanthorrhoeaceae[k]	M	14°	2	P	15,974	16·3	32·6	65·2	440	O	*Agave* sp.[ab]	FC:PI
90	*Aloe speciosa* Baker	No	Xanthorrhoeaceae[k]	M	14°	2	P	14,112	14·4	28·8	57·6	440	O	*Agave* sp.[ab]	FC:PI
91	*Aloe spicata* L.f.	No	Xanthorrhoeaceae[k]	M	14°	2	P	14,259	14·6	29·1	58·2	440	O	*Agave* sp.[ab]	FC:PI
92	*Aloe striata* Haw.	No	Xanthorrhoeaceae[k]	M	14°	2	P	18,914	19·3	38·6	77·2	440	O	*Agave* sp.[ab]	FC:PI
93	*Aloe suprafoliata* Pole-Evans	No	Xanthorrhoeaceae[k]	M	14°	2	P	14,014	14·3	28·6	57·2	440	O	*Agave* sp.[ab]	FC:PI

94	*Aloe suzannae* Decary	No	Xanthorrhoeaceae[k]	M	14[o]	2	P	16,317	16·7	33·3	66·6	440	O	*Agave* sp.[ab]	FC:PI
95b	*Aloe tenuior* Haw.	No	Xanthorrhoeaceae[k]	M	14[o]	2	P	10,633	10·9	21·7	43·4	440	O	*Agave* sp.[ab]	FC:PI
96	*Aloe trichosantha* Berger	No	Xanthorrhoeaceae[k]	M	14[o]	2	P	18,179	18·6	37·1	74·2	440	O	*Agave* sp.[ab]	FC:PI
97	*Aloe vanbalenii* Pillans	No	Xanthorrhoeaceae[k]	M	14[o]	2	P	13,965	14·3	28·5	57·0	440	O	*Agave* sp.[ab]	FC:PI
98a	*Aloe variegata* L. ''Ausana''	No	Xanthorrhoeaceae[k]	M	14[o]	2	P	16,268	16·6	33·2	66·4	440	O	*Agave* sp.[ab]	FC:PI
98b	*Aloe variegata* L.	No	Xanthorrhoeaceae[k]	M	14[o]	2	P	16,562	16·9	33·8	67·6	440	O	*Agave* sp.[ab]	FC:PI
99	*Aloe vera* (L.) Burm.f.	No	Xanthorrhoeaceae[k]	M	14[o]	2	P	16,072	16·4	32·8	65·6	440	O	*Agave* sp.[ab]	FC:PI
100	*Alstonia macrophylla* Wall. ex G.Don.	No	Apocynaceae	E	—[n]	—[p]	P	718	0·7	1·5	2·9	454	O	B[c]	Fe
101c	*Alstroemeria aurea* Graham[h]	No	Alstroemeriaceae	M	16	2	P	24,843	25·4	50·7	101·4	436	O	B	FC:PI
101d	*Alstroemeria aurea* Graham[h]	No	Alstroemeriaceae	M	16	2	P	27,097	27·7	55·3	110·6	436	O	B	FC:PI
102	*Alstroemeria aurea* Graham[h]	No	Alstroemeriaceae	M	24	3	P	—[t]	—[t]	80·9	161·8	436	O	B	FC:PI
103d	*Alstroemeria ligtu* L. ssp. *incarnata* L.[h]	No	Alstroemeriaceae	M	16	2	P	34,300	35·0	70·0	140·0	436	O	B	FC:PI
103e	*Alstroemeria ligtu* L. ssp. *simsii*[h]	No	Alstroemeriaceae	M	16	2	P	31,948	32·6	65·2	130·4	436	O	B	FC:PI
103f	*Alstroemeria ligtu* L. ssp. *simsii*[h]	No	Alstroemeriaceae	M	16	2	P	38,661	39·5	78·9	157·8	436	O	B	FC:PI
103g	*Alstroemeria ligtu* L. ssp. *ligtu*[h]	No	Alstroemeriaceae	M	16	2	P	34,006	34·7	69·4	138·8	436	O	B	FC:PI
103h	*Alstroemeria ligtu* L. ssp. *ligtu*[h]	No	Alstroemeriaceae	M	16	2	P	33,369	34·1	68·1	136·2	436	O	B	FC:PI
104c	*Alstroemeria magnifica* Herb. ssp. *magnifica*[h]	No	Alstroemeriaceae	M	16	2	P	17,885	18·3	36·5	73·0	436	O	B	FC:PI
104d	*Alstroemeria magnifica* Herb. ssp. *magnifica*[h]	No	Alstroemeriaceae	M	16	2	P	20,531	21·0	41·9	83·8	436	O	B	FC:PI
105	*Alstroemeria magnifica* Herb. ssp. *magnifica*[h]	No	Alstroemeriaceae	M	24	3	P	—[t]	—[t]	61·6	123·2	436	O	B	FC:PI
106	*Amborella trichopoda* Baill.	No	Amborellaceae	BA	26[o]	—[p]	P	870	0·9	1·8	3·6	381	O	K	FC:PI
107	*Amoreuxia wrightii* A.Gray	No	Cochlospermaceae	E	c.12-14	2	P	164	0·2	0·3	0·7	378	O	J	Fe
108	*Anthemis altissima*[l]	No	Compositae[j]	E	—[n]	—[p]	—[q]	7,742	7·9	15·8	31·6	457[bm]	O	B[d]	Fe
109	*Anthemis montana*[l]	No	Compositae[j]	E	—[n]	—[p]	—[q]	8,281	8·5	16·9	33·8	457[bm]	O	B[d]	Fe
110	*Anthurium grande* Host.	No	Araceae	M	28	—[p]	P	13,252	13·5	27·0	54·1	411	O	B[c]	Fe
111	*Anthurium tetragonum* Schott	No	Araceae	M	30	—[p]	P	7,485	7·6	15·3	30·6	411	O	B[c]	Fe
112	*Aphyllanthes monspeliensis* L.	No	Asparagaceae	M	c. 32	—[p]	P	635	0·6	1·3	2·6	380	O	J	FC:PI
113	*Arabidopsis korshynskyi*[l]	No	Cruciferae[j]	E	—[n]	—[p]	—[q]	245	0·3	0·5	1·0	457[bm]	O	B[d]	Fe
114a	*Arabidopsis thaliana* (L.) Heynh. ecotype Columbia	No	Cruciferae	E	10	2	A	157	0·2	0·3	0·6	461	O	*Caeno.*[f]	FC:PI
114g	*Arabidopsis thaliana* (L.) Heynh. ecotype Columbia	No	Cruciferae	E	10	2	A	164	0·2	0·3	0·7	461	O	*Gallus*[f]	FC:PI
114h	*Arabidopsis thaliana* (L.) Heynh. ecotype Columbia	No	Cruciferae	E	10	2	A	150	0·2	0·3	0·6	461	O	*Dros.*[f]	FC:PI
114i	*Arabidopsis thaliana* (L.) Heynh.	—[m]	Cruciferae	E	10	2	A	125[be]	0·1[be]	0·3[be]	0·5[be]	448[be]	O	—	GS
114j	*Arabidopsis thaliana* (L.) Heynh. ecotype Columbia	No	Cruciferae	E	10	2	A	167	0·2	0·3	0·7	463	O	*Gallus*[f]	FC:DAPI
114k	*Arabidopsis thaliana* (L.) Heynh. ecotype Columbia	No	Cruciferae	E	10	2	A	162	0·2	0·3	0·7	463	O	*Gallus*[f]	FC:HO
114l	*Arabidopsis thaliana* (L.) Heynh. ecotype Columbia	No	Cruciferae	E	10	2	A	157	0·2	0·3	0·6	463	O	*Gallus*[f]	FC:MI
114m	*Arabidopsis thaliana* (L.) Heynh. line Landsberg erecta	No	Cruciferae	E	10	2	A	51	0·05	0·10	0·21	464	O	—	RK
115a	*Arachis duranensis* Krapov. & W.C.Gregory[h]	No	Leguminosae[j]	E	20	2	A	1,243	1·3	2·5	5·1	396	O	G[c]	FC:PI
115b	*Arachis duranensis* Krapov. & W.C.Gregory[h]	No	Leguminosae[j]	E	20	2	A	1,324	1·4	2·7	5·4	396	O	G[c]	FC:PI
115c	*Arachis duranensis* Krapov. & W.C.Gregory[h]	No	Leguminosae[j]	E	20	2	A	1,333	1·4	2·7	5·4	396	O	G[c]	Fe
116a	*Arachis hypogaea* L.	No	Leguminosae	E	40	4	A	2,813	2·9	5·7	11·5	395[aj]	O	G[c]	Fe

APPENDIX. *(continued, the superscript letters refer to notes preceding this table)*

Entry number[g]	Species	Voucher	Family	Higher group[#]	2n‡	Ploidy level (*x*)	Life cycle type[§]	DNA amount 1C (Mbp[s])	DNA amount 1C (pg)	DNA amount 2C (pg)	DNA amount 4C (pg)	Original ref.[a]	Present amount[†]	Standard species[*b1]	Method[††]
116b	*Arachis hypogaea* L.	No	Leguminosae	E	40	4	A	2,898	3·0	5·9	11·8	395[aj]	O	G[c]	FC:PI
116r	*Arachis hypogaea* L.	No	Leguminosae[j]	E	40°	4	A	1,568	1·6	3·2	6·4	457[bm]	O	B[d]	Fe
117a	*Arachis monticola* Krapov. & Rigoni	No	Leguminosae	E	40	4	A	2,891	3·0	5·9	11·8	395[aj]	O	G[c]	Fe
117b	*Arachis monticola* Krapov. & Rigoni	No	Leguminosae	E	40	4	A	2,930	3·0	6·0	12·0	395[aj]	O	G[c]	FC:PI
118	*Archidendron monadelphum* (Roxb.) I.C. Neilsen	No	Leguminosae	E	—[n]	—[p]	P	1,470	1·5	3·0	6·0	454	O	B[c]	Fe
119c	*Artemisia absinthium* L.	No	Compositae[j]	E	18	2	P	4,175	4·3	8·5	17·0	386	O	G-120d	FC:PI
120d	*Artemisia annua* L.	No	Compositae[j]	E	18	2	A	1,715	1·8	3·5	7·0	386	O	G[c]	FC:PI
121	*Artemisia barrelieri* Besser	No	Compositae[j]	E	36	4	P	6,350	6·5	13·0	25·9	386	O	G[c]	FC:PI
122	*Artemisia caerulescens* L. ssp. *gallica* (Willd.) K.Persson	No	Compositae[j]	E	18	2	P	3,263	3·3	6·7	13·3	386	O	G[c]	FC:PI
123	*Artemisia campestris* L.	No	Compositae[j]	E	18	2	P	2,876	2·9	5·9	11·7	386	O	G[c]	FC:PI
124	*Artemisia campestris* L.	No	Compositae[j]	E	36	4	P	5,390	5·5	11·0	22·0	386	O	G[c]	FC:PI
125	*Artemisia cana* Pursh.	No	Compositae[j]	E	72	8	P	12,569	12·8	25·7	51·3	386	O	G[c]	FC:PI
126	*Artemisia chamaemelifolia* Vill.	No	Compositae[j]	E	18	2	P	2,960	3·0	6·0	12·1	386	O	G[c]	FC:PI
127	*Artemisia crithmifolia* L.	No	Compositae[j]	E	54	6	P	7,644	7·8	15·6	31·2	386	O	G[c]	FC:PI
128	*Artemisia dracunculus* L.	No	Compositae[j]	E	90	10	P	11,378	11·6	23·2	46·4	386	O	G[c]	FC:PI
129	*Artemisia fragrans* Willd.	No	Compositae[j]	E	18	2	P	2,622	2·7	5·4	10·7	386	O	G[c]	FC:PI
130	*Artemisia herba-alba* Asso ssp. *valentina* (Lam.) Mascl.	No	Compositae[j]	E	18	2	P	3,219	3·3	6·6	13·1	386	O	G[c]	FC:PI
131	*Artemisia herba-alba* Asso ssp. *herba-alba*	No	Compositae[j]	E	36	4	P	6,115	6·2	12·5	25·0	386	O	G[c]	FC:PI
132c	*Artemisia judaica* L.	No	Compositae[j]	E	16	2	P	5,645	5·8	11·5	23·0	386	O	G[c]	FC:PI
133	*Artemisia lucentica* O.Bolos, Valles & Vigo in O.Bolos & Vigo	No	Compositae[j]	E	16	2	P	3,763	3·8	7·7	15·4	386	O	G-120d	FC:PI
134	*Artemisia molinieri* Quezel, Barbero & R.Loisel	No	Compositae[j]	E	18	2	P	2,920	3·0	6·0	11·9	386	O	G[c]	FC:PI
135	*Artemisia monosperma* Delile	No	Compositae[j]	E	36	4	P	5,400	5·5	11·0	22·0	386	O	G[c]	FC:PI
136	*Artemisia splendens* Willd.	No	Compositae[j]	E	32	4	P	6,659	6·8	13·6	27·2	386	O	G[c]	FC:PI
137	*Artemisia thuscula* Cav.	No	Compositae[j]	E	18	2	P	5,155	5·3	10·5	21·0	386	O	G[c]	FC:PI
138	*Artemisia tournefortiana* Reichenb.	No	Compositae[j]	E	18	2	AB	3,278	3·3	6·7	13·4	386	O	G[c]	FC:PI
139	*Artemisia tridentata* Nutt. ssp. *spiciformis* Kartesz & Gandhi	No	Compositae[j]	E	18	2	P	4,008	4·1	8·2	16·4	386	O	G-120d	FC:PI
140	*Artemisia umbelliformis* Lam. ssp. *umbelliformis*	No	Compositae[j]	E	34	4	P	6,081	6·2	12·4	24·8	386	O	G[c]	FC:PI
141b	*Artemisia vulgaris* L.	No	Compositae[j]	E	16	2	P	2,979	3·0	6·1	12·2	386	O	G[c]	FC:PI
142	*Artemisia vulgaris* L.	No	Compositae[j]	E	34	4	P	4,773	4·9	9·7	19·5	386	O	G[c]	FC:PI
143b	*Arum maculatum* L.	No	Araceae	M	56°	8	P	10,682	10·9	21·8	43·6	457[bm]	O	B[d]	Fe
144	*Asarum europaeum* L.	No	Aristolochiaceae	BA	—[n]	—[p]	P	4,753	4·9	9·7	19·4	457[bm]	O	B[d]	Fe
145	*Astelia fragrans* Colenso	No	Asteliaceae	M	c. 60	8	P	1,240	1·3	2·5	5·1	380	O	K	FC:PI
146	*Atalantia ceylanica* (Arn.) Oliv.)	No	Rutaceae	E	18°	2	P	515	0·5	1·1	2·1	426	O	*Gallus*[f]	FC:PI

147	*Austrobaileya scandens* C.T.White	No	Austrobaileyaceae	BA	44°	—[p]	P	9,327	9·5	19·0	38·1	381	O	G	FC:PI
148	*Averrhoa carambola* L.	No	Oxalidaceae	E	—[n]	—[p]	P	235	0·2	0·5	1·0	454	O	B[c]	Fe
149	*Azadirachta indica* A.Juss	No	Meliaceae	E	28°	—[p]	P	385	0·4	0·8	1·6	454	O	B[c]	Fe
150	*Bauhinia hookeri* (F.Muell.) Pedley	No	Leguminosae	E	26°	—[p]	P	620	0·6	1·3	2·5	454	O	B[c]	Fe
151b	*Bauhinia purpurea* L.	No	Leguminosae	E	28°	2	P	573	0·6	1·2	2·3	454	O	B[c]	Fe
152	*Bauhinia tomentosa* L.	No	Leguminosae	E	28°	2	P	613	0·6	1·3	2·5	454	O	B[c]	Fe
153	*Bellevalia rixii* P.Wendalbo	No	Asparagaceae	M	8	2	P	9,102	9·3	18·6	37·2	465	O	B	Fe
154	*Berberidopsis corallina* Hook. f.	No	Berberidopsidaceae	E	c. 42	6	P	252	0·3	0·5	1·0	379	O	J	Fe
155	*Berrya cordifolia* (Willd.) Burret	No	Malvaceae	E	—[n]	—[p]	P	549	0·6	1·1	2·2	454	O	B[c]	Fe
156a	*Bixa orellana* L.	No	Bixaceae	E	14	2	P	191	0·2	0·4	0·8	379	O	J	Fe
156b	*Bixa orellana* L.	No	Bixaceae	E	14°	2	P	203	0·2	0·4	0·8	454	O	B[c]	Fe
157	*Blandfordia punicea* Sweet.	No	Blandfordiaceae	M	68	4	P	7,970	8·1	16·3	32·5	380	O	G	Fe
158	*Bombax ceiba* L.	No	Malvaceae	E	92°	—[p]	P	1,590	1·6	3·2	6·5	454	O	B[c]	Fe
159	*Boswellia serrata* Roxb.	No	Burseraceae	E	22°	—[p]	P	684	0·7	1·4	2·8	454	O	B[c]	Fe
160	*Brachychiton discolor* F.Muell	No	Malvaceae	E	40°	—[p]	P	1,132	1·2	2·3	4·6	454	O	B[c]	Fe
161a	*Brachypodium distachyon* (L.) P.Beauv.	No	Gramineae	M	10	2	A	355	0·4	0·7	1·5	465	O	K	FC:PI
161b	*Brachypodium distachyon* (L.) P.Beauv.	—[m]	Gramineae	M	10	2	A	294	0·3	0·6	1·2	460[bh]	O	J	Fe
162e	*Brassica napus* L.	No	Cruciferae[j]	E	38°	4	AB	1,568	1·6	3·2	6·4	457[bm]	O	B[d]	Fe
163b	*Bromus arvensis* L.	No	Gramineae	M	14	2	A	5,699	5·8	11·6	23·3	391[af]	O	H-164b	FC:PI
164b	*Bromus carinatus* Hooker & Arnott cv. Broma	No	Gramineae	M	56	8	P	11,241	11·5	22·9	45·9	391[af]	O	H[c]	FC:PI
165c	*Bromus erectus* Hudson	No	Gramineae	M	56	8	P	12,079	12·3	24·7	49·3	391[af]	O	H[c]	FC:PI
166c	*Bromus hordeaceus* L.	No	Gramineae	M	28	4	A	11,285	11·5	23·0	46·1	391[af]	O	H[c]	FC:PI
167b	*Bromus inermis* Leysser	No	Gramineae	M	56	8	P	12,025	12·3	24·5	49·1	391[af]	O	H[c]	FC:PI
168	*Bromus willdenowii* Knuth	No	Gramineae	M	42	6	P	6,365	6·5	13·0	26·0	391[af]	O	H[c]	FC:PI
169	*Buchloe dactyloides* (Nutt.) Engelm.	No	Gramineae	M	40	4	P	779	0·8	1·6	3·2	417	O	*Gallus*[f]	FC:PI
170	*Buddleja globosa* Hope	No	Buddlejaceae	E	38	2	P	840	0·9	1·7	3·4	378	O	J	Fe
171	*Bulbine alooides* Willd.	No	Xanthorrhoeaceae	M	14	2	P	10,601	10·8	21·6	43·3	465	O	B	Fe
172	*Bulbine fallax* Poelln.	No	Xanthorrhoeaceae	M	14	2	P	11,201	11·4	22·9	45·7	465	O	B	Fe
173	*Bulbine lagopus* (Thunb.) N.E.Brown	No	Xanthorrhoeaceae	M	—[n]	—[p]	P	7,938	8·1	16·2	32·4	465	O	B	Fe
174	*Bulbine praemorsa* Spreng.	No	Xanthorrhoeaceae	M	14	2	P	12,213	12·5	24·9	49·9	465	O	B	Fe
175a	*Bunias erucago* L.	No	Cruciferae	E	14	2	A	2,029	2·1	4·1	8·3	393	O	G[c]	Fe
175b	*Bunias erucago* L.	No	Cruciferae	E	14	2	A	2,136	2·2	4·4	8·7	393	O	*Glycine*[e]	FC:PI
176a	*Bunias orientalis* L.	No	Cruciferae	E	14	2	P	2,538	2·6	5·2	10·4	393	O	G[c]	Fe
176b	*Bunias orientalis* L.	No	Cruciferae	E	14	2	P	2,636	2·7	5·4	10·8	393	O	*Glycine*[e]	FC:PI
177	*Buxus papillosa* C.K. Schneid.	No	Buxaceae	E	—[n]	—[p]	P	1,389	1·4	2·8	5·7	454	O	B[c]	Fe
178	*Buxus sempervirens*[l]	No	Buxaceae	E	28	2 or 4	P	794	0·8	1·6	3·2	380	O	K	FC:PI
179	*Byblis liniflora* Salisb.	No	Byblidaceae	E	32	2	A	870	0·9	1·8	3·6	378	O	J	Fe
180	*Cajanus albicans* (Wight. & Am.) Maesen	No	Leguminosae	E	22	2	A	1,259	1·3	2·6	5·1	443[bc]	O	B[c]	Fe
181	*Cajanus mollis* (Benth.) Maesen	No	Leguminosae	E	22	2	B	804	0·8	1·6	3·3	443[bc]	O	B[c]	Fe
182	*Cajanus sericeus* (Benth. ex Bak.) Maesen	No	Leguminosae	E	22	2	P	1,414	1·4	2·9	5·8	443[bc]	O	B[c]	Fe
183	*Caladium bicolor* Vent. var. red polka	No	Araceae	M	32	—[p]	A	5,407	5·5	11·0	22·1	411	O	B[c]	Fe
184	*Caladium bicolor* Vent. var. red polka large	No	Araceae	M	66	—[p]	A	9,927	10·1	20·3	40·5	411	O	B[c]	Fe
185	*Calceolaria acutifolia* Witasek	No	Scrophulariaceae	E	—[n]	—[p]	—[q]	1,348	1·4	2·8	5·5	465	O	J	Fe
186	*Calceolaria gracilis*[l]	No	Scrophulariaceae	E	—[n]	—[p]	—[q]	1,335	1·4	2·7	5·5	465	O	J	Fe
187	*Calibrachoa calycina* (Sendtn.) Wijsman	No	Solanaceae	E	18	2	P	1,504	1·5	3·1	6·1	387[ae]	O	*Gallus*-398p	FC:PI
188	*Calibrachoa dusenii* (R.E.Fr.) Stehmann & Semir.	No	Solanaceae	E	18	2	P	1,401	1·4	2·9	5·7	387[ae]	O	*Gallus*-398p	FC:PI
189	*Calibrachoa eglandulata* Stehmann & Semir.	No	Solanaceae	E	18°	2	P	1,411	1·4	2·9	5·8	387[ae]	O	*Gallus*-398p	FC:PI
190	*Calibrachoa elegans* (Miers) Stehmann & Semir.	No	Solanaceae	E	18	2	P	1,563	1·6	3·2	6·4	387[ae]	O	*Gallus*-398p	FC:PI
191	*Calibrachoa ericaefolia* (R.E.Fr.) Wijsman	No	Solanaceae	E	18	2	P	1,436	1·5	2·9	5·9	387[ae]	O	*Gallus*-398p	FC:PI
192	*Calibrachoa heterophylla* (Sendtn.) Wijsman	No	Solanaceae	E	18°	2	P	1,455	1·5	3·0	5·9	387[ae]	O	*Gallus*-398p	FC:PI
193	*Calibrachoa linearis* (Hook.) Wijsman	No	Solanaceae	E	18	2	P	1,485	1·5	3·0	6·1	387[ae]	O	*Gallus*-398p	FC:PI
194	*Calibrachoa linoides* (Sendtn.) Wijsman	No	Solanaceae	E	18	2	P	1,397	1·4	2·9	5·7	387[ae]	O	*Gallus*-398p	FC:PI

APPENDIX. *(continued, the superscript letters refer to notes preceding this table)*

Entry number[g]	Species	Voucher	Family	Higher group[#]	2n‡	Ploidy level (*x*)	Life cycle type[§]	DNA amount 1C (Mbp[s])	1C (pg)	2C (pg)	4C (pg)	Original ref.[a]	Present amount[†]	Standard species[*b1]	Method[††]
195	*Calibrachoa macrodactylon* (L.B.Sm. & Downs) Wijsman	No	Solanaceae	E	18	2	P	1,480	1·5	3·0	6·0	387[ae]	O	*Gallus*-398p	FC:PI
196	*Calibrachoa micrantha* (R.E.Fr.) Stehmann & Semir.	No	Solanaceae	E	18	2	P	1,411	1·4	2·9	5·8	387[ae]	O	*Gallus*-398p	FC:PI
197	*Calibrachoa parviflora* (Juss.) Wijsman	No	Solanaceae	E	18	2	A	936	1·0	1·9	3·8	387[ae]	O	*Gallus*-398p	FC:PI
198	*Calibrachoa pygmaea* (R.E.Fr.) Wijsman	No	Solanaceae	E	18	2	A	764	0·8	1·6	3·1	387[ae]	O	*Gallus*-398p	FC:PI
199	*Calibrachoa rupestris* (Dusen) Wijsman	No	Solanaceae	E	18[o]	2	P	1,597	1·6	3·3	6·5	387[ae]	O	*Gallus*-398p	FC:PI
200	*Calibrachoa selloviana* (Sendtn.) Wijsman	No	Solanaceae	E	18	2	P	1,455	1·5	3·0	5·9	387[ae]	O	*Gallus*-398p	FC:PI
201	*Calibrachoa sendtneriana* (R.E.Fr.) Stehmann & Semir.	No	Solanaceae	E	18[o]	2	P	1,450	1·5	3·0	5·9	387[ae]	O	*Gallus*-398p	FC:PI
202	*Calibrachoa serrulata* (L.B.Sm. & Downs) Stehmann & Semir.	No	Solanaceae	E	18	2	P	1,446	1·5	3·0	5·9	387[ae]	O	*Gallus*-398p	FC:PI
203	*Calibrachoa spathulata* (L.B.Sm. & Downs) Stehmann & Semir.	No	Solanaceae	E	18	2	P	1,416	1·4	2·9	5·8	387[ae]	O	*Gallus*-398p	FC:PI
204	*Calibrachoa thymifolia* (A. St.-Hil.) Stehmann & Semir.	No	Solanaceae	E	18	2	P	1,485	1·5	3·0	6·1	387[ae]	O	*Gallus*-398p	FC:PI
205	*Callistemon citrinus* (Curtis) Skeels	No	Myrtaceae	E	22[o]	—[p]	P	1,014	1·0	2·1	4·1	454	O	B[c]	Fe
206	*Callistemon rigidus* R.Br.	No	Myrtaceae	E	—[n]	—[p]	P	1,526	1·6	3·1	6·2	454	O	B[c]	Fe
207	*Camellia sinensis* Kuntze	No	Theaceae	E	30	2	P	3,824	3·9	7·8	15·6	379	O	G	Fe
208	*Canna indica*[l]	No	Cannaceae	M	18	2	P	706	0·7	1·4	2·9	379	O	J	Fe
209a	*Cannabis sativa* L. (female)	No	Cannabaceae	E	20	2	A	818[am]	0·8[am]	1·7[am]	3·3[am]	414	O	*Arab.*[e]	FC:DAPI
209b	*Cannabis sativa* L. (male)	No	Cannabaceae	E	20	2	A	843[am]	0·9[am]	1·7[am]	3·4[am]	414	O	*Arab.*[e]	FC:DAPI
210	*Canotia holacantha* Torr.	No	Celastraceae	E	30	2	P	181	0·2	0·4	0·7	378	O	J	Fe
211b	*Capsella bursa-pastoris* (L.) Medic.	No	Cruciferae[j]	E	32[o]	4	A	686	0·7	1·4	2·8	457[bm]	O	B[d]	Fe
212h	*Capsicum annuum* L. cv. Doux Long des Landes	No	Solanaceae	E	24	2	—[q]	3,734	3·8	7·6	15·2	434	O	G[c]	FC:PI
213c	*Capsicum baccatum* L. ssp. *pendulum*	No	Solanaceae	E	24	2	—[q]	4,111	4·2	8·4	16·8	434[ay]	O	G-212h	FC:PI
213d	*Capsicum baccatum* L. ssp. *baccatum*	No	Solanaceae	E	24	2	—[q]	4,131	4·2	8·4	16·9	434[ay]	O	G-212h	FC:PI
214	*Capsicum cardenasii* Heiser & Smith	No	Solanaceae	E	24[o]	2	—[q]	4,395	4·5	9·0	17·9	434	O	G-212h	FC:PI
215	*Capsicum chacoense* A.T.Hunz.	No	Solanaceae	E	24[o]	2	—[q]	3,753	3·8	7·7	15·3	434	O	G-212h	FC:PI
216b	*Capsicum chinense* Jacq.	No	Solanaceae	E	24	2	—[q]	3,940	4·0	8·0	16·1	434[ay]	O	G-212h	FC:PI
217b	*Capsicum eximium* A.T.Hunz.	No	Solanaceae	E	24[o]	2	—[q]	4,263	4·4	8·7	17·4	434[ay]	O	G-212h	FC:PI
218b	*Capsicum frutescens* L.	No	Solanaceae	E	24[o]	2	—[q]	3,891	4·0	7·9	15·9	434[ay]	O	G-212h	FC:PI
219	*Capsicum praetermissum* Heiser & Smith	No	Solanaceae	E	24[o]	2	—[q]	4,474	4·6	9·1	18·3	434	O	G-212h	FC:PI
220b	*Capsicum pubescens* R. & P.	No	Solanaceae	E	24[o]	2	—[q]	4,763	4·9	9·7	19·4	434[ay]	O	G-212h	FC:PI
221	*Capsicum tovarii* Eshbaugh, Smith & Nickrent	No	Solanaceae	E	24[o]	2	—[q]	3,886	4·0	7·9	15·9	434	O	G-212h	FC:PI
222a	*Cardamine amara* L.	No	Cruciferae	E	16	2	P	238	0·2	0·5	1·0	465	O	*Lycopers.*[c]	FC:PI
223	*Castanospermum australe* A.Cunn. & C.Fraser	No	Leguminosae	E	—[n]	—[p]	P	554	0·6	1·1	2·3	454	O	B[c]	Fe
224	*Casuarina glauca* Sieb. ex Spring.	No	Casuarinaceae	E	18[o]	2	P	343	0·4	0·7	1·4	452	O	*Petunia*[e]	FC:PI
225	*Catunaregam spinosa* (Thunb.) Trivengadum	No	Rubiaceae	E	22[o]	—[p]	P	343	0·4	0·7	1·4	454	O	B[c]	Fe
226b	*Centaurea scabiosa*[l]	No	Compositae	E	—[n]	—[p]	P	1,254	1·3	2·6	5·1	465	O	J	Fe
227	*Cephalotus follicularis* Labill.	No	Cephalotaceae	E	20[o]	2	P	625	0·6	1·3	2·6	378	O	J	Fe
228a	*Cerastium alpinum* L.	No	Caryophyllaceae	E	72	4	P	1,813	1·9	3·7	7·4	427	O	*Cerastium*[e]	FC:DAPI
228b	*Cerastium alpinum* L.	No	Caryophyllaceae	E	72	4	P	1,970	2·0	4·0	8·0	427	O	B[c]	Fe
229	*Cerastium arcticum* Lange s. str.	No	Caryophyllaceae	E	108	6	P	3,126	3·2	6·4	12·8	427	O	*Cerastium*[e]	FC:DAPI

230	*Cerastium arvense* L. ssp. *glandulosum* (Kit.) Soo	No	Caryophyllaceae	E	36	2[au]	P	666	0·7	1·4	2·7	427	O	*Cerastium*[e]	FC:DAPI
231	*Cerastium arvense* L. ssp. *arvense*	No	Caryophyllaceae	E	72	4	P	1,274	1·3	2·6	5·2	427	O	*Cerastium*[e]	FC:DAPI
232a	*Cerastium banaticum* (Rochel) Heuff.	No	Caryophyllaceae	E	36	2[au]	P	1,470	1·5	3·0	6·0	427	O	B[c]	Fe
232b	*Cerastium banaticum* (Rochel) Heuff.	No	Caryophyllaceae	E	36	2[au]	P	1,529	1·6	3·1	6·2	427	O	*Cerastium*[e]	FC:DAPI
233	*Cerastium carinthiacum* Vest	No	Caryophyllaceae	E	36	2[au]	P	1,480	1·5	3·0	6·0	427	O	*Cerastium*[e]	FC:DAPI
234a	*Cerastium eriophorum* Kit. in Schult.	No	Caryophyllaceae	E	36	2[au]	P	1,264	1·3	2·6	5·2	427	O	B[c]	Fe
234b	*Cerastium eriophorum* Kit. in Schult.	No	Caryophyllaceae	E	36	2[au]	P	1,274	1·3	2·6	5·2	427	O	*Nicot.*[e]	FC:DAPI
235b	*Cerastium fontanum* Baumg.	No	Caryophyllaceae	E	144	8	P	3,469	3·5	7·1	14·2	427	O	*Cerastium*[e]	FC:DAPI
236a	*Cerastium latifolium* L.	No	Caryophyllaceae	E	36	2[au]	P	1,421	1·5	2·9	5·8	427	O	B[c]	Fe
236b	*Cerastium latifolium* L.	No	Caryophyllaceae	E	36	2[au]	P	1,470	1·5	3·0	6·0	427	O	*Cerastium*[e]	FC:DAPI
237a	*Cerastium transsylvanicum* Schur ex Griseb. & Schenk	No	Caryophyllaceae	E	108	6	P	3,038	3·1	6·2	12·4	427	O	*Cerastium*[e]	FC:DAPI
237b	*Cerastium transsylvanicum* Schur ex Griseb. & Schenk	No	Caryophyllaceae	E	108	6	P	3,048	3·1	6·2	12·4	427	O	B[c]	Fe
238	*Ceratophyllum demersum* L.	No	Ceratophyllaceae	BA	c.70	6	P	674	0·7	1·4	2·8	381	O	J	Fe
239	*Chenopodium album* L.[h]	No	Amaranthaceae	E	18°	2	A	750	0·8	1·5	3·1	455	O	B[c]	Fe
240	*Chenopodium album* L.[h]	No	Amaranthaceae	E	36°	4	A	1,597	1·6	3·3	6·5	455	O	B[c]	Fe
241b	*Chenopodium album* L.[h]	No	Amaranthaceae	E	54°	6	A	2,423	2·5	4·9	9·9	455	O	B[c]	Fe
242	*Chenopodium berlandieri* (Saff.) Wilson & Heiser ssp. *nuttalliae*[h]	No	Amaranthaceae	E	36°	4	A	1,446	1·5	3·0	5·9	455	O	B[c]	Fe
243	*Chenopodium bushianum* Aellen	No	Amaranthaceae	E	36°	4	A	1,558	1·6	3·2	6·4	455	O	B[c]	Fe
244	*Chenopodium ficifolium* Sm.	No	Amaranthaceae	E	18°	2	A	649	0·7	1·3	2·7	455	O	B[c]	Fe
245	*Chenopodium giganteum* D.Don	No	Amaranthaceae	E	54°	6	A	2,151	2·2	4·4	8·8	455	O	B[c]	Fe
246	*Chenopodium murale* L.	No	Amaranthaceae	E	18°	2	A	610	0·6	1·2	2·5	455	O	B[c]	Fe
247	*Chenopodium opulifolium* Schrad. ex Koch & Ziz	No	Amaranthaceae	E	36°	4	A	1,303	1·3	2·7	5·3	455	O	B[c]	Fe
248b	*Chenopodium pallidicaule* Aellen	No	Amaranthaceae	E	18°	2	A	617	0·6	1·3	2·5	455	O	B[c]	Fe
249b	*Chenopodium quinoa* Willd.[h]	No	Amaranthaceae	E	36°	4	A	1,585	1·6	3·2	6·5	455	O	B[c]	Fe
250	*Chenopodium ugandae* (Aell.) Aell.	No	Amaranthaceae	E	32°	—[p]	A	1,401	1·4	2·9	5·7	455	O	B[c]	Fe
251	*Chenopodium vulvaria* L.	No	Amaranthaceae	E	18°	2	A	622	0·6	1·3	2·5	455	O	B[c]	Fe
252	*Chloranthus spicatus* Mak.	No	Chloranthaceae	BA	30	—[p]	P	3,526	3·6	7·2	14·4	381	O	G	FC:PI
253	*Chorisia speciosa* St. Hill	No	Malvaceae	E	86°	—[p]	P	845	0·9	1·7	3·5	454	O	B[c]	Fe
254	*Cicca acida* (L.) Merr.	No	Euphorbiaceae	E	—[n]	—[p]	P	938	1·0	1·9	3·8	454	O	B[c]	Fe
255	*Cicer songaricum* Steph. ex DC.	No	Leguminosae	E	16	2	P	1,328	1·4	2·7	5·4	435	O	B[c]	Fe
256	*Cienfuegosia tripartita* H.B.K. Gurke	—[m]	Malvaceae	E	20	2	—[q]	931	1·0	1·9	3·8	444[bd]	O	G[b2]	FC:PI
257	*Cienfuegosia yucatanensis* Millspaugh	—[m]	Malvaceae	E	22	2	—[q]	980	1·0	2·0	4·0	444[bd]	O	G[b2]	FC:PI
258	*Cistus albanicus* E.F.Warburg ex Heywood	No	Cistaceae	E	18°	2	P	2,617	2·7	5·3	10·7	404	O	*Raphanus*[e]	FC:PI
259	*Cistus albidus* L.	No	Cistaceae	E	18°	2	P	2,342	2·4	4·8	9·6	404	O	*Raphanus*[e]	FC:PI
260	*Cistus clusii* Dunal	No	Cistaceae	E	18°	2	P	2,587	2·6	5·3	10·6	404	O	*Raphanus*[e]	FC:PI
261	*Cistus creticus* L.	No	Cistaceae	E	18°	2	P	2,127	2·2	4·3	8·7	404	O	*Raphanus*[e]	FC:PI
262	*Cistus crispus* L.	No	Cistaceae	E	18°	2	P	1,921	2·0	3·9	7·8	404	O	*Raphanus*[e]	FC:PI
263	*Cistus heterophyllus* Desf. ssp. *carthaginensis* (Pau) Crespo & Mateo	No	Cistaceae	E	18°	2	P	2,362	2·4	4·8	9·6	404	O	*Raphanus*[e]	FC:PI
264	*Cistus ladanifer* L.	No	Cistaceae	E	18°	2	P	2,181	2·2	4·5	8·9	404	O	*Raphanus*[e]	FC:PI
265	*Cistus laurifolius* L.	No	Cistaceae	E	18°	2	P	2,185	2·2	4·5	8·9	404	O	*Raphanus*[e]	FC:PI
266	*Cistus libanotis* L.	No	Cistaceae	E	18°	2	P	2,827	2·9	5·8	11·5	404	O	*Raphanus*[e]	FC:PI
267	*Cistus monspeliensis* L.	No	Cistaceae	E	18°	2	P	2,881	2·9	5·9	11·8	404	O	*Raphanus*[e]	FC:PI
268	*Cistus osbeckiaefolius* Webb ex Pitard & Proust	No	Cistaceae	E	18°	2	P	2,024	2·1	4·1	8·3	404	O	*Raphanus*[e]	FC:PI
269	*Cistus parviflorus* Lam.	No	Cistaceae	E	18°	2	P	2,430	2·5	5·0	9·9	404	O	*Raphanus*[e]	FC:PI
270	*Cistus populifolius* L.	No	Cistaceae	E	18°	2	P	2,102	2·1	4·3	8·6	404	O	*Raphanus*[e]	FC:PI
271	*Cistus psilosepalus* Sweet	No	Cistaceae	E	18°	2	P	2,558	2·6	5·2	10·4	404	O	*Raphanus*[e]	FC:PI
272	*Cistus salviifolius* L.	No	Cistaceae	E	18°	2	P	2,332	2·4	4·8	9·5	404	O	*Raphanus*[e]	FC:PI

APPENDIX. *(continued, the superscript letters refer to notes preceding this table)*

Entry number[g]	Species	Voucher	Family	Higher group[#]	2n‡	Ploidy level (*x*)	Life cycle type[§]	DNA amount 1C (Mbp[s])	1C (pg)	2C (pg)	4C (pg)	Original ref.[a]	Present amount[†]	Standard species[*b1]	Method[††]
273	*Cistus symphytifolius* Lam.	No	Cistaceae	E	18°	2	P	2,406	2·5	4·9	9·8	404	O	*Raphanus*[e]	FC:PI
274b	*Citrus aurantium* L.	No	Rutaceae	E	18°	2	P	431	0·4	0·9	1·8	426	O	*Gallus*[f]	FC:PI
275b	*Citrus grandis* (L.) Osbeck	No	Rutaceae	E	18°	2	P	377	0·4	0·8	1·5	426	O	*Gallus*[f]	FC:PI
276b	*Citrus limon* (L.) Burm. f.[i]	No	Rutaceae	E	18°	2	P	392	0·4	0·8	1·6	426	O	*Gallus*[f]	FC:PI
277	*Citrus limonia* Osbeck cv. Brome Rangpur	No	Rutaceae	E	18°	2	P	402	0·4	0·8	1·6	426	O	*Gallus*[f]	FC:PI
278b	*Citrus paradisi* Macfad.	No	Rutaceae	E	18°	2	P	392	0·4	0·8	1·6	426	O	*Gallus*[f]	FC:PI
279	*Citrus reshni* Hort. ex Tanaka	No	Rutaceae	E	18°	2	P	402	0·4	0·8	1·6	426	O	*Gallus*[f]	FC:PI
280e	*Citrus sinensis* (L.) Osbeck cv. Sargoins Grosse Ronde[h]	No	Rutaceae	E	18°	2	P	372	0·4	0·8	1·5	426	O	*Gallus*[f]	FC:PI
280f	*Citrus sinensis* (L.) Osbeck cv. Pineapple[h]	No	Rutaceae	E	18°	2	P	417	0·4	0·9	1·7	426	O	*Gallus*[f]	FC:PI
280g	*Citrus sinensis* (L.) Osbeck	No	Rutaceae	E	18°	2	P	588	0·6	1·2	2·4	457[bm]	O	B[d]	Fe
281	*Citrus volkameriana* Ten. & Pasq.	No	Rutaceae	E	18°	2	P	387	0·4	0·8	1·6	426	O	*Gallus*[f]	FC:PI
282	*Coccoloba diversifolia* Jacq.	No	Polygonaceae	E	—[n]	—[p]	P	1,127	1·2	2·3	4·6	454	O	B[c]	Fe
283h	*Coffea arabica* L.	—[m]	Rubiaceae	E	44	4	P	1,279	1·3	2·6	5·2	424	O	K[c]	FC:PI
283i	*Coffea arabica* L.	No	Rubiaceae	E	44°	4	P	1,122	1·1	2·3	4·6	454	O	B[c]	Fe
284c	*Coffea brevipes* Hiern.	—[m]	Rubiaceae	E	22	2	P	760	0·8	1·6	3·1	424	O	K[c]	FC:PI
285d	*Coffea canephora* Pierre. ex Froehn.	—[m]	Rubiaceae	E	22	2	P	755	0·8	1·5	3·1	424	O	K[c]	FC:PI
286c	*Coffea congensis* Froehn.	—[m]	Rubiaceae	E	22	2	P	794	0·8	1·6	3·2	424	O	K[c]	FC:PI
287d	*Coffea eugenioides* S.Moore	—[m]	Rubiaceae	E	22	2	P	681	0·7	1·4	2·8	424	O	K[c]	FC:PI
288c	*Coffea humilis* A.Cheval.	—[m]	Rubiaceae	E	22	2	P	872	0·9	1·8	3·6	424	O	K[c]	FC:PI
289d	*Coffea liberica* L. ssp. *dewevrei* Wild & Dur. Hiern	No	Rubiaceae	E	22	2	P	703	0·7	1·4	2·9	401	O	*Petunia*[e]	FC:PI
289e	*Coffea liberica* L.	—[m]	Rubiaceae	E	22	2	P	823	0·8	1·7	3·4	424	O	K[c]	FC:PI
290d	*Coffea pseudozanguebariae* D.M.Bridson	—[m]	Rubiaceae	E	22	2	P	534	0·5	1·1	2·2	424	O	K[c]	FC:PI
291c	*Coffea racemosa*[l]	—[m]	Rubiaceae	E	22	2	P	466	0·5	1·0	1·9	424	O	K[c]	FC:PI
292c	*Coffea sessiliflora* D.M.Bridson	—[m]	Rubiaceae	E	22	2	P	510	0·5	1·0	2·1	424	O	K[c]	FC:PI
293	*Coffea* sp. F. Bridson[y]	—[m]	Rubiaceae	E	22	2	P	652	0·7	1·3	2·7	424	O	K[c]	FC:PI
294	*Coffea* sp. Moloundou[y]	—[m]	Rubiaceae	E	22	2	P	828	0·8	1·7	3·4	424	O	K[c]	FC:PI
295c	*Coffea stenophylla* G.Don.	—[m]	Rubiaceae	E	22	2	P	662	0·7	1·4	2·7	424	O	K[c]	FC:PI
296b	*Colocasia antiquorum* Schott var. 1[i]	No	Araceae	M	32	—[p]	AP	4,951	5·1	10·1	20·2	411	O	B[c]	Fe
297	*Commiphora mossambicensis* Engl.	No	Burseraceae	E	26	2	P	613	0·6	1·3	2·5	379	O	J	Fe
298	*Coriaria myrtifolia* L.	No	Coriariaceae	E	c. 72	8	P	326	0·3	0·7	1·3	378	O	J	Fe
299	*Cosmos atrosanguineus*[l]	No	Compositae	E	48	—[p]	P	7,191	7·3	14·7	29·4	465	O	F	Fe
300c	*Crepis biennis* L.[h]	No	Compositae	E	c. 40	10	B	7,448	7·6	15·2	30·4	394[ah]	O	G[c]	CIA
300d	*Crepis biennis* L.[h]	No	Compositae	E	c. 40	10	B	7,928	8·1	16·2	32·4	394[ah]	O	G[c]	CIA
300e	*Crepis biennis* L.[h]	No	Compositae	E	c. 40	10	B	8,173	8·3	16·7	33·4	394[ah]	O	G[c]	Fe
300f	*Crepis biennis* L.[h]	No	Compositae	E	c. 40	10	B	8,555	8·7	17·5	34·9	394[ah]	O	G[c]	Fe
301a	*Crepis bithynica* var. *pirinica* Acht.[i]	No	Compositae	E	10	2	P	3,156	3·2	6·4	12·9	394	O	G[c]	Fe
301b	*Crepis bithynica* var. *bithynica* Boiss.[i]	No	Compositae	E	10	2	P	3,244	3·3	6·6	13·2	394	O	G[c]	Fe
302h	*Crepis capillaris* (L.) Wallr.	No	Compositae[j]	E	6°	2	A	2,597	2·7	5·3	10·6	457[bm]	O	B[d]	Fe
303a	*Crepis conyzaefolia* (Gouan) A.Kerner[i]	No	Compositae	E	8	2	P	5,400	5·5	11·0	22·0	394	O	G[c]	Fe
303b	*Crepis conyzaefolia* (Gouan) A.Kerner[i]	No	Compositae	E	8	2	P	5,576	5·7	11·4	22·8	394	O	E[c]	FC:PI
304a	*Crepis paludosa* (L.) Moench[i]	No	Compositae	E	12	2	P	4,077	4·2	8·3	16·6	394	O	G[c]	Fe
304b	*Crepis paludosa* (L.) Moench[i]	No	Compositae	E	12	2	P	4,361	4·5	8·9	17·8	394	O	E[c]	FC:PI
305b	*Crepis pulchra* L.[h]	No	Compositae	E	8	2	A	4,459	4·6	9·1	18·2	394	O	G[c]	CIA
305c	*Crepis pulchra* L.[h]	No	Compositae	E	8	2	A	5,449	5·6	11·1	22·2	394[ai]	O	G[c]	CIA

305d	*Crepis pulchra* L.[h]	No	Compositae	E	8	2	A	4,851	5·0	9·9	19·8	394	O	G[c]	Fe
305e	*Crepis pulchra* L.[h]	No	Compositae	E	8	2	A	5,400	5·5	11·0	22·0	394[ai]	O	G[c]	Fe
305f	*Crepis pulchra* L.[h]	No	Compositae	E	8	2	A	5,380	5·5	11·0	22·0	394	O	E[c]	FC:PI
305g	*Crepis pulchra* L.[h]	No	Compositae	E	8	2	A	5,988	6·1	12·2	24·4	394	O	E[c]	FC:PI
306a	*Crepis sancta* (L.) Babc.[h]	No	Compositae	E	10	2	A	2,048	2·1	4·2	8·4	394[ah]	O	G[c]	Fe
306b	*Crepis sancta* (L.) Babc.[h]	No	Compositae	E	10	2	A	2,176	2·2	4·4	8·9	394[ah]	O	G[c]	CIA
307	*Crepis schachtii* Babc.[i]	No	Compositae	E	10	2	P	2,764	2·8	5·6	11·3	394	O	G[c]	Fe
308b	*Crepis setosa* Haller f.[i]	No	Compositae	E	8	2	A	1,695	1·7	3·5	6·9	394	O	G[c]	CIA
309a	*Crepis viscidula* Froel.[i]	No	Compositae	E	12	2	P	4,283	4·4	8·7	17·5	394	O	G[c]	CIA
309b	*Crepis viscidula* Froel.[i]	No	Compositae	E	12	2	P	4,782	4·9	9·8	19·5	394	O	E[c]	FC:PI
310b	*Crepis zacintha* (L.) Babc.[i]	No	Compositae	E	6	2	A	1,058	1·1	2·2	4·3	394	O	G[c]	CIA
311	*Crocus biflorus* Mill.	No	Iridaceae	M	8[ao]	2	P	4,253	4·3	8·7	17·4	419	O	*Homo*[f]	FC:PI
312	*Crocus cartwrightianus* Herb.[i]	No	Iridaceae	M	16	2	P	3,886	4·0	7·9	15·9	419	O	*Homo*[f]	FC:PI
313	*Crocus etruscus* Parl.	No	Iridaceae	M	8	2	P	3,553	3·6	7·3	14·5	419	O	*Homo*[f]	FC:PI
314	*Crocus sativus* L.[i]	No	Iridaceae	M	24	3	P	—[t]	—[t]	11·8	23·6	419	O	*Homo*[f]	FC:PI
315	*Crocus thomasii* Ten.	No	Iridaceae	M	16	2	P	4,258	4·3	8·7	17·4	419	O	*Homo*[f]	FC:PI
316	*Cyclamen hederifolium*[l]	No	Primulaceae	E	—[n]	—[p]	P	2,923	3·0	6·0	11·9	465	O	G	FC:PI
317a	*Cyclamen trochopteranthum* O.Schwarz[h]	No	Primulaceae	E	30	—[p]	P	10,373	10·6	21·2	42·3	465	O	G	Fe
317b	*Cyclamen trochopteranthum* O.Schwarz[h]	No	Primulaceae	E	30	—[p]	P	13,458	13·7	27·5	54·9	465	O	G	Fe
318b	*Cynodon dactylon* (L.) Pers.	No	Gramineae	M	36	4	P	956	1·0	2·0	3·9	417	O	*Gallus*[f]	FC:PI
318c	*Cynodon dactylon* (L.) Pers. var. *dactylon*	No	Gramineae	M	36	4	P	1,103	1·1	2·3	4·5	438[ba]	O	*Sus*[f]	FC:PI
319	*Cynodon dactylon* (L.) Pers. var. *dactylon*	No	Gramineae	M	54	6	P	1,436	1·5	2·9	5·9	438[ba]	O	*Ictal.*[f]	FC:PI
320a	*Cynodon transvaalensis* Burtt-Davy	No	Gramineae	M	18	2	P	505	0·5	1·0	2·1	417	O	*Gallus*[f]	FC:PI
320b	*Cynodon transvaalensis* Burtt-Davy	No	Gramineae	M	18	2	P	544	0·6	1·1	2·2	438[ba]	O	*Ictal.*[f]	FC:PI
321	*Dalbergia horrida* Dennst.	No	Leguminosae	E	20	2	P	1,928	2·0	3·9	7·9	445	O	G	Fe
322a	*Dalbergia lanceolaria* Lin. f.	No	Leguminosae	E	20	2	P	1,431	1·5	2·9	5·8	445	O	G	Fe
323a	*Dalbergia latifolia* Roxb.	No	Leguminosae	E	20	2	P	1,681	1·7	3·4	6·9	445	O	G	Fe
324	*Dalbergia malabarica* Prain.	No	Leguminosae	E	20	2	P	1,847	1·9	3·8	7·5	445	O	G	Fe
325	*Dalbergia melanoxylon* Guill & Perr.	No	Leguminosae	E	20	2	P	1,806	1·8	3·7	7·4	445	O	G	Fe
326	*Dalbergia paniculata* Roxb.	No	Leguminosae	E	20	2	P	1,551	1·6	3·2	6·3	445	O	G	Fe
327	*Dalbergia rubiginosa* Roxb.	No	Leguminosae	E	20	2	P	1,803	1·8	3·7	7·4	445	O	G	Fe
328	*Dalbergia sissoides* Grah.	No	Leguminosae	E	20	2	P	1,764	1·8	3·6	7·2	445	O	G	Fe
329a	*Dalbergia sissoo* Roxb. ex DC.	No	Leguminosae	E	20	2	P	1,585	1·6	3·2	6·5	445	O	G	Fe
329b	*Dalbergia sissoo* Roxb. ex DC.	No	Leguminosae	E	20°	2	P	691	0·7	1·4	2·8	454	O	B[c]	Fe
330	*Dalbergia volubilis* Roxb.	No	Leguminosae	E	20	2	P	1,901	1·9	3·9	7·8	445	O	G	Fe
331	*Damasonium alisma* Mill.	No	Alismataceae	M	—[n]	—[p]	A	23,143	23·6	47·2	94·5	465	O	B	FC:PI
332	*Dasypogon hookeri* Drumm.	No	Dasypogonaceae	M	14	2	P	426	0·4	0·9	1·7	380	O	J	FC:PI
333	*Dasypyrum hordeaceum* (Cosson & Durieu) Candargy	No	Gramineae	M	28	4	P	10,288	10·5	21·0	42·0	431	C	—[aw]	Fe
334d	*Dasypyrum villosum (=Haynaldia villosa)* (L.) P. Candargy[h]	No	Gramineae	M	14	2	A	10,408	10·6	21·2	42·5	430	O	C[c]	Fe
334e	*Dasypyrum villosum (=Haynaldia villosa)* (L.) P. Candargy[h]	No	Gramineae	M	14	2	A	6,262	6·4	12·8	25·6	430	O	C[c]	Fe
335b	*Decaisnea fargesii* Franch.	No	Lardizabalaceae[k]	E	40°	2	P	2,450	2·5	5·0	10·0	457[bm]	O	B[d]	Fe
336	*Deutzia prunifolia* Rehder	No	Hydrangeaceae	E	52	4	P	1,835	1·9	3·7	7·5	378	O	J	Fe
337	*Dictamnus albus* L.	No	Rutaceae	E	36°	—[p]	P	3,381	3·5	6·9	13·8	457[bm]	O	B[d]	Fe
338	*Dieffenbachia picta* Schott	No	Araceae	M	36	—[p]	P	12,083	12·3	24·7	49·3	411	O	B[c]	Fe
339	*Diospyros discolor* Willd.	No	Ebenaceae	E	30°	—[p]	P	1,174	1·2	2·4	4·8	454	O	B[c]	Fe
340	*Diospyros malabarica* Kost.	No	Ebenaceae	E	30°	—[p]	P	1,436	1·5	2·9	5·9	454	O	B[c]	Fe
341	*Dissotis canescens* Hook. f.	No	Melastomataceae	E	c. 28-32	—[p]	P	181	0·2	0·4	0·7	378	O	J	Fe
342a	*Doritis pulcherrima* Lindl.	No	Orchidaceae	M	38	2	P	6,610	6·7	13·5	27·0	447	O	G[b2]	FC:PI
343	*Doryanthes palmeri* W. Hill ex Benth.	No	Doryanthaceae	M	48	—[p]	P	3,239	3·3	6·6	13·2	380	O	G	FC:PI
344	*Drimys vickeriana* A.C. Smith	No	Winteraceae	BA	—[n]	—[p]	P	1,105	1·1	2·3	4·5	381	O	K	FC:PI
345	*Drypetes roxburghii* Wall.	No	Putranjavaceae[k]	E	42°	—[p]	P	1,002	1·0	2·0	4·1	449[bf]	O	B[c]	Fe

APPENDIX. *(continued, the superscript letters refer to notes preceding this table)*

Entry number[g]	Species	Voucher	Family	Higher group[#]	2n‡	Ploidy level (*x*)	Life cycle type[§]	DNA amount 1C (Mbp[s])	1C (pg)	2C (pg)	4C (pg)	Original ref.[a]	Present amount[†]	Standard species[*b1]	Method[††]
346	*Ehretia laevis* (Rottler ex G.Don) Roxb.	No	Boraginaceae	E	—[n]	—[p]	P	3,533	3·6	7·2	14·4	454	O	B[c]	Fe
347	*Eremochloa ophiuroides* (Munro) Hack.	No	Gramineae	M	18	2	P	813	0·8	1·7	3·3	417	O	*Gallus*[f]	FC:PI
348	*Eriocaulon aquaticum*[l]	No	Eriocaulaceae	M	32	4	P	4,101	4·2	8·4	16·7	380	O	G	FC:PI
349	*Escallonia rubra*[l]	No	Escalloniaceae	E	24	2	P	414	0·4	0·8	1·7	380	O	J	Fe
350	*Eucnide grandiflora* Rose	No	Loasaceae	E	c. 38-40	2 or 6	P	588	0·6	1·2	2·4	378	O	J	Fe
351	*Eucommia ulmoides* Oliver	No	Eucommiaceae	E	34	2	P	725	0·7	1·5	3·0	379	O	G	Fe
352a	*Fagus sylvatica* L. var. *tortuosa* Pepin Willk.	No	Fagaceae	E	24°	2	P	544	0·6	1·1	2·2	433	O	*Petunia*[e]	FC:PI
352b	*Fagus sylvatica* L.	No	Fagaceae	E	24°	2	P	544	0·6	1·1	2·2	433	O	*Petunia*[e]	FC:PI
352c	*Fagus sylvatica* L. var. *purpurea* Ait.	No	Fagaceae	E	24°	2	P	549	0·6	1·1	2·2	433	O	*Petunia*[e]	FC:PI
352d	*Fagus sylvatica* L. var. *pendula* Lodd.	No	Fagaceae	E	24°	2	P	554	0·6	1·1	2·3	433	O	*Petunia*[e]	FC:PI
353d	*Festuca arundinacea* Schreb.	No	Gramineae	M	42	6	P	7,639	7·8	15·6	31·2	417	O	*Nicot.*[e]	FC:PI
354	*Festuca longifolia* Thuill.	No	Gramineae	M	42	6	P	6,223	6·4	12·7	25·4	417	O	F[c]	FC:PI
355	*Firmiana colorata* (Roxb.) R.Br.	No	Malvaceae	E	40°	—[p]	P	1,615	1·6	3·3	6·6	454	O	B[c]	Fe
356	*Flagellaria guineensis* Schum.	No	Flagellariaceae	M	38°	2	P	880	0·9	1·8	3·6	380	O	K	FC:PI
357	*Flemingia bracteata* Wight	No	Leguminosae	E	22	2	P	1,570	1·6	3·2	6·4	443[bc]	O	B[c]	Fe
358	*Fortunella hindsii* Swing.	No	Rutaceae	E	36°	4	P	622	0·6	1·3	2·5	426	O	*Gallus*[f]	FC:PI
359	*Fouquieria splendens* Engelm.	No	Fouquieriaceae	E	24	4	P	519	0·5	1·1	2·1	378	O	J	Fe
360	*Fragaria* x *ananassa* cv. Redcoat Duch.	—[m]	Rosaceae	E	56	8	P	598	0·6	1·2	2·4	442	O	*Gallus*[f]	FC:M
361a	*Gagea lutea* (L.) Ker Gawl.	No	Liliaceae	M	72	6	P	19,355	19·8	39·5	79·0	413	O	B[c]	Fe
361b	*Gagea lutea* (L.) Ker Gawl.	No	Liliaceae	M	72	6	P	19,825	20·2	40·5	80·9	413	O	B[c]	FC:EB
362	*Gardenia resiniflua* Hiern	No	Rubiaceae	E	—[n]	—[p]	P	1,269	1·3	2·6	5·2	454	O	B[c]	Fe
363	*Garrya fremontii* Torr.	No	Garryaceae	E	c. 20	2	P	1,490	1·5	3·0	6·1	380	O	*Lycopers.*[c]	FC:PI
364j	*Glycine max* (L.) Merr. strain T215[h]	No	Leguminosae	E	40°	2	A	1,161	1·2	2·4	4·7	423[as]	O	F[c]	FC:PI
364k	*Glycine max* (L.) Merr. strain PI423·894[h]	No	Leguminosae	E	40°	2	A	1,215	1·2	2·5	5·0	423[as]	O	F[c]	FC:PI
364l	*Glycine max* (L.) Merr.[h]	—[m]	Leguminosae	E	40°	2	A	1,250	1·3	2·6	5·1	432[ax]	C	*Glycine*[e]	FC:PI
364m	*Glycine max* (L.) Merr.[h]	—[m]	Leguminosae	E	40°	2	A	1,401	1·4	2·9	5·7	432[ax]	C	*Glycine*[e]	FC:PI
365	*Goodenia mimuloides* S.Moore	No	Goodeniaceae	E	16	2	A	507	0·5	1·0	2·1	379	O	G	Fe
366	*Gossypioides herbaceum* L.	—[m]	Malvaceae	E	26°	2	—[q]	1,813	1·9	3·7	7·4	444[bd]	O	G[b2]	FC:PI
367	*Gossypioides raimondii* Ulbrich	—[m]	Malvaceae	E	26°	2	—[q]	980	1·0	2·0	4·0	444[bd]	O	G[b2]	FC:PI
368	*Gunnera manicata* Linden	No	Gunneraceae	E	34	2	P	7,286	7·4	14·9	29·7	379	O	F	Fe
369	*Gymnostoma deplancheana* (Miq.) L.Johnson	No	Moraceae[k]	E	16°	2	P	368	0·4	0·8	1·5	452	O	*Petunia*[e]	FC:PI
370	*Haldina cordifolia* (Roxb.) Ridsdale	No	Rubiaceae	E	44°	4	P	1,296	1·3	2·6	5·3	454	O	B[c]	Fe
371	*Hampea appendiculata* (J. Donnell-Smith) Standley	—[m]	Malvaceae	E	26°	2	—[q]	2,891	3·0	5·9	11·8	444[bd]	O	G[b2]	FC:PI
372	*Hanguana malayana* Merrill	No	Hanguanaceae	M	c. 170	—[p]	P	1,612	1·6	3·3	6·6	380	O	F	Fe
373a	*Hedera canariensis* Willd.	No	Araliaceae	E	48°	2	P	1,372	1·4	2·8	5·6	429	O	*Glycine*[e]	FC:PI
373b	*Hedera canariensis* Willd.	No	Araliaceae	E	48°	2	P	1,509	1·5	3·1	6·2	429	O	G[c]	CIA
374a	*Hedera colchica* C.Koch.	No	Araliaceae	E	192	8	P	5,341	5·5	10·9	21·8	429	O	*Glycine*[e]	FC:PI
374b	*Hedera colchica* C.Koch.	No	Araliaceae	E	192	8	P	5,586	5·7	11·4	22·8	429	O	G[c]	CIA
375e	*Hedera helix* L.	No	Araliaceae	E	48	2	P	1,460	1·5	3·0	6·0	429[av]	O	G[c]	CIA
375f	*Hedera helix* L.	No	Araliaceae	E	48	2	P	1,372	1·4	2·8	5·6	429[av]	O	*Glycine*[e]	FC:PI
375g	*Hedera helix* L. f. *arborescens* C.K. Schneider	No	Araliaceae	E	48	2	P	1,509	1·5	3·1	6·2	429	O	G[c]	CIA
375h	*Hedera helix* L. f. *arborescens* C.K. Schneider	No	Araliaceae	E	48	2	P	1,382	1·4	2·8	5·6	429	O	*Glycine*[e]	FC:PI
376r	*Helianthus annuus* L.	No	Compositae	E	34	2	A	3,577	3·7	7·3	14·6	403	O	G	FC:PI
377	*Heliconia rostrata* Ruiz & Pav.	No	Heliconiaceae	M	24	2	P	441	0·5	0·9	1·8	379	O	J	Fe

378	*Helleborus argutifolius* Viv.	No	Ranunculaceae	E	32	2	P	9,261	9·5	18·9	37·8	383[z]	O	*Agave*[e]	FC:PI
379a	*Helleborus atrorubens* Waldst. & Kit. 'Cupreus'[i]	No	Ranunculaceae	E	32	2	P	14,504	14·8	29·6	59·2	383[z]	O	*Agave*[e]	FC:PI
379b	*Helleborus atrorubens* Waldst. & Kit.[i]	No	Ranunculaceae	E	32	2	P	15,092	15·4	30·8	61·6	383[z]	O	*Agave*[e]	FC:PI
380	*Helleborus cyclophyllus* (A.Br.) Boiss.	No	Ranunculaceae	E	32	2	P	14,651	15·0	29·9	59·8	383[z]	O	*Agave*[e]	FC:PI
381	*Helleborus dumetorum* Waldst. & Kit.	No	Ranunculaceae	E	32	2	P	15,876	16·2	32·4	64·8	383[z]	O	*Agave*[e]	FC:PI
382a	*Helleborus foetidus* L. 'Wester Flisk'	No	Ranunculaceae	E	32	2	P	11,417	11·7	23·3	46·6	383[z]	O	*Agave*[e]	FC:PI
382b	*Helleborus foetidus* L.[i]	No	Ranunculaceae	E	32	2	P	11,466	11·7	23·4	46·8	383[z]	O	*Agave*[e]	FC:PI
383	*Helleborus lividus* Aiton	No	Ranunculaceae	E	32	2	P	9,310	9·5	19·0	38·0	383[z]	O	*Agave*[e]	FC:PI
384a	*Helleborus multifidus* Vis. ssp. *hercegovinus* (Martinis) B.Mathew	No	Ranunculaceae	E	32	2	P	14,504	14·8	29·6	59·2	383[z]	O	*Agave*[e]	FC:PI
384b	*Helleborus multifidus* Vis. ssp. *istriacus* (Schiffner) Merxm & Podl.	No	Ranunculaceae	E	32	2	P	14,749	15·1	30·1	60·2	383[z]	O	*Agave*[e]	FC:PI
384c	*Helleborus multifidus* Vis. ssp. *multifidus*	No	Ranunculaceae	E	32	2	P	14,798	15·1	30·2	60·4	383[z]	O	*Agave*[e]	FC:PI
384d	*Helleborus multifidus* Vis. ssp. *bocconei siculus*	No	Ranunculaceae	E	32	2	P	15,043	15·4	30·7	61·4	383[z]	O	*Agave*[e]	FC:PI
384e	*Helleborus multifidus* Vis.ssp. *bocconei* (Tenore) B.Mathew	No	Ranunculaceae	E	32	2	P	15,092	15·4	30·8	61·6	383[z]	O	*Agave*[e]	FC:PI
385a	*Helleborus niger* L. (double flower)[i]	No	Ranunculaceae	E	32	2	P	13,720	14·0	28·0	56·0	383[z]	O	*Agave*[e]	FC:PI
385b	*Helleborus niger* L.[i]	No	Ranunculaceae	E	32	2	P	13,867	14·2	28·3	56·6	383[z]	O	*Agave*[e]	FC:PI
385c	*Helleborus niger* L. ssp. *macranthus* (Freyn) Schiffner[i]	No	Ranunculaceae	E	32	2	P	14,406	14·7	29·4	58·8	383[z]	O	*Agave*[e]	FC:PI
386	*Helleborus odorus* Waldst. & Kit.[i]	No	Ranunculaceae	E	32	2	P	15,043	15·4	30·7	61·4	383[z]	O	*Agave*[e]	FC:PI
387a	*Helleborus orientalis* Lamarck ssp. *orientalis*[i]	No	Ranunculaceae	E	32	2	P	14,553	14·9	29·7	59·4	383[z]	O	*Agave*[e]	FC:PI
387b	*Helleborus orientalis* Lamarck[i]	No	Ranunculaceae	E	32	2	P	14,725	15·0	30·1	60·1	383[z]	O	*Agave*[e]	FC:PI
387c	*Helleborus orientalis* Lamarck ssp. *guttatus* (A.Br. & Sauer) B.Mathew[i]	No	Ranunculaceae	E	32	2	P	14,749	15·1	30·1	60·2	383[z]	O	*Agave*[e]	FC:PI
387d	*Helleborus orientalis* Lamarck ssp. *abchasicus* (A.Br.) B.Mathew[i]	No	Ranunculaceae	E	32	2	P	14,798	15·1	30·2	60·4	383[z]	O	*Agave*[e]	FC:PI
387e	*Helleborus orientalis* Lamarck 'Kochii'[i]	No	Ranunculaceae	E	32	2	P	14,994	15·3	30·6	61·2	383[z]	O	*Agave*[e]	FC:PI
388	*Helleborus purpurascens* Waldst. & Kit.	No	Ranunculaceae	E	32	2	P	14,945	15·3	30·5	61·0	383[z]	O	*Agave*[e]	FC:PI
389	*Helleborus thibetanus* Franchet	No	Ranunculaceae	E	32	2	P	17,493	17·9	35·7	71·4	383[z]	O	*Agave*[e]	FC:PI
390a	*Helleborus torquatus*Archer Hind 'Dido' (double flowers)[i]	No	Ranunculaceae	E	32	2	P	14,602	14·9	29·8	59·6	383[z]	O	*Agave*[e]	FC:PI
390b	*Helleborus torquatus* Archer Hind[i]	No	Ranunculaceae	E	32	2	P	14,749	15·1	30·1	60·2	383[z]	O	*Agave*[e]	FC:PI
390c	*Helleborus torquatus* Archer Hind 'Croaticus'[i]	No	Ranunculaceae	E	32	2	P	14,700	15·0	30·0	60·0	383[z]	O	*Agave*[e]	FC:PI
391	*Helleborus vesicarius* Aucher	No	Ranunculaceae	E	32	2	P	13,867	14·2	28·3	56·6	383[z]	O	*Agave*[e]	FC:PI
392a	*Helleborus viridis* L. ssp. *viridis*	No	Ranunculaceae	E	32	2	P	14,896	15·2	30·4	60·8	383[z]	O	*Agave*[e]	FC:PI
392b	*Helleborus viridis* L. ssp. *occidentalis* (Reut.) Schiffner	No	Ranunculaceae	E	32	2	P	15,092	15·4	30·8	61·6	383[z]	O	*Agave*[e]	FC:PI
393	*Hernandia nymphaeifolia* (C.Presl.) Kubitzki	No	Hernandiaceae	BA	—[n]	—[p]	P	2,340	2·4	4·8	9·6	454	O	B[c]	Fe
394	*Herniaria glabra* Linn.	No	Caryophyllaceae	E	18	2	AP	515	0·5	1·1	2·1	465	O	J	Fe
395b	*Hieracium aurantiacum* L.	No	Compositae[j]	E	36°	4	P	3,626	3·7	7·4	14·8	457[bm]	O	B[d]	Fe
396	*Holoptelea integrifolia* Planch.	No	Ulmaceae	E	28°	—[p]	P	666	0·7	1·4	2·7	454	O	B[c]	Fe
397	*Homalomena rubescens* Kunth	No	Araceae	M	34	—[p]	AP	8,955	9·1	18·3	36·6	411	O	B[c]	Fe
398p	*Hordeum vulgare* L. cv. New Golden	No	Gramineae	M	14°	2	A	5,096	5·2	10·4	20·8	387[ae]	O	*Gallus*[f]	FC:PI
399	*Hosta capitata* (Koidzumi) Nakai	No	Asparagaceae[k]	M	60	2	P	9,457	9·7	19·3	38·6	384[aa]	O	*Agave* sp.[ab]	FC:PI
400	*Hosta clausa* var. *normalis* F.Maekawa	No	Asparagaceae[k]	M	60	2	P	9,408	9·6	19·2	38·4	384[aa]	O	*Agave* sp.[ab]	FC:PI
401	*Hosta clausa* Nakai var. *clausa*	No	Asparagaceae[k]	M	90	3	P	—[t]	—[t]	28·5	57·0	384[aa]	O	*Agave* sp.[ab]	FC:PI
402	*Hosta gracillima* F.Maekawa	No	Asparagaceae[k]	M	60	2	P	10,829	11·1	22·1	44·2	384[aa]	O	*Agave* sp.[ab]	FC:PI
403	*Hosta hypoleuca* Murata	No	Asparagaceae[k]	M	60	2	P	12,495	12·8	25·5	51·0	384[aa]	O	*Agave* sp.[ab]	FC:PI
404	*Hosta jonesii* M.Chung	No	Asparagaceae[k]	M	60	2	P	8,575	8·8	17·5	35·0	384[aa]	O	*Agave* sp.[ab]	FC:PI
405	*Hosta kikutii* F.Maekawa	No	Asparagaceae[k]	M	60	2	P	11,172	11·4	22·8	45·6	384[aa]	O	*Agave* sp.[ab]	FC:PI
406	*Hosta kiyosumiensis* F.Maekawa	No	Asparagaceae[k]	M	60	2	P	11,907	12·2	24·3	48·6	384[aa]	O	*Agave* sp.[ab]	FC:PI

APPENDIX. *(continued, the superscript letters refer to notes preceding this table)*

Entry number[g]	Species	Voucher	Family	Higher group[#]	2n‡	Ploidy level (*x*)	Life cycle type[§]	DNA amount 1C (Mbp[s])	1C (pg)	2C (pg)	4C (pg)	Original ref.[a]	Present amount[†]	Standard species[*b1]	Method[††]
407	*Hosta longipes* var. *longipes* Matsumura	No	Asparagaceae[k]	M	60	2	P	12,740	13·0	26·0	52·0	384[aa]	O	*Agave* sp.[ab]	FC:PI
408	*Hosta longissima* Honda	No	Asparagaceae[k]	M	60	2	P	9,604	9·8	19·6	39·2	384[aa]	O	*Agave* sp.[ab]	FC:PI
409	*Hosta minor* Nakai 'Gosan'	No	Asparagaceae[k]	M	60	2	P	8,428	8·6	17·2	34·4	384[aa]	O	*Agave* sp.[ab]	FC:PI
410	*Hosta plantaginea* (Lamarck) Ascherson	No	Asparagaceae[k]	M	60	2	P	12,103	12·4	24·7	49·4	384[aa]	O	*Agave* sp.[ab]	FC:PI
411	*Hosta pulchella* N.Fujita	No	Asparagaceae[k]	M	60	2	P	10,633	10·9	21·7	43·4	384[aa]	O	*Agave* sp.[ab]	FC:PI
412	*Hosta pycnophylla* F.Maekawa	No	Asparagaceae[k]	M	60	2	P	10,878	11·1	22·2	44·4	384[aa]	O	*Agave* sp.[ab]	FC:PI
413b	*Hosta rectifolia* Nakai	No	Asparagaceae[k]	M	60	2	P	10,437	10·7	21·3	42·6	384[aa]	O	*Agave* sp.[ab]	FC:PI
414	*Hosta rupifraga* Nakai	No	Asparagaceae[k]	M	60	2	P	12,985	13·3	26·5	53·0	384[aa]	O	*Agave* sp.[ab]	FC:PI
415	*Hosta shikokiana* N.Fujita	No	Asparagaceae[k]	M	60	2	P	11,221	11·5	22·9	45·8	384[aa]	O	*Agave* sp.[ab]	FC:PI
416	*Hosta sieboldiana* var. *sieboldiana* (Hooker) Engler	No	Asparagaceae[k]	M	60	2	P	11,564	11·8	23·6	47·2	384[aa]	O	*Agave* sp.[ab]	FC:PI
417	*Hosta sieboldii* P.O.(Paxton) Ingram	No	Asparagaceae[k]	M	60	2	P	11,025	11·3	22·5	45·0	384[aa]	O	*Agave* sp.[ab]	FC:PI
418	*Hosta tibae* F.Maekawa	No	Asparagaceae[k]	M	60	2	P	8,624	8·8	17·6	35·2	384[aa]	O	*Agave* sp.[ab]	FC:PI
419	*Hosta tsushimensis* N.Fujita	No	Asparagaceae[k]	M	60	2	P	8,477	8·7	17·3	34·6	384[aa]	O	*Agave* sp.[ab]	FC:PI
420	*Hosta ventricosa* Stearn	No	Asparagaceae[k]	M	120	4	P	19,208	19·6	39·2	78·4	384[aa]	O	*Agave* sp.[ab]	FC:PI
421	*Hosta venusta* F.Maekawa	No	Asparagaceae[k]	M	60	2	P	8,477	8·7	17·3	34·6	384[aa]	O	*Agave* sp.[ab]	FC:PI
422	*Hosta yingeri* S.B.Jones	No	Asparagaceae[k]	M	60	2	P	9,359	9·6	19·1	38·2	384[aa]	O	*Agave* sp.[ab]	FC:PI
423a	*Hydrangea anomala* D.Don ssp. *petiolaris* Sieb. & Zucc.	No	Hydrangeaceae	E	36	2	P	1,328	1·4	2·7	5·4	397	O	G[c]	FC:EB
423b	*Hydrangea anomala* D.Don ssp. *anomala* McClint.	No	Hydrangeaceae	E	36	2	P	1,534	1·6	3·1	6·3	397	O	G[c]	FC:EB
424	*Hydrangea arborescens* L.	No	Hydrangeaceae	E	36	2	P	1,132	1·2	2·3	4·6	397	O	G[c]	FC:EB
425a	*Hydrangea aspera* Don. ssp. *robusta* McClint. *(=H. longipes Franch.)*	No	Hydrangeaceae	E	34	2	P	1,480	1·5	3·0	6·0	397	O	G[c]	FC:EB
425b	*Hydrangea aspera* Don. ssp. *sargentiana* (Rehder) McClint.	No	Hydrangeaceae	E	34	2	P	1,529	1·6	3·1	6·2	397	O	G[c]	FC:EB
425c	*Hydrangea aspera* Don. ssp. *strigosa* McClint.	No	Hydrangeaceae	E	34	2	P	1,700	1·7	3·5	6·9	397	O	G[c]	FC:EB
425d	*Hydrangea aspera* Don. ssp. *aspera* McClint.	No	Hydrangeaceae	E	36	2	P	2,323	2·4	4·7	9·5	397	O	G[c]	FC:EB
426	*Hydrangea heteromalla* D.Don	No	Hydrangeaceae	E	36	2	P	1,446	1·5	3·0	5·9	397	O	G[c]	FC:EB
427	*Hydrangea involucrata* Sieb.	No	Hydrangeaceae	E	30	2	P	2,450	2·5	5·0	10·0	397	O	G[c]	FC:EB
428a	*Hydrangea macrophylla* (Thunb.) Ser. ssp. *serrata* (Thunb.) Makino	No	Hydrangeaceae	E	36	2	P	1,887	1·9	3·9	7·7	397	O	G[c]	FC:EB
428b	*Hydrangea macrophylla* (Thunb.) Ser. ssp. *macrophylla* McClint.	No	Hydrangeaceae	E	36	2	P	2,107	2·2	4·3	8·6	397	O	G[c]	FC:EB
429	*Hydrangea paniculata* Sieb.	No	Hydrangeaceae	E	36	2	P	1,847	1·9	3·8	7·5	397	O	G[c]	FC:EB
430	*Hydrangea quercifolia* Bartr.	No	Hydrangeaceae	E	36	2	P	956	1·0	2·0	3·9	397	O	G[c]	FC:EB
431a	*Hydrangea scandens* (L.f.) ssp. *scandens* McClint.	No	Hydrangeaceae	E	36	2	P	1,803	1·8	3·7	7·4	397	O	G[c]	FC:EB
431b	*Hydrangea scandens* (L.f.) ssp. *luikinensis* (Nakai) McClint.	No	Hydrangeaceae	E	36	2	P	1,872	1·9	3·8	7·6	397	O	G[c]	FC:EB
432	*Hydrangea seemannii* Riley	No	Hydrangeaceae	E	36	2	P	1,024	1·0	2·1	4·2	397	O	G[c]	FC:EB
433	*Hypericum hirsutum*[l]	No	Hypericaceae	E	—[n]	—[p]	P	147	0·2	0·3	0·6	465	O	J	Fe
434	*Inga dulcis* (Roxb.) Willd.	No	Leguminosae	E	—[n]	—[p]	P	402	0·4	0·8	1·6	454	O	B[c]	Fe
435a	*Iris stenophylla* Hausskn. ex Baker[h]	No	Iridaceae	M	24	2	P	8,359	8·5	17·1	34·1	465	O	B	Fe
435b	*Iris stenophylla* Hausskn. ex Baker[h]	No	Iridaceae	M	26	2	P	10,743	11·0	21·9	43·9	465	O	B	Fe
435c	*Iris stenophylla* Hausskn. ex Baker[h]	No	Iridaceae	M	26	2	P	11,439	11·7	23·3	46·7	465	O	B	Fe

436	*Ixiolirion ledebourii* Fisch. & Mey.	No	Ixioliriaceae	M	c. 24	2	P	995	1·0	2·0	4·1	380	O	J	Fe
437	*Ixora arborea* Roxb. ex Sm.	No	Rubiaceae	E	—[n]	—[p]	P	1,365	1·4	2·8	5·6	454	O	B[c]	Fe
438	*Jacquinia aristata* Jacq.	No	Theophrastaceae	E	38	2	P	593	0·6	1·2	2·4	378	O	J	Fe
439	*Kentranthus ruber* Druce	No	Valerianaceae	E	32	4	P	407	0·4	0·8	1·7	379	O	G	Fe
440	*Khaya senegalensis* (Desr.) A.Juss.	No	Meliaceae	E	—[n]	—[p]	P	853	0·9	1·7	3·5	454	O	B[c]	Fe
441	*Kigelia africana* (Lam.) Benth.	No	Bignoniaceae	E	—[n]	—[p]	P	1,700	1·7	3·5	6·9	454	O	B[c]	Fe
442	*Kirkia acuminata* Oliver	No	Kirkiaceae	E	c. 30	2	P	319	0·3	0·7	1·3	378	O	J	Fe
443	*Lagerstroemia tomentosa* C.Presl. Presl.	No	Lythraceae	E	—[n]	—[p]	P	965	1·0	2·0	3·9	454	O	B[c]	Fe
444	*Lantana camara* L.	No	Verbenaceae	E	22°	—[p]	P	2,697	2·8	5·5	11·0	454	O	B[c]	Fe
445	*Lapageria rosea* Ruiz & Pav.	No	Philesiaceae	M	30 + 1B	2	P	6,644	6·8	13·6	27·1	380	O	G	Fe
446b	*Lathyrus amphicarpos* L.	—[m]	Leguminosae	E	14	2	A	5,123	5·2	10·5	20·9	412	O	—[v]	Fe
447e	*Lathyrus annuus* L.	—[m]	Leguminosae	E	14	2	A	6,429	6·6	13·1	26·2	412	O	—[v]	Fe
447f	*Lathyrus annuus* L.	—[m]	Leguminosae	E	14	2	A	6,282	6·4	12·8	25·6	418	O	G[c]	FC:PI
448j	*Lathyrus aphaca* L.	—[m]	Leguminosae	E	14	2	A	4,528	4·6	9·2	18·5	418	O	C & E[c]	FC:PI
449b	*Lathyrus chloranthus* Boiss.	—[m]	Leguminosae	E	14	2	A	5,944	6·1	12·1	24·3	412	O	—[v]	Fe
450f	*Lathyrus cicera* L.	—[m]	Leguminosae	E	14	2	A	5,194	5·3	10·6	21·2	418	O	G[c]	FC:PI
451e	*Lathyrus clymenum* L.	—[m]	Leguminosae	E	14	2	A	4,297	4·4	8·8	17·5	418	O	C & E[c]	FC:PI
451f	*Lathyrus clymenum* L.	—[m]	Leguminosae	E	14	2	A	6,399	6·5	13·1	26·1	412	O	—[v]	Fe
452	*Lathyrus gmelinii* Fritsch	—[m]	Leguminosae	E	14	2	P	8,791	9·0	17·9	35·9	412	O	—[v]	Fe
453b	*Lathyrus grandiflorus* Sibth. & Sm.	—[m]	Leguminosae	E	14	2	P	8,724	8·9	17·8	35·6	412	O	—[v]	Fe
454b	*Lathyrus heterophyllus* L.	—[m]	Leguminosae	E	14	2	P	8,639	8·8	17·6	35·3	412	O	—[v]	Fe
455	*Lathyrus laevigatus* (Waldst. & Kit.)	—[m]	Leguminosae	E	14	2	P	11,008	11·2	22·5	44·9	412	O	—[v]	Fe
456c	*Lathyrus maritimus* Bigelow	—[m]	Leguminosae	E	14	2	P	6,777	6·9	13·8	27·7	412	O	—[v]	Fe
457e	*Lathyrus nissolia* L.	—[m]	Leguminosae	E	14	2	A	4,853	5·0	9·9	19·8	412	O	—[v]	Fe
458e	*Lathyrus ochrus* (L.) DC	—[m]	Leguminosae	E	14	2	A	4,542	4·6	9·3	18·5	418	O	C & E[c]	FC:PI
459i	*Lathyrus odoratus* L.	No	Leguminosae[j]	E	14°	2	A	8,134	8·3	16·6	33·2	457[bm]	O	B[d]	Fe
460f	*Lathyrus sativus* L.	—[m]	Leguminosae	E	14	2	A	6,551	6·7	13·4	26·7	418	O	G[c]	FC:PI
460g	*Lathyrus sativus* L.	—[m]	Leguminosae	E	14	2	A	6,899	7·0	14·1	28·2	412	O	—[v]	Fe
461f	*Lathyrus sylvestris* L.	—[m]	Leguminosae	E	14	2	P	10,104	10·3	20·6	41·2	412	O	—[v]	Fe
462g	*Lathyrus tingitanus* L.	—[m]	Leguminosae	E	14	2	A	7,693	7·9	15·7	31·4	418	O	G[c]	FC:PI
462h	*Lathyrus tingitanus* L.	—[m]	Leguminosae	E	14	2	A	7,691	7·8	15·7	31·4	412	O	—[v]	Fe
465	*Lawsonia inermis* L.	No	Lythraceae	E	c. 30-34	4	P	333	0·3	0·7	1·4	378	O	J	Fe
464	*Lebronnecia kokioides* Fosberg	—[m]	Malvaceae	E	26	2	—[q]	1,764	1·8	3·6	7·2	444[bd]	O	G[b2]	FC:PI
465	*Lemna minor* L.	No	Araceae	M	126	6	P	1,426	1·5	2·9	5·8	400	O	G	Fe
466	*Leucaena collinsii* Britton & Rose	No	Leguminosae	E	52, ?56°	2	P	529	0·5	1·1	2·2	425	O	—[at]	FC:EB
467b	*Leucaena confertiflora* S.Zarate	No	Leguminosae	E	112°	4	P	828	0·8	1·7	3·4	425	O	—[at]	FC:EB
468	*Leucaena cuspidata* Standley	No	Leguminosae	E	—[n]	—[p]	P	686	0·7	1·4	2·8	425	O	—[at]	FC:EB
469	*Leucaena diversifolia* (Schltdl. Benth.	No	Leguminosae	E	104	4	P	1,328	1·4	2·7	5·4	425	O	—[at]	FC:EB
470c	*Leucaena esculenta* (Sesse & Moc. ex DC) Benth.	No	Leguminosae	E	52 (?56, ?112)	—[p]	P	706	0·7	1·4	2·9	425	O	—[at]	FC:EB
471	*Leucaena greggii* S.Watson	No	Leguminosae	E	56°	2	P	887	0·9	1·8	3·6	425	O	—[at]	FC:EB
472	*Leucaena involucrata* S.Zarate	No	Leguminosae	E	—[n]	—[p]	P	1,122	1·1	2·3	4·6	425	O	—[at]	FC:EB
473c	*Leucaena lanceolata* S.Watson	No	Leguminosae	E	52	2	P	706	0·7	1·4	2·9	425	O	—[at]	FC:EB
474	*Leucaena lempirana* C.E.Hughes	No	Leguminosae	E	—[n]	—[p]	P	426	0·4	0·9	1·7	425	O	—[at]	FC:EB
475b	*Leucaena leucocephala* (Lam.) De Wit.	No	Leguminosae	E	104	4	P	1,455	1·5	3·0	5·9	425	O	—[at]	FC:EB
476	*Leucaena macrophylla* Benth.	No	Leguminosae	E	?52°	—[p]	P	299	0·3	0·6	1·2	425	O	—[at]	FC:EB
477	*Leucaena magnifica* (C.E.Hughes) C.E.Hughes	No	Leguminosae	E	?52°	—[p]	P	500	0·5	1·0	2·0	425	O	—[at]	FC:EB
478	*Leucaena matudae* (S.Zarate) C.E.Hughes	No	Leguminosae	E	?52°	—[p]	P	519	0·5	1·1	2·1	425	O	—[at]	FC:EB
479	*Leucaena multicapitula* Schery	No	Leguminosae	E	?52°	—[p]	P	470	0·5	1·0	1·9	425	O	—[at]	FC:EB
480	*Leucaena pallida* Britton & Rose	No	Leguminosae	E	104 (?110/112)°	4	P	774	0·8	1·6	3·2	425	O	—[at]	FC:EB
481	*Leucaena pueblana* Britton & Rose	No	Leguminosae	E	—[n]	—[p]	P	490	0·5	1·0	2·0	425	O	—[at]	FC:EB
482	*Leucaena pulverulenta* (Schltdl.) Benth.	No	Leguminosae	E	56	2	P	686	0·7	1·4	2·8	425	O	—[at]	FC:EB
483	*Leucaena retusa* Benth.	No	Leguminosae	E	56°	2	P	764	0·8	1·6	3·1	425	O	—[at]	FC:EB

APPENDIX. *(continued, the superscript letters refer to notes preceding this table)*

Entry number[g]	Species	Voucher	Family	Higher group[#]	2n‡	Ploidy level (*x*)	Life cycle type[§]	DNA amount 1C (Mbp[s])	1C (pg)	2C (pg)	4C (pg)	Original ref.[a]	Present amount[†]	Standard species[*b1]	Method[††]
484	*Leucaena salvadorensis* Standley ex Britton & Rose	No	Leguminosae	E	?56°	—[p]	P	887	0·9	1·8	3·6	425	O	—[at]	FC:EB
485	*Leucaena shannonii* J.D.Smith	No	Leguminosae	E	52°	2	P	691	0·7	1·4	2·8	425	O	—[at]	FC:EB
486	*Leucaena trichandra* (Zucc.) Urban	No	Leguminosae	E	52 (?56)°	2	P	764	0·8	1·6	3·1	425	O	—[at]	FC:EB
487	*Leucaena trichodes* (Jacq.) Benth.	No	Leguminosae	E	52°	2	P	539	0·6	1·1	2·2	425	O	—[at]	FC:EB
488	*Limnanthes douglasii* R. Br.	No	Limnanthaceae	E	10	2	A	1,362	1·4	2·8	5·6	379	O	J	Fe
489	*Litsea glutinosa* (Lour.) C.B. Robinson	No	Lauraceae	BA	48°	—[p]	P	2,766	2·8	5·6	11·3	454	O	B[c]	Fe
490c	*Lolium perenne* L.	No	Gramineae	M	14	2	P	2,773	2·8	5·7	11·3	417	O	*Gallus*[f]	FC:PI
491	*Loranthus europaeus*[l]	No	Loranthaceae[k]	E	—[n]	—[p]	—[q]	8,085	8·3	16·5	33·0	457[bm]	O	B[d]	Fe
492b	*Lupinus angustifolius* L.	No	Leguminosae	E	38, 42, 44	—[p]	A	752·[an]	0·8[an]	1·5[an]	3·1[an]	416	C	—[an]	FC:PI
493	*Lupinus atlanticus* Gladst.	No	Leguminosae	E	38	—[p]	A	1,458·[an]	1·5[an]	3·0[an]	6·0[an]	416	C	—[an]	FC:PI
494	*Lupinus cosentinii* Guss.	No	Leguminosae	E	32	—[p]	A	1,126·[an]	1·1[an]	2·3[an]	4·6[an]	416	C	—[an]	FC:PI
495	*Lupinus digitatus* Forssk.	No	Leguminosae	E	36	—[p]	A	1,286·[an]	1·3[an]	2·6[an]	5·3[an]	416	C	—[an]	FC:PI
496	*Lupinus micranthus* Guss.	No	Leguminosae	E	52	—[p]	A	461·[an]	0·5[an]	0·9[an]	1·9[an]	416	C	—[an]	FC:PI
497	*Lupinus palaestinus* Boiss.	No	Leguminosae	E	42	—[p]	A	1,201·[an]	1·2[an]	2·5[an]	4·9[an]	416	C	—[an]	FC:PI
498c	*Lupinus pilosus* Murr.	No	Leguminosae	E	42	—[p]	A	1,201·[an]	1·2[an]	2·5[an]	4·9[an]	416	C	—[an]	FC:PI
499c	*Luzula campestris* (L.) DC.	No	Juncaceae	M	12	—[u]	P	1,443	1·5	2·9	5·9	420	O	B[c]	Fe
500c	*Luzula elegans* Guthnick	No	Juncaceae	M	6	—[u]	P	1,512	1·5	3·1	6·2	420	O	B[c]	Fe
501d	*Luzula luzuloides* (Lam.) Dandy & Wilmott	No	Juncaceae	M	12	—[u]	P	1,722·[ap]	1·8[ap]	3·5[ap]	7·0[ap]	420	O	B[c]	Fe
502d	*Luzula nivea* Lam. & DC.	No	Juncaceae	M	12	—[u]	P	1,482·[ap]	1·5[ap]	3·0[ap]	6·1[ap]	420	O	B[c]	Fe
503c	*Luzula pedemontana* Boiss & Reut.	No	Juncaceae	M	30	—[u]	P	1,717	1·8	3·5	7·0	420	O	B[c]	Fe
504c	*Luzula pediformis* DC.	No	Juncaceae	M	12	—[u]	P	1,583	1·6	3·2	6·5	420	O	B[c]	Fe
505	*Luzula spicata* DC.	No	Juncaceae	M	24	—[u]	P	1,904	1·9	3·9	7·8	420	O	B[c]	Fe
506	*Luzula sudetica* DC.	No	Juncaceae	M	48	—[u]	P	1,686	1·7	3·4	6·9	420	O	B[c]	Fe
507k	*Lycopersicon esculentum* Mill. cv. Gardener's Delight	No	Solanaceae	E	—[n]	—[p]	A	980	1·0	2·0	4·0	382	O	H[c]	FC:PI
508b	*Malva sylvestris* L.	—[m]	Malvaceae	E	42°	6	P	1,470	1·5	3·0	6·0	444[bd]	O	G[b2]	FC:PI
509b	*Mangifera indica* L.	No	Anacardiaceae	E	40°	4	P	882	0·9	1·8	3·6	454	O	B[c]	Fe
510	*Matthiola incana*[l]	No	Cruciferae[j]	E	—[n]	—[p]	—[q]	2,597	2·7	5·3	10·6	457[bm]	O	B[d]	Fe
511a	*Melaleuca leucadendra* L.	No	Myrtaceae	E	22°	—[p]	P	1,110	1·1	2·3	4·5	449bf	O	B[c]	Fe
512	*Melampyrum arvense* Linn.	No	Orobanchaceae	E	—[n]	—[p]	P	8,073	8·2	16·5	33·0	465	O	G	FC:PI
513	*Melia azedarach* L.	No	Meliaceae	E	28°	—[p]	P	421	0·4	0·9	1·7	454	O	B[c]	Fe
514	*Melianthus major* L.	No	Melianthaceae	E	36, 38°	2 or 4	P	627	0·6	1·3	2·6	378	O	J	Fe
515	*Mentha longifolia*[l]	No	Labiatae	E	24	2	P	385	0·4	0·8	1·6	465	O	J	Fe
516	*Merrilliodendron megacarpum* (Hemsl.) Sleum.	No	Icacinaceae	E	30	2	P	1,071	1·1	2·2	4·4	380	O	K	FC:PI
517	*Mimusops elengi* L.	No	Sapotaceae	E	24°	—[p]	P	274	0·3	0·6	1·1	454	O	B[c]	Fe
518a	*Monstera deliciosa* Liebm.	No	Araceae	M	50	—[p]	P	9,384	9·6	19·2	38·3	411	O	B[c]	Fe
519	*Monstera obliqua* Miq.	No	Araceae	M	44	—[p]	P	8,822	9·0	18·0	36·0	411	O	B[c]	Fe
520	*Montinia caryophyllacea* Thunb.	No	Montiniaceae	E	24	2	P	554	0·6	1·1	2·3	380	O	J	Fe
521d	*Musa acuminata* Colla ssp. *banksii*	—[m]	Musaceae	M	22	2	P	600	0·6	1·2	2·5	402	O	*Glycine*[e]	FC:PI
521e	*Musa acuminata* Colla ssp. *siamea*	—[m]	Musaceae	M	22	2	P	618	0·6	1·3	2·5	402	O	*Glycine*[e]	FC:PI
521f	*Musa acuminata* Colla ssp. *banksii*[h]	No	Musaceae	M	22°	2	P	588	0·6	1·2	2·4	410	O	*Petunia*[e]	FC:EB
521g	*Musa acuminata* Colla ssp. *malaccensis* Accession Selangor[h]	No	Musaceae	M	22°	2	P	598	0·6	1·2	2·4	410	O	*Petunia*[e]	FC:EB
521h	*Musa acuminata* Colla ssp. *banksii*[h]	No	Musaceae	M	22°	2	P	637	0·7	1·3	2·6	410	O	*Petunia*[e]	FC:EB

521i	*Musa acuminata* Colla ssp. *siamea* Accession Siam[h]	No	Musaceae	M	22	2	P	652	0·7	1·3	2·7	410	O	*Petunia*[e]	FC:EB
521j	*Musa acuminata* Colla ssp. *truncata*	—[m]	Musaceae	M	22	2	P	626	0·6	1·3	2·6	421[aq]	O	*Glycine*[e]	FC:PI
521k	*Musa acuminata* Colla genotype PPC	—[m]	Musaceae	M	22	2	P	610	0·6	1·2	2·5	421[aq]	O	*Glycine*[e]	FC:PI
522c	*Musa balbisiana* Colla	—[m]	Musaceae	M	22	2	P	556	0·6	1·1	2·3	421	O	*Glycine*[e]	FC:PI
522d	*Musa balbisiana* Colla	—[m]	Musaceae	M	22	2	P	549	0·6	1·1	2·2	402	O	*Glycine*[e]	FC:PI
522e	*Musa balbisiana* Colla Accession Tani (1120)	No	Musaceae	M	22°	2	P	568	0·6	1·2	2·3	410	O	*Petunia*[e]	FC:EB
523	*Musa ornata* Roxb.	No	Musaceae	M	22°	2	P	603	0·6	1·2	2·5	410	O	*Petunia*[e]	FC:EB
524	*Musa violascens*[l]	—[m]	Musaceae	M	20	2	P	691	0·7	1·4	2·8	421	O	*Glycine*[e]	FC:PI
525	*Muscari adilii* M.B. Guner & H. Duman	No	Asparagaceae	M	18	2	P	2,550	2·6	5·2	10·4	465	O	G	Fe
526	*Muscari mcbeathianum*[l]	No	Asparagaceae	M	18	2	P	2,989	3·1	6·1	12·2	465	O	B	Fe
527	*Myoporum mauritianum* A. DC.	No	Myoporaceae	E	72	8	P	1,904	1·9	3·9	7·8	379	O	G	Fe
528	*Myrica gale* Linn.	No	Myricaceae	E	16, 48, 80, 96°	—[p]	P	409	0·4	0·8	1·7	379	O	J	Fe
529	*Myrsine africana* L.	No	Myrsinaceae	E	46	—[p]	P	1,205	1·2	2·5	4·9	380	O	J	Fe
530	*Narthecium ossifragum* Huds.	No	Nartheciaceae	M	26°	2	P	404	0·4	0·8	1·7	380	O	J	FC:PI
531	*Navarretia squarrosa* Hook. & Arn.	No	Polemoniaceae	E	18	2	A	1,289	1·3	2·6	5·3	378	O	J	Fe
532	*Nelumbo nucifera* Gaertn.	No	Nelumbonaceae	E	16	2	P	238	0·2	0·5	1·0	379	O	J	Fe
533	*Nemophila menziesii* Hook. & Arn.	No	Boraginaceae	E	18	2	A	1,220	1·2	2·5	5·0	465	O	J	Fe
534	*Nepenthes pervillei* Blume	No	Nepenthaceae	E	—[n]	—[p]	P	274	0·3	0·6	1·1	378	O	J	Fe
535k	*Nicotiana tabacum* L.	No	Solanaceae	E	48°	4	A	7,546	7·7	15·4	30·8	457[bm]	O	B[d]	Fe
536	*Nyctanthes arbor-tristis* L.	No	Oleaceae	E	44°	—[p]	P	1,203	1·2	2·5	4·9	454	O	B[c]	Fe
537	*Odontites lutea*[l]	No	Orobanchaceae	E	—[n]	—[p]	P	554	0·6	1·1	2·3	465	O	J	Fe
538	*Odontites verna* Dum.	No	Orobanchaceae	E	c. 18	2	P	559	0·6	1·1	2·3	465	O	J	Fe
539	*Odontostomum hartwegii* Torr.	No	Techophilaeaceae	M	20	2	P	2,506	2·6	5·1	10·2	380	O	G	FC:PI
540	*Oenothera ammophila* Focke	No	Onagraceae	E	14	2	BP	1,142	1·2	2·3	4·7	439	O	*Sorghum*[e]	FC:PI
541	*Oenothera biennis* L.	No	Onagraceae	E	14	2	BP	1,196	1·2	2·4	4·9	439	O	*Sorghum*[e]	FC:PI
542	*Olea africana* Mill.	No	Oleaceae	E	46	2	P	1,548	1·6	3·2	6·3	462	O	*Sorghum*[e]	Fe
543	*Olea cuspidata* Wall.	No	Oleaceae	E	46	2	P	2,029	2·1	4·1	8·3	462	O	*Sorghum*[e]	Fe
544a	*Olea europaea* L. cv. Dolce Agogia[h]	No	Oleaceae	E	46	2	P	1,911	2·0	3·9	7·8	462	O	*Sorghum*[e]	Fe
544b	*Olea europaea* L. cv. Pendolino[h]	No	Oleaceae	E	46	2	P	2,283	2·3	4·7	9·3	462	O	*Sorghum*[e]	Fe
545	*Olea ferruginea* Royale	No	Oleaceae	E	46	2	P	1,813	1·9	3·7	7·4	462	O	*Sorghum*[e]	Fe
546	*Olea indica* Klein	No	Oleaceae	E	46	2	P	1,646	1·7	3·4	6·7	462	O	*Sorghum*[e]	Fe
547r	*Oryza sativa* L. ssp. *indica*	No	Gramineae	M	24	2	A	466	0·5	1·0	1·9	450[bg]	O	—	GS
547s	*Oryza sativa* L. ssp. *indica* cv. IR8	—[m]	Gramineae	M	24	2	A	440	0·4	0·9	1·8	389	O	*Arab.*[e]	FC:PI
547t	*Oryza sativa* L. ssp. *japonica* cv. Nipponbare	—[m]	Gramineae	M	24	2	A	401	0·4	0·8	1·6	389	O	*Arab.*[e]	FC:PI
547u	*Oryza sativa* L. ssp. *japonica* cv. Nipponbare	No	Gramineae	M	24	2	A	420	0·4	0·9	1·7	451[bh]	O	—	GS
548	*Oxalis boliviana* Britton	No	Oxalidaceae	E	—[n]	—[p]	P	469	0·5	1·0	1·9	456[bk]	O	*Gallus*[f]	FC:PI
549	*Oxalis coralleoides* R.Knuth	No	Oxalidaceae	E	16°	2	P	521	0·5	1·1	2·1	456[bk]	O	*Gallus*[f]	FC:PI
550	*Oxalis cuzcensis* R.Knuth	No	Oxalidaceae	E	16°	2	AP	575	0·6	1·2	2·3	456[bk]	O	*Gallus*[f]	FC:PI
551	*Oxalis herrerae* R.Knuth	No	Oxalidaceae	E	16°	2	P	454	0·5	0·9	1·9	456[bk]	O	*Gallus*[f]	FC:PI
552	*Oxalis humbertii* R.Knuth	No	Oxalidaceae	E	16°	2	P	510	0·5	1·0	2·1	456[bk]	O	*Gallus*[f]	FC:PI
553	*Oxalis lotoides* Kunth	No	Oxalidaceae	E	16°	2	P	432	0·4	0·9	1·8	456[bk]	O	*Gallus*[f]	FC:PI
554a	*Oxalis lucumayensis* R.Knuth ssp. *lucumayensis*	No	Oxalidaceae	E	16°	2	P	455	0·5	0·9	1·9	456[bk]	O	*Gallus*[f]	FC:PI
554b	*Oxalis lucumayensis* R.Knuth ssp. *subiens* Lourteig	No	Oxalidaceae	E	16°	2	P	483	0·5	1·0	2·0	456[bk]	O	*Gallus*[f]	FC:PI
555	*Oxalis marcapatensis* R.Knuth	No	Oxalidaceae	E	16°	2	P	440	0·4	0·9	1·8	456[bk]	O	*Gallus*[f]	FC:PI
556	*Oxalis medicaginea* Kunth	No	Oxalidaceae	E	16°	2	P	417	0·4	0·9	1·7	456[bk]	O	*Gallus*[f]	FC:PI
557	*Oxalis megalorrhiza* Jacquin	No	Oxalidaceae	E	14 or 18°	2	P	399	0·4	0·8	1·6	456[bk]	O	*Gallus*[f]	FC:PI
558	*Oxalis mollis* Kunth	No	Oxalidaceae	E	16°	2	P	437	0·4	0·9	1·8	456[bk]	O	*Gallus*[f]	FC:PI
559	*Oxalis oulophora* Lourteig	No	Oxalidaceae	E	16°	2	P	433	0·4	0·9	1·8	456[bk]	O	*Gallus*[f]	FC:PI
560	*Oxalis paucartambensis* R.Knuth	No	Oxalidaceae	E	16°	2	P	470	0·5	1·0	1·9	456[bk]	O	*Gallus*[f]	FC:PI
561a	*Oxalis peduncularis* Kunth[h]	No	Oxalidaceae	E	16°	2	P	454	0·5	0·9	1·9	456[bk]	O	*Gallus*[f]	FC:PI

APPENDIX. *(continued, the superscript letters refer to notes preceding this table)*

Entry number[g]	Species	Voucher	Family	Higher group[#]	2n‡	Ploidy level (*x*)	Life cycle type[§]	DNA amount 1C (Mbp[s])	1C (pg)	2C (pg)	4C (pg)	Original ref.[a]	Present amount[†]	Standard species[*b1]	Method[††]
561b	*Oxalis peduncularis* Kunth var. *pilosa*[h]	No	Oxalidaceae	E	16[o]	2	P	570	0·6	1·2	2·3	456[bk]	O	*Gallus*[f]	FC:PI
562	*Oxalis petrophila* R.Knuth	No	Oxalidaceae	E	16[o]	2	P	482	0·5	1·0	2·0	456[bk]	O	*Gallus*[f]	FC:PI
563	*Oxalis phaeotricha* Diels	No	Oxalidaceae	E	32[o]	4	P	820	0·8	1·7	3·3	456[bk]	O	*Gallus*[f]	FC:PI
564	*Oxalis picchensis* R.Knuth	No	Oxalidaceae	E	32[o]	4	P	821	0·8	1·7	3·4	456[bk]	O	*Gallus*[f]	FC:PI
565a	*Oxalis ptychoclada* Diels	No	Oxalidaceae	E	16[o]	2	P	434	0·4	0·9	1·8	456[bk]	O	*Gallus*[f]	FC:PI
565b	*Oxalis ptychoclada* Diels var. *trichocarpa* Lourteig	No	Oxalidaceae	E	16[o]	2	P	466	0·5	1·0	1·9	456[bk]	O	*Gallus*[f]	FC:PI
566	*Oxalis san-miguelii* R.Knuth	No	Oxalidaceae	E	16[o]	2	P	428	0·4	0·9	1·7	456[bk]	O	*Gallus*[f]	FC:PI
567	*Oxalis* sp. cfr. *melilotoides* Zuccarini[y]	No	Oxalidaceae	E	16[o]	2	P	456	0·5	0·9	1·9	456[bk]	O	*Gallus*[f]	FC:PI
568	*Oxalis* sp. cfr. *teneriensis* R. Knuth[y]	No	Oxalidaceae	E	16[o]	2	P	473	0·5	1·0	1·9	456[bk]	O	*Gallus*[f]	FC:PI
569a	*Oxalis spiralis* R. & P. ex G.Don[h]	No	Oxalidaceae	E	16[o]	2	AP	520	0·5	1·1	2·1	456[bk]	O	*Gallus*[f]	FC:PI
569b	*Oxalis spiralis* R. & P. ex G.Don[h]	No	Oxalidaceae	E	16[o]	2	AP	656	0·7	1·3	2·7	456[bk]	O	*Gallus*[f]	FC:PI
570	*Oxalis tabaconasensis* R.Knuth	No	Oxalidaceae	E	16[o]	2	P	515	0·5	1·1	2·1	456[bk]	O	*Gallus*[f]	FC:PI
571	*Oxalis tuberosa* Molina	No	Oxalidaceae	E	64[o]	8	P	1,722	1·8	3·5	7·0	456[bl]	O	*Gallus*[f]	FC:PI
572	*Oxalis unduavensis* (Rusby) R.Knuth	No	Oxalidaceae	E	16[o]	2	P	505	0·5	1·0	2·1	456[bk]	O	*Gallus*[f]	FC:PI
573	*Oxalis urubambensis* R.Knuth	No	Oxalidaceae	E	16[o]	2	P	431	0·4	0·9	1·8	456[bk]	O	*Gallus*[f]	FC:PI
574	*Oxalis vulcanicola* Donn. Sm.	No	Oxalidaceae	E	16[o]	2	P	434	0·4	0·9	1·8	456[bk]	O	*Gallus*[f]	FC:PI
575a	*Paeonia caucasica* (Schipcz.) Schipcz.[h]	—[m]	Paeoniaceae	E	10	2	P	15,592	15·9	31·8	63·6	459	C	—[bq]	Fe
575b	*Paeonia caucasica* (Schipcz.) Schipcz.[h]	—[m]	Paeoniaceae	E	10	2	P	16,087	16·4	32·8	65·7	459	C	—[bq]	Fe
576a	*Paeonia daurica* Andr.[h]	—[m]	Paeoniaceae	E	10	2	P	11,804	12·0	24·1	48·2	459	C	—[bq]	Fe
576b	*Paeonia daurica* Andr.[h]	—[m]	Paeoniaceae	E	10	2	P	12,970	13·2	26·5	52·9	459	C	—[bq]	Fe
577a	*Paeonia lagodechiana* Kem.-Nath.[h]	—[m]	Paeoniaceae	E	10	2	P	11,981	12·2	24·5	48·9	459	C	—[bq]	Fe
577b	*Paeonia lagodechiana* Kem.-Nath.[h]	—[m]	Paeoniaceae	E	10	2	P	14,009	14·3	28·6	57·2	459	C	—[bq]	Fe
578a	*Paeonia macrophylla* (Albov) Lomak.[h]	—[m]	Paeoniaceae	E	20	4	P	29,449	30·1	60·1	120·2	459	C	—[bq]	Fe
578b	*Paeonia macrophylla* (Albov) Lomak.[h]	—[m]	Paeoniaceae	E	20	4	P	30,086	30·7	61·4	122·8	459	C	—[bq]	Fe
579b	*Paeonia mlokosewitschi* Lomak.[h]	—[m]	Paeoniaceae	E	10	2	P	16,790	17·1	34·3	68·5	459	C	—[bq]	Fe
579c	*Paeonia mlokosewitschi* Lomak.[h]	—[m]	Paeoniaceae	E	10	2	P	17,571	17·9	35·9	71·7	459	C	—[bq]	Fe
580b	*Paeonia officinalis* L.[h]	—[m]	Paeoniaceae	E	20	4	P	25,995	26·5	53·1	106·1	459	C	—[bq]	Fe
581a	*Paeonia ruprechtiana* Kem.-Nath.[h]	—[m]	Paeoniaceae	E	10	2	P	15,224	15·5	31·1	62·1	459	C	—[bq]	Fe
581b	*Paeonia ruprechtiana* Kem.-Nath.[h]	—[m]	Paeoniaceae	E	10	2	P	17,331	17·7	35·4	70·7	459	C	—[bq]	Fe
582a	*Paeonia steveniana* Kem.-Nath.[h]	—[m]	Paeoniaceae	E	20	4	P	27,955	28·5	57·1	114·1	459	C	—[bq]	Fe
582b	*Paeonia steveniana* Kem.-Nath.[h]	—[m]	Paeoniaceae	E	20	4	P	29,939	30·6	61·1	122·2	459	C	—[bq]	Fe
583b	*Paeonia tenuifolia* L.[h]	—[m]	Paeoniaceae	E	10	2	P	7,700	7·9	15·7	31·4	459	C	—[bq]	Fe
583c	*Paeonia tenuifolia* L.[h]	—[m]	Paeoniaceae	E	10	2	P	11,598	11·8	23·7	47·3	459	C	—[bq]	Fe
584a	*Paeonia tomentosa* (Lomak.) N.Busch[h]	—[m]	Paeoniaceae	E	20	4	P	25,260	25·8	51·6	103·1	459	C	—[bq]	Fe
584b	*Paeonia tomentosa* (Lomak.) N.Busch[h]	—[m]	Paeoniaceae	E	20	4	P	27,391	28·0	55·9	111·8	459	C	—[bq]	Fe
585a	*Paeonia wittmanniana* Hartwiss ex Lindl.[h]	—[m]	Paeoniaceae	E	20	4	P	27,514	28·1	56·2	112·3	459	C	—[bq]	Fe
585b	*Paeonia wittmanniana* Hartwiss ex Lindl.[h]	—[m]	Paeoniaceae	E	20	4	P	31,042	31·7	63·4	126·7	459	C	—[bq]	Fe
586d	*Papaver rhoeas* L.	No	Papaveraceae	E	14[o]	2	A	2,548	2·6	5·2	10·4	457[bm]	O	B[d]	Fe
587	*Parmentiera cereifera* Seem.	No	Bignoniaceae	E	—[n]	—[p]	P	647	0·7	1·3	2·6	454	O	B[c]	Fe
588	*Paspalum notatum* Flugge.	No	Gramineae	M	20	2	P	706	0·7	1·4	2·9	417	O	*Gallus*[f]	FC:PI
589	*Peltophorum pterocarpum* (DC.) Baker ex K.Heyne	No	Leguminosae	E	26[o]	—[p]	P	777	0·8	1·6	3·2	454	O	B[c]	Fe
590a	*Petroselinum crispum* cv. Champion Moss Curled[l]	No	Umbelliferae	E	—[n]	—[p]	P	2,205	2·3	4·5	9·0	382	O	*Lycopers.*[c]	FC:PI

	Petunia – Some taxa once included in *Petunia* are now included in *Calibrachoa* (see footnote ae)													
591	*Petunia alpicola* L.B.Sm. & Downs	No	Solanaceae	E	18	2	P	1,450	1·5	3·0	5·9	387[ae]	O	*Gallus*-398p FC:PI
592	*Petunia altiplana* T.Ando & Hashim.	No	Solanaceae	E	14	2	P	1,274	1·3	2·6	5·2	387[ae]	O	*Gallus*-398p FC:PI
593b	*Petunia axillaris* (Lam.) Britton, Sterns & Poggenb. ssp. *axillaris*	No	Solanaceae	E	14	2	P	1,436	1·5	2·9	5·9	387[ae]	O	*Gallus*-398p FC:PI
593c	*Petunia axillaris* (Lam.) Britton, Sterns & Poggenb. ssp. *subandina*	No	Solanaceae	E	14°	2	P	1,465	1·5	3·0	6·0	387[ae]	O	*Gallus*-398p FC:PI
593d	*Petunia axillaris* (Lam.) Britton, Sterns & Poggenb. ssp. *parodii*	No	Solanaceae	E	14	2	P	1,470	1·5	3·0	6·0	387[ae]	O	*Gallus*-398p FC:PI
594	*Petunia bajeensis* T.Ando & Hashim.	No	Solanaceae	E	14°	2	P	1,450	1·5	3·0	5·9	387[ae]	O	*Gallus*-398p FC:PI
595	*Petunia bonjardinensis* T.Ando & Hashim.	No	Solanaceae	E	14	2	P	1,421	1·5	2·9	5·8	387[ae]	O	*Gallus*-398p FC:PI
596	*Petunia exserta* Stehmann.	No	Solanaceae	E	14°	2	P	1,539	1·6	3·1	6·3	387[ae]	O	*Gallus*-398p FC:PI
597	*Petunia guarapuavensis* T.Ando & Hashim.	No	Solanaceae	E	14	2	P	1,499	1·5	3·1	6·1	387[ae]	O	*Gallus*-398p FC:PI
598	*Petunia helianthemoides* Sendtn.	No	Solanaceae	E	18	2	P	1,436	1·5	2·9	5·9	387[ae]	O	*Gallus*-398p FC:PI
599e	*Petunia hybrida* Vilm. cv. Pearl Sky Blue	No	Solanaceae	E	14°	2	P	1,441	1·5	2·9	5·9	387[ae]	O	*Gallus*-398p FC:PI
600a	*Petunia integrifolia* (Hook.) Schinz & Thell. ssp. *inflata* (R.E.Fr.)	No	Solanaceae	E	14	2	A	1,333	1·4	2·7	5·4	387[ae]	O	*Gallus*-398p FC:PI
600b	*Petunia integrifolia* (Hook.) Schinz & Thell. ssp. *integrifolia* var. *integrifolia*	No	Solanaceae	E	14	2	P	1,436	1·5	2·9	5·9	387[ae]	O	*Gallus*-398p FC:PI
600c	*Petunia integrifolia* (Hook.) Schinz & Thell. ssp. *integrifolia* var. *depauperata* (R.E.Fr.)	No	Solanaceae	E	14	2	P	1,490	1·5	3·0	6·1	387[ae]	O	*Gallus*-398p FC:PI
601	*Petunia interior* T.Ando & Hashim.	No	Solanaceae	E	14	2	P	1,455	1·5	3·0	5·9	387[ae]	O	*Gallus*-398p FC:PI
602	*Petunia kleinii* L.B.Sm. & Downs	No	Solanaceae	E	18	2	P	1,436	1·5	2·9	5·9	387[ae]	O	*Gallus*-398p FC:PI
603	*Petunia littoralis* L.B. Sm. & Downs	No	Solanaceae	E	14	2	P	1,455	1·5	3·0	5·9	387[ae]	O	*Gallus*-398p FC:PI
604	*Petunia mantiqueirensis* T.Ando & Hashim.	No	Solanaceae	E	14°	2	P	1,524	1·6	3·1	6·2	387[ae]	O	*Gallus*-398p FC:PI
605	*Petunia occidentalis* R.E.Fr.	No	Solanaceae	E	14	2	A	1,362	1·4	2·8	5·6	387[ae]	O	*Gallus*-398p FC:PI
606	*Petunia pubescens* (Spreng.) R.E.Fr.	No	Solanaceae	E	18	2	P	1,446	1·5	3·0	5·9	387[ae]	O	*Gallus*-398p FC:PI
607	*Petunia reitzii* L.B.Sm. & Downs.	No	Solanaceae	E	14	2	P	1,406	1·4	2·9	5·7	387[ae]	O	*Gallus*-398p FC:PI
608	*Petunia riograndensis* T.Ando & Hashim.	No	Solanaceae	E	14°	2	P	1,460	1·5	3·0	6·0	387[ae]	O	*Gallus*-398p FC:PI
609	*Petunia saxicola* L.B.Sm. & Downs	No	Solanaceae	E	14	2	P	1,411	1·4	2·9	5·8	387[ae]	O	*Gallus*-398p FC:PI
610	*Petunia scheideana* L.B.Sm. & Downs	No	Solanaceae	E	14	2	P	1,436	1·5	2·9	5·9	387[ae]	O	*Gallus*-398p FC:PI
611	*Petunia variabilis*R.E.Fr.	No	Solanaceae	E	18	2	P	1,441	1·5	2·9	5·9	387[ae]	O	*Gallus*-398p FC:PI
612	*Phalaenopsis amboinensis* J. J. Smith	No	Orchidaceae	M	38	2	P	7,036	7·2	14·4	28·7	447	O	G[b2] FC:PI
613	*Phalaenopsis aphrodite* Rchb.f.	No	Orchidaceae	M	38	2	P	1,372	1·4	2·8	5·6	447	O	G[b2] FC:PI
614	*Phalaenopsis bellina* (Rchb. f.) Cristenson	No	Orchidaceae	M	38	2	P	7,365	7·5	15·0	30·1	447	O	G[b2] FC:PI
615	*Phalaenopsis cornu-cervi* (Breda) Bl & Rchb.f.	No	Orchidaceae	M	38	2	P	3,156	3·2	6·4	12·9	447	O	G[b2] FC:PI
616a	*Phalaenopsis equestris* (Schauer) Rchb.f.	No	Orchidaceae	M	38	2	P	1,651	1·7	3·4	6·7	447	O	G[b2] FC:PI
617	*Phalaenopsis fasciata* Rchb.f.	No	Orchidaceae	M	38	2	P	3,214	3·3	6·6	13·1	447	O	G[b2] FC:PI
618	*Phalaenopsis gigantea* J.J.Smith	No	Orchidaceae	M	38	2	P	2,587	2·6	5·3	10·6	447	O	G[b2] FC:PI
619a	*Phalaenopsis lueddemanniana* Rchb.f.	No	Orchidaceae	M	38	2	P	3,180	3·2	6·5	13·0	447	O	G[b2] FC:PI
620	*Phalaenopsis mannii* Rchb.f.	No	Orchidaceae	M	38	2	P	6,615	6·8	13·5	27·0	447	O	G[b2] FC:PI
621	*Phalaenopsis mariae* Burb. ex Warn. & Wms.	No	Orchidaceae	M	38	2	P	3,175	3·2	6·5	13·0	447	O	G[b2] FC:PI
622	*Phalaenopsis micholitzii* Rolfe	No	Orchidaceae	M	38	2	P	3,180	3·2	6·5	13·0	447	O	G[b2] FC:PI
623	*Phalaenopsis modesta* J.J.Smith	No	Orchidaceae	M	38	2	P	2,524	2·6	5·2	10·3	447	O	G[b2] FC:PI
624	*Phalaenopsis parishii* Rchb.f.	No	Orchidaceae	M	38	2	P	8,139	8·3	16·6	33·2	447	O	G[b2] FC:PI
625	*Phalaenopsis pulchra* (Rchb.f.) Sweet	No	Orchidaceae	M	38	2	P	3,121	3·2	6·4	12·7	447	O	G[b2] FC:PI
626	*Phalaenopsis sanderiana* Rchb.f.[i]	No	Orchidaceae	M	38	2	P	1,372	1·4	2·7	5·6	447	O	G[b2] FC:PI
627	*Phalaenopsis stuartiana* Rchb.f.	No	Orchidaceae	M	38	2	P	1,534	1·6	3·1	6·3	447	O	G[b2] FC:PI
628	*Phalaenopsis sumatrana* Korth. & Rchb.f.	No	Orchidaceae	M	38	2	P	3,244	3·3	6·6	13·2	447	O	G[b2] FC:PI
629	*Phalaenopsis venosa* Shim & Fowl.	No	Orchidaceae	M	38	2	P	4,665	4·8	9·5	19·0	447	O	G[b2] FC:PI
630c	*Phaseolus acutifolius* var. *latifolius* G.Freeman	—[m]	Leguminosae	E	22°	2	A	794	0·8	1·6	3·2	390	O	*Petunia*[e] FC:DAPI

APPENDIX. *(continued, the superscript letters refer to notes preceding this table)*

Entry number[g]	Species	Voucher	Family	Higher group[#]	2n‡	Ploidy level (*x*)	Life cycle type[§]	DNA amount 1C (Mbp[s])	1C (pg)	2C (pg)	4C (pg)	Original ref.[a]	Present amount[†]	Standard species[*b1]	Method[††]
630d	*Phaseolus acutifolius* var. *tenuifolius* (Wood & Standl) A.Gray	—[m]	Leguminosae	E	22°	2	A	799	0·8	1·6	3·3	390	O	*Petunia*[e]	FC:DAPI
630e	*Phaseolus acutifolius* var. *acutifolius* A.Gray	—[m]	Leguminosae	E	22°	2	A	862	0·9	1·8	3·5	390	O	*Petunia*[e]	FC:DAPI
631	*Phaseolus angustissimus* A.Gray	—[m]	Leguminosae	E	22°	2	—[q]	647	0·7	1·3	2·6	390	O	*Petunia*[e]	FC:DAPI
632e	*Phaseolus coccineus* L.	—[m]	Leguminosae	E	22°	2	P	784	0·8	1·6	3·2	390	O	*Petunia*[e]	FC:DAPI
632f	*Phaseolus coccineus* L. ssp. *Purpurascens*	—[m]	Leguminosae	E	22°	2	P	794	0·8	1·6	3·2	390	O	*Petunia*[e]	FC:DAPI
632g	*Phaseolus coccineus* L. ssp. *coccineus* cv. Hammond's Dwarf Scarlet[h]	—[m]	Leguminosae	E	22°	2	P	794	0·8	1·6	3·2	390	O	*Petunia*[e]	FC:DAPI
632h	*Phaseolus coccineus* L. ssp. *coccineus* cv. Preisgewinner[h]	—[m]	Leguminosae	E	22°	2	P	809	0·8	1·7	3·3	390	O	*Petunia*[e]	FC:DAPI
632i	*Phaseolus coccineus* L.	No	Leguminosae[j]	E	22°	2	P	1,715	1·8	3·5	7·0	457[bm]	O	B[d]	Fe
633b	*Phaseolus filiformis* Benth.	—[m]	Leguminosae	E	22°	2	P	691	0·7	1·4	2·8	390	O	*Petunia*[e]	FC:DAPI
634b	*Phaseolus glabellus* Piper	—[m]	Leguminosae	E	22°	2	P	1,024	1·0	2·1	4·2	390	O	*Petunia*[e]	FC:DAPI
635	*Phaseolus grayanus* Wood. & Standl	—[m]	Leguminosae	E	22°	2	—[q]	931	1·0	1·9	3·8	390	O	*Petunia*[e]	FC:DAPI
636b	*Phaseolus hintonii* Delgado	—[m]	Leguminosae	E	22°	2	P	715	0·7	1·5	2·9	390	O	*Petunia*[e]	FC:DAPI
637	*Phaseolus leptostachys* var. *leptostachys* Benth.	—[m]	Leguminosae	E	22°	2	—[q]	613	0·6	1·3	2·5	390	O	*Petunia*[e]	FC:DAPI
638d	*Phaseolus lunatus* L. var. *lunatus* cv. Early Thorogreen[h]	—[m]	Leguminosae	E	22°	2	P	691	0·7	1·4	2·8	390	O	*Petunia*[e]	FC:DAPI
638e	*Phaseolus lunatus* L. var. *silvester* Baudet	—[m]	Leguminosae	E	22°	2	P	696	0·7	1·4	2·8	390	O	*Petunia*[e]	FC:DAPI
638f	*Phaseolus lunatus* L. var. *lunatus* cv. Henderson Bush[h]	—[m]	Leguminosae	E	22°	2	P	701	0·7	1·4	2·9	390	O	*Petunia*[e]	FC:DAPI
639b	*Phaseolus marechalli* Delgado	—[m]	Leguminosae	E	22°	2	P	784	0·8	1·6	3·2	390	O	*Petunia*[e]	FC:DAPI
640	*Phaseolus micranthus* Hook. & Arn.	—[m]	Leguminosae	E	22°	2	—[q]	588	0·6	1·2	2·4	390	O	*Petunia*[e]	FC:DAPI
641	*Phaseolus microcarpus* Mart.	—[m]	Leguminosae	E	22°	2	—[q]	505	0·5	1·0	2·1	390	O	*Petunia*[e]	FC:DAPI
642b	*Phaseolus neglectus* Herm.	—[m]	Leguminosae	E	22°	2	—[q]	941	1·0	1·9	3·8	390	O	*Petunia*[e]	FC:DAPI
643	*Phaseolus parviflorus* G.Freytag	—[m]	Leguminosae	E	22°	2	—[q]	637	0·7	1·3	2·6	390	O	*Petunia*[e]	FC:DAPI
644b	*Phaseolus pluriflorus* Marechal	—[m]	Leguminosae	E	22°	2	—[q]	1,068	1·1	2·2	4·4	390	O	*Petunia*[e]	FC:DAPI
645b	*Phaseolus polyanthus* Greenm.	—[m]	Leguminosae	E	22°	2	P	799	0·8	1·6	3·3	390	O	*Petunia*[e]	FC:DAPI
646g	*Phaseolus vulgaris* L. cv. Kentucky Wonder[h]	—[m]	Leguminosae	E	22°	2	A	686	0·7	1·4	2·8	390	O	*Petunia*[e]	FC:DAPI
646h	*Phaseolus vulgaris* L. var. *aborigineus* (Burk.) Baudet	—[m]	Leguminosae	E	22°	2	A	720	0·7	1·5	2·9	390	O	*Petunia*[e]	FC:DAPI
646i	*Phaseolus vulgaris* L. var. *mexicanus*	—[m]	Leguminosae	E	22°	2	A	735	0·8	1·5	3·0	390	O	*Petunia*[e]	FC:DAPI
646j	*Phaseolus vulgaris* L. cv. Sanilac	—[m]	Leguminosae	E	22°	2	A	750	0·8	1·5	3·1	390	O	*Petunia*[e]	FC:DAPI
646k	*Phaseolus vulgaris* L.	No	Leguminosae[j]	E	22°	2	A	1,666.[bn]	1·7[bn]	3·4[bn]	6·8[bn]	457[bm]	O	B[d]	Fe
647b	*Phaseolus xanthotrichus* Piper var. *xanthotrichus*	—[m]	Leguminosae	E	22°	2	P	662	0·7	1·4	2·7	390	O	*Petunia*[e]	FC:DAPI
647c	*Phaseolus xanthotrichus* Piper	—[m]	Leguminosae	E	22°	2	P	848	0·9	1·7	3·5	390	O	*Petunia*[e]	FC:DAPI
648	*Philodendron erubescens* C.Koch & Bousche	No	Araceae	M	42	—[p]	P	5,174	5·3	10·6	21·1	411	O	B[c]	Fe
649	*Philodendron selloum* C.Koch	No	Araceae	M	36	—[p]	P	4,895	5·0	10·0	20·0	411	O	B[c]	Fe
650	*Philodendron squamiferum* Poepp. & Endl.	No	Araceae	M	30	—[p]	P	4,557	4·7	9·3	18·6	411	O	B[c]	Fe
651	*Phormium tenax*[l]	No	Hemerocallidaceae	M	32	2	P	740	0·8	1·5	3·0	379	O	J	Fe
652	*Pinguicula primuliflora* C.E.Wood & Godfrey	No	Lentibulariaceae	E	22	2	P	669	0·7	1·4	2·7	378	O	J	Fe
653	*Piptocalyx moorei* Oliver	No	Trimeniaceae	BA	16°	2	P	4,001	4·1	8·2	16·3	381	O	G	FC:PI
654b	*Pistia stratiotes* L.	No	Araceae[k]	M	28	2	P	250	0·3	0·5	1·0	400	O	G	Fe
655c	*Pisum abyssinicum* A.Braun[h]	No	Leguminosae	E	14	2	A	4,371	4·5	8·9	17·8	458[bp]	C[bp]	G[c]	FC:EB
655d	*Pisum abyssinicum* A.Braun[h]	No	Leguminosae	E	14	2	A	4,751	4·8	9·7	19·4	458[bp]	C[bp]	G[c]	FC:EB

656c	*Pisum elatius* Steven ex M.Bieb.[h]	No	Leguminosae	E	14	2	A	4,231	4·3	8·6	17·3	458[bp]	C[bp]	G[c]	FC:EB
656d	*Pisum elatius* Steven ex M.Bieb.[h]	No	Leguminosae	E	14	2	A	4,978	5·1	10·2	20·3	458[bp]	C[bp]	G[c]	FC:EB
657b	*Pisum fulvum* Sibth. & Smith	No	Leguminosae	E	14	2	A	4,716	4·8	9·6	19·3	458[bp]	C[bp]	G[c]	FC:EB
658c	*Pisum humile* Boiss & Noë[h]	No	Leguminosae	E	14	2	A	4,258	4·3	8·7	17·4	458[bp]	C[bp]	G[c]	FC:EB
658d	*Pisum humile* Boiss & Noë[h]	No	Leguminosae	E	14	2	A	4,809	4·9	9·8	19·6	458[bp]	C[bp]	G[c]	FC:EB
659	*Pittosporum tenuifolium* Gaertn.	No	Pittosporaceae	E	24	2	P	453	0·5	0·9	1·9	379	O	G	Fe
660	*Planchonella eerwah* (F.M. Bailey) van Royen	No	Sapotaceae	E	c. 24	2	P	527	0·5	1·1	2·2	380	O	J	Fe
661	*Plantago afra* L.	No	Plantaginaceae	E	12	2	A	1,129	1·2	2·3	4·6	388	O	B[c]	Fe
662	*Plantago arenaria* W. & K.	No	Plantaginaceae	E	12	2	A	1,115	1·1	2·3	4·6	388	O	B[c]	Fe
663	*Plantago coronopus* L.	No	Plantaginaceae	E	10	2	AP	845	0·9	1·7	3·5	388	O	B[c]	Fe
664	*Plantago indica* L.	No	Plantaginaceae	E	12	2	—[q]	1,088	1·1	2·2	4·4	388	O	B[c]	Fe
665b	*Plantago lagopus* L.	No	Plantaginaceae	E	12	2	—[q]	1,046	1·1	2·1	4·3	388	O	B[c]	Fe
666c	*Plantago lanceolata* L.	No	Plantaginaceae	E	12	2	P	1,299	1·3	2·7	5·3	388	O	B[c]	Fe
667c	*Plantago major* L.	No	Plantaginaceae	E	12	2	P	867	0·9	1·8	3·5	388	O	B[c]	Fe
668	*Plantago psyllium* L.	No	Plantaginaceae	E	12	2	—[q]	1,142	1·2	2·3	4·7	388	O	B[c]	Fe
669	*Plantago serraria* L.	No	Plantaginaceae	E	10	2	—[q]	882	0·9	1·8	3·6	388	O	B[c]	Fe
670	*Plantago stepposa* K.	No	Plantaginaceae	E	24	4	—[q]	1,593	1·6	3·3	6·5	388	O	B[c]	Fe
671	*Platanus orientalis* L.	No	Platanaceae	E	42	2	P	1,274	1·3	2·6	5·2	379	O	J	Fe
672	*Poa pratensis* L.	No	Gramineae	M	58-62	—[p]	P	4,155	4·2	8·5	17·0	417	O	*Gallus*[f]	FC:PI
673	*Poncirus trifoliata* (L.) Raf.	No	Rutaceae	E	18°	2	P	377	0·4	0·8	1·5	426	O	*Gallus*[f]	FC:PI
674	*Prosopis cineraria* (L.) Druce	No	Leguminosae	E	52°	—[p]	P	1,252	1·3	2·6	5·1	454	O	B[c]	Fe
675	*Protium serratum* (Wall. ex Colebr.)	No	Burseraceae	E	—[n]	—[p]	P	924	0·9	1·9	3·8	454	O	B[c]	Fe
676	*Pterospermum lanceifolium* Roxb.	No	Malvaceae	E	38°	—[p]	P	786	0·8	1·6	3·2	454	O	B[c]	Fe
677	*Pterostyrax psilophylla* Diels ex Perkins	No	Styracaceae	E	24	2	P	867	0·9	1·8	3·5	380	O	J	Fe
678	*Punica granatum* L.	No	Sonneratiaceae	E	16°	2	P	706	0·7	1·4	2·9	454	O	B[c]	Fe
679	*Reseda luteola* L.	No	Resedaceae	E	26	2	B	500	0·5	1·0	2·0	378	O	J	Fe
680	*Rhapidophora montana* Schott	No	Araceae	M	30	—[p]	P	9,829	10·0	20·1	40·1	411	O	B[c]	Fe
681	*Rhapidophora peepla* Schott	No	Araceae	M	18	—[p]	P	8,984	9·2	18·3	36·7	411	O	B[c]	Fe
682	*Rhipogonum papuanum* C.T. White	No	Rhipogonaceae	M	30	2	P	10,922	11·1	22·3	44·6	380	O	G	Fe
683	*Rhodocoma gigantea* (Kunth) H.P. Linder	No	Restionaceae	M	—[n]	—[p]	P	728	0·7	1·5	3·0	380	O	J	FC:PI
684	*Rhodohypoxis milloides* (Baker) Hilliard & B.L. Burtt	No	Hypoxidaceae	M	24 + 1-2B	4	P	1,394	1·4	2·8	5·7	379	O	J	Fe
685c	*Rhoeo discolor* Hance	No	Commelinaceae	M	12°	2	P	7,987	8·2	16·3	32·6	457[bm]	O	B[d]	Fe
686	*Rhoiacarpos capensis* A. DC.	No	Santalaceae	E	—[n]	—[p]	P	304	0·3	0·6	1·2	379	O	J	Fe
687	*Rhynchosia cyanosperma* Benth. Ex Baker	No	Leguminosae	E	22	2	B	2,727	2·8	5·6	11·1	443[bc]	O	B[c]	Fe
688	*Rhynchosia minima* (L.) DC.	No	Leguminosae	E	22	2	P	1,227	1·3	2·5	5·0	443[bc]	O	B[c]	Fe
689	*Ribes glutinosum*[l]	No	Grossulariaceae	E	16	2	P	534	0·5	1·1	2·2	379	O	J	Fe
690	*Roridula gorgonias* Planch.	No	Roridulaceae	E	12	2	P	186	0·2	0·4	0·8	379	O	G	Fe
691c	*Ruta graveolens* L.	No	Rutaceae	E	—[n]	—[p]	P	735	0·8	1·5	3·0	457[bm]	O	B[d]	Fe
692	*Salix alba* L.[h]	—[m]	Salicaceae	E	76[ad]	4[ad]	P	809	0·8	1·7	3·3	385[ac]	O	*Lycopers.*[c]	FC:PI
693	*Salix atrocinerea* Brot.[h]	—[m]	Salicaceae	E	76[ad]	4[ad]	P	804	0·8	1·6	3·3	385[ac]	O	*Lycopers.*[c]	FC:PI
694b	*Salix caprea* L.[h]	—[m]	Salicaceae	E	38[ad]	2[ad]	P	470	0·5	1·0	1·9	385[ac]	O	*Lycopers.*[c]	FC:PI
695	*Salix cinerea* L.[h]	—[m]	Salicaceae	E	76[ad]	4[ad]	P	828	0·8	1·7	3·4	385[ac]	O	*Lycopers.*[c]	FC:PI
696	*Salix elaeagnos* Scop.[h]	—[m]	Salicaceae	E	38[ad]	2[ad]	P	417	0·4	0·9	1·7	385[ac]	O	*Lycopers.*[c]	FC:PI
697	*Salix fragilis* L.[h]	—[m]	Salicaceae	E	76[ad]	4[ad]	P	843	0·9	1·7	3·4	385[ac]	O	*Lycopers.*[c]	FC:PI
698	*Salix purpurea* L.[h]	—[m]	Salicaceae	E	38[ad]	2[ad]	P	461	0·5	0·9	1·9	385[ac]	O	*Lycopers.*[c]	FC:PI
699	*Salix pyrenaica* Gouan[h]	—[m]	Salicaceae	E	38[ad]	2[ad]	P	470	0·5	1·0	1·9	385[ac]	O	*Lycopers.*[c]	FC:PI
700	*Salix triandra* L.[h]	—[m]	Salicaceae	E	38[ad]	2[ad]	P	387	0·4	0·8	1·6	385[ac]	O	*Lycopers.*[c]	FC:PI
701	*Salix viminalis* L.[h]	—[m]	Salicaceae	E	38[ad]	2[ad]	P	402	0·4	0·8	1·6	385[ac]	O	*Lycopers.*[c]	FC:PI
702	*Salix viminalis* L.[h]	—[m]	Salicaceae	E	76[ad]	4[ad]	P	794	0·8	1·6	3·2	385[ac]	O	*Lycopers.*[c]	FC:PI
703a	*Sambucus nigra* L.	No	Adoxaceae[k]	E	36°	2	P	14,945.[bo]	15·3[bo]	30·5[bo]	61·0[bo]	457[bm]	O	B[d]	Fe
704	*Santalum album* L.	No	Santalaceae	E	20°	—[p]	P	282	0·3	0·6	1·2	454	O	B[c]	Fe
705b	*Saxifraga granulata* L. ssp. *granulata*	No	Saxifragaceae	E	22	—[p]	P	662	0·7	1·4	2·7	453	O	G[c]	FC:EB
706	*Saxifraga granulata* L.	No	Saxifragaceae	E	—[bj]	—[p]	P	1,122	1·1	2·3	4·6	453	O	G[c]	FC:EB

APPENDIX. *(continued, the superscript letters refer to notes preceding this table)*

Entry number[g]	Species	Voucher	Family	Higher group[#]	2n‡	Ploidy level (*x*)	Life cycle type[§]	DNA amount 1C (Mbp[s])	1C (pg)	2C (pg)	4C (pg)	Original ref.[a]	Present amount[†]	Standard species[*b1]	Method[††]
707a	*Saxifraga granulata* L.	No	Saxifragaceae	E	52	—[p]	P	2,332	2·4	4·8	9·5	453	O	G[c]	FC:EB
707b	*Saxifraga granulata* L. ssp. *fernandesii* Redondo & Horjales[i]	No	Saxifragaceae	E	44-56	—[p]	P	1,735	1·8	3·5	7·1	453[bi]	O	G[c]	FC:EB
708	*Schisandra rubriflora*[l]	No	Schisandraceae	BA	—[n]	—[p]	P	8,938	9·1	18·2	36·5	381	O	G	FC:PI
709	*Schleichera oleosa* (Lour.) Oken	No	Sapindaceae	E	32°	—[p]	P	1,142	1·2	2·3	4·7	454	O	B[c]	Fe
710b	*Scilla indica* (Roxb.) Baker (cytotype II)	No	Asparagaceae	M	30	—[p]	P	3,504	3·6	7·2	14·3	422[ar]	O	B[c]	Fe
710c	*Scilla indica* (Roxb.) Baker (cytotype I)[h]	No	Asparagaceae	M	30	—[p]	P	5,701	5·8	11·6	23·3	422[ar]	O	B[c]	Fe
711	*Scilla nervosa* (Burch.) J.P.Jessop	No	Asparagaceae	M	38	—[p]	P	3,964	4·0	8·1	16·2	422	O	B[c]	Fe
712f	*Scilla siberica* Haw. in Andr.	No	Asparagaceae	M	12	2	P	30,135	30·8	61·5	123·0	422	O	B[c]	Fe
713	*Scilla talosii* D.Tzanoudakis & Kypriotakis	No	Asparagaceae	M	c. 150	—[p]	P	45,840	46·8	93·6	187·1	465	O	B	Fe
714c	*Scilla vindobonensis* Speta	No	Asparagaceae	M	18	3	P	—[t]	—[t]	17·9	35·7	422	O	B[c]	Fe
715	*Scindapsus pictus* Hassk	No	Araceae	M	60	—[p]	P	11,517	11·8	23·5	47·0	411	O	B[c]	Fe
716	*Sedum acre* L.	No	Crassulaceae	E	—[n]	—[p]	P	1,225	1·3	2·5	5·0	457[bm]	O	B[d]	Fe
717	*Sedum album* L.	—[m]	Crassulaceae	E	34	2	P	142	0·1	0·3	0·6	398	O	—[w]	—[r]
718	*Sedum forsterianum* Sm.	—[m]	Crassulaceae	E	24	2	P	451	0·5	0·9	1·8	398	O	—[w]	—[r]
719	*Sedum montanum* Song. & Perrier	—[m]	Crassulaceae	E	34	2	P	515	0·5	1·1	2·1	398	O	—[w]	—[r]
720a	*Sedum obtusifolium* C.A.Meyer	—[m]	Crassulaceae	E	12	2	P	206	0·2	0·4	0·8	398	O	—[w]	—[r]
720b	*Sedum obtusifolium* C.A.Meyer	—[m]	Crassulaceae	E	12	2	P	206	0·2	0·4	0·8	399	O	B-723b	Fe
721	*Sedum obtusifolium* C.A.Meyer	—[m]	Crassulaceae	E	30	5	P	—[t]	—[t]	1·7	3·4	399	O	B-723b	Fe
722	*Sedum ochroleucum* Chaix	—[m]	Crassulaceae	E	34	2	P	446	0·5	0·9	1·8	398	O	—[w]	—[r]
723a	*Sedum rupestre* L. ssp. *erectum*	—[m]	Crassulaceae	E	64	4	P	1,014	1·0	2·1	4·1	398	O	—[w]	—[r]
723b	*Sedum rupestre* L. ssp. *rupestre*	—[m]	Crassulaceae	E	—[n]	—[p]	P	2,244	2·3	4·6	9·2	399	O	B	Fe
724	*Sedum sediforme* (Jacq.) Pau	—[m]	Crassulaceae	E	32	2	P	568	0·6	1·2	2·3	398	O	—[w]	—[r]
725	*Sedum spurium* Bieb.	—[m]	Crassulaceae	E	28	4	P	1,735	1·8	3·5	7·1	399	O	B-723b	Fe
726	*Sedum spurium* Bieb.	—[m]	Crassulaceae	E	42	6	P	2,764	2·8	5·6	11·3	399	O	B-723b	Fe
727a	*Sedum stellatum* L.	—[m]	Crassulaceae	E	10	2	P	289	0·3	0·6	1·2	399	O	B-723b	Fe
727b	*Sedum stellatum* L.	—[m]	Crassulaceae	E	10	2	P	289	0·3	0·6	1·2	398	O	—[w]	—[r]
728a	*Sedum stoloniferum* S.G.Gmelin	—[m]	Crassulaceae	E	14	2	P	309	0·3	0·6	1·3	399	O	B-723b	Fe
728b	*Sedum stoloniferum* S.G.Gmelin	—[m]	Crassulaceae	E	14	2	P	309	0·3	0·6	1·3	398	O	—[w]	—[r]
729	*Senecio viscosus* L.	No	Compositae[j]	E	—[n]	—[p]	A	1,519	1·6	3·1	6·2	457[bm]	O	B[d]	Fe
730	*Sesamum alatum* Thonn.	No	Pedaliaceae	E	26	2	A	1,651	1·7	3·4	6·7	446	O	G	Fe
731	*Sesamum capense* Burm.	No	Pedaliaceae	E	26	2	A	1,188	1·2	2·4	4·9	446	O	G	Fe
732	*Sesamum indicum* L.	No	Pedaliaceae	E	26	2	A	951	1·0	1·9	3·9	446	O	G	Fe
733	*Sesamum laciniatum* Klein.	No	Pedaliaceae	E	32	4	A	1,154	1·2	2·4	4·7	446	O	G	Fe
734	*Sesamum latifolium* Gillett.	No	Pedaliaceae	E	32	4	A	933	1·0	1·9	3·8	446	O	G	Fe
735	*Sesamum mulayanum* Nair.	No	Pedaliaceae	E	26	2	A	870	0·9	1·8	3·6	446	O	G	Fe
736	*Sesamum occidentale* Regel.	No	Pedaliaceae	E	64	8	A	1,551	1·6	3·2	6·3	446	O	G	Fe
737	*Sesamum radiatum* Schumach.	No	Pedaliaceae	E	64	8	A	1,306	1·3	2·7	5·3	446	O	G	Fe
738	*Sesamum schinzianum* Aschers.	No	Pedaliaceae	E	64	8	A	1,343	1·4	2·7	5·5	446	O	G	Fe
739	*Sesamum triphyllum* Welw. ex Aschers.	No	Pedaliaceae	E	c. 26	2	A	524	0·5	1·1	2·1	378	O	J	Fe
740b	*Sesleria albicans* Kit. ex Schult.[h]	No	Gramineae[j]	M	28°	4	P	4,748	4·8	9·7	19·4	428	O	*Homo*[f]	FC:PI
740c	*Sesleria albicans* Kit. ex Schult.[h]	No	Gramineae[j]	M	28°	4	P	4,827	4·9	9·9	19·7	428	O	*Homo*[f]	FC:PI
741	*Severinia buxifolia* (Poir.) Ten.	No	Rutaceae	E	18°	2	P	328	0·3	0·7	1·3	426	O	*Gallus*[f]	FC:PI
742	*Silene chalcedonica* L.	No	Caryophyllaceae	E	24	2	P	3,229	3·3	6·6	13·2	437	O	*Lycopers.*[c]	FC:PI
743c	*Silene latifolia* Poiret (female)	No	Caryophyllaceae	E	24	2	AP	2,808	2·9	5·7	11·5	437[az]	O	*Lycopers.*[c]	FC:PI
743d	*Silene latifolia* Poiret (male)	No	Caryophyllaceae	E	24	2	AP	2,867	2·9	5·9	11·7	437[az]	O	*Lycopers.*[c]	FC:PI

744	*Silene pendula* L.	No	Caryophyllaceae	E	24	2	A	1,152	1·2	2·4	4·7	437	O	H[c]	FC:PI
745	*Silene vulgaris* (Moench) Garcke	No	Caryophyllaceae	E	24	2	P	1,103	1·1	2·3	4·5	437	O	H[c]	FC:PI
746a	*Simmondsia chinensis* (Link) C.K.Schneid.	No	Simmondsiaceae	E	48-50	—[p]	P	723	0·7	1·5	3·0	465	O	J	Fe
747	*Spirodela polyrrhiza* (L.) Schleid.	No	Araceae[k]	M	80	4	P	292	0·3	0·6	1·2	400	O	G	Fe
748	*Spirodela punctata* (G.F.W.Meyer) Thompson	No	Araceae	M	46	2	P	363	0·4	0·7	1·5	400	O	G	Fe
749	*Stemona tuberosa* Lour.	No	Stemonaceae	M	—[n]	—[p]	P	715	0·7	1·5	2·9	379	O	J	Fe
750	*Stenotaphrum secundatum* (Walt.) Kuntze.	No	Gramineae	M	18	2	P	529	0·5	1·1	2·2	417	O	*Gallus*[f]	FC:PI
751	*Strelitzia nicolai* Regel & C. Koch	No	Strelitziaceae	M	14, 22°	2	P	566	0·6	1·2	2·3	379	O	J	Fe
752	*Streptocarpus cyaneus* S. Moore	No	Gesneriaceae	E	c. 30	2 or 4	P	662	0·7	1·4	2·7	378	O	J	Fe
753	*Stylidium adnatum* R. Br.	No	Stylidiaceae	E	30	2	P	1,495	1·5	3·1	6·1	378	O	J	Fe
754	*Stylobasium spathulatum* Desf.	No	Surianaceae	E	30	2	P	1,284	1·3	2·6	5·2	378	O	J	Fe
755	*Syngonium albo-lineatum* Bull	No	Araceae	M	22	—[p]	AP	4,628	4·7	9·4	18·9	411	O	B[c]	Fe
756	*Syngonium podophyllum* Schott	No	Araceae	M	24	—[p]	AP	4,755	4·9	9·7	19·4	411	O	B[c]	Fe
757	*Tabebuia argentea* (Bureau & K.Schum.) Britton	No	Bignoniaceae	E	—[n]	—[p]	P	782	0·8	1·6	3·2	454	O	B[c]	Fe
758	*Tamarindus indica* L.	No	Leguminosae	E	26°	—[p]	P	821	0·8	1·7	3·4	454	O	B[c]	Fe
759	*Tecoma stans* (L.) Juss. ex Kunth	No	Bignoniaceae	E	36°	—[p]	P	593	0·6	1·2	2·4	454	O	B[c]	Fe
760	*Thespesia lampas* (Cavanilles) Dalzell ex Dalzell & Gibson	—[m]	Malvaceae	E	26°	2	—[q]	1,568	1·6	3·2	6·4	444[bd]	O	G[b2]	FC:PI
761a	*Thespesia populnea* (L.) Solander ex Correa	—[m]	Malvaceae	E	26	2	P	4,018	4·1	8·2	16·4	444[bd]	O	G[b2]	FC:PI
761b	*Thespesia populnea* (L.) Solander ex Correa	No	Malvaceae	E	26°	2	P	3,011	3·1	6·1	13·3	454	O	B[c]	Fe
762	*Thespesia thespesioides* (R.Brown ex Bentham) Fryxell	—[m]	Malvaceae	E	26	2	—[q]	1,568	1·6	3·2	6·4	444[bd]	O	G[b2]	FC:PI
763	*Triteleia laxa* Benth.	No	Asparagaceae	M	28°	4	P	10,435	10·6	21·3	42·6	380	O	B	FC:PI
764	*Trochodendron aralioides* Siebold & Zucc.	No	Trochodendraceae	E	38	2	P	1,872	1·9	3·8	7·6	380	O	*Lycopers.*[c]	FC:PI
765	*Typhonium cuspidatum* Decne.	No	Araceae	M	16	—[p]	A	5,064	5·2	10·3	20·7	411	O	B[c]	Fe
766	*Typhonium trilobatum* Schott	No	Araceae	M	40	—[p]	A	6,453	6·6	13·2	26·3	411	O	B[c]	Fe
767	*Vicia canescens* Lab.	No	Leguminosae	E	10	2	P	3,058	3·1	6·2	12·5	409	O	B[c]	Fe
768a	*Vicia cracca* L. ssp. *tenuifolia*	No	Leguminosae	E	14	2	P	5,797	5·9	11·8	23·7	409	O	B[c]	Fe
768b	*Vicia cracca* L. ssp. *cracca*	No	Leguminosae	E	14	2	P	6,409[al]	6·5[al]	13·1[al]	26·2[al]	409	O	B[c]	Fe
769a	*Vicia epetiolaris* Burk.[h]	No	Leguminosae[j]	E	14	2	A	4,067	4·2	8·3	16·6	415	O	B	Fe
769b	*Vicia epetiolaris* Burk.[h]	No	Leguminosae[j]	E	14	2	A	4,533	4·6	9·3	18·5	415	O	B	Fe
770b	*Vicia eristalioides* Maxted	No	Leguminosae	E	14	2	A	9,452	9·6	19·3	38·6	406	O	*Vicia narb.*[e]	Fe
771r	*Vicia faba* L.	No	Leguminosae[j]	E	12°	2	A	12,740	13·0	26·0	52·0	457[bm]	O	B[d]	Fe
771s	*Vicia faba* L. var. *equina*	No	Leguminosae	E	12	2	A	14,377	14·7	29·3	58·7	408	O	C[d]	Fe
771t	*Vicia faba* L. 'Futura RZ'	—[m]	Leguminosae	E	—[n]	—[p]	A	12,985	13·3	26·5	53·0	384[aa]	O	*Homo*[f]	FC:PI
772a	*Vicia galilaea* Plitm. & Zoh.	No	Leguminosae	E	14	2	A	6,392	6·5	13·0	26·1	408	O	C[d]	Fe
772b	*Vicia galilaea* Plitm. & Zoh.	No	Leguminosae	E	14	2	A	7,904	8·1	16·1	32·3	409	O	B[c]	Fe
773d	*Vicia graminea* Sm.[i]	No	Leguminosae[j]	E	14	2	AB	4,969	5·1	10·1	20·3	415	O	B	Fe
774b	*Vicia hyaeniscyamus* Mout.	No	Leguminosae	E	14	2	A	7,654	7·8	15·6	31·2	408	O	C[d]	Fe
775e	*Vicia hybrida* L.	No	Leguminosae	E	12	2	A	8,306	8·5	17·0	33·9	409	O	B[c]	Fe
776e	*Vicia hyrcanica* Fisch. & Mey.	No	Leguminosae	E	12	2	A	7,634	7·8	15·6	31·2	409	O	B[c]	Fe
777c	*Vicia johannis* Tamamsch.	No	Leguminosae	E	14	2	A	6,145	6·3	12·5	25·1	408	O	C[d]	Fe
778b	*Vicia kalakhensis* Khattab, Maxted & Bisby	No	Leguminosae	E	14	2	A	10,344	10·6	21·1	42·2	406	O	*Vicia narb.*[e]	Fe
779	*Vicia macrograminea* Burk.	No	Leguminosae[j]	E	14	2	BP	5,821	5·9	11·9	23·8	415	O	B	Fe
780d	*Vicia melanops* Sibth. & Sm.	No	Leguminosae	E	10	2	A	6,764[ak]	6·9[ak]	13·8[ak]	27·6[ak]	408	O	C[d]	Fe
781	*Vicia nana* Vog.	No	Leguminosae[j]	E	14	2	A	4,376	4·5	8·9	17·9	415	O	B	Fe
782a	*Vicia pampicola* Burk.[h]	No	Leguminosae[j]	E	14	2	A	4,640	4·7	9·5	18·9	415	O	B	Fe
782b	*Vicia pampicola* Burk.[h]	No	Leguminosae[j]	E	14	2	A	5,223	5·3	10·7	21·3	415	O	B	Fe
783d	*Vicia peregrina* L.	No	Leguminosae	E	14	2	A	9,540	9·7	19·5	38·9	409	O	B[c]	Fe
784d	*Vicia pisiformis* L.[h]	No	Leguminosae	E	12	2	P	6,223	6·4	12·7	25·4	407	O	C[d]	Fe
784e	*Vicia pisiformis* L.[h]	No	Leguminosae	E	12	2	P	8,038	8·2	16·4	32·8	407	O	C[d]	Fe
785v	*Vicia sativa* L. line 20·1[i]	No	Leguminosae	E	12	2	A	1,882	1·9	3·8	7·7	409	O	B[c]	Fe
785w	*Vicia sativa* L. line 31[i]	No	Leguminosae	E	12	2	A	2,445	2·5	5·0	10·0	409	O	B[c]	Fe

APPENDIX. *(continued, the superscript letters refer to notes preceding this table)*

Entry number[g]	Species	Voucher	Family	Higher group[#]	2n‡	Ploidy level (*x*)	Life cycle type[§]	DNA amount 1C (Mbp[s])	DNA amount 1C (pg)	DNA amount 2C (pg)	DNA amount 4C (pg)	Original ref.[a]	Present amount[†]	Standard species[*b1]	Method[††]
785x	*Vicia sativa* L. ssp. *amphicarpa*	No	Leguminosae	E	12	2	A	2,102	2·1	4·3	8·6	409	O	B[c]	Fe
785y	*Vicia sativa* L. ssp. *nigra* var. *nigra*	No	Leguminosae	E	12	2	A	2,337	2·4	4·8	9·5	409	O	B[c]	Fe
786e	*Vicia sepium* L.	No	Leguminosae	E	14	2	P	4,719	4·8	9·6	19·3	409	O	B[c]	Fe
787c	*Vicia serratifolia* Jacq.	No	Leguminosae	E	14	2	A	9,700	9·9	19·8	39·6	405	O	C[c]	Fe
788d	*Viscum album* L.	No	Loranthaceae[k]	E	20°	2	P	52,430	53·5	107·0	214·0	457[bm]	O	B[d]	Fe
789	*Vitex negundo* L.	No	Lamiaceae	E	34°	—[p]	P	1,590	1·6	3·2	6·5	454	O	B[c]	Fe
790	*Vitex pinnata* L.	No	Lamiaceae	E	—[n]	—[p]	P	1,411	1·4	2·9	5·8	454	O	B[c]	Fe
791	*Voacanga grandifolia* (Miq.) Rolfe	No	Apocynaceae	E	—[n]	—[p]	P	358	0·4	0·7	1·5	454	O	B[c]	Fe
792	*Wolffia arrhiza* (L.) Horkel ex Wimmer	No	Araceae	M	42	2	P	1,600	1·6	3·3	6·5	400	O	G	Fe
793	*Wolffiella oblonga* (Phil.) Hegelm.	No	Araceae	M	42	2	P	742	0·8	1·5	3·0	400	O	G	Fe
794	*Xanthorrhoea preisii* Endl.	No	Xanthorrhoeaceae	M	22	2	P	1,014	1·0	2·1	4·1	380	O	J	Fe
795	*Xanthosoma sagittifolium* (L.) Schott	No	Araceae	M	38	—[p]	P	8,609	8·8	17·6	35·1	411	O	B[c]	Fe
796	*Xeronema callistemon* W.R.B. Oliv.	No	Xeronemataceae	M	34	2 or 4	P	3,210	3·3	6·6	13·1	380	O	G	FC:PI
797	*Xerophyta humilis* Th. Dur. & Schinz.	No	Velloziaceae	M	48°	4 or 8	P	532	0·5	1·1	2·2	378	O	J	Fe
798	*Ximenia americana* Linn.	No	Olacaceae	E	26	2	P	1,595	1·6	3·3	6·5	379	O	J	Fe
799	*Xiphidium caeruleum* Aubl. var. *caeruleum*	No	Haemodoraceae	M	38°	2	P	767	0·8	1·6	3·1	378	O	J	Fe
800	*Xyris gracilis* ssp. *gracilis*[l]	No	Xyridaceae	M	26°	2	P	6,867	7·0	14·0	28·0	380	O	B	FC:PI
801bx	*Zea mays* ssp. *mays* L. line opaque 2[h]	No	Gramineae[j]	M	20	4	A	3,262	3·3	6·7	13·3	392	O	B	Fe
801by	*Zea mays* ssp. *mays* L. race Altiplano[h]	No	Gramineae[j]	M	20	4	A	2,454	2·5	5·0	10·0	392[ag]	O	B-801bx	Fe
801bz	*Zea mays* ssp. *mays* L. race Blanco y ocho rayas[h]	No	Gramineae[j]	M	20	4	A	3,311	3·4	6·8	13·5	392[ag]	O	B-801bx	Fe
801ca	*Zea mays* L.	No	Gramineae[j]	M	20°	4	A	3,283	3·4	6·7	13·4	457[bm]	O	B[d]	Fe
802	*Zizyphus glabrata* Heyne	No	Rhamnaceae	E	24°	—[p]	P	1,517	1·5	3·1	6·2	454	O	B[c]	Fe
803	*Zostera marina*[l]	No	Zosteraceae	M	12°	2	P	309	0·3	0·6	1·3	380	O	J	Fe
804	*Zoysia japonica* Steud.	No	Gramineae	M	40	4	P	421	0·4	0·9	1·7	417	O	*Gallus*[f]	FC:PI

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