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Nuclear DNA Amounts in Angiosperms and their Modern Uses—807 New Estimates

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CONTENTS

The DNA amount in the unreplicated haploid nucleus of an organism is known as its C-value. C-values differ about 1000-fold among angiosperms and are characteristic of taxa. The data are used in many biological fields, so they should be easily available. Values for 2802 angiosperm species (1 %) were estimated during 1950–1997, and five collected lists of C-values were published for reference purposes during 1976–1997. Numbers of new angiosperm C-values published recently remained high, necessitating a further supplementary list. This paper lists DNA C-values for 807 angiosperm species from 70 original sources, including 520 (75·2 %) from sources published after 1996, and 691 for species not included in any of the previous five lists. There is a continuing need to estimate accurate DNA C-values for plant taxa, as shown in a workshop on this biodiversity topic sponsored by *Annals of Botany* and held at Kew in 1997. Its key aim was to identify major gaps in our knowledge of plant DNA amounts and to recommend targets and priorities for new work to fill them. A target of estimating first C-values for the next 1 % of angiosperm species in 5 years was set. The proportion of such C-values in the present work (85·6 %) is very high; and the number being published (approx. 220 per annum) has never been exceeded. In 1997, C-values were still unknown for most (68 %) families, so a target of complete coverage was set. This paper includes first C-values for 12 families, but as less than 2 % of such values listed here targeted new families, the need to improve familial representation remains.

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

INTRODUCTION

The DNA amount in the unreplicated haploid or gametic nucleus of an organism is referred to as its C-value (Swift, 1950), irrespective of the ploidy level of the taxon. C-value equals genome size in diploid species, but always exceeds genome size(s) in polyploid species. Nuclear DNA C-values differ by approx. 1000-fold among angiosperms, ranging from about 0·1 pg to about 125 pg, and tend to be characteristic for a taxon. C-values are used in many

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biological fields, so they should be easily available for reference and analysis. Five collected lists of nuclear DNA amounts have been published for reference purposes (Bennett and Smith, 1976, 1991; Bennett *et al.*, 1982; Bennett and Leitch, 1995, 1997). These were recently pooled into one combined list with C-values for 2802 species from 306 original sources. A first version of the Angiosperm DNA C-values database was published electronically in April 1997, and a new relational version (release 2.0) went live in October 1998 (http://www.rbgkew.org.uk/cval/database1.html). The number of new angiosperm C-values published recently has continued to be high, necessitating the production of a further supplementary list. This paper lists DNA C-values for 807 angiosperm species from 70 original sources, including 520 (75·2 %) from sources published or communicated after 1996, and 691 for species not included in the previous five lists.

The Angiosperm Genome Size Workshop, September 1997

Nuclear DNA C-value and genome size are important biodiversity characters. As with other factors it is important to know how much information is available, who needs it, and also to assess what it is used for and the impact of those uses (Bennett, 1998). A preliminary analysis of these questions was presented by Bennett and Leitch (1995). This led to informal discussions among a small international group of interested scientists, and later to a workshop and discussion meeting held at the Royal Botanic Gardens, Kew (RBG, Kew) in September 1997 which was sponsored by *Annals of Botany*. These were attended by about 90 scientists from 15 countries with special expertise or interest in generating and using information on plant nuclear DNA amounts, and were highly focused on the questions listed above. Fourteen papers from the discussion meeting were published in a special issue 'Genome size in plants' in *Annals of Botany* volume 82 (Supplement A) in 1998 (Bennett and Leitch, 1998). A report on the workshop's recommendations was given orally to participants at the discussion meeting, but its valuable work merits wider exposure. This paper, listing angiosperm C-values published mainly in 1997–1999, is a suitable vehicle in which to mention some key conclusions of that 1997 workshop. One recommendation was to hold a similar workshop in about 5 years to assess progress in the field. Half of that period has already elapsed, and new work on plant C-values undertaken since the 1997 workshop has begun to be published. It is timely, therefore, (1) to mention the main targets for new work agreed in 1997; (2) to assess progress towards the 5-year goals set; and (3) to monitor how plant DNA C-value information is being used.

One useful measure of interest in angiosperm DNA C-values comes from calculating the numbers of estimates communicated per year, and establishing any trend in this factor. Analysis of such estimates for the 3493 species listed in the pooled Angiosperm DNA C-values database and the present work shows a continuing strong increase in the mean number per year of total estimates and the mean number of 'prime' estimates (usually the first) for species listed for all but one of eight successive 5 year periods

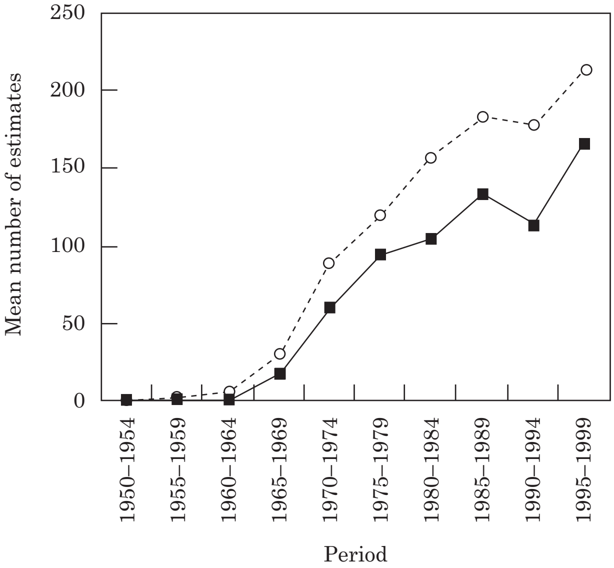

FIG. 1. Mean number per year of total (- - -○- - -) and 'prime' (—■—) DNA C-value estimates communicated in ten successive 5 year periods between 1950 and 1999. Based on analysis of 3493 DNA C-values pooled from the Angiosperm DNA C-values database (Bennett *et al.*, 1997) and this paper.

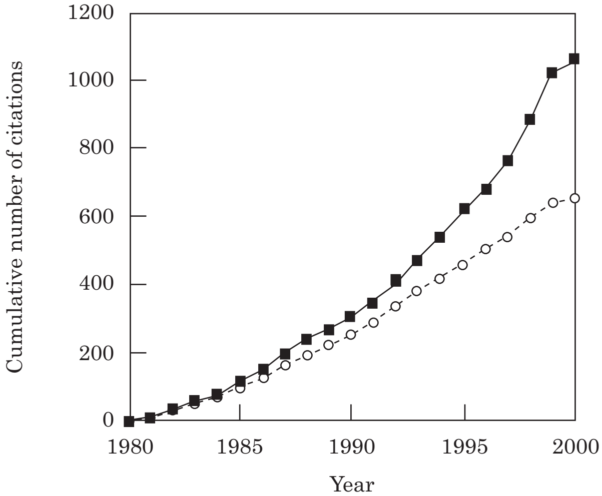

FIG. 2. Cumulative number of citations for the first nuclear DNA reference list (Bennett and Smith, 1976) (- - -○- - -) and for all DNA lists (—■—) i.e. Bennett and Smith (1976, 1991), Bennett *et al.* (1982), and Bennett and Leitch (1995, 1997) between 1980 and May 2000.

during 1960 to 1999 (Fig. 1). For example, the mean total number of new estimates per year rose over ten-fold, from about 18 in the 1960s to almost 200 in the 1990s. Clearly interest in C-values, as judged by the mean annual output of new data, continues to increase.

A further measure of the use of C-value estimates comes from how often they are cited. Analysis of the Science Citation Index shows that the first collected list (Bennett and Smith, 1976) has now been cited over 650 times, including 239 times in the last 5 years (1995–1999) (Fig. 2). Moreover, by 1999 the two most recently published lists (Bennett and Leitch, 1995, 1997) already had 94 and 22 citations listed, respectively. Altogether the various lists have been cited over 1060 times.

The Angiosperm DNA C-values database available on the internet (http://www.rbgkew.org.uk/cval/database1.html) has automatic logging of the e-mail address, taxonomic query, and number of species' C-values supplied (including zero), for all enquiries. The log shows that there were 6955 successful scientific enquiries in the first 18 months, and over 10 000 in the 16 months after release 2.0 went live in October 1998. So there is also a large and growing use of C-value data by this means.

Examining the database log and the Science Citations Index of DNA C-value reference lists reveals a wide range of countries and disciplines using these data. C-value enquiries logged in 1999 came from at least 43 countries on five continents. Moreover, since 1995 the DNA C-value reference lists were cited, or provided data used for comparative studies at levels ranging from the biosphere to genome organization and the size of introns, and in many diverse disciplines including: taxonomy and systematics (Kiehn, 1995; Ebert *et al.*, 1996; Cox *et al.*, 1998; Ohri *et al.*, 1998); genome evolution and phylogeny (Bennetzen and Kellogg, 1997; Bennetzen *et al.*, 1998; Kellogg, 1998; Leitch *et al.*, 1998; Voytas and Naylor, 1998; Vinogradov, 1999); ecology and the environment (MacGillivray and Grime, 1995; Bennett *et al.*, 1998); genomics (Dunford *et al.*, 1995; Moore, 1995; Foote *et al.*, 1997; Geisler *et al.*, 1999; Somerville and Somerville, 1999); plant breeding (Riera Lizarazu *et al.*, 1996); cell and molecular biology (Dean and Schmidt, 1995; Jeddeloh and Richards, 1996; Vershinin and Heslop-Harrison, 1998); conservation (Rejmanek, 1996; Bennett and Leitch, 2000); and physiology and development (Butterfass, 1995; Xia Xh, 1995; Bharathan, 1996; Convey, 1996; Raven, 1999). Some of these uses are described in more detail below. Several authors have recently noted a need for additional C-value data for more plant species in order to extend their comparative studies. For example, specific needs were for more grass taxa (Jasienski and Bazzaz, 1995), and for more higher order taxa among angiosperms (Leitch *et al.*, 1998).

IDENTIFYING GAPS IN OUR KNOWLEDGE OF PLANT C-VALUES

Given the broad and growing demand for plant DNA C-values it is clearly important to monitor what is known, and to recognize what is unknown and needed most (Bennett, 1998). Consequently, a first key aim of the 1997 workshop was to identify major gaps in our knowledge of plant DNA C-values and to recommend targets and priorities for new work to fill them by international collaboration. Presentations on regional floras, and analysis of representation of data in the Angiosperm DNA C-values database, highlighted huge gaps in our knowledge, both in terms of the low numbers of species represented, but also in terms of systematic, life form, ecological and geographic representation. For example, a first DNA C-value estimate was still unavailable for the large majority (approx. 68 %) of angiosperm families (Table 1).

TABLE 1. *The level of representation at different taxonomic levels for the 2802 species listed in the Angiosperm DNA C-values database in September 1997*

Taxonomic level	Number recognized	Number with DNA C-values available	Representation (%)
Families	approx. 475*	151	approx. 31·8
Genera	approx. 13 479*	772	approx. 5·7
Species	approx. 250 000†	2802	approx. 1·1

* Brummitt (1992); †Mabberley (1997).

TABLE 2. *The level of representation of C-value data for non-angiosperm plants in September 1997*

Group	Number of species recognized	Number of species with DNA C-values available	Representation (%)
Gymnosperms	approx. 730*	117	approx. 16·03
Pteridophytes	approx. 9250†	39	approx. 0·42
Bryophytes	approx. 18 400‡	18	approx. 0·10

* Murray (1998); † Mabberley (1997); ‡ Schofield (1995).

At the workshop Murray reviewed our knowledge of C-values in non-angiosperm plants where, in some groups, there were not 'intermittent gaps' but almost 'one continuous gap' (Table 2). Representation was much better for gymnosperms than angiosperms, as values were published for approx. 16 % of gymnosperm species (Murray, 1998) compared with approx. 1 % for angiosperms. The situation was worse for pteridophytes (approx. 0·42 %), and almost no C-value data were known for bryophytes (approx. 0·1 %), although locating data for these two groups had proved very difficult [e.g. 23 of the 39 C-values known for pteridophytes were published only in a Ph.D thesis (Bouchard, 1976)].

The workshop concluded that this level of ignorance was unsafe and unacceptable. New targeted work was essential to improve representation of both the angiosperm flora and of the other least-known plant groups. The difficulties encountered in locating DNA amount data for review at the workshop clearly demonstrated the value of user-friendly reference works. Thus, there was a clear need to bring together DNA amount data for species in other groups besides angiosperms, and make them easily accessible in one plant C-values database.

Long-term and 5-year targets were set. The ideal of a C-value for every taxon is unrealistic. However, estimates for 10–20 % of plants seemed both ultimately achievable and adequate for all conceivable uses, provided these were carefully targeted to represent the various taxonomic groups, geographical regions, and life forms in the global flora. C-values for about 2800 (approx. 1 %) angiosperm species had been estimated in the last 40 years. However, a 5-year target of estimating first C-values for the next 1 % of angiosperm species (i.e. an additional 2500 species) by 2002 seemed possible and was therefore recommended. Meeting this target would require on average at least 500 first C-value estimates per year.

FILLING MAJOR GAPS IN OUR KNOWLEDGE OF PLANT C-VALUES

Recent progress towards meeting the targets for angiosperms

Only 33 months elapsed between closing the angiosperm C-value list for Bennett and Leitch (1997) in January 1997, and for the present work in October 1999. This paper lists first DNA C-values for 691 angiosperm species known to us (520 published in papers dated 1997–1999), so an average of at least 165 first estimates for such species was published per annum in this period. On past record this is an underestimate, as about 25 % of the values estimated in such a period are missed or uncommunicated, but are included in a later supplement (N.B. 520/691 = 75·3 %). If so, at least 220 first estimates were published in each recent year. How does this compare with the long-term historical rate, recent trends, and with the target set at the 1997 workshop?

The total number of angiosperm species whose C-values are listed in the pooled Angiosperm DNA C-values database and the present work is 3493, published since 1960 at an average rate of about 85 per year. Numbers fluctuate considerably between years (Bennett and Leitch, 1995). However, analysis shows a continuing strong increase in the mean number of 'prime' estimates (usually the first) for species (Fig. 1) listed in the four successive decades from 1960–1999. The mean total number of 'new/prime' estimates per year rose steadily from 8·6 in the 1960s to almost 140 in the 1990s, reaching 165·4 in 1995–99, and 203 in 1998–99. Thus, the output of such values is rising in the long term, and increasingly so in recent years.

Clearly, good progress has been made towards achieving the target set at the 1997 workshop. First C-value estimates for angiosperm species are being published at the highest rate known (approx. 220 per annum), but even at this record rate the total number of such values estimated by 2002 (approx. 1100) would be < 50 % of the minimum (2500) target set. To reach this target, output of first C-value estimates for angiosperms must triple to about 600 per annum in 2000–2002. Normally at least 2 years elapse between planning C-value research and publishing new data. Work influenced by the September 1997 workshop would not appear before late 1999, so its impact on annual output should be very minimal so far. Whether the target set in 1997 has been influential in raising the annual output of first C-values for angiosperm species significantly above the historical trend may be unclear before 2002.

It is also important to monitor other qualitative aspects of new C-value estimates. Bennett and Leitch (1995) noted a need for new work to focus on obtaining first C-values for species rather than unnecessarily multiplying DNA estimates for taxa whose C-values are already well known. Analysis shows (Fig. 3) that while the proportion of C-values for 'new' taxa tended to fall (from approx. 80 % to approx. 60 %) in the 1970s and 1980s, it has tended to rise again (from approx. 60 to approx. 80 %) in the 1990s, since this problem was first noted. Indeed the proportion of such C-values in the present Appendix (691/807 = 85·6 %) is encouragingly high.

Bennett and Leitch (1995) noted that none of the 269 original references to DNA C-values listed was from China, and this remained so for 306 original references listed before the 1997 workshop. However, the present work includes values for taxa of *Vicia* from North East China (Li and Liu, 1996) and for grain amaranths (Sun *et al.*, 1999), both by first authors in China. It also lists the first estimates contributed with first authors of original sources from several other countries including: Bulgaria (Dimitrova *et al.*, 1999), Croatia (Zoldoš *et al.*, 1998), Finland (Antonius and Ahokas, 1996; Bukhari, 1997; Keskitalo *et al.*, 1998) and Turkey (Akpinar and Yildes, 1999), besides Ethiopia (Ayele *et al.*, 1996) and Colombia (Martínez *et al.*, 1994). Such work is now less concentrated in a few first world countries like the UK (down from 29·7 % of 306 original sources previously, to 11·4 % for the present Appendix), but Africa remains an unexplored continent. 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 report work done in Europe or the USA. More encouragingly, C-values for 42 *Lonchocarpus* (Leguminosae) taxa represent the first large sample (31 % of species) from a tropical arboreal genus (Palomino and Sousa, 2000). Moreover, nuclear DNA amounts for 41 primitive dicot species (Morawetz and Samuel, pers. comm.) more than doubled our knowledge of C-values in this important phylogenetic group as values for only 31 species were known previously.

Bennett and Leitch (1997) also noted a need to target new work to achieve better systematic representation, as no estimate was available for about 68 % of angiosperm families. The 1997 workshop confirmed this, and set a

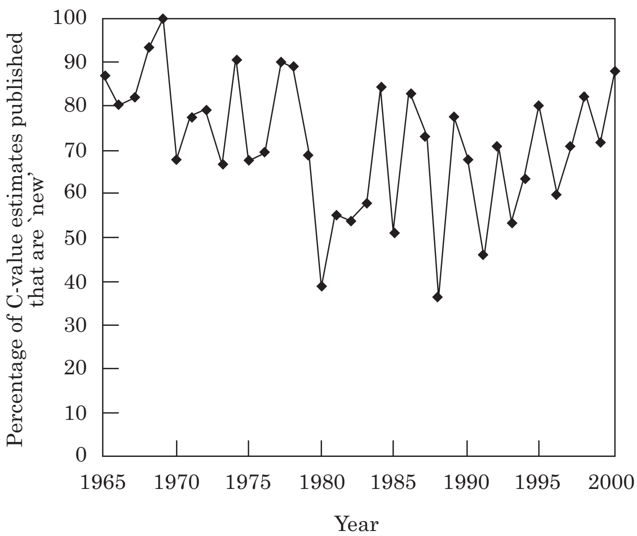

FIG. 3. Percentage of DNA C-value estimates published or communicated during 1965–2000 that are first values for species listed in the Angiosperm DNA C-values database (Bennett *et al.*, 1997) or the present work.

target of complete familial coverage by 2002. The present Appendix lists first C-values for 12 families unrepresented on previous lists (namely: Anemarrhenaceae, Calycanthaceae, Canellaceae, Chloranthaceae, Eupomatiaceae, Hernandiaceae, Juglandaceae, Monimiaceae, Myristicaceae, Paeoniaceae, Phytolaccaceae and Schisandraceae). This is useful progress, but it shows that less than 2 % of the 691 first C-value estimates for angiosperms listed in the present Appendix were targeted on new families. The need to improve representation at the family level remains, so work targeted to fill this gap for 50 unrepresented families by 2001 is ongoing at RBG, Kew.

Recent progress towards meeting the target for non-angiosperms

The 1997 workshop concluded that new work on other plant groups besides angiosperms was essential, and there was a clear need to bring together published C-value data for these groups and to make them easily accessible. Soon afterwards a list of DNA C-values for 117 gymnosperm species was published (Murray, 1998), making them available in a user-friendly form as a reference source for the first time. These data, with their associated information were presented in a table similar to that used for angiosperm C-values in recent papers (Bennett and Leitch, 1995, 1997). This standard format was adopted to help users move easily from one to the other, and to facilitate combining them into a unified plant DNA C-values database in 2000.

Murray (1998) listed C-values for 12 out of 17 gymnosperm families, noting that systematic coverage was very uneven, and that 'the order Gnetales would appear to be a group where more measurements of genome size are needed if any meaningful phylogenetic relationship in genome size is to be revealed'. Few C-values have been estimated for gymnosperms since 1997. Hall *et al.* (2000) give values for 11 *Pinus* taxa from Central America, which include eight species not previously listed by Murray (1998). Estimates for six previously unlisted *Ephedra* species (Gnetales) were also made (Winfield and Leitch, unpubl. res.). Thus, scope remains to improve the systematic coverage of gymnosperms, with first C-values for the five as yet unrepresented families being addressed at RBG, Kew as a prime target.

Published estimates of C-values for pteridophytes remained rare in the 1990s. Tan and Thompson (1990) gave C-values for several subgroups in the genus *Pteridium* (including *P. aquilinum* and *P. esculentum*). Recently C-values for eight species in the Aspleniaceae (Redondo *et al.*, 1999*a*) and three *Polypodium* species (Redondo *et al.*, 1999*b*) were published. The need for targeted work on C-values in pteridophytes seems undiminished.

The most significant recent advance in systematic coverage is for mosses (Bryatae) where estimates for only about ten species were known before 1997 (Reski *et al.*, 1994; Renzaglia *et al.*, 1995). Since 1997, estimates for a further 34 species were published (Lamparter *et al.*, 1998; Temsch *et al.*, 1998, 1999; Zouhair and Lecocq, 1998). Voglmayr (2000) estimated C-values for 289 accessions of 138 different moss taxa in 34 families in a carefully targeted study whose main aim was to cover a representative spectrum of moss taxa. This benchmark study showed that 1C-values in these bryophytes varied only about 12-fold (from 0·174 to 2·16 pg), which is remarkable compared with about 1000-fold variation in angiosperms. Moreover, the relative constancy of C-values in many genera and families suggests that the incidence of secondary polyploidy among mosses is much lower than has been claimed (Ramsay, 1983; Voglmayr, 2000). These results agree with those obtained by Renzaglia *et al.* (1995) for 17 bryophyte species (hornworts, liverworts and mosses) showing only 24-fold variation. Renzaglia *et al.* (1995) suggested that selection for a narrow range of low C-values may act on the reduced efficiency of biflagellate motile sperm cells with increasing ploidy level and/or DNA C-values.

Together, the new work already completed or known to be in hand suggests that the recommendations of the 1997 workshop will have been influential in achieving some significant improvement in our knowledge of, and access to, DNA C-values in non-angiosperm groups. Thus, by 2001 we plan to release a first electronic plant DNA C-values database combining data for at least 325 species of pteridophytes, bryophytes and gymnosperms, and about 3500 angiosperms.

TECHNICAL TRENDS AND LIMITING FACTORS IN C-VALUE WORK

Recent trends in methods of choice for plant C-value estimation

Limited space precludes an analysis of all the technical recommendations of the 1997 workshop, so discussion here is limited to a few key points. Further details are given on the web [http://www.rbgkew.org.uk/cval/conference.html (under Angiosperm Genome Size Discussion Meeting)].

Several authors have discussed the choice of material(s) for use as calibration standard(s) to estimate C-values in plants, and/or the reliability of their assumed C-values (Bennett and Smith, 1976; Price *et al.*, 1980; Greilhuber and Ebert, 1994; Bennett and Leitch, 1995; Johnston *et al.*, 1999). Bennett and Leitch (1995) stated: (1) that ideally only one strain of a standard species from a single source should be used to improve comparability between laboratories; (2) for technical reasons several species are needed whose DNA C-values are distributed at suitable intervals over the large range of C-values known for plants; and (3) such calibration standards should all be calibrated against one base calibration standard. This 'ideal' is approached by the use of *Allium cepa* 'Ailsa Craig' and of defined cultivars of several other species all calibrated against it (Bennett and Smith, 1976). As noted by Bennett *et al.* (2000), *Allium cepa* has been informally adopted by common usage as the main calibration standard for C-value estimations in angiosperms. At least 143 (= 46·7 %) of 306 original sources of data listed in Bennett *et al.* (1997) used *A. cepa* with an assumed 4C DNA amount of 67·1 (or 67·0) pg, as a calibration standard.

Calibration standards are of fundamental importance for accurate plant C-value estimations. Indeed, many discrepancies in C-values reported for the same species probably reflect problems associated with the choice and use of calibration standards rather than genuine intraspecific variation. C-values for chicken red blood cells (CRBC) vary between authorities and breeds. Moreover, CRBC show different hydrolysis curves from plants (Johnston *et al.*, 1999). In view of these problems the 1997 workshop recommended that animal standards, such as CRBC, should not be used as calibration standards for estimating plant C-values.

The characteristics of ideal plant calibration standards were discussed. It was agreed that they should be diploid (to minimize variation owing to aneuploidy), single cultivars of a species, easily available from more than one source, stable, and suitable for both flow cytometry and Feulgen microdensitometry. Three basic standards conforming to these criteria were recommended at the workshop (*Allium cepa* 'Ailsa Craig', *Hordeum vulgare* 'Sultan', and *Pisum sativum* 'Minerva Maple'). Collaborative work to identify and agree other suitable calibration standards is needed. Candidates included: *Raphanus sativus*, *Lycopersicon esculentum* and *Vicia faba*.

Analysis shows that 77·2 % of DNA estimates in the Appendix of the present work were made using a plant calibration standard, but 22·8 % used an animal calibration standard. Thus, the recommendation made by Price *et al.* (1980) and confirmed at the 1997 workshop is only partly followed as yet. However, while 97·1 % of estimates based on an animal calibration standard used one species (chicken), estimates based on plant standards used many taxa for calibration [see (b) and (e) in 'Notes to the Appendix'], and no one species predominated. Analysis of the data in the Appendix shows that 237 such estimates (25·7 %) used *Hordeum vulgare*, 235 (25·6 %) used *Allium cepa*, but only 55 (6·0 %) used *Pisum sativum*. Thus, > 57 % of such estimates used the three plant species recommended in 1997 as calibration standards.

Work to improve further the accuracy and reliability of, and confidence in, plant calibration standards has begun (e.g. Johnston *et al.*, 1999; Bennett *et al.*, 2000). It has also been suggested that extra calibration standards are needed which readily produce seed in tropical conditions (Guerra, pers. comm. 1998). Recommended standards which thrive in temperate environments (e.g. *Pisum sativum*, *Allium cepa* and *Hordeum vulgare*) can be difficult to maintain in tropical conditions.

A key observation regarding flow cytometry was that co-chopping of tissues from a calibration standard and an unknown is essential, as using an external standard to estimate C-values can cause unacceptable errors (Price, pers. comm. 1998). The 1997 workshop also recommended that the non-base specific intercalating stain propidium iodide be used as the fluorochrome of choice for DNA estimations by flow cytometry, at a concentration of 50 to 70 ppm. Analysis of the fluorochromes used to estimate C-values among the 447 taxa in the Appendix studied using flow cytometry (Table 3) shows that 390 and 50 (i.e. over 98 %) used propidium iodide or ethidium bromide, respectively, while only four and three used mithramycin or DAPI, respectively. These proportions represent a major shift from earlier work (Table 3). Thus, the advice to use non-base specific fluorochromes rather than base specific fluorochromes (Doležel *et al.*, 1992, 1998; Bennett and Leitch, 1995) which was recommended as best practice by the recent workshop, is now widely followed. Moreover, the use of propidium iodide (as the fluorochrome of first choice) outstrips that of ethidium bromide by almost 8 : 1, which may reflect health and safety concerns as the latter is a known frame shift and UV-sensitive mutagen in man.

Bennett and Leitch (1995, 1997) compared strengths and weaknesses of flow cytometry and Feulgen microdensitometry as the two main modern methods of choice for estimating DNA C-values in angiosperms, and described trends in their use. Analysis of the data for 919 C-value estimates in the present Appendix shows that 472 (51·4 %) were obtained using Feulgen microdensitometry and 437 (48·6 %) using flow cytometry. These proportions are similar to those for 469 estimates listed by Bennett and Leitch (1995) for original data published during 1990–1994, namely 51 % flow cytometry and 49 % Feulgen microdensitometry, but show a reduction in the proportion estimated by Feulgen microdensitometry from 65·6 % for 629 taxa listed by Bennett and Leitch (1997). Nevertheless, these new data continue to confirm the conclusion (Bennett and Leitch, 1997) that despite its potential, flow cytometry is unlikely to replace Feulgen microdensitometry for estimating DNA C-values in the short term. Indeed, Feulgen methods will probably be preferred in many places, although an important imminent problem was identified at the workshop.

The 'obsolescence time bomb' threatening plant C-value research

A major factor likely to limit progress in plant C-value research is the 'obsolescence time bomb' of ageing microdensitometers. Several workers noted that the equipment they used for Feulgen microdensitometry was considered

TABLE 3. *Analysis of the type of fluorochrome used to estimate C-values by flow cytometry in plant taxa listed in Bennett and Leitch (1995, 1997) and this paper*

	Number of C-values		
Fluorochrome	Bennett and Leitch (1995)	Bennett and Leitch (1997)	This paper
Base-specific			
DAPI	27 (9 %)	34 (23 %)	3 (1 %)
Mithromycin	35 (12 %)	0 (0 %)	4 (1 %)
Subtotal	62 (21 %)	34 (23 %)	7 (2 %)
Intercalating			
Ethidium bromide	37 (13 %)	13 (9 %)	50 (11 %)
Propidium iodide	195 (66 %)	104 (69 %)	390 (87 %)
Subtotal	232 (79 %)	117 (77 %)	440 (98 %)
Total	294 (100 %)	151 (100 %)	447 (100 %)

DAPI, 4′,6-diamidino-2-phenylindole.

obsolete and close to irreparable failure. For example, a high proportion of new C-value estimates were estimated using Vickers M85 microdensitometers made in the 1980s but now unsupported by the manufacturer. Without replacements there was already a serious risk that C-value estimation may cease in several countries (Mexico, Argentina etc.), so preventing regional and global targets from being met. Specialist replacement microdensitometers, developed mainly for medical purposes, are expensive, probably prohibitively so, especially for developing countries. Two alternative technologies considered were flow cytometry, provided that a rugged, low-cost machine suited for conditions in developing countries becomes available, and computerized image analysis systems. In 1997 the latter seemed too expensive for most users, but recently several papers have presented C-value estimates for angiosperms (Dimitrova *et al.*, 1999), bryophytes (Temsch *et al.*, 1998) and fungi (Voglmayr and Greilhuber, 1998), obtained using a basic video-based image analysis method. Unlike flow cytometry, where nuclei are unseen by the operator and chromosome numbers must be checked in separate cytological studies, this method is highly advantageous, allowing chromosome number and ploidy level to be assessed directly in Feulgen-stained nuclei on the same slide used to estimate C-values. Thus, Feulgen staining seems likely to continue as a method of choice but will increasingly use computerized image analysis techniques.

Connecting C-values given only in arbitrary units with the database

About 10 % of all angiosperm DNA estimates have been published only in arbitrary units and do not connect with a database for taxa given in absolute units. Action to avoid wasting so much potential information is worthwhile. The importance of including a taxon of known C-value as a calibration standard in work to study DNA amounts in taxa where this is unknown to maximize the value of the work has often been noted (Bennett and Smith, 1976, 1991). Analysis of the new data in the Appendix shows that the practice of publishing relative DNA amounts in arbitrary units alone is now generally defunct. Data from only two original references giving DNA amounts in arbitrary units are included in the Appendix. However, both were published in 1984. These data for 37 *Carex* and 12 Marantaceae species were all converted to absolute values in our laboratory [see Appendix footnotes (ao) and (ap)]. Overall, using this approach, we have brought absolute C-values for 490 species (14 % of the total) onto the quantitative list since 1976, and this contributes 'prime' values for 343 species (9·8 % of the total) in the Angiosperm DNA C-values database and the present work. More opportunities to increase substantially our knowledge of C-values in this way seem unlikely, as we are unaware of further references giving significant numbers of prime DNA estimates in arbitrary units alone. However, we would welcome information of references or unpublished data of any further bodies of such data if, as seems likely, some examples still exist.

MODERN USES OF PLANT C-VALUE AND GENOME SIZE DATA

DNA C-values in modern molecular practice

DNA C-value remains a key character in biology and biodiversity. Genome size has many important practical implications at many different levels. For example, species with large DNA amounts (i.e. 1C greater than 20 pg) can be problematic when studying genome diversity using the standard AFLP^{TM} technique [designed for genomes of 500–6000 Mbp (approx. 0·5–6 pg); Perkin-Elmer, 1996] with three selective bases on each primer, and it may be necessary to increase the number of selective bases or to change the restriction enzymes. AFLP traces for *Cypripedium calceolus* using the standard protocol are suboptimal (Fay and Cowan, pers. comm.) as a result of its large DNA amount (1C = 32·4 pg—see Appendix). Similar problems have been encountered by Han *et al.* (1999) in *Alstroemeria* species (1C = approx. 22 pg), and by Costa *et al.* (2000) in *Pinus pinaster* (1C = 24 pg).

Moreover, possession of a very small DNA content has been a major factor in determining which taxa were chosen as the first candidates for genome sequencing, and which chromosome(s) in the karyotypes of various organisms were sequenced first. *Arabidopsis thaliana* was the first plant chosen for genome sequencing, partly because it had one of the smallest C-values known for an angiosperm (NSF, 1990; Anderson, 1991). A grass in the genus *Brachypodium* (e.g. diploid *B. distachyon*—1C = 0·25–0·3 pg) was proposed as a first monocot for genome sequencing on similar grounds (Bablak *et al.*, 1995; Catalan *et al.*, 1995), but rice (*Oryza sativa*, 1C = approx. 0·5 pg) was chosen because it has the smallest C-value among the world's major cereal crops (Sasaki, 1998; Somerville and Somerville, 1999). In 1999 DNA sequences were published for the first human chromosome (number 22) as part of the human genome project (Dunham *et al.*, 1999), chosen because it is one of the smallest human chromosomes. Among autosomes only chromosome 21 is smaller (Little, 1999) and its DNA sequence was also recently published (Hattori *et al.*, 2000).

Estimates of the 1C-value for *Arabidopsis thaliana*, often taken for convenience by molecular biologists as about 100 Mbp (= approx. 0·1 pg), have increased from about 70 Mbp (Leutwiler *et al.*, 1984; Marie and Brown, 1993) to 130–155 Mbp (Arumuganathan and Earle, 1991; Somerville and Somerville, 1999), or higher (1C = approx. 0·19 pg: Doležel *et al.*, 1998), and hence towards the values obtained by Feulgen microdensitometry (0·175 pg = 170 Mbp, re-estimated by Bennett and Smith, 1991; 0·167 pg = 162 Mbp, Krisai and Greilhuber, 1997). Summing DNA sequences for each *A. thaliana* chromosome will soon yield a first angiosperm C-value based on this new approach, but it will still be a best estimate based on assumptions, as several segments containing repeated DNA sequences will remain unsequenced as gaps.

DNA C-values and mechanisms in genome size evolution

Genome sizes range over five orders of magnitude in eukaryotes (Cavalier-Smith, 1985), and approx. 1000-fold in angiosperms (Bennett and Smith, 1976). However, we are still unsure in theory or practice what are the smallest and largest C-values and/or genome sizes for taxa in different groups of organisms. Leutwiler *et al.* (1984) put the theoretical minimum C-value for an angiosperm at about 1C = 0·025 pg (assuming 15 000 different genes and an average of 1·5 kb of DNA per gene) and suggested that diploid *Arabidopsis thaliana* (assumed 1C = 0·07 pg) approached that limit within three–four fold. However, it was recently shown that duplications cover considerably more than half of the genome and at least 30 % of *A. thaliana* genes are duplicated, raising the intriguing possibility that it could be a degenerate tetraploid (Blanc *et al.*, 2000). If so, diploids with only half the C-value of *A. thaliana* may exist, approaching the theoretical minimum more closely. The report that *Rosa wichuriana* had a 1C DNA amount of only 0·05 pg (Bennett and Smith, 1991) must now be discounted as an artefact, perhaps caused by self-tanning, as Yokoya *et al.* (2000) recently estimated this taxon as 1C = 0·55 pg. Another angiosperm C-value below 0·1 pg is known (1C = 0·05 pg for the crucifer *Cardamine amara*; S.R. Band pers. comm.—listed in Bennett and Smith, 1991), but its validity needs confirmation. With estimates available for only about 1 % of species, the full range of C-values and genome sizes in angiosperms is still uncertain (Bennett, 1998) and may include taxa with amounts significantly larger or smaller than those already known.

What determines C-value size, and how genome size is controlled, is an ongoing debate (Beaton and Cavalier-Smith, 1999). In particular there is considerable interest in the molecular mechanisms responsible for the gain or loss of DNA. Kubis *et al.* (1998) proposed that changes in nucleosome structure and size (including potentially species-specific modifications such as histone acetylation under genetic control) may be a driver to directional changes in DNA amount. They found small differences in the average size of repeated DNA sequences coiled around nucleosomes between wheat and rye (Vershinin and Heslop-Harrison, 1998). If one repeated sequence is more stable in packing around a particular nucleosome structure and size, then its amplification could be favoured over others, leading to the gain or loss of DNA.

There is considerable new evidence for the role of retrotransposons and satellite DNA in enlarging the amount of repeated sequences and therefore DNA C-value. Elegant work on *Zea mays* has described how different retrotransposons have sequentially inserted one within another, in 'Russian doll' fashion, and then spread in its genomes (SanMiguel *et al.*, 1998). This phenomenon can be used as a type of molecular clock to study the sequence and timing of such events in genome evolution (Voytas and Naylor, 1998). Knowledge of this process, coupled with some phylogenetic comparisons for grasses, led Bennetzen and Kellogg (1997) to ask if plants have a one-way ticket to genomic obesity. This idea was based on the current 'absence of a known mechanism that could substantially reduce nuclear DNA content in plants'. However, they noted that a failure to identify such processes 'does not indicate of course that such a mechanism is not present'. C-values may often tend to grow by such processes until selection acts on some nucleotypic character(s) related with C-value (Bennett, 1987*a*).

There is also good reason to believe that C-values can often decrease during evolution, although better knowledge is needed of the molecular mechanisms involved. Evidence that DNA loss can occur has been seen at the cytological level. Deletion of segments of heterochromatin from *Secale* chromosomes, known to contain highly repeated DNA sequences visible in the light microscope, were seen in *Triticale*, leading to a reduced C-value detectable by Feulgen microdensitometry (Gustafson *et al.*, 1983). Such losses, each equivalent to one–three complete *Arabidopsis* genomes, need not be detrimental to fitness. Indeed, the resulting line may be improved, as judged by the award of plant breeders rights (Bennett, 1985). Such loss was due to chromosome breakage, and may be associated with incomplete late DNA replication, although the precise molecular mechanism is uncertain. Work on insects gives an interesting insight into DNA loss at the molecular level. Petrov *et al.* (2000) tested the hypothesis that some variation in genome size can be attributed to differences in the pattern of insertion and deletion (indel) mutations among organisms. They compared the indel spectrum in *Laupala* crickets, whose genome size is 11 times larger than that of *Drosophila*. DNA loss of non-transposing copies of a 'dead on arrival' pseudogene was 40 times slower in the former than in the latter. They concluded that some differences in haploid genome size may result from variation in the rate of spontaneous loss of non-essential DNA.

An interesting question meriting further research concerns the proportion and parts of the genome that are dispensable in taxa with specialist life styles. Insights into molecular mechanisms influencing genome size evolution may be obtained from studies of genomes in highly specialized taxa, such as parasites and symbionts. Gilson and McFadden (1997) reported that the vestigial nucleus of a chlorarachniophyte endosymbiont, termed the nucleomorph, had a haploid genome size of 380 kbp—then 'the smallest eukaryotic genomes known'. [The smallest eukaryote genome known now is 225 kbp (Beaton and Cavalier-Smith, 1999) in the microsporidian *Encephalitozoon intestinalis*.] They described its stripped-down eukaryotic genome, only a little larger than some chloroplast genomes, as the quintessence of compactness whose features included overlapping genes. Intensive reductive pressures had apparently squeezed spliceosome-type introns down to only 18–20 bases in length. Comparing nuclear and nucleomorph genome sizes shows such reductive pressures in natural selection can readily eliminate functionless nuclear DNA, refuting 'selfish' and 'junk' theories of secondary DNA (Beaton and Cavalier-Smith, 1999).

Comparisons of related diploids and polyploids may also increase our knowledge of changes in DNA amount and of the mechanisms involved. All else being equal, the DNA amounts for polyploids are expected to increase in direct proportion to ploidy level. Tetraploids and hexaploids are expected to show double and treble the mean C-value for diploids. This expectation is obeyed in many polyploid series, especially those newly formed, but the literature abounds with examples where genome size in polyploids is smaller than expected. While some of these are technical artefacts, others seem real (Ohri and Khoshoo, 1986). Moreover, analysis of 2452 angiosperm taxa of known ploidy showed that mean C-values for diploids and polyploids were more similar than expected. DNA amount did not increase in direct proportion with ploidy level, and mean DNA amount per basic genome actually decreased with increasing ploidy in many cases. Polyploidy is often associated with selection and adaptation for rapid cell development, which in turn is correlated with small C-values and genome size, as in ephemeral weeds such as *Arabidopsis thaliana* (Bennett *et al*., 1998). If so, DNA loss may commonly occur from constituent genomes in many polyploids after their formation. The alternative explanation, that C-value and genome size increase in diploids but not in their derived polyploids seems unlikely. While the case for reduced genome size in many polyploids seems strong, more work is needed to confirm this at the molecular level and to describe the sequences involved.

Recent work has focused on how repetitive DNA sequences (both tandem and dispersed repeats) evolve in polyploids. Evidence from several polyploids including wheat (*Triticum*) and cotton (*Gossypium*) showed that they behave in a dynamic and varied manner undergoing various types of concerted evolution—the non-independent evolution of sequences at multiple loci (Wendel *et al*., 1995; Hanson *et al*., 1998). The mechanisms involved are not well understood but include unequal crossing over, gene amplification, gene conversion and replicative transposition. The extent to which intensive selection for a reduced genome size could drive concerted evolution has yet to be investigated but may help explain how changes in genome size following polyploidy could occur. The report by Liu *et al*. (1998) that allopolyploid formation in synthetic wheat is accompanied by rapid and non-random elimination of certain low copy non-coding DNA sequences in a genome-specific manner provides direct evidence that loss of DNA from genomes in polyploids does occur. Chenuil *et al*. (1997) noted that polyploid barbel fish (*Barbus*) had fewer and shorter microsatellites than their diploid relatives. They suggested that a bias in the mismatch repair system towards deletion could account for this, providing an efficient way of eliminating excess DNA in polyploids. Further, it was recently suggested that following polyploidy, extensive methylation and other gene silencing mechanisms are activated, in part, to repress the spread of transposable elements (Matzke and Matzke, 1998). Such methylated sequences could themselves also become targets for elimination, providing a further way to remove excess DNA from genomes in polyploids.

C-value variation and constancy—a new C-value paradox?

Differences in nuclear DNA amounts among organisms arise as variation between individuals within species. However, views on the incidence and magnitude of extant intraspecific variation in C-values remain hotly debated (Bennett and Leitch, 1995, 1997). New evidence on this issue is too extensive to review here, but many reported examples were unrepeatable using the same materials (e.g. Greilhuber and Obermayer, 1997, 1998; Baranyi and Greilhuber, 1999) and probably reflect technical artefacts of one sort or another (Greilhuber, 1998). Consequent on such studies, the idea of the plastic genome has been questioned, at least with respect to its gross size (Greilhuber and Obermayer, 1998) though not with respect to its constituent DNA sequences, as the concept of relative genome size constancy within species has recently received new support (Baranyi and Greilhuber, 1999; Bennett *et al*., 2000).

Part of the current interest in C-values and what determines genome size focuses on a tension between the massive variation in DNA amounts existing between taxa within the angiosperms, and the surprisingly high degree of genome constancy found in many widely distributed species, including the base calibration standard for estimating C-values—*Allium cepa* (Bennett *et al*., 2000). In view of the molecular mechanisms now known which can rapidly generate considerable variation in DNA C-value and genome size (Kubis *et al*., 1998; SanMiguel *et al*., 1998), the degree of C-value constancy found in many species is remarkable, and needs explanation. Indeed, it is arguable that such constancy would not be expected without some mechanism(s) to select for constancy (or against drift) in C-value, which thereby controls variation in C-value back towards some encoded norm for each species. Were it not so, the frequency and extent of intraspecific variation in DNA amount would surely be much larger, and the observed degree of species DNA constancy would present a new C-value paradox (Bennett *et al*., 2000). Genome size is widely perceived as free to vary, changes being undetected and uncorrected by internal control mechanisms. Yet many results challenge this view, suggesting instead that DNA amount may normally be subject to innate controls by 'counting' mechanisms which somehow detect, quantify and regulate genomic size characters within quite tightly defined or preselected limits (Bennett, 1987*b*; Bennett *et al*., 2000).

Thus, C-value and genome size can be perceived as characters subject to a tight genotypic control, rather than as merely the end product of the interaction of evolutionary drift and natural selection against the consequences of disadvantageous obesity. DNA C-value can be perceived as a genetically set 'mould' within whose constraint different families of repeated sequences may compete and vary rapidly in identity and copy number, subject to their competitive strengths as preferred replicators, etc. This view sees nuclear DNA not only or just as the genotype, but as the environment of the essential information encoded in its genes, with its own ecology represented by different competing species of non-essential repetitive DNA elements.

Using C-values to probe phylogenetic dimensions

C-values are increasingly useful in a phylogenetic context. Much research has looked for evolutionary trends in DNA amount at the species, genus and family level, but most studies were flawed by the lack of a rigorous phylogenetic framework on which to analyse the data. However, there is a phylogenetic component to genome size variation which needs evaluation before any evolutionary significance of C-value variation can be explained fully (Bharathan, 1996). New availability for angiosperms of both a DNA C-values database and a consensus higher level phylogeny recently opened the way for such studies, super-imposing data from the former on the latter (Cox *et al*., 1998; Kellogg, 1998; Leitch *et al*., 1998), which support a range of interesting conclusions. Leitch *et al*. (1998) compared C-value data for 152 families covering all four major subdivisions and 15 out of 20 higher level groups among angiosperms. Every higher level group for which data were available contained species with small C-values (3·5 pg or less) and (with one exception) very small C-values (1·4 pg or less). Species with large C-values (14·0 pg or more) were found in only six groups, while only two had very large C-values (35·0 pg or more). It seems that ancestral angiosperm genomes were small, whereas very large C-values represent a derived condition that arose at least twice in angiosperm evolution, in the higher eudicots and in the monocots (Bharathan, 1996; Leitch *et al*., 1998). Such analysis not only provides information on the direction of genome size evolution in different plant groups but, as noted above, it can also provide a framework essential for directing studies on the mechanism(s) and timing of genome size changes at many taxonomic levels ranging from grass tribes (Kellogg, 1998), to species such as *Zea mays* (SanMiguel *et al*., 1998; Voytas and Naylor, 1998).

DNA amounts as predictors and indicators

Nuclear DNA amount shows nucleotypic correlations with many widely different phenotypic and phenological characters at cell, tissue and organismic levels. C-value is, therefore, an important fundamental factor involved in scaling of living systems. The extensive literature on nucleotypic correlations is reviewed elsewhere (Bennett, 1973, 1987*a*; Cavalier-Smith, 1985). The 70 new original sources listed in the Appendix report or confirm several relationships between nuclear DNA amounts and widely different characters, including C-value and genomic chromosome volume in *Zingiber officinale* cultivars (Rai *et al*., 1997) and C-value and nuclear size in *Hedysarum* taxa (Akpinar and Yildez, 1999). Among relationships with reproductive characters, C-value was directly correlated with chiasma frequency in *Mammillaria* species (Das *et al*., 1997); and pollen diameter significantly correlated to DNA content for populations of *Armeria maritima* (Vekemans *et al*., 1996) 'confirming the relationship between genome size and pollen size (Bennett, 1972), but at the intraspecific level'. Baranyi and Greilhuber (1999) found significant negative correlations between genome size and first month of flowering for *Allium* taxa, confirming the hypothesis (Grime and Mowforth, 1982) that species flowering very early in spring have large genomes. Significant negative correlations were also noted between DNA amount per nucleus or per genome and the probability of being a recognized weed species (Bennett *et al*., 1998). Correlations vary in 'tightness', but are often surprisingly close for biological systems and more reminiscent of chemical or physical relationships (Bennett, 1977). The closer the correlation between a character and C-value, the greater the utility of C-value data as a predictor.

C-values as ecological or environmental indicators

Clearly interest in C-values is not limited to biological matters internal to organisms, such as genome evolution, but extends to a broad range of external ecological issues and environmental concerns (Grime, 1983, 1996, 1998). Thus, DNA amounts are known to correlate with plant life histories (Bennett, 1972, 1987*a*), the geographical distribution of crop plants (Bennett, 1976), plant phenology (Grime and Mowforth, 1982; Grime *et al*., 1985), biomass (Jasienski and Bazzaz, 1995), sensitivity of growth to environmental variables such as temperature and frost (Grime, 1983; MacGillivray and Grime, 1995), besides predicting changes in vegetation caused by long-term changes such as global warming (Grime, 1990, 1996). Moreover, C-value has been suggested as a prime predictor of the likely responses of vegetation to man-made catastrophes such as nuclear winter (Grime, 1986), or other nuclear incidents. Experimental results relating plant DNA amounts with known doses of ionizing radiation (Sparrow and Miksche, 1961; Underbrink and Pond, 1976) obtained at the Brookhaven National Laboratory in the 1960s and 1970s, were used to predict the effects of radiation on vegetation in the Ukraine after the accident at Chernobyl in 1986 (Van't Hof, pers. comm.).

Using inferred C-values to reveal paleobiological trends

Not only do C-values have predictive value based on their close relationships with phenotypic characters (Bennett, 1996, 1998), but conversely such correlations allow C-values to be predicted from such characters. For example, it seems possible to infer the genome content of fossils, as cell size is proportional to quantity of DNA. If so, in prospect is the possibility of investigating changes in genome size through geological time and on a macroevolutionary scale encompassing the origin of major groups and the effects of extinctions. A pioneering survey of inferred variation in genome content in fossils was based on measurements of epithelial cells in extinct conodonts over a period of 270 million years (Conway Morris and Harper, 1988). These inferred C-values in extinct taxa vary by at least one, and perhaps two orders of magnitude (approx. 1–150 pg). Even when they entered their final Triassic decline, inferred C-values remained widely variable, showing no evidence that conodont extinction was linked to increasingly small genome size. Relationships between cell size and DNA amount also mean that sizes of defined cell types (such as stomatal guard cells) can be used to estimate DNA amounts in fossil plants, and to track evolutionary trends in C-values over geological time (Masterson, 1994).

DNA amounts and their conservation interest

We face a mass extinction of biodiversity, losing plant species at 10 000 times the normal rate (May *et al*., 1995). Knowledge of C-values and genome sizes may also be significant for conservation. Whether relationships exist between genome size and species loss is unknown, but it seems likely. Slow-developing gymnosperm taxa with long minimum generation times, which produce relatively few large seeds, are probably at increased risk of extinction (Rejmanek, 1996). These characters, obligately associated with very high C-values, occur in many perennial monocots. Massive C-values may identify over-specialized end products of evolutionary lineages with slim chances of a return from extreme genomic obesity, and also confer increased chances of extinction (Bennett and Leitch, 2000). Prospects for survival may reflect genome size more than C-value, and hence may be modified by ploidy level. We need to know if, for a given high C-value, diploids and polyploids are equally at risk. If so, because allopolyploidy is common, the loss of genomes may be proportionally more than the loss of species. However, if polyploids are more adaptable, and more likely to survive than parental diploids, as many have argued, then the proportion of polyploids among surviving taxa in the angiosperm flora will increase, while mean genome size (taken as C-value divided by ploidy level) will decrease during a wave of extinction.

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Notes to the Appendix

The Appendix appears on pp. 878–906.

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 ‘Notes to the Appendix’. 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) and Bennett and Smith (1991; references 108–163), ‘Notes to the Appendix’ by Bennett and Leitch (1995; references 165–269), and in ‘Notes to the Appendix’ by Bennett and Leitch (1997; references 270–306).

(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. The 11 standard species and their 4C DNA amounts are shown 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

TABLE 4. *The 11 angiosperm species recommended for use as calibration standards*

Key	Standard species	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

(e.g. F is *Hordeum vulgare*, etc.). If a species was first calibrated using a standard species listed in Table 4, 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 J (*V. radiata*) was used to calibrate *Carex ciliatomarginata* (species 198 in the Appendix) which was then used as an intermediate assumed standard to calibrate other *Carex* species given by Nishikawa *et al*. (1984; Ref. 357). The calibration standard for such *Carex* species is therefore given as J-198.

(b2) In Ref. 338, Keskitalo *et al*. (1998) used *Hordeum vulgare* 'Sultan' as the calibration standard but assumed a 4C DNA value of 21·88 pg (Valkonen, 1994) instead of 22·24 pg which is the value given in Bennett and Smith (1976). The 4C value of *H. vulgare* 'Sultan' used by Keskitalo *et al*. (Ref. 338) was estimated using *Gallus* as the calibration standard with an assumed 4C DNA content of 4·66 pg. Similarly, in Refs 348 (Grauke *et al*., pers. comm.), 349 (Wendel *et al*., pers. comm.), and 373 (Bennett *et al*., pers. comm.) *Pisum sativum* 'Minerva Maple' was used as the calibration standard but with a 4C value of 19·12 pg (Johnston *et al*., 1999) instead of 19·46 pg, the value given in Bennett and Smith (1976). The 4C value of *P. sativum* 'Minerva Maple' used in Refs 348, 349, and 373 was estimated using *H. vulgare* 'Sultan' as the calibration standard with an assumed 4C DNA content of 22·24 pg.

(c) In several of the references listed in 'Original references for DNA values' the authors used a cultivar of a standard species different from that listed in note (b1) above. Thus for *Allium cepa* the following cultivars were used instead of 'Ailsa Craig': 'Alice' (Ref. 371), 'Wolska' (Ref. 326), 'Deshi' (Refs 324, 334), 'Frühstamn' (Refs 350, 360), 'Kantar Topu' (Ref. 363), 'Stuttgart Riesen' (Ref. 341) and 'Madras Local' (Ref. 364). For *Zea mays*, cultivars 'Va35' and 'CE-777' were used instead of 'W64A' in Refs 311, 344 and 370 respectively. For *Pisum sativum*, the following cultivars were used instead of 'Minerva Maple': 'Express Long' (Ref. 342) and 'Kleine Rheinländerin' (Refs 350, 360, 361). For *Hordeum vulgare*, the cultivar 'Stark' was used in Refs 343, 345, and 368 and the cultivar 'Ditta' was used in Ref. 371 instead of 'Sultan'. For *Vicia faba*, the cultivar 'Aquadulce' was used instead of PBI inbred line 6 in Ref. 310. In Ref. 343, the cultivar 'Arapahoe' of *Triticum aestivum* was used instead of 'Chinese Spring'. In Ref. 329 plants from the Palmerston North population in New Zealand of *Senecio vulgaris* were used instead of the PBI population.

In some cases the C-value of the cultivar used was assumed or estimated to be the same as that of the standard species listed in note (b1). 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 (b1). For example Ref. 342 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. Similarly Refs 350, 360 and 361 used the cultivar 'Kleine Rheinländerin' with a 4C DNA amount of 17·68 pg. Other examples of this include a low assumed value for *Hordeum vulgare* 'Stark' (4C = 21·36 pg used in Refs 343, 345, 368) relative to the 4C DNA amount of 'Sultan' (22·24 pg).

(d) In Ref. 313 (Ceccarelli *et al*., 1998) the cultivar of *Vicia faba* used as a calibration standard was not given even though the authors assumed the same 4C value as for PBI inbred line 6 (i.e. 53·3 pg). If this species exhibits intraspecific variation then such assumptions may be incorrect. In Ref. 344 (Hopping, 1994) the cultivar of *Hordeum vulgare* used as the calibration standard was not given. Hopping (loc. cit.) estimated the 4C DNA amount for the material to be 20·14 pg.

(e) In a number of original references for DNA values the authors used a plant species not listed in note (b) as a calibration standard. These are listed in Table 5.

(f) Several papers listed in 'Original references for DNA values' used animal cells as the calibration standards. Thus Refs 307, 309, 320, 337, 339, 351, 352, 358, 362, 365, 367 all 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. 331 blood cells from the catfish *Ictalurus punctatus* were used as a calibration standard with an assumed 4C value of 4·00 pg (Tiersch *et al*., 1989); this is abbreviated to *Ictal*. in column 15 of the Appendix.

If a species was first calibrated using an animal species, then the original animal species is identified first and the intermediate standard species used to calibrate those species listed with it is denoted by its number in column 1 of the

TABLE 5. *Plant species used as a calibration standard but not listed in note (b1)*

Original ref.	Plant calibration standard used	Assumed 4C DNA amount (pg)		Abbreviation used in column 15 of Appendix
308	*Medicago sativa* ssp. × *varia* 'Rambler'	6·94	(Blondon *et al*., 1994)	*Medic.*
314, 318, 323, 330, 366	*Petunia hybrida* 'P × Pc6'	5·7	(Marie and Brown, 1993)	*Petunia*
325	*Petunia hybrida* cv. not given	5·7	(Marie and Brown, 1993)	*Petunia*
	Lycopersicon esculentum			*Lycopers.*
328, 332	'Stupické polni rané'	3·92	(Doležel *et al*., 1992)	
330, 356	'Montfavet 63/5'	4·02	(Marie and Brown, 1993)	
331	'Rutgers'	4·0	(no reference given)	
360, 361, 369	*Glycine max* 'Ceresia'	4·54	(Greilhuber and Obermayer, 1997)	*Glycine*
335	*Citrus limon* 'Lisbon'	1·58	(Ollitrault *et al*., 1994)	*Citrus*

Appendix. For example, in Ref. 352, Bräutigam and Bräutigam (1996) used *Gallus* with an assumed 4C DNA amount of 4·66 pg to calibrate *Hieracium lactucella* (species 388 in the Appendix) which was then used as an internal standard to estimate the DNA C-values of other *Hieracium* species given by Bräutigam and Bräutigam (loc. cit.). The calibration standard for these *Hieracium* species is given as *Gallus*-388. Similary, Ollitrault *et al*. (1994, Ref. 358) used *Gallus* to estimate the DNA C-value of *Citrus* 'Tahiti Lime' (species 236 in the Appendix) which was then used to estimate the DNA C-values of other *Citrus* species listed in Ref. 358. The calibration standard for these *Citrus* species is given as *Gallus*-236.

(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) 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 be automatically chosen to represent the species 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 DNA 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 (e.g. *Coffea* species listed in Ref. 309 by Cros *et al*., 1994).

(i) A range of nuclear 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 the 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 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; 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 464 flowering plant families [Angiosperm Phylogeny Group (APG), 1998]. The familial names used in the APG classification are followed in the Appendix of this paper. Thus, although Bukhari (1997, Ref. 320) placed the genera *Acacia* and *Prosopis* in Mimosaceae, recent molecular and non-molecular phylogenetic data recognize that this family (although monophyletic) is embedded within the Leguminosae (APG, 1998) so Leguminosae is given as the family in the Appendix. This also agrees with previous DNA C-value lists (i.e. Bennett and Leitch, 1995, 1997) where both *Acacia* and *Prosopis* were listed under Leguminosae. Similarly, the APG (1998) now recognizes that Chenopodiaceae is embedded within the Amaranthaceae, so *Chenopodium album* which was placed in Chenopodiaceae in Ref. 375 (Bennett *et al*., 1998) is listed under Amaranthaceae 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) DNA amounts are often given in picograms (pg) or megabase pairs (Mbp). Hitherto, collected lists of DNA amounts by Bennett and co-authors gave DNA amounts only in picograms, noting a conversion factor from Strauss (1971) of 1 pg = 965 Mbp. The Appendix of the present work gives a range of C-values in picograms for each taxon as before, except that the 3C value is omitted here as this value is rarely used today. (3C values are easily obtained from the data given, but to minimize rounding errors they should be calculated as 0·75 of the 4C value, rather than three times the 1C value.)

The present work also gives 1C values in Mbp for the first time (see column 9 of the Appendix). Please note that the factor used to convert picograms to Mbp differs from that given previously. Thus, a value of 1 pg = 980 Mbp (Cavalier-Smith, 1985) was used, rather than that from Strauss (1971) mentioned above.

When converting picogram values to base pairs it is often permissible to use the rough approximation 1 pg $\approx$ 1 million base pairs $\approx$ 1000 Mbp. The conversion factor used in the present work (1 pg = 980 Mbp) is more accurate, but it is also an approximation. Different factors for converting picograms and daltons may reflect authors using different approximations for the atomic weights of elements in DNA (i.e. 1 or 1·00797 for hydrogen), or assuming different states of the DNA molecule (i.e. dissociated or non-dissociated). Assuming the following atomic weights (H = 1·00797; C = 12.0115; N = 14·0067; O = 15·9994; and P = 30·9738), 1 dalton = $1{\cdot}65979 \times 10^{-24}$ g), and an AT : GC base ratio of 1 : 1, then a more accurate factor for converting pg to Mbp is 1 pg = 978·3 Mbp for dissociated DNA and 975·0 Mbp for non-dissociated DNA. The molecular weights of the nucleotide pairs are, for A-T, 615·39361 and 617·40955 in dissociated and non-dissociated DNA, respectively, and for C-G 616·38119 and 618·39713 in dissociated and non-dissociated DNA, respectively. The AT:GC base ratios vary between taxa, e.g. the % GC ranges from 38·0 to 45·4 % in angiosperms (Marie and Brown, 1993). As noted above the molecular weights of the nucleotide pairs A-T and G-C differ slightly (by about 0·15 %). Thus, small additional errors are caused by variation in AT:GC ratios of the nuclear DNA among different taxa. While the values for A-T and C-G differ slightly, the difference is insufficient to require a different conversion factor for transforming pg to Mbp in taxa with different DNA base pair ratios. The resulting error (no more than 0·15 %) is similar to the accepted error of 0·5 % caused by the approximation which rounds 1 pg = 975 Mbp to 1 pg = 980 Mbp for non-dissociated DNA.

(t) In Refs 307, 332, 351, 363, 366 and 370, 1C DNA values are given in Mbp calculated from DNA estimates expressed in picograms using a factor other than 1 pg = 980 Mbp. Refs 307, 332, 351 and 370 used a conversion factor of 1 pg = 965 Mbp, whereas Ref. 363 used 1 pg = 912 Mbp. For each of these original references, the 1C DNA values in Mbp were re-calculated using the factor 1 pg = 980 Mbp [see note (s)] before listing in column 9 of the Appendix.

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

(v) In several original references the DNA C-value of a taxon to be used as an internal standard was determined from a regression of nuclear fluorescence *vs.* nuclear DNA content for a few calibration standards whose DNA C-values were already known. For example, Morgan *et al.* (1995, Ref. 315) and Morgan *et al.* (1998, Ref. 316) obtained the regression from *Zea mays* inbred line Va35, *Hordeum vulgare* 'Sultan' and *Triticum aestivum* 'Chinese Spring' with assumed 4C DNA values of 10·30, 21·88 and 69·26 pg, respectively (but note that all of these 4C DNA amounts are non-standard values compared with 4C values given for these species in note (b1) above). Morgan *et al.* (1995, Ref. 315) used this regression to determine the nuclear DNA content of *Avena sativa* 'Awapuni' (4C = 50·10 pg) which was added to *Limonium* extractions to serve as an internal standard. The calibration standard was abbreviated to *Avena* in column 15 of the Appendix. Morgan *et al.* (1998, Ref. 316) also used this regression to determine the DNA content of *Secale cereale* 'Rahu' (4C = 31·78 pg) which was added to *Limonium* extractions as an internal standard. Yokoya *et al.* (1999, Ref. 346) used a similar approach to obtain their regression from *Vigna radiata* 'Berken' (4C = 2·12 pg), *Lycopersicon esculentum* 'Stupické polni rané' (4C = 3·92 pg), *Glycine max* 'Polanka' (4C = 5·00 pg) and *Hordeum vulgare* 'Sultan' (4C = 22·24 pg). They used this regression to determine the DNA content of *Petroselinum crispum* 'Champion Moss Curled' (4C = 8·92 pg) which was added to many *Rosa* samples studied by flow cytometry as an internal standard. This calibration standard was abbreviated to *Petrosel.* in column 15 of the Appendix.

(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; Bennett and Leitch, 1995, 1997). The reason(s) for this is unknown. Thus this C-value should 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) Jones *et al.* (1998, Ref. 307) and Jones and Kuehnle (1998, Ref. 362) estimated the 4C DNA amount of *Dendrobium moschatum* as 7·0 pg. This value differs considerably from the 4C value of 18·6 pg obtained by Narayan *et al.* (1989). The discrepancy was noted by Jones *et al.* (1998) who stated 'The reason for this is unknown but could arise from differences between varieties or between methods of DNA content analysis'.

(aa) Cremonini *et al.* (1994, Ref. 310) studied C-values in *Dasypyrum villosum* (syn. *Haynaldia villosa*) and reported 4C amounts of 23·7 and 19·1 pg for yellow and brown caryopses respectively. They used *Vicia faba* as the calibration standard, but did not state the assumed 4C DNA amount. Cremonini *et al.* (loc. cit.) stated that their values contradicted a previous report by Bennett (1972). However, the 3C value (19·6 pg) given by Bennett (1972) was later corrected and a recalibrated value (4C = 21·4 pg) was given by Bennett and Smith (1976) using *Hordum vulgare* 'Sultan' (4C DNA amount = 22·24 pg) as the calibration standard. Contrary to Cremonini *et al.* (1994) the most recent 4C estimate for *Dasypyrum villosum* given by Bennett and Smith (1976) does not contradict their results, but is within their range of reported values (19·1–23·7 pg) and identical with their mean of 21·4 pg.

(ab) In Ref. 311 (Lindsay *et al.*, 1994), the DNA amount was estimated in *Eustoma grandiflorum* 'Hakusen' using flow cytometry. Although no chromosome counts were made it was assumed that the DNA content from the flow cytometric histograms corresponded to the 2C value. Only if this assumption is correct is the C-value valid.

(ac) Horjales *et al.* (1995, Ref. 314) checked the chromosome number (2n = 42) cytologically in their hexaploid plants. However, their claim that DNA measurements made by flow cytometry, without such counts, offer a reliable method to detect ploidy level/chromosome number routinely (see their English abstract) in these materials may be premature. The 2C DNA amounts for diploid and tetraploid *Dactylis glomerata* estimated by flow cytometry in Horjales *et al.* (1995) are about half as large as those reported for this taxon by several previous authors using Feulgen microdensitometry (Table 6).

TABLE 6. *2C DNA amounts for diploid and polyploid* Dactylis glomerata

Original ref.	2n	2C DNA amount (pg)	Method
1 (Bennett, 1972)	14	9·8	Fe
154 (Band, pers. comm., 1984)	14	8·7	Fe
275 (Creber *et al*., 1994)	14	6·6	Fe
314 (Horjales *et al*., 1995)	14	3·5	FC: DAPI
117 (Schifino and Winge, 1983)	28	12·4	Fe
275 (Creber *et al*., 1994)	28	11·2	Fe
371 (Greilhuber and Baranyi, 1999)	28	8·3	Fe
371 (Greilhuber and Baranyi, 1999)	28	8·2	FC: PI
314 (Horjales *et al*., 1995)	28	6·4	FC: DAPI
314 (Horjales *et al*., 1995)	42	8·8	FC: DAPI

The reason(s) for this divergence is uncertain. Schifino and Winge (1983) expressed reservations about the reliability of their measurements including those for *D. glomerata* (see footnote 'o' in Bennett and Smith, 1991) while Creber *et al*. (1994) claimed considerable intraspecific variation in C-values in this species estimated by Feulgen microdensitometry. However, Creber *et al*. (loc. cit.) also reported that *D. glomerata* needed a considerably longer hydrolysis time (62 min at 25°C with 5 M HCl) than the standard species *Hordeum vulgare* (20 min in otherwise the same conditions), an observation that Greilhuber and Baranyi (1999) could not reproduce. These observations suggest that C-value estimates for *D. glomerata* taxa should be treated with caution until the nature and extent of the variation is determined.

(ad) The genus *Prospero* Salisb. was first used to describe a natural group of species formerly in the genus *Scilla* L. sharing the synapomorphy of a certain micropyle type not found in other related taxa (Ebert, 1993). The species included in this genus were *P. autumnalis* (= *Scilla autumnalis*) and *P. obtusifolia* (= *Scilla obtusifolia*), although given the considerable morphological and chromosomal variation described in the genus, other species have since been described (e.g. see Ebert *et al*., 1996, Ref. 321). Given the variation encountered and the taxonomic uncertainties surrounding the delimitation of the species in the genus *Prospero*, Ebert *et al*. (loc. cit.) used the name *P. autumnalis* s.l. to describe the material of *P. autumnalis* rather than *P. autumnalis* (L.) Speta, which they considered to belong to the widely-distributed tetraploid which occurs in Italy and parts of France.

Genome size data for 15 accessions of *P. autumnalis* s.l. with either 2n = 12 or 2n = 14 were reported. Significant differences in C-values between populations were found. Consequently only the lowest and highest DNA amounts for each chromosome number are given in the Appendix.

(ae) Hopkins *et al*. (1996, Ref. 331) estimated nuclear DNA contents in 34 different populations of switchgrass (*Panicum virgatum*) with ploidy levels of 4, 6 or 8x. In the Appendix only the largest and smallest DNA amounts are given for each ploidy level. The mean 4C nuclear DNA contents for verified tetraploid and octoploid populations were estimated to be 6·2 and 10·4 pg, respectively.

(af) In Ref. 332, Ayele *et al*. (1996) stated 'To our knowledge, the genomic size of *Eragrostis tef* has not been reported'. They were the first to use flow cytometry for this purpose, but they did not make the first estimate for this species. Their 4C nuclear DNA contents of 2·96–3·02 pg for four cultivars are similar to the 4C value of 2·70 pg given by Bennett and Smith (1976). Surprisingly, Ayele *et al*. (loc. cit.) seemed unaware of this earlier estimate, yet they cited Bennett and Smith (1976) for a different reason when listing their DNA values for the Ethiopian cereal, tef, in their Table 1.

(ag) The range of C-values (4C = 37·0–57·4 pg) given for eight species of *Euphorbia* by Vosa and Bassi (1991, Ref. 333) differ considerably (i.e. sometimes more than ten-fold) from two estimates of *Euphorbia pulcherrima* by Galbraith *et al*. (1983: 4C = 5·2 pg estimated by flow cytometry using mithromycin), and Bennett *et al*. (Ref. 373 in this paper: 4C = 6·6 pg estimated by flow cytometry using propidium iodide). Vosa and Bassi (loc. cit.) did not estimate a C-value for *E. pulcherrima* nor did they comment on the large difference between their values for *Euphorbia* taxa and that of Galbraith *et al*. (1983). While up to nine-fold variation in C-values has been reported within a genus (e.g. *Crepis*; Jones and Brown, 1976) it is uncommon and so further work is needed to confirm that such large differences in C-values within the genus *Euphorbia* are real.

(ah) The range of C-values (4C = 18·4–27·8 pg) for seven species of Cactaceae in the genus *Mammillaria* given by Das *et al*. (1997, Ref. 334) is more than two-fold greater than three other estimates for *Mammillaria* species by Barlow (pers. comm., cited in Bennett and Smith, 1976; *M. bocasana* 4C = 8·2 pg and *M. woodsii* 4C = 6·2 pg estimated by Feulgen microdensitometry), and Palomino *et al*. (1999, Ref. 328 in this paper: *M. san-angelensis* 4C = 6·4 pg estimated by flow cytometry using propidium iodide). In particular, the 4C estimate of *M. bocasana* given by Das *et al*. (loc. cit.) of 19·5 pg was 2·4-fold greater than the value reported by Barlow (loc. cit.) for the same species (4C = 8·2 pg). The values in Ref. 334 also fall outside the range of C-values reported for eight other diploid species of Cactaceae (4C = 4·1–7·8 pg) given by Barlow (loc. cit.) and De Rocher *et al*. (1990). The reason(s) for this discrepancy is unknown, thus the C-value estimates of Ref. 334 should be viewed with caution until the question is resolved.

(ai) Ref. 336 (Baranyi and Greilhuber, 1999) estimated the C-values of 57 accessions or cultivars of 28 different *Allium* species. Variation in DNA content of 1·08-fold or less was reported for all species except *A. carinatum* where C-values for different accessions varied by 1·10-fold. The authors suggested that a real difference in DNA amount existed between diploid *A. carinatum* accessions. The C-value variation reported for the 27 other species was not statistically significant and Baranyi and Greilhuber (loc. cit.) proposed that the data 'give an indication of the variation in measurement values that is to be expected between investigators working with the same material, technique and instrumentation at a given sample size'. Consequently the mean DNA C-values are given in the

Appendix for all species except diploid *A. carinatum* where the highest and lowest values are listed.

(aj) Baranyi and Greilhuber (1999, Ref. 336) estimated the 4C DNA amount of *Allium cepa* var. *viviparum* to be 57·5 pg. This estimate is very similar to the 4C value of 59·8 pg for the F_1 hybrid *A. cepa* × *A. fistulosum* reported by Evans *et al.* (1972). Both values differ considerably from other reported 4C values of *A. cepa* which range from 65·4–69·5 pg [listed in Bennett and Smith (1976) and Bennett and Leitch (1995, 1997)]. The similarity in DNA values between *A. cepa* var. *viviparum* and *A. cepa* × *A. fistulosum* support the theory that the former is an ancient hybrid of the latter (van Raamsdonk and de Vries, 1992), and the considerable difference in C-value between *A. cepa* var. *viviparum* and the other *A. cepa* estimates suggest that this variety is more taxonomically distinct from *A. cepa* than is currently recognized by its nomenclature. Further work is needed to investigate this.

(ak) Valkonen (1994, Ref. 337) estimated the C-values of three species of *Solanum* from Section Etuberosa under two different temperature regimes [18°C and 25/22°C (day/night)]. He found that *S. fernandezianum* grew vigorously and produced flowers at 18°C whereas growth was poor at 25/22°C. In contrast, *S. brevidens* and *S. etuberosum* grew well at 25/22°C but poorly at 18°C with the plants remaining stunted. These results were shown to reflect the different natural habitats of the species. DNA C-values were estimated at each temperature. For *S. brevidens* and *S. etuberosum*, a small decrease in DNA amount was reported at 18°C compared with 25/22°C. In contrast, DNA amount increased in *S. fernandezianum* grown at 18°C compared with 25/22°C. To reflect the different temperature requirements of the three species the highest DNA amounts recorded for *S. brevidens* and *S. etuberosum* grown at 25/22°C are given in the Appendix whereas for *S. fernandezianum* the DNA amount for plants grown at 18°C is listed.

(al) In Ref. 343, Vogel *et al.* (1999) used the genomically-based nomenclature system of Dewey (1984) and Barkworth and Dewey (1985). In these two papers, tables are presented showing the genomically-based nomenclature together with common synonyms and traditional nomenclature. To check for synonyms in previously published lists of DNA C-values (i.e. Bennett and Smith, 1976, 1991; Bennett *et al.*, 1982; Bennett and Leitch, 1995, 1997), a species name listed by Vogel *et al.* (loc. cit.) was located in the genomically-based nomenclature list of Dewey (1984) or Barkworth and Dewey (1985) and then the common synonyms given were checked against previously published DNA lists. For example, *Thinopyrum elongatum*, listed by Vogel *et al.* (loc. cit.), has the common synonym *Agropyron elongatum* (Dewey, 1984) which was listed by Bennett and Smith (1976). Synonyms could not be checked for 15 species given in Vogel *et al.* (loc. cit.) because they were not listed by Dewey (1984) or Barkworth and Dewey (1985).

(am) Lu *et al.* (1998, Ref. 345) reported DNA C-values for two tetraploid and four octoploid populations of switchgrass (*Panicum virgatum*) which were cytologically analysed. Since the DNA C-values given for each ploidy level differed by less than 10 % and intraspecific variation was not reported, only the mean DNA amount for the two ploidy levels is given in the Appendix. The mean 4C DNA amount for the two tetraploid populations of 6·2 pg agreed well with values in Ref. 331 by Hopkins *et al.* (1996; 4C = 4·3–6·6 pg, 20 populations analysed).

However, Lu *et al.* (1998) reported that their results for four octoploid populations (mean 4C = 12·26 pg, range = 12·12–12·44 pg) were higher than those of Hopkins *et al.* (loc. cit.; mean 4C = 10·20 pg, range 9·40–12·00 pg) who analysed 12 octoploid populations. Lu *et al.* suggested that technical differences accounted for the discrepancy. For example, different calibration standards were used. Hopkins *et al.* used catfish (*Ictalurus punctatus*) blood cells and tomato (*Lycopersicon esculentum)*, both with an assumed 4C value of 4·0 pg, whereas Lu *et al.* used barley (*Hordeum vulgare* 'Stark') with an assumed 4C value of 21·36 pg. Interestingly, Lu *et al.* (1998) also reported that the mean 4C DNA content of 100 plants from each of three different octoploid cultivars estimated by flow cytometry but not analysed cytogenetically, were 11·80, 11·84 and 12·00 pg. These values do overlap with the data from Hopkins *et al.* (1996) but this was not noted by Lu *et al.* (1998).

(an) Bräutigam and Bräutigam (1996, Ref. 352) gave DNA amounts for nine *Hieracium* species in arbitrary units relative to *H. lactucella* that was used as an internal standard. Following correspondence with the authors, the absolute 4C DNA amount of *H. lactucella* was determined as 3·65 pg using *Gallus* as a calibration standard with an assumed 2C DNA amount of 2·33 pg. It was therefore possible to convert the relative DNA values for the remaining *Hieracium* taxa into absolute amounts by multiplying the peak ratio value given in column 3 of Table 2 in Ref. 352 by 3·65. The absolute DNA amounts are given in the Appendix. Although the relative DNA value for *H. stoloniflorum* was given in Ref. 352, its absolute DNA amount was omitted from the Appendix following the authors' request.

The DNA amounts for *Hieracium* species listed by Bräutigam and Bräutigam (loc. cit.) included two species measured previously (i) *H. piloselloides*, 4C = 4·3 pg, estimated by Bachmann, Price and Bierweiler and listed in Bennett and Smith (1976), and (ii) *H. pilosella*, 4C = 17·0 pg, estimated by Band and listed in Bennett and Smith (1991). These values differ from those given in Ref. 352 of 4C = 14·7 and 12·6 pg respectively but the discrepancies were not noted so the reason(s) is unknown.

(ao) 4C DNA amounts for several Marantaceae taxa given in Table 1 of Sharma and Mukhopadhyay (1984, Ref. 355) in arbitrary units (a.u.) were converted to absolute amounts using the conversion faction 1 pg = 12 a.u. This factor was obtained as the mean ratio of the estimates for *Maranta bicolor* (0·1734 a.u.) and *Stromanthe sanguinea* (0·2254 a.u.) obtained by Sharma and Mukhopadhyay (1984) and by L. Hanson at RBG, Kew (4C = 2·09 pg and 2·68 pg, respectively). Root-tips of *Maranta bicolor* and *Stromanthe sanguinea* were taken from plants at RBG, Kew in 1999, and their 4C DNA amounts estimated by Feulgen microdensitometry as 2·09 pg and 2·68 pg, respectively, using *Vigna radiata* 'Berken' (4C = 2·12 pg) as a calibration

APPENDIX. *Chromosome number, ploidy level, life-cycle type, and nuclear DNA content in 807 angiosperm species (the superscript letters refer to notes concerning this table)*

Entry number[g]	Species	Voucher	Family	Monocot or dicot	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†
1	*Abelmoschus esculentus* (L.) Moench	No	Malvaceae	D	120	—[p]	A	1,666	1.7	3.3	6.6	373	O	G[b2]	FC:PI
2	*Abutilon theophrasti* Medik.	Yes	Malvaceae	D	42	6	A	1,372	1.4	2.8	5.6	375	O	F	Fe
3	*Acacia albida* (Del.)[j]	No	Leguminosae[k]	D	26	2	P	588	0.6	1.2	2.3	320	O	*Gallus*[f]	FC:PI
4	*Acacia aulacocarpa* A.Cunn. ex Benth.	No	Leguminosae	D	26	2	P	1,470	1.5	3.0	6.0	364	O	B[c]	Fe
5	*Acacia auriculaeformis* A.Cunn. ex Benth.	No	Leguminosae	D	26	2	P	1,078	1.1	2.2	4.4	364	O	B[c]	Fe
6	*Acacia bancrofti* Maiden	No	Leguminosae	D	26	2	P	1,470	1.5	2.9	5.8	364	O	B[c]	Fe
7	*Acacia caffra* (Thunb.) Willd.	No	Leguminosae[k]	D	26	2	P	588	0.6	1.1	2.2	320	O	*Gallus*[f]	FC:PI
8	*Acacia cincinnata* F.Muell.	No	Leguminosae	D	26	2	P	1,862	1.9	3.9	7.7	364	O	B[c]	Fe
9	*Acacia concurrens* Pedley	No	Leguminosae	D	26	2	P	1,470	1.5	3.1	6.1	364	O	B[c]	Fe
10	*Acacia crassa* Pedley	No	Leguminosae	D	26	2	P	1,470	1.5	2.9	5.8	364	O	B[c]	Fe
11	*Acacia crassicarpa* A.Cunn. ex Benth.	No	Leguminosae	D	26	2	P	1,372	1.4	2.7	5.5	364	O	B[c]	Fe
12b	*Acacia dealbata* Link var. *dealbata*	No	Leguminosae[k]	D	26	2	P	784	0.8	1.6	3.1	320	O	*Gallus*[f]	FC:PI
13	*Acacia drepanolobium* Harm. ex Sios.	No	Leguminosae[k]	D	52	4	P	588	0.6	1.1	2.3	320	O	*Gallus*[f]	FC:PI
14	*Acacia falcata*[l]	No	Leguminosae	D	26	2	P	1,470	1.5	3.0	6.0	364	O	B[c]	Fe
15	*Acacia falciformis* DC.	No	Leguminosae	D	26	2	P	1,176	1.2	2.3	4.7	364	O	B[c]	Fe
16b	*Acacia farnesiana* Willd.	No	Leguminosae	D	52	4	P	1,470	1.5	3.1	6.1	364	O	B[c]	Fe
17	*Acacia fimbriata* A.Cunn. ex G.Don	No	Leguminosae	D	26	2	P	1,764	1.8	3.6	7.2	364	O	B[c]	Fe
18a	*Acacia holosericea* A.Cunn. ex G.Don	No	Leguminosae	D	52	4	P	1,666	1.7	3.5	7.0	364	O	B[c]	Fe
18b	*Acacia holosericea* A.Cunn. ex G.Don.	No	Leguminosae[k]	D	52	4	P	1,666	1.7	3.3	6.6	320	O	*Gallus*[f]	FC:PI
19	*Acacia hylonoma* L.Pedley	No	Leguminosae	D	26	2	P	1,372	1.4	2.8	5.6	364	O	B[c]	Fe
20	*Acacia implexa* Benth.	No	Leguminosae[k]	D	26	2	P	784	0.8	1.6	3.2	320	O	*Gallus*[f]	FC:PI
21	*Acacia irrorata* Sieber	No	Leguminosae	D	26	2	P	1,764	1.8	3.6	7.1	364	O	B[c]	Fe
22	*Acacia iteaphylla* F.Muell. ex Benth.	No	Leguminosae	D	26	2	P	1,862	1.9	3.8	7.7	364	O	B[c]	Fe
23	*Acacia leiocalyx* (Domin) Pedley	No	Leguminosae	D	26	2	P	1,568	1.6	3.2	6.3	364	O	B[c]	Fe
24	*Acacia leptocarpa* A.Cunn. ex Benth.	No	Leguminosae	D	26	2	P	1,176	1.2	2.4	4.9	364	O	B[c]	Fe
25	*Acacia longispicata* Benth.	No	Leguminosae	D	26	2	P	1,862	1.9	3.8	7.5	364	O	B[c]	Fe

26	*Acacia maidenii* F.Muell.	No	Leguminosae	D	26	2	P	1,470	1.5	2.9	5.8	364	O	B[c]	Fe
27	*Acacia mangium* Willd.	No	Leguminosae	D	26	2	P	1,078	1.1	2.3	4.6	364	O	B[c]	Fe
28	*Acacia mearnsii* Willd.	No	Leguminosae[k]	D	26	2	P	686	0.7	1.4	2.8	320	O	*Gallus*[f]	FC:PI
29b	*Acacia melanoxylon* Roxb.	No	Leguminosae[k]	D	26	2	P	686	0.7	1.5	3.0	320	O	*Gallus*[f]	FC:PI
30	*Acacia mellifera* (Vahal) Benth.[i]	No	Leguminosae[k]	D	26	2	P	588	0.6	1.2	2.4	320	O	*Gallus*[f]	FC:PI
31a	*Acacia nilotica* (L.) Willd. ex Del. var. *indica*[i]	No	Leguminosae[k]	D	52	4	P	490	0.5	1.1	2.2	320	O	*Gallus*[f]	FC:PI
31b	*Acacia nilotica* (L.) Willd. ex Del. var. *nilotica*	No	Leguminosae[k]	D	52	4	P	588	0.6	1.1	2.2	320	O	*Gallus*[f]	FC:PI
31c	*Acacia nilotica* (L.) Willd. ex Del. var. *tomentosa*	No	Leguminosae[k]	D	52	4	P	588	0.6	1.1	2.2	320	O	*Gallus*[f]	FC:PI
32	*Acacia nilotica* (L.) Willd. ex Del. var. *adstringens*	No	Leguminosae[k]	D	104	8	P	1,078	1.1	2.2	4.4	320	O	*Gallus*[f]	FC:PI
33	*Acacia nubica* Benth.[i]	No	Leguminosae[k]	D	56	4	P	882	0.9	1.7	3.4	320	O	*Gallus*[f]	FC:PI
34	*Acacia orites* Pedley	No	Leguminosae	D	26	2	P	1,470	1.5	2.9	5.8	364	O	B[c]	Fe
35	*Acacia podalyriifolia* A.Cunn.	No	Leguminosae	D	26	2	P	1,666	1.7	3.3	6.6	364	O	B[c]	Fe
36	*Acacia polycantha* Willd.	No	Leguminosae[k]	D	52	4	P	588	0.6	1.1	2.2	320	O	*Gallus*[f]	FC:PI
37	*Acacia pycnantha* Benth.	No	Leguminosae	D	26	2	P	1,764	1.8	3.6	7.1	364	O	B[c]	Fe
38	*Acacia radiana* (Savi.) Brenan	No	Leguminosae[k]	D	78	6	P	980	1.0	1.9	3.8	320	O	*Gallus*[f]	FC:PI
39b	*Acacia radiana* (Savi.) Brenan	No	Leguminosae[k]	D	104	8	P	980	1.0	2.1	4.2	320	O	*Gallus*[f]	FC:PI
40b	*Acacia senegal* (L.) Willd.[i]	No	Leguminosae[k]	D	26	2	P	588	0.6	1.2	2.3	320	O	*Gallus*[f]	FC:PI
41a	*Acacia seyal* (Del.) var. *fistula*	No	Leguminosae[k]	D	104	8	P	1,078	1.1	2.1	4.3	320	O	*Gallus*[f]	FC:PI
41b	*Acacia seyal* (Del.) var. *seyal*	No	Leguminosae[k]	D	104	8	P	1,078	1.1	2.2	4.4	320	O	*Gallus*[f]	FC:PI
42	*Acacia sieberana* DC.	No	Leguminosae[k]	D	26	2	P	588	0.6	1.2	2.4	320	O	*Gallus*[f]	FC:PI
43	*Acacia simsii* A.Cunn. ex Benth.	No	Leguminosae	D	26	2	P	2,058	2.1	4.2	8.4	364	O	B[c]	Fe
44	*Acacia sophorae* Benth.	No	Leguminosae[k]	D	26	2	P	784	0.8	1.7	3.3	320	O	*Gallus*[f]	FC:PI
45a	*Acacia tortilis* (Forssk.) Hayne[i]	No	Leguminosae[k]	D	52	4	P	490	0.5	1.1	2.1	320	O	*Gallus*[f]	FC:PI
45b	*Acacia tortilis* (Forssk.) Hayne ssp. *spiracarpa*	No	Leguminosae[k]	D	52	4	P	490	0.5	1.1	2.2	320	O	*Gallus*[f]	FC:PI
45c	*Acacia tortilis* (Forssk.) Hayne[i]	No	Leguminosae[k]	D	52	4	P	784	0.8	1.6	3.3	320	O	*Gallus*[f]	FC:PI
46	*Acacia tortilis* (Forssk.) Hayne ssp. *radiana*	No	Leguminosae[k]	D	104	8	P	1,078	1.1	2.2	4.4	320	O	*Gallus*[f]	FC:PI
47	*Achillea abrotanoides* Vis.	Yes	Compositae	D	18	2	P	2,744	2.8	5.5	11.1	326	O	B[c]	Fe
48	*Achillea ageratifolia* (Sibth. & Sm.) Boiss.	Yes	Compositae	D	18	2	P	2,842	2.9	5.8	11.6	326	O	B[c]	Fe

‡ 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.

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

Entry number[g]	Species	Voucher	Family	Monocot or dicot	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††
49	*Achillea ageratum* L.	Yes	Compositae	D	18	2	P	2,940	3.0	6.0	12.0	326	O	B[c]	Fe
50	*Achillea asiatica* Serg.	Yes	Compositae	D	36	4	P	4,900	5.0	9.9	19.8	326	O	B[c]	Fe
51	*Achillea asplenifolia* Vent.	Yes	Compositae	D	18	2	P	3,038	3.1	6.2	12.5	326	O	B[c]	Fc
52	*Achillea biebersteinii* Afanasiev	Yes	Compositae	D	18	2	P	2,548	2.6	5.3	10.5	326	O	B[c]	Fe
53	*Achillea borealis* Bong.	Yes	Compositae	D	54	6	P	7,252	7.4	14.9	29.7	326	O	B[c]	Fc
54	*Achillea chamaemelifolia* Pourr.	Yes	Compositae	D	18	2	P	3,332	3.4	6.8	13.5	326	O	B[c]	Fe
55	*Achillea clavenae* L.	Ycs	Compositac	D	18	2	P	2,940	3.0	6.1	12.2	326	O	B[c]	Fe
56	*Achillea clypeolata* Sibth. & Sm.	Yes	Compositae	D	18	2	P	2,646	2.7	5.4	10.8	326	O	B[c]	Fe
57	*Achillea collina* J.Becker ex Reichenb.	Yes	Compositae	D	36	4	P	4,900	5.0	9.9	19.8	326	O	B[c]	Fe
58	*Achillea compacta* Willd.	Yes	Compositae	D	18	2	P	2,450	2.5	4.9	9.8	326	O	B[c]	Fe
59	*Achillea crithmifolia* Waldst. & Kit.	Yes	Compositae	D	18	2	P	2,450	2.5	4.9	9.8	326	O	B[c]	Fe
60	*Achillea crithmifolia* Waldst. & Kit.	Yes	Compositae	D	36	4	P	5,096	5.2	10.5	21.0	326	O	B[c]	Fe
61	*Achillea distans* Waldst. & Kit.	Yes	Compositae	D	54	6	P	8,526	8.7	17.5	35.0	326	O	B[c]	Fe
62	*Achillea erba-rotta* All.	Yes	Compositae	D	18	2	P	2,646	2.7	5.4	10.7	326	O	B[c]	Fe
63	*Achillea filipendulina* Lam.	Yes	Compositae	D	18	2	P	2,842	2.9	5.8	11.6	326	O	B[c]	Fe
64	*Achillea glaberrima* Klok.	Yes	Compositae	D	18	2	P	2,744	2.8	5.7	11.3	326	O	B[c]	Fe
65	*Achillea grandifolia* Friv.	Yes	Compositae	D	18	2	P	3,234	3.3	6.6	13.1	326	O	B[c]	Fe
66	*Achillea impatiens* L.	Yes	Compositae	D	18	2	P	3,038	3.1	6.1	12.2	326	O	B[c]	Fe
67	*Achillea lanulosa* Nutt.	Yes	Compositae	D	36	4	P	4,998	5.1	10.1	20.2	326	O	B[c]	Fe
68	*Achillea ligustica* All.	Yes	Compositae	D	18	2	P	3,136	3.2	6.5	13.0	326	O	B[c]	Fe
69	*Achillea lingulata* Waldst. & Kit.	Ycs	Compositae	D	18	2	P	3,234	3.3	6.5	13.1	326	O	B[c]	Fe
70	*Achillea macrophylla* L.	Yes	Compositae	D	18	2	P	3,038	3.1	6.2	12.4	326	O	B[c]	Fe
71b	*Achillea millefolium* L.	Yes	Compositae	D	54	6	P	7,154	7.3	14.7	29.4	326	O	B[c]	Fe
71c	*Achillea millefolium* L. ssp. *sudetica*	Yes	Compositae	D	54	6	P	7,840	8.0	15.9	31.8	326	O	B[c]	Fe
72	*Achillea nobilis* L.	Yes	Compositae	D	18	2	P	2,646	2.7	5.3	10.7	326	O	B[c]	Fe
73	*Achillea ochroleuca* Ehrh.	Yes	Compositae	D	18	2	P	2,842	2.9	5.8	11.6	326	O	B[c]	Fe
74a	*Achillea pannonica* Scheele Ligota Dolna population[h]	Yes	Compositae	D	72	8	P	9,310	9.5	19.1	38.2	326	O	B[c]	Fe
74b	*Achillea pannonica* Scheele Busko population[h]	Yes	Compositae	D	72	8	P	10,094	10.3	20.6	41.3	326	O	B[c]	Fe
75	*Achillea ptarmica* L.	Yes	Compositae	D	18	2	P	2,842	2.9	5.8	11.6	326	O	B[c]	Fe
76	*Achillea salicifolia* Bess.	Yes	Compositae	D	18	2	P	3,038	3.1	6.3	12.5	326	O	B[c]	Fe
77	*Achillea setacea* Waldst. & Kit.	Yes	Compositae	D	18	2	P	2,842	2.9	5.9	11.7	326	O	B[c]	Fe
78	*Achillea sibirica* Ledeb.	Yes	Compositae	D	36	4	P	4,998	5.1	10.3	20.5	326	O	B[c]	Fe
79	*Achillea stricta* Schleich. ex Grembli (Koch)	Yes	Compositae	D	54	6	P	7,252	7.4	14.9	29.8	326	O	B[c]	Fe
80	*Achillea sulphurea* Boiss.	Yes	Compositae	D	18	2	P	2,646	2.7	5.5	10.9	326	O	B[c]	Fe
81	*Achillea tanacetifolia* All.	Yes	Compositae	D	54	6	P	7,546	7.7	15.5	30.9	326	O	B[c]	Fe

82	*Achillea teretifolia* Willd.	Yes	Compositae	D	18	2	P	2,548	2.6	5.1	10.2	326	O	B[c]	Fe
83	*Achillea tomentosa* L.	Yes	Compositae	D	18	2	P	2,940	3.0	6.0	11.9	326	O	B[c]	Fe
84	*Achillea vermicularis* Trin.	Yes	Compositae	D	18	2	P	2,842	2.9	5.8	11.5	326	O	B[c]	Fe
85	*Actinidia arguta* (Sieb. & Zucc.) Planch. ex Miq. var. *arguta*	No	Actinidiaceae	D	116[o]	4	P	1,470	1.5	3.1	6.2	344	O	F[d]	FC:PI
86	*Actinidia chinensis* Planch. var. *chinensis*	No	Actinidiaceae	D	58[o]	2	P	784	0.8	1.5	3.1	344	O	F[d] & H[c]	FC:PI
87	*Actinidia deliciosa* (A.Chev.) C.F.Liang & A.R.Furguson var. *deliciosa*	No	Actinidiaceae	D	174[o]	6	P	2,156	2.2	4.4	8.9	344	O	F[d]	FC:PI
88	*Actinidia eriantha* Benth.	No	Actinidiaceae	D	c.174[o]	6	P	745	0.8	1.5	3.0	344	O	F[d]	FC:PI
89	*Actinidia kolomikta* (Maxim.& Rupr.) Maxim.	No	Actinidiaceae	D	c.174[o]	6	P	681	0.7	1.4	2.8	344	O	F[d]	FC:PI
90	*Actinidia polygama* (Sieb. & Zucc.) Maxim.	No	Actinidiaceae	D	c.174[o]	6	P	769	0.8	1.6	3.1	344	O	F[d]	FC:PI
91	*Ada ocanensis* (Lindl.) N.H.Williams	No	Orchidaceae	M	—[n]	—[p]	P	3,626	3.7	7.4	14.8	377	O	F	Fe
92	*Agropyron cristatum* (L.) Gaertner[i]	No	Gramineae[j]	M	14	2	P	6,958	7.1	14.3	28.5	343[al]	O	A[c] & F[c]	FC:PI
93	*Agropyron desertorum* (Fischer ex Link) Shultes[i]	No	Gramineae[j]	M	28	4	P	12,936	13.2	26.4	52.8	343[al]	O	A[c] & F[c]	FC:PI
94	*Agropyron mongolicum* Keng[i]	No	Gramineae[j]	M	14	2	P	7,644	7.8	15.6	31.1	343[al]	O	A[c] & F[c]	FC:PI
95c	*Allium aflatunense* B.Fedtsch.	Yes	Alliaceae	M	16	2	P	21,148	21.6	43.2	86.3	336[ai]	O	C	Fe
96c	*Allium angulosum* L.	Yes	Alliaceae	M	16	2	P	13,680	14.0	27.9	55.8	336[ai]	O	C	Fe
97c	*Allium carinatum* L. ssp. *carinatum*[h & ai]	Yes	Alliaceae	M	16	2	P	15,077	15.4	30.8	61.5	336[ai]	O	C	Fe
97d	*Allium carinatum* L. ssp. *carinatum*[h & ai]	Yes	Alliaceae	M	16	2	P	16,479	16.8	33.6	67.2	336[ai]	O	C	Fe
98b	*Allium carinatum* L. ssp. *carinatum*	Yes	Alliaceae	M	24	3	P	22,300	22.8	45.5	91.0	336[ai]	O	C	Fe
99j	*Allium cepa* L.	Yes	Alliaceae	M	16	2	P	16,469	16.8	33.6	67.2	336[ai]	O	C	Fe
100b	*Allium cepa* L. var. *viviparum*[aj]	Yes	Alliaceae	M	16	2	P	14,078	14.4	28.7	57.5	336[ai]	O	C	Fe
101d	*Allium cernuum* Roth.	Yes	Alliaceae	M	14	2	P	22,432	22.9	45.8	91.6	336[ai]	O	C	Fe
102d	*Allium christophii* Trautv.	Yes	Alliaceae	M	16	2	P	20,521	20.9	41.9	83.8	336[ai]	O	C	Fe
103e	*Allium fistulosum* L.	Yes	Alliaceae	M	16	2	P	11,638	11.9	23.8	47.5	336[ai]	O	C	Fe
104c	*Allium flavum* L. ssp. *flavum*	Yes	Alliaceae	M	16	2	P	12,515	12.8	25.5	51.1	336[ai]	O	C	Fe
105	*Allium flavum* L. ssp. *flavum*	Yes	Alliaceae	M	32	4	P	19,968	20.4	40.8	81.5	336[ai]	O	C	Fe
106e	*Allium galanthum* Kar. & Kir.	Yes	Alliaceae	M	16	2	P	14,612	14.9	29.8	59.6	336[ai]	O	C	Fe
107c	*Allium giganteum* Regel	Yes	Alliaceae	M	16	2	P	20,168	20.6	41.2	82.3	336[ai]	O	C	Fe
108	*Allium hirtifolium* Boiss.	Yes	Alliaceae	M	16	2	P	21,041	21.5	42.9	85.9	336[ai]	O	C	Fe
109d	*Allium karataviense* Regel	Yes	Alliaceae	M	18	2	P	19,443	19.8	39.7	79.4	336[ai]	O	C	Fe
110d	*Allium moly* L.	Yes	Alliaceae	M	14	2	P	22,266	22.7	45.4	90.9	336[ai]	O	C	Fe
111	*Allium nutans* L.	Yes	Alliaceae	M	66	8	P	46,530	47.5	95.0	189.9	336[ai]	O	C	Fe
112c	*Allium obliquum* L.	Yes	Alliaceae	M	16	2	P	10,618	10.8	21.7	43.3	336[ai]	O	C	Fe
113b	*Allium oleraceum* L.	Yes	Alliaceae	M	40	5	P	29,581	30.2	60.4	120.7	336[ai]	O	C	Fc
114c	*Allium oreophilum* Meyer	Yes	Alliaceae	M	16	2	P	20,825	21.3	42.5	85.0	336[ai]	O	C	Fe

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

Entry number[g]	Species	Voucher	Family	Monocot or dicot	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††
115c	*Allium paradoxum* (Bieb.) G.Don	Yes	Alliaceae	M	16	2	P	25,745	26.3	52.5	105.1	336[ai]	O	C	Fe
116f	*Allium porrum* L.	Yes	Alliaceae	M	32	4	P	26,592	27.1	54.3	108.5	336[ai]	O	C	Fe
117d	*Allium sativum* L.	Yes	Alliaceae	M	16	2	P	16,508	16.8	33.7	67.4	336[ai]	O	C	Fe
118d	*Allium schoenoprasum* L.	Yes	Alliaceae	M	16	2	P	7,473	7.6	15.3	30.5	336[ai]	O	C	Fe
119b	*Allium senescens* L. ssp. *montanum*	Yes	Alliaceae	M	32	4	P	22,452	22.9	45.8	91.6	336[ai]	O	C	Fe
120	*Allium siculum* Ucria	Yes	Alliaceae	M	18	2	P	34,712	35.4	70.8	141.7	336[ai]	O	C	Fe
121b	*Allium sphaerocephalon* L. ssp. *sphaerocephalon*	Yes	Alliaceae	M	16	2	P	12,275	12.5	25.1	50.1	336[ai]	O	C	Fe
122	*Allium sphaerocephalon* L.	Yes	Alliaceae	M	24	3	P	19,654	20.1	40.1	80.2	336[ai]	O	C	Fe
123c	*Allium stipitatum* Regel	Yes	Alliaceae	M	16	2	P	21,070	21.5	43.0	86.0	336[ai]	O	C	Fe
124c	*Allium tuberosum* Rottl. ex Spreng.	Yes	Alliaceae	M	32	4	P	31,448	32.1	64.2	128.4	336[ai]	O	C	Fe
125d	*Allium ursinum* L. ssp. *ursinum*	Yes	Alliaceae	M	14	2	P	29,567	30.2	60.3	120.7	336[ai]	O	C	Fe
126	*Amaranthus caudatus* L.	No	Amaranthaceae	D	32	2	A	588	0.6	1.3	2.5	359	O	H	FC:PI
127b	*Amaranthus cruentus* L.	No	Amaranthaceae	D	32	2	A	588	0.6	1.3	2.5	359	O	H	FC:PI
128b	*Amaranthus hybridus* L.	No	Amaranthaceae	D	32	2	A	588	0.6	1.3	2.5	359	O	H	FC:PI
129c	*Amaranthus hypochondriacus* L.	No	Amaranthaceae	D	32	2	A	588	0.6	1.3	2.5	359	O	H	FC:PI
130	*Amaranthus powellii* S.Wats.	No	Amaranthaceae	D	32	2	A	588	0.6	1.2	2.4	359	O	H	FC:PI
131	*Amaranthus quitensis* H.B. & K.	No	Amaranthaceae	D	32	2	A	588	0.6	1.2	2.4	359	O	H	FC:PI
132	*Amaranthus retroflexus* L.	Yes	Amaranthaceae	D	32	2	A	882	0.9	1.7	3.4	375	O	F	Fe
133	*Amaranthus spinosus* L.	Yes	Amaranthaceae	D	34	2	A	980	1.0	1.9	3.8	375	O	F	Fe
134b	*Amaranthus tricolor* L.	No	Amaranthaceae	D	32	2	A	882	0.9	1.8	3.6	359	O	H	FC:PI
135	*Amsinckia douglasiana* A.DC.	Yes	Boraginaceae	D	—[n]	—[p]	A	980	1.0	2.0	4.0	377	O	F	Fe
136	*Amsinckia furcata* Suksdorf	Yes	Boraginaceae	D	—[n]	—[p]	A	1,274	1.3	2.6	5.2	377	O	F	Fe
137	*Amsinckia spectabilis* Fisch. & Mey. *var. microcarpa*	Yes	Boraginaceae	D	—[n]	—[p]	A	1,078	1.1	2.2	4.4	377	O	F	Fe
138	*Anagallis arvensis* L. cv. caerulea	Yes	Primulaceae	D	40	4	A	1,764	1.8	3.5	7.0	375	O	F	Fe
139c	*Andropogon gerardii* Vitman	No	Gramineae	M	60	6	P	3,528	3.6	7.2	14.3	367	O	*Gallus*[f]	FC:MI
140	*Andropogon gerardii* Vitman	No	Gramineae	M	70	7	P	4,214	4.3	8.6	17.3	367	O	*Gallus*[f]	FC:MI
141b	*Andropogon gerardii* Vitman	No	Gramineae	M	80	8	P	4,900	5.0	10.0	20.1	367	O	*Gallus*[f]	FC:MI
142	*Andropogon gerardii* Vitman	No	Gramineae	M	90	9	P	5,096	5.2	10.3	20.7	367	O	*Gallus*[f]	FC:MI
143	*Anemarrhena asphodeloides* Bunge	Yes	Anemarrhenaceae	M	22	2	P	2,842	2.9	5.8	11.5	317	O	B	Fe
144	*Annona cacans* Warm.	Yes	Annonaceae	D	14	2	P	980	1.0	2.0	4.0	341	O	B[c]	Fe
145	*Annona glabra* L.	Yes	Annonaceae	D	28	4	P	1,274	1.3	2.7	5.4	341	O	B[c]	Fe
146	*Annona lutescens* Saff.	Yes	Annonaceae	D	28	4	P	980	1.0	2.0	4.0	341	O	B[c]	Fe
147b	*Annona reticulata* L.	Yes	Annonaceae	D	14	2	P	784	0.8	1.7	3.3	341	O	B[c]	Fe
148	*Annona sericea*[l]	Yes	Annonaceae	D	—[n]	—[p]	P	686	0.7	1.4	2.7	341	O	B[c]	Fe
149	*Ansellia africana* Lindl.	No	Orchidaceae	M	42[o]	—[p]	P	1,813[t]	1.6	3.7	7.4	307	O	*Gallus*[f]	FC:PI
150b	*Anthemis tinctoria* L.	Yes	Compositae	D	18	2	P	3,964	4.0	8.1	16.2	326	O	B[c]	Fe
151c	*Antirrhinum majus* L.	Yes	Scrophulariaceae	D	16	2	P	515	0.5	1.1	2.1	377	O	J	Fe

152	*Apera spica-venti* (L.) Beauv.	Yes	Gramineae	M	14	2	A	5,292	5.4	10.8	21.6	375	O	F	Fe
153f	*Arabidopsis thaliana* (L.) Heynh.	—[m]	Cruciferae	D	10[o]	2	A	164	0.2	0.3	0.7	350	O	B[c] & G[c]	Fe
154b	*Armeria maritima* (Mill.) Willd.[h]	Yes	Plumbaginaceae	D	18	2	P	4,018	4.1	8.2	16.4	318	O	*Petunia*[f]	FC:EB
154c	*Armeria maritima* (Mill.) Willd.[h]	Yes	Plumbaginaceae	D	18	2	P	4,508	4.6	9.1	18.2	318	O	*Petunia*[f]	FC:EB
155b	*Artemisia absinthium* L.	Yes	Compositae	D	18	2	P	3,726	3.8	7.6	15.2	326	O	B[c]	Fe
156	*Asimina triloba* (L.) Dun.	Yes	Annonaceae	D	—[n]	—[p]	P	784	0.8	1.6	3.2	341	O	B[c]	Fe
157	*Barkeria lindleyana* Batem. ex Lindl.	No	Orchidaceae	M	—[n]	—[p]	P	1,612[t]	1.7	3.3	6.6	307	O	*Gallus*[f]	FC:PI
158	*Berberis bidentata* Lechl.	Yes	Berberidaceae	D	28	2	P	784	0.8	1.5	3.0	353	O	B	Fe
159	*Berberis buxifolia* Lam.	Yes	Berberidaceae	D	56	4	P	2,940	3.0	6.1	12.1	353	O	B	Fe
160	*Berberis cabrerae* Job	Yes	Berberidaceae	D	28	2	P	784	0.8	1.7	3.3	353	O	B	Fe
161	*Berberis chillanensis* (Schn.) Sragne	Yes	Berberidaceae	D	28	2	P	882	0.9	1.7	3.4	353	O	B	Fe
162	*Berberis darwinii* Hook.	Yes	Berberidaceae	D	28	2	P	1,568	1.6	3.1	6.2	353	O	B	Fe
163	*Berberis empetrifolia* Lam.	Yes	Berberidaceae	D	28	2	P	1,764	1.8	3.6	7.3	353	O	B	Fe
164	*Berberis heterophylla* Juss	Yes	Berberidaceae	D	56	4	P	3,038	3.1	6.2	12.4	353	O	B	Fe
165	*Berberis linearifolia* Phil.	Yes	Berberidaceae	D	28	2	P	1,666	1.7	3.4	6.8	353	O	B	Fe
166	*Berberis montana* Gay.	Yes	Berberidaceae	D	28	2	P	882	0.9	1.7	3.4	353	O	B	Fe
167	*Berberis parodii* Job	Yes	Berberidaceae	D	28	2	P	1,568	1.6	3.1	6.3	353	O	B	Fe
168	*Berberis serrato-dentata* Lechl.	Yes	Berberidaceae	D	28	2	P	882	0.9	1.8	3.7	353	O	B	Fe
169	*Borago officinalis* L.	No	Boraginaceae	D	16[o]	2	A	1,666	1.7	3.5	7.0	373	O	G[b2]	FC:PI
170	*Brachycome dichromosomatica* C.R.Carter	Yes	Compositae	D	4	2	A	1,078	1.1	2.2	4.5	376	O	J	Fe
171	*Brahea dulcis*[l]	Yes	Palmae	M	—[n]	—[p]	P	27,582	28.1	56.3	112.6	377	O	B	Fe
172	*Brassia maculata R.Br.*	No	Orchidaceae	M	60[o]	—[p]	P	1,832[t]	1.6	3.7	7.4	307	O	*Gallus*[f]	FC:PI
173	*Brassia verrucosa* Lindl.	Yes	Orchidaceae	M	52-60[o]	—[p]	P	3,822	3.9	7.8	15.7	377	O	F	Fe
174	*Broughtonia sanguinea* (Sw.) R.Br.	No	Orchidaceae	M	40[o]	—[p]	P	1,039[t]	1.1	2.1	4.2	307	O	*Gallus*[f]	FC:PI
175	*Bulbophyllum cocoinum* Batem. ex Lindl.	No	Orchidaceae	M	38[o]	—[p]	P	2,621[t]	2.7	5.4	10.8	307	O	*Gallus*[f]	FC:PI
176	*Cadetia taylori* (F.Muell.) Schltr.	No	Orchidaceae	M	—[n]	—[p]	P	936[t]	1.0	1.9	3.8	307	O	*Gallus*[f]	FC:PI
177d	*Cajanus cajan* (L.) Huth	Yes	Leguminosae[j]	D	22	2	P	784	0.8	1.6	3.3	360[ar]	O	*Glycine*[e]	FC:PI
177e	*Cajanus cajan* (L.) Huth	Yes	Leguminosae[j]	D	22	2	P	882	0.9	1.7	3.4	360[ar]	O	B[c] & G[c]	Fe
178	*Calamus caesius* Blume	Yes	Palmae	M	—[n]	—[p]	P	1,470	1.5	2.9	5.8	377	O	B	Fe
179	*Calamus subinermis* Wendl. ex Becc.	Yes	Palmae	M	—[n]	—[p]	P	2,058	2.1	4.3	8.6	377	O	B	Fe
180	*Calathea bachemiana* E.Morr.	No	Marantaceae	M	26	2	P	392	0.4	0.8	1.5	355	C	J[ao]	Fe
181	*Calathea clossoni*[l]	No	Marantaceae	M	26	2	P	392	0.4	0.8	1.5	355	C	J[ao]	Fe
182	*Calathea insignis* Petersen	No	Marantaceae	M	28	2	P	392	0.4	0.8	1.6	355	C	J[ao]	Fe
183	*Calathea kegeliana*[l]	No	Marantaceae	M	28	2	P	490	0.5	1.1	2.1	355	C	J[ao]	Fe
184	*Calathea lietzei E.Morr.*	No	Marantaceae	M	24	2	P	392	0.4	0.8	1.6	355	C	J[ao]	Fe
185	*Calathea ornata* Koern. var. *rosea-lineata*	No	Marantaceae	M	28	2	P	392	0.4	0.9	1.8	355	C	J[ao]	Fe
186a	*Calathea picturata* C.Koch. & Linden. var. *vandenheckii*	No	Marantaceae	M	26	2	P	392	0.4	0.8	1.5	355	C	J[ao]	Fe

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

Entry number[g]	Species	Voucher	Family	Monocot or dicot	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††
186b	*Calathea picturata* C.Koch. & Linden. var. *argentea*	No	Marantaceae	M	26	2	P	392	0.4	0.8	1.6	355	C	J[ao]	Fe
187	*Calathea princeps* Regel.	No	Marantaceae	M	24	2	P	294	0.3	0.6	1.3	355	C	J[ao]	Fe
188	*Calathea undulata* Regel.	No	Marantaceae	M	24	2	P	392	0.4	0.8	1.6	355	C	J[ao]	Fe
189	*Calathea zebrina* Lindl.	No	Marantaceae	M	26	2	P	392	0.4	0.7	1.4	355	C	J[ao]	Fe
190	*Calycanthus chemonanthis*[l]	Yes	Calycanthaceae	D	—[n]	—[p]	P	980	1.0	2.0	3.9	341	O	B[c]	Fe
191	*Cananga odorata* Hook.f. & Thomson	Yes	Annonaceae	D	16	2	P	784	0.8	1.6	3.1	341	O	B[c]	Fe
192	*Canella winterana* (L.) Gaertner.	Yes	Canellaceae	D	—[n]	—[p]	P	5,684	5.8	11.7	23.3	341	O	B[c]	Fe
193	*Carex blepharicarpa* Franch.	Yes	Cyperaceae	M	30	—[u]	P	490	0.5	0.9	1.8	357	C[ap]	J-198	Fe
194	*Carex bostrychostigma* Maxim.	Yes	Cyperaceae	M	46	—[u]	P	588	0.6	1.1	2.2	357	C[ap]	J-198	Fe
195	*Carex brownii* Tuckerm.[h & ap]	Yes	Cyperaceae	M	72	—[u]	P	196	0.2	0.4	0.9	357	C[ap]	J-198	Fe
196	*Carex capillacea* Boott[h & ap]	Yes	Cyperaceae	M	60-66	—[u]	P	294	0.3	0.5	1.0	357	C[ap]	J-198	Fe
197	*Carex chrysolepis* Franch. & Sav.	Yes	Cyperaceae	M	28	—[u]	P	392	0.4	0.8	1.6	357	C[ap]	J-198	Fe
198	*Carex ciliatomarginata* Nakai	Yes	Cyperaceae	M	12[o]	2	P	588	0.6	1.1	2.3	377	O	J	Fe
199	*Carex conica* Boott[i & ap]	Yes	Cyperaceae	M	36	—[u]	P	490	0.5	0.9	1.8	357	C[ap]	J-198	Fe
200	*Carex curviollis*[l]	Yes	Cyperaceae	M	56	—[u]	P	294	0.3	0.7	1.4	357	C[ap]	J-198	Fe
201	*Carex dolichostachya* Hayata var. *glaberrima*	Yes	Cyperaceae	M	62-70	—[u]	P	392	0.4	0.8	1.6	357	C[ap]	J-198	Fe
202	*Carex foliosissima* F.Schmidt	Yes	Cyperaceae	M	30	—[u]	P	490	0.5	1.0	2.1	357	C[ap]	J-198	Fe
203	*Carex humilis*[l] ssp. *lanceolata*	Yes	Cyperaceae	M	72	4[u]	P	686	0.7	1.5	2.9	357	C[ap]	J-198	Fe
204	*Carex ischnostachya* Steud.	Yes	Cyperaceae	M	62	—[u]	P	294	0.3	0.6	1.1	357	C[ap]	J-198	Fe
205	*Carex kiotensis* Franch. & Sav.	Yes	Cyperaceae	M	74	—[u]	P	294	0.3	0.6	1.2	357	C[ap]	J-198	Fe
206	*Carex kobomugi* Ohwi	Yes	Cyperaceae	M	88	—[u]	P	196	0.2	0.5	0.9	357	C[ap]	J-198	Fe
207	*Carex laticeps* C.B.Clarke	Yes	Cyperaceae	M	58	—[u]	P	294	0.3	0.7	1.3	357	C[ap]	J-198	Fe
208	*Carex makinoensis*[l]	Yes	Cyperaceae	M	30	—[u]	P	392	0.4	0.8	1.6	357	C[ap]	J-198	Fe
209	*Carex maximowiczii*[l]	Yes	Cyperaceae	M	68-74	—[u]	P	294	0.3	0.6	1.2	357	C[ap]	J-198	Fe
210a	*Carex morrowii* Boott var. *albo-marginata*	Yes	Cyperaceae	M	30	—[u]	P	490	0.5	1.0	2.0	357	C[ap]	J-198	Fe
210b	*Carex morrowii* Boott var. *temnolepis*	Yes	Cyperaceae	M	38	—[u]	P	490	0.5	1.0	2.0	357	C[ap]	J-198	Fe
210c	*Carex morrowii* Boott	Yes	Cyperaceae	M	38	—[u]	P	490	0.5	1.0	2.0	357	C[ap]	J-198	Fe
211	*Carex nubigera*[l] ssp. *albata*[h & ap]	Yes	Cyperaceae	M	112	2[u]	P	196	0.2	0.3	0.6	357	C[ap]	J-198	Fe
212	*Carex oahuensis* Hillebr. ssp. *robusta*	Yes	Cyperaceae	M	62	—[u]	P	294	0.3	0.5	1.1	357	C[ap]	J-198	Fe
213	*Carex omiana* Franch. & Sav.	Yes	Cyperaceae	M	48-58	—[u]	P	294	0.3	0.6	1.2	357	C[ap]	J-198	Fe
214	*Carex oxyandra* Kudo[i & ap]	Yes	Cyperaceae	M	20	—[u]	P	392	0.4	0.8	1.7	357	C[ap]	J-198	Fe
215	*Carex pachygyna* Franch. & Sav.	Yes	Cyperaceae	M	12	2	P	686	0.7	1.5	3.0	357	C[ap]	J-198	Fe
216	*Carex paxii* Kukenthal[h & ap]	Yes	Cyperaceae	M	76	2[u]	P	196	0.2	0.3	0.6	357	C[ap]	J-198	Fe

217a	*Carex pisiformis* Boott ssp. *stenostachya var. ikegamiana*	Yes	Cyperaceae	M	58	—[u]	P	294	0.3	0.7	1.3	357	C[ap]	J-198	Fe
217b	*Carex pisiformis* Boott ssp. *stenostachya*	Yes	Cyperaceae	M	58	—[u]	P	294	0.3	0.7	1.3	357	C[ap]	J-198	Fe
217c	*Carex pisiformis* Boott ssp. *alterniflora*	Yes	Cyperaceae	M	60-84	—[u]	P	294	0.3	0.7	1.3	357	C[ap]	J-198	Fe
217d	*Carex pisiformis* Boott	Yes	Cyperaceae	M	68	—[u]	P	392	0.4	0.7	1.4	357	C[ap]	J-198	Fe
217e	*Carex pisiformis* Boott ssp. *duvaliana*	Yes	Cyperaceae	M	76	—[u]	P	294	0.3	0.6	1.3	357	C[ap]	J-198	Fe
218	*Carex pumila*[l]	Yes	Cyperaceae	M	82	—[u]	P	294	0.3	0.6	1.1	357	C[ap]	J-198	Fe
219	*Carex reinii* Franch. & Sav.	Yes	Cyperaceae	M	26	—[u]	P	490	0.5	1.0	2.0	357	C[ap]	J-198	Fe
220	*Carex sendaica* Franch. ssp. *nakiri*	Yes	Cyperaceae	M	62	—[u]	P	294	0.3	0.7	1.3	357	C[ap]	J-198	Fe
221	*Carex shimidzensis* Franch.	Yes	Cyperaceae	M	68	—[u]	P	294	0.3	0.6	1.3	357	C[ap]	J-198	Fe
222	*Carex siderosticta* Hance	Yes	Cyperaceae	M	24	4	P	1,176	1.2	2.4	4.7	357	C[ap]	J-198	Fe
223	*Carex thunbergii* Steud.[h & ap]	Yes	Cyperaceae	M	78-90	—[u]	P	294	0.3	0.6	1.2	357	C[ap]	J-198	Fe
224	*Carex tristachya* Thunb. ssp. *pocilliformis*[h & ap]	Yes	Cyperaceae	M	—[n]	—[p]	P	294	0.3	0.6	1.2	357	C[ap]	J-198	Fe
225	*Carya illinoensis* C.Koch	No	Juglandaceae	D	32[o]	2	P	784	0.8	1.7	3.3	348	O	G[b2]	FC:PI
226	*Cassia obtusifolia* L.	Yes	Leguminosae	D	—[n]	—[p]	A	980	1.0	2.0	4.0	375	O	F	Fe
227a	*Cattleya bowringiana* O'Brien f. *alba*	No	Orchidaceae	M	40, 42[o]	—[p]	P	2,440[t]	2.5	5.0	10.0	307	O	*Gallus*[f]	FC:PI
227b	*Cattleya bowringiana* O'Brien var. *coerulea*	No	Orchidaceae	M	—[n]	—[p]	P	2,445[t]	2.5	5.0	10.0	307	O	*Gallus*[f]	FC:PI
228	*Cattleya forbesii* Lindl.	No	Orchidaceae	M	54-60[o]	—[p]	P	1,612[t]	1.7	3.3	6.6	307	O	*Gallus*[f]	FC:PI
229a	*Cattleya walkeriana* Gardn.	No	Orchidaceae	M	40[o]	—[p]	P	2,925[t]	3.0	6.0	12.0	307	O	*Gallus*[f]	FC:PI
229b	*Cattleya walkeriana* Gardn. var. *coerulea* Hort.	No	Orchidaceae	M	40[o]	—[p]	P	2,602[t]	2.7	5.3	10.6	307	O	*Gallus*[f]	FC:PI
230a	*Cattleya walkeriana* Gardn. f. *alba* Hort. 'Limerick'	No	Orchidaceae	M	c.60[o]	—[p]	P	3,984[t]	4.1	8.1	16.2	307	O	*Gallus*[f]	FC:PI
230b	*Cattleya walkeriana* Gardn. f. *semi-alba* Hort. 'Puanani'	No	Orchidaceae	M	—[n]	—[p]	P	3,577[t]	3.7	7.3	14.6	307	O	*Gallus*[f]	FC:PI
231a	*Cattleya walkeriana* Gardn. f. *alba* Hort. 'Pendentive'	No	Orchidaceae	M	c.80[o]	—[p]	P	4,067[t]	4.3	8.6	17.2	307	O	*Gallus*[f]	FC:PI
231b	*Cattleya walkeriana* Gardn. var. *coerulea* Hort. 'Chouju'	No	Orchidaceae	M	—[n]	—[p]	P	4,552[t]	4.7	9.3	18.6	307	O	*Gallus*[f]	FC:PI
232	*Cenchrus echinatus*[l]	Yes	Gramineae	M	—[n]	—[p]	A	2,548	2.6	5.1	10.2	375	O	F	Fe
233	*Chenopodium album L.*	Yes	Amaranthaceae[k]	D	54	6	A	2,254	2.3	4.7	9.3	375	O	F	Fe
234	*Chloranthus officinalis* Mal.	Yes	Chloranthaceae	D	30	—[p]	P	2,842	2.9	5.8	11.6	341	O	B[c]	Fe
235	*Cienfuegosia hitchcockii* (Ulbrich ex Kearney) O.J.Blanchard	No	Malvaceae	D	20[o]	2	P	1,176	1.2	2.3	4.6	349	O	G[b2]	FC:PI
236	*Citrus* cv. Tahiti lime	No	Rutaceae	D	27[o]	3	P	573	0.6	1.2	2.3	358	O	*Gallus*[f]	FC:PI
237	*Citrus aurantifolia* Swingle[aq]	No	Rutaceae	D	18[o]	2	P	392	0.4	0.8	1.5	358	O	*Gallus*-236[f]	FC:PI

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

Entry number[g]	Species	Voucher	Family	Monocot or dicot	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††
238	*Citrus aurantium* L.	No	Rutaceae	D	18[o]	2	P	392	0.4	0.8	1.5	358	O	*Gallus*-236[f]	FC:PI
239	*Citrus grandis*[l & aq]	No	Rutaceae	D	18[o]	2	P	392	0.4	0.8	1.6	358	O	*Gallus*-236[f]	FC:PI
240	*Citrus limon* (L.) Burm. f.[aq]	No	Rutaceae	D	18[o]	2	P	392	0.4	0.8	1.6	358	O	*Gallus*-236[f]	FC:PI
241	*Citrus medica* L.[aq]	No	Rutaceae	D	18[o]	2	P	392	0.4	0.8	1.6	358	O	*Gallus*-236[f]	FC:PI
242	*Citrus paradisi* Macfad[aq]	No	Rutaceae	D	18[o]	2	P	392	0.4	0.8	1.6	358	O	*Gallus*-236[f]	FC:PI
243b	*Citrus reticulata* Blanco[aq]	No	Rutaceae	D	18[o]	2	P	392	0.4	0.7	1.5	358	O	*Gallus*-236[f]	FC:PI
244d	*Citrus sinensis* Osbeck	No	Rutaceae	D	18[o]	2	P	392	0.4	0.8	1.5	358	O	*Gallus*-236[f]	FC:PI
245	*Cleisostoma subulatum* Bl.	No	Orchidaceae	M	38[o]	—[p]	P	3,136[t]	3.2	6.4	12.8	307	O	*Gallus*[f]	FC:PI
246	*Coccothrinax fragrans* Burret	Yes	Palmae	M	—[n]	—[p]	P	6,370	6.5	12.9	25.9	377	O	B	Fe
247	*Cochlearia pyrenaica* DC.	—[m]	Cruciferae	D	12[o]	2	B-P	392	0.4	0.8	1.6	350	O	B[c] & G[c]	Fe
248	*Cochlioda noezliana* Rolfe	Yes	Orchidaceae	M	—[n]	—[p]	P	3,430	3.5	6.9	13.9	377	O	F	Fe
249	*Coelogyne pastulata* Pfitz.	No	Orchidaceae	M	—[n]	—[p]	P	2,685[t]	2.8	5.5	11.0	307	O	*Gallus*[f]	FC:PI
250f	*Coffea arabica* L.[h]	No	Rubiaceae	D	44[o]	4	P	1,176	1.2	2.3	4.6	309	O	*Gallus*[f]	FC:PI
250g	*Coffea arabica* L.[h]	No	Rubiaceae	D	44[o]	4	P	1,372	1.4	2.7	5.4	309	O	*Gallus*[f]	FC:PI
251	*Coffea bertrandii* A.Cheval.	No	Rubiaceae	D	22[o]	2	P	784	0.8	1.7	3.3	309	O	*Gallus*[f]	FC:PI
252a	*Coffea brevipes* Hiern.[h]	No	Rubiaceae	D	22[o]	2	P	686	0.7	1.4	2.8	309	O	*Gallus*[f]	FC:PI
252b	*Coffea brevipes* Hiern.[h]	No	Rubiaceae	D	22[o]	2	P	882	0.9	1.7	3.4	309	O	*Gallus*[f]	FC:PI
253b	*Coffea canephora* Pierre. ex Froehn.[h]	No	Rubiaceae	D	22[o]	2	P	588	0.6	1.2	2.4	309	O	*Gallus*[f]	FC:PI
253c	*Coffea canephora* Pierre. ex Froehn.[h]	No	Rubiaceae	D	22[o]	2	P	784	0.8	1.6	3.2	309	O	*Gallus*[f]	FC:PI
254a	*Coffea congensis* Froehn.[h]	No	Rubiaceae	D	22[o]	2	P	686	0.7	1.4	2.8	309	O	*Gallus*[f]	FC:PI
254b	*Coffea congensis* Froehn.[h]	No	Rubiaceae	D	22[o]	2	P	882	0.9	1.8	3.6	309	O	*Gallus*[f]	FC:PI
255b	*Coffea eugenioides* S.Moore.[h]	No	Rubiaceae	D	22[o]	2	P	686	0.7	1.3	2.6	309	O	*Gallus*[f]	FC:PI
255c	*Coffea eugenioides* S.Moore.[h]	No	Rubiaceae	D	22[o]	2	P	686	0.7	1.4	2.8	309	O	*Gallus*[f]	FC:PI
256	*Coffea farafanganensis* Leroy	No	Rubiaceae	D	22[o]	2	P	686	0.7	1.3	2.7	309	O	*Gallus*[f]	FC:PI
257a	*Coffea humilis* A.Cheval.[h]	No	Rubiaceae	D	22[o]	2	P	686	0.7	1.4	2.8	309	O	*Gallus*[f]	FC:PI
257b	*Coffea humilis* A.Cheval.[h]	No	Rubiaceae	D	22[o]	2	P	882	0.9	1.8	3.6	309	O	*Gallus*[f]	FC:PI
258a	*Coffea liberica* L.[h]	No	Rubiaceae	D	22[o]	2	P	686	0.7	1.3	2.6	309	O	*Gallus*[f]	FC:PI
258b	*Coffea liberica* L.[h]	No	Rubiaceae	D	22[o]	2	P	980	1.0	1.9	3.8	309	O	*Gallus*[f]	FC:PI
258c	*Coffea liberica* var. *dewevrei* Lebrun	—[m]	Rubiaceae	D	—[n]	—[p]	P	686	0.7	1.4	2.8	325	O	*Petunia*[f]	FC:PI

259	*Coffea millotii* Leroy	No	Rubiaceae	D	22[o]	2	P	882	0.9	1.7	3.4	309	O	*Gallus*[f]	FC:PI
260a	*Coffea pseudozanguebariae* D.M.Bridson[h]	No	Rubiaceae	D	22[o]	2	P	490	0.5	1.0	2.0	309	O	*Gallus*[f]	FC:PI
260b	*Coffea pseudozanguebariae* D.M.Bridson[h]	No	Rubiaceae	D	22[o]	2	P	686	0.7	1.3	2.6	309	O	*Gallus*[f]	FC:PI
260c	*Coffea pseudozanguebariae* D.M.Bridson	—[m]	Rubiaceae	D	—[n]	—[p]	P	588	0.6	1.1	2.3	325	O	*Petunia*[f]	FC:PI
261a	*Coffea racemosa*[h&l]	No	Rubiaceae	D	22[o]	2	P	490	0.5	0.9	1.8	309	O	*Gallus*[f]	FC:PI
261b	*Coffea racemosa*[h&l]	No	Rubiaceae	D	22[o]	2	P	588	0.6	1.1	2.2	309	O	*Gallus*[f]	FC:PI
262	*Coffea salvatrix* Swynn. & Philipson.	No	Rubiaceae	D	22[o]	2	P	784	0.8	1.5	3.0	309	O	*Gallus*[f]	FC:PI
263a	*Coffea sessiliflora* D.M.Bridson[h]	No	Rubiaceae	D	22[o]	2	P	392	0.4	0.9	1.7	309	O	*Gallus*[f]	FC:PI
263b	*Coffea sessiliflora* D.M.Bridson[h]	No	Rubiaceae	D	22[o]	2	P	588	0.6	1.1	2.3	309	O	*Gallus*[f]	FC:PI
264a	*Coffea stenophylla* G.Don.[h]	No	Rubiaceae	D	22[o]	2	P	588	0.6	1.2	2.4	309	O	*Gallus*[f]	FC:PI
264b	*Coffea stenophylla* G.Don.[h]	No	Rubiaceae	D	22[o]	2	P	784	0.8	1.5	3.0	309	O	*Gallus*[f]	FC:PI
265	*Convolvulus arvensis* L.	Yes	Convolvulaceae	D	48	—[p]	P	1,764	1.8	3.6	7.1	375	O	F	Fe
266b	*Crepis foetida* L. ssp. *commutata*	Yes	Compositae[j]	D	10	2	A	1,931	2.0	3.9	7.9	361[as]	O	G[c]	Fe
266c	*Crepis foetida* L. ssp. *commutata*	Yes	Compositae[j]	D	10	2	A	1,940	2.0	4.0	7.9	361[as]	O	*Glycine*[e]	FC:PI
266d	*Crepis foetida* L. ssp. *foetida*	Yes	Compositae[j]	D	10	2	A	2,136	2.2	4.4	8.7	361[as]	O	G[c]	Fe
266e	*Crepis foetida* L. ssp. *foetida*	Yes	Compositae[j]	D	10	2	A	2,185	2.2	4.5	8.9	361[as]	O	*Glycine*[e]	FC:PI
266f	*Crepis foetida* L. ssp. *rhoeadifolia*	Yes	Compositae[j]	D	10	2	A	2,107	2.2	4.3	8.6	361[as]	O	G[c]	Fe
266g	*Crepis foetida* L. ssp. *rhoeadifolia*	Yes	Compositae[j]	D	10	2	A	2,127	2.2	4.3	8.7	361[as]	O	*Glycine*[e]	FC:PI
267	*Cymbidium sinense* (Jacks.) Willd	No	Orchidaceae	M	40[o]	—[p]	P	3,092[t]	3.2	6.3	12.6	307	O	*Gallus*[f]	FC:PI
268	*Cymbopetalum bailonii* R.E.Fr.	Yes	Annonaceae	D	18	2	P	784	0.8	1.6	3.2	341	O	B[c]	Fe
269	*Cymbopetalum brasiliense* (Vell.) & Benth.	Yes	Annonaceae	D	27	—[p]	P	2,450	2.5	4.9	9.9	341	O	B[c]	Fe
270	*Cynodon dactylon* (L.) Pers.	Yes	Gramineae	M	—[n]	—[p]	P	784	0.8	1.6	3.2	375	O	F	Fe
271	*Cyperus esculentus* L.	Yes	Cyperaceae	M	c.128	—[p]	P	588	0.6	1.2	2.4	375	O	F	Fe
272	*Cyperus iria* L.	Yes	Cyperaceae	M	c.128	—[p]	A	784	0.8	1.6	3.2	375	O	F	Fe
273	*Cyperus rotundus*[l]	Yes	Cyperaceae	M	—[n]	—[p]	P	490	0.5	0.9	1.8	375	O	F	Fe
274	*Cypripedium calceolus* L.	—[m]	Orchidaceae	M	20-22[o]	—[p]	P	31,703	32.4	64.7	129.4	377	O	B	Fe
275	*Cypripedium henryi* Rolfe	—[m]	Orchidaceae	M	—[n]	—[p]	P	38,024	38.8	77.7	155.3	377	O	B	Fe
276	*Cypripedium japonicum* Thunb. var. *formosanum*	—[m]	Orchidaceae	M	20[o]	—[p]	P	31,360	32.0	64.1	128.1	377	O	B	Fe
277	*Cypripedium macranthos* Sw.	—[m]	Orchidaceae	M	20[o]	—[p]	P	36,652	37.4	74.8	149.6	377	O	B	Fe
278	*Cypripedium molle* Lindl.	Yes	Orchidaceae	M	20	2	P	4,052	4.1	8.3	16.5	377	O	B	Fe
279f	*Dactylis glomerata* L.	Yes	Gramineae[j]	M	14[o]	2	P	1,666[ac]	1.7[ac]	3.5[ac]	6.9[ac]	314	O	*Petunia*[f]	FC:DAPI
280d	*Dactylis glomerata* L.	Yes	Gramineae	M	28	4	P	4,038	4.1	8.2	16.5	371	O	F[c]	FC:PI
280e	*Dactylis glomerata* L.	Yes	Gramineae	M	28	4	P	4,067	4.2	8.3	16.6	371	O	B[c]	Fe
280f	*Dactylis glomerata* L.	Yes	Gramineae[j]	M	28[o]	4	P	3,136[ac]	3.2[ac]	6.4[ac]	12.8[ac]	314	O	*Petunia*[f]	FC:DAPI
281	*Dactylis glomerata* L.	Yes	Gramineae[j]	M	42[o]	6	P	4,312[ac]	4.4[ac]	8.8[ac]	17.6[ac]	314	O	*Petunia*[f]	FC:DAPI
282	*Dactyloctenium aegyptium*[l]	Yes	Gramineae	M	—[n]	—[p]	A-P	1,862	1.9	3.8	7.5	375	O	F	Fe
283	*Daemonorops angustifolius*[l]	Yes	Palmae	M	—[n]	—[p]	P	1,764	1.8	3.7	7.3	377	O	B	Fe

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

Entry number[g]	Species	Voucher	Family	Monocot or dicot	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††
284b	*Dasypyrum villosum* (L.) P. Candargy (= *Haynaldia villosa*)[h]	Yes	Gramineae	M	14	2	A	4,704	4.8	9.6	19.1	310[aa]	O	C[c]	Fe
284c	*Dasypyrum villosum* (L.) P. Candargy (= *Haynaldia villosa*)[h]	Yes	Gramineae	M	14	2	A	5,782	5.9	11.9	23.7	310[aa]	O	C[c]	Fe
285	*Dendrobium affine* (Deane) Steud.	No	Orchidaceae	M	38[o]	2	P	911[t]	1.0	1.9	3.8	307	O	*Gallus*[f]	FC:PI
286	*Dendrobium antennatum* Lindl.	No	Orchidaceae	M	38[o]	2	P	1,357[t]	1.4	2.8	5.6	307	O	*Gallus*[f]	FC:PI
287	*Dendrobium atroviolaceum* Rolfe	No	Orchidaceae	M	38[o]	2	P	1,259[t]	1.3	2.6	5.2	307	O	*Gallus*[f]	FC:PI
288	*Dendrobium bellatulum* Rolfe	No	Orchidaceae	M	38[o]	2	P	1,308[t]	1.3	2.6	5.2	307	O	*Gallus*[f]	FC:PI
289	*Dendrobium bicaudatum* Reinw.	No	Orchidaceae	M	38[o]	2	P	1,181[t]	1.2	2.4	4.8	307	O	*Gallus*[f]	FC:PI
290	*Dendrobium bigibbum* Lindl.	No	Orchidaceae	M	38[o]	2	P	877[t]	0.9	1.8	3.6	307	O	*Gallus*[f]	FC:PI
291	*Dendrobium bracteosum* Rchb.f.	No	Orchidaceae	M	38[o]	2	P	1,729[t]	1.8	3.5	7.0	307	O	*Gallus*[f]	FC:PI
292	*Dendrobium bullenianum* Rchb.f.	No	Orchidaceac	M	38[o]	2	P	1,764[t]	1.8	3.6	7.2	307	O	*Gallus*[f]	FC:PI
293	*Dendrobium canaliculatum* R.Br.	No	Orchidaceae	M	38[o]	2	P	1,328[t]	1.4	2.7	5.4	307	O	*Gallus*[f]	FC:PI
294	*Dendrobium conanthum* Schltr.	No	Orchidaceae	M	38[o]	2	P	1,103[t]	1.2	2.3	4.6	307	O	*Gallus*[f]	FC:PI
295	*Dendrobium cruentum* Rchb.f.	No	Orchidaceae	M	38[o]	2	P	749[t]	0.8	1.5	3.0	307	O	*Gallus*[f]	FC:PI
296	*Dendrobium crumenatum* Sw.	No	Orchidaceae	M	38[o]	2	P	1,279[t]	1.3	2.6	5.2	307	O	*Gallus*[f]	FC:PI
297	*Dendrobium discolor* Lindl.	No	Orchidaceae	M	38[o]	2	P	828[t]	0.9	1.7	3.4	307	O	*Gallus*[f]	FC:PI
298	*Dendrobium forbesii* Ridl.	No	Orchidaceae	M	38[o]	2	P	936[t]	1.0	1.9	3.8	307	O	*Gallus*[f]	FC:PI
299	*Dendrobium formosum* Roxb. ex Lindl.	No	Orchidaceae	M	40[o]	2	P	848[t]	0.9	1.7	3.4	307	O	*Gallus*[f]	FC:PI
300a	*Dendrobium gouldii* Rchb.f.	No	Orchidaceae	M	38[o]	2	P	1,024[t]	1.1	2.1	4.2	307	O	*Gallus*[f]	FC:PI
300b	*Dendrobium gouldii* Rchb.f.	No	Orchidaceae	M	38	2	P	1,078	1.1	2.1	4.2	362	O	*Gallus*[f]	FC:PI
301	*Dendrobium helix* Cribb	No	Orchidaceae	M	38[o]	2	P	1,136[t]	1.2	2.3	4.6	307	O	*Gallus*[f]	FC:PI
302	*Dendrobium lasianthera* J.J.Sm.	No	Orchidaceae	M	38[o]	2	P	1,039[t]	1.1	2.1	4.2	307	O	*Gallus*[f]	FC:PI
303	*Dendrobium lindleyi* Steud.	No	Orchidaceae	M	38[o]	2	P	1,176[t]	1.2	2.4	4.8	307	O	*Gallus*[f]	FC:PI
304	*Dendrobium macrophyllum* A.Rich.	No	Orchidaceae	M	38[o]	2	P	921[t]	1.0	1.9	3.8	307	O	*Gallus*[f]	FC:PI
305b	*Dendrobium moschatum* (Buch.-Ham.) Sw.	No	Orchidaceae	M	38[o]	2	P	1,705[t]	1.8[z]	3.5[z]	7.0[z]	307	O	*Gallus*[f]	FC:PI
305c	*Dendrobium moschatum* (Buch.-Ham.) Sw.	No	Orchidaceae	M	38[o]	2	P	1,666	1.7[z]	3.5[z]	7.0[z]	362	O	*Gallus*[f]	FC:PI
306	*Dendrobium parishii* Rchb.f.	No	Orchidaceae	M	38[o]	2	P	1,181[t]	1.2	2.4	4.8	307	O	*Gallus*[f]	FC:PI
307a	*Dendrobium phalaenopsis* Fitzg.	No	Orchidaceae	M	38[o]	2	P	970[t]	1.0	2.0	4.0	307	O	*Gallus*[f]	FC:PI
307b	*Dendrobium phalaenopsis* Fitzg. var. *compactum*	No	Orchidaceae	M	38	2	P	1,176	1.2	2.4	4.7	362	O	*Gallus*[f]	FC:PI
308	*Dendrobium polysema* Schltr.	No	Orchidaceae	M	38[o]	2	P	1,485[t]	1.5	3.0	6.0	307	O	*Gallus*[f]	FC:PI
309	*Dendrobium pulchellum* Roxb. ex Lindl.	No	Orchidaceae	M	38[o]	2	P	1,558[t]	1.6	3.2	6.4	307	O	*Gallus*[f]	FC:PI
310	*Dendrobium rhodostictum* F.Muell. & Kranzl.	No	Orchidaceae	M	38[o]	2	P	1,440[t]	1.5	2.9	5.8	307	O	*Gallus*[f]	FC:PI

311	*Dendrobium samoense* Cribb	No	Orchidaceae	M	38[o]	2	P	1,984[t]	2.1	4.1	8.2	307	O	*Gallus*[f]	FC:PI
312	*Dendrobium schulleri* J.J.Sm.	No	Orchidaceae	M	38[o]	2	P	961[t]	1.0	2.0	4.0	307	O	*Gallus*[f]	FC:PI
313	*Dendrobium signatum* Rchb.f.	No	Orchidaceae	M	38[o]	2	P	1,430[t]	1.5	2.9	5.8	307	O	*Gallus*[f]	FC:PI
314a	*Dendrobium smillieae* F.Muell.	No	Orchidaceae	M	38[o]	2	P	1,544[t]	1.6	3.2	6.4	307	O	*Gallus*[f]	FC:PI
314b	*Dendrobium smillieae* F.Muell.	No	Orchidaceae	M	38	2	P	1,568	1.6	3.2	6.3	362	O	*Gallus*[f]	FC:PI
315	*Dendrobium spectabile* (Bl.) Miq.	No	Orchidaceae	M	38[o]	2	P	2,073[t]	2.1	4.2	8.4	307	O	*Gallus*[f]	FC:PI
316	*Dendrobium stratiotes* Rchb.f.	No	Orchidaceae	M	38[o]	2	P	1,641[t]	1.7	3.4	6.8	307	O	*Gallus*[f]	FC:PI
317	*Dendrobium streblocerus* Rchb.f.	No	Orchidaceae	M	38[o]	2	P	1,828[t]	1.9	3.7	7.4	307	O	*Gallus*[f]	FC:PI
318	*Dendrobium strepsiceros* J.J.Sm.	No	Orchidaceae	M	38[o]	2	P	1,431[t]	1.5	2.9	5.8	307	O	*Gallus*[f]	FC:PI
319	*Dendrobium tangerinum* Cribb	No	Orchidaceae	M	38[o]	2	P	1,073[t]	1.1	2.2	4.4	307	O	*Gallus*[f]	FC:PI
320	*Dendrobium taurinum* J.J.Sm.	No	Orchidaceae	M	38[o]	2	P	940[t]	1.0	1.9	3.8	307	O	*Gallus*[f]	FC:PI
321	*Dendrobium violaceoflavens* Thomson	No	Orchidaceae	M	38[o]	2	P	1,318[t]	1.4	2.7	5.4	307	O	*Gallus*[f]	FC:PI
322	*Digitaria ascendens* Rendle.	Yes	Gramineae	M	—[n]	—[p]	A-P	1,470	1.5	3.0	6.0	375	O	F	Fe
323	*Digitaria sanguinalis* (L.) Scop.	Yes	Gramineae	M	54	6	A	1,176	1.2	2.4	4.8	375	O	F	Fe
324	*Doritis pulcherrima* Lindl.	No	Orchidaceae	M	38[o]	—[p]	P	4,532[t]	4.7	9.3	18.6	307	O	*Gallus*[f]	FC:PI
325	*Dypsis lutescens* (H. Wendl.) H.Beentje & J.Dransfield	Yes	Palmae	M	—[n]	—[p]	P	1,470	1.5	3.1	6.1	377	O	B	Fe
326	*Echinochloa colonum* (L.) Link.	Yes	Gramineae	M	—[n]	—[p]	A	1,372	1.4	2.7	5.4	375	O	F	Fe
327	*Eclipta prostrata* (L.) Mant.	Yes	Compositae	D	22	2	A-P	1,568	1.6	3.1	6.2	375	O	F	Fe
328	*Elymus abolinii* (Drob.) Tzvelev	No	Gramineae[j]	M	28	4	P	9,212	9.4	18.7	37.4	343[al]	O	A[c] & F[c]	FC:PI
329	*Elymus alatavicus* (Drob.) A.Löve	No	Gramineae[j]	M	42	6	P	14,896	15.2	30.3	60.6	343[al]	O	A[c] & F[c]	FC:PI
330b	*Elymus canadensis* L.	No	Gramineae[j]	M	28	4	P	10,388	10.6	21.1	42.2	343[al]	O	A[c] & F[c]	FC:PI
331	*Elymus caninus* L.[i]	No	Gramineae[j]	M	28	4	P	8,428	8.6	17.1	34.2	343[al]	O	A[c] & F[c]	FC:PI
332	*Elymus ciliaris* (Trin.) Tzvelev	No	Gramineae[j]	M	28	4	P	8,526	8.7	17.3	34.7	343[al]	O	A[c] & F[c]	FC:PI
333	*Elymus dahuricus* Turez ex Griseb.[i]	No	Gramineae[j]	M	42	6	P	12,936	13.2	26.4	52.9	343[al]	O	A[c] & F[c]	FC:PI
334	*Elymus glaucus* Buckley[i]	No	Gramineae[j]	M	28	4	P	9,114	9.3	18.6	37.2	343[al]	O	A[c] & F[c]	FC:PI
335	*Elymus lanceolatus* (Schribner & Smith) Gould[i]	No	Gramineae[j]	M	28	4	P	8,232	8.4	16.9	33.7	343[al]	O	A[c] & F[c]	FC:PI
336	*Elymus mutabilis* (Drob.) Tzvelev[i]	No	Gramineae[j]	M	28	4	P	8,526	8.7	17.4	34.8	343[al]	O	A[c] & F[c]	FC:PI
337	*Elymus sibiricus* L.[i]	No	Gramineae[j]	M	—[n]	—[p]	P	8,134	8.3	16.6	33.2	343[al]	O	A[c] & F[c]	FC:PI
338	*Elymus trachycaulus* (Link) Gould ex Shinners[i]	No	Gramineae[j]	M	28	4	P	9,408	9.6	19.1	38.3	343[al]	O	A[c] & F[c]	FC:PI
339	*Epidendrum steinbachii* Ames	No	Orchidaceae	M	—[n]	—[p]	P	1,407[t]	1.5	2.9	5.8	307	O	*Gallus*[f]	FC:PI
340	*Epilobium ciliatum* Rafin.	Yes	Onagraceae	D	36	2	P	490	0.5	1.1	2.1	375	O	F	Fe
341	*Epilobium tetragonum*[l]	Yes	Onagraceae	D	36	2	P	588	0.6	1.2	2.3	375	O	F	Fe
342b	*Eragrostis tef* (Zucc.) Trotter cv. Trotterian[i]	No	Gramineae	M	40[o]	4	A	784[t]	0.8	1.5	3.0	332[af]	O	*Lycopers.*[e]	FC:PI
343	*Erianthus arundinaceus*[l]	No	Gramineae	M	60	6	P	3,528	3.6	7.3	14.5	342	O	G[c]	FC:EB
344	*Erycina diaphana* Schltr.	Yes	Orchidaceae	M	56[o]	—[p]	P	1,862	1.9	3.8	7.7	377	O	F	Fe
345	*Eschscholzia californica* Cham.	No	Papaveraceae	D	12[o]	2	A	1,078	1.1	2.2	4.5	373	O	G[b2]	FC:PI
346	*Euphorbia globosa* Sims	No	Euphorbiaceae	D	20	2	P	9,212[ag]	9.4[ag]	18.7[ag]	37.4[ag]	333	O	B	Fe
347	*Euphorbia hirta* L.	Yes	Euphorbiaceae	D	—[n]	—[p]	A	686	0.7	1.3	2.6	375	O	F	Fe
348	*Euphorbia meloformis* Ait.	No	Euphorbiaceae	D	20	2	P	14,014[ag]	14.3[ag]	28.6[ag]	57.2[ag]	333	O	B	Fe

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

Entry number[g]	Species	Voucher	Family	Monocot or dicot	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††
349	*Euphorbia nesemannii* R.A.Dyer	No	Euphorbiaceae	D	20	2	P	13,132[ag]	13.4[ag]	26.9[ag]	53.7[ag]	333	O	B	Fe
350	*Euphorbia obesa* Hook.f.	No	Euphorbiaceae	D	20	2	P	13,034[ag]	13.3[ag]	26.5[ag]	53.0[ag]	333	O	B	Fe
351	*Euphorbia pentagona* Haw.	No	Euphorbiaceae	D	20	2	P	9,114[ag]	9.3[ag]	18.5[ag]	37.0[ag]	333	O	B	Fe
352	*Euphorbia polygona* Haw.	No	Euphorbiaceae	D	20	2	P	14,112[ag]	14.4[ag]	28.7[ag]	57.4[ag]	333	O	B	Fe
353	*Euphorbia pugniformis* Boiss.	No	Euphorbiaceae	D	20	2	P	9,212[ag]	9.4[ag]	18.8[ag]	37.6[ag]	333	O	B	Fe
354	*Euphorbia pulcherrima* Willd ex Klotzsch	No	Euphorbiaceae	D	28	4	P	1,666	1.7	3.3	6.6	373	O	G[b2]	FC:PI
355	*Euphorbia valida* N.E.Br.	No	Euphorbiaceae	D	20	2	P	13,916[ag]	14.2[ag]	28.3[ag]	56.6[ag]	333	O	B	Fe
356	*Eupomatia benettii* F.Muell.	Yes	Eupomatiaceae	D	20	—[p]	P	1,078	1.1	2.2	4.3	341	O	B[c]	Fe
357	*Eupomatia laurina* R.Br.	Yes	Eupomatiaceae	D	20	—[p]	P	1,176	1.2	2.4	4.9	341	O	B[c]	Fe
358	*Eustoma grandiflorum* (Griesbach) Schinners cv. Hakusen	No	Gentianaceae	D	72[o]	8	A-B	1,568[ab]	1.6[ab]	3.3[ab]	6.5[ab]	311	O	H[c]	FC:PI
359	*Fragaria moschata* Duchesne	Yes	Rosaceae	D	42	6	P	686	0.3	0.7	1.4	339	O	*Gallus*[f]	FC:PI
360	*Fragaria virginiana* Duchesne	Yes	Rosaceae	D	56	8	P	784	0.4	0.8	1.6	339	O	*Gallus*[f]	FC:PI
361	*Fragaria viridis* Duchesne	Yes	Rosaceae	D	14	2	P	105	0.1	0.2	0.4	339	O	*Gallus*[f]	FC:PI
362	*Friesodielsia obovata* (Benth.) Verdcourt	Yes	Annonaceae	D	—[n]	—[p]	P	392	0.4	0.8	1.7	341	O	B[c]	Fe
363	*Froesiodendron surinamense*[l]	Yes	Annonaceae	D	—[n]	—[p]	P	980	1.0	2.0	4.1	341	O	B[c]	Fe
364	*Galinsoga parviflora* Cav.lc.	Yes	Compositae	D	16	2	A	1,274	1.3	2.5	5.0	375	O	F	Fe
365	*Gasteria brachyphylla* (Salm-Dyck) E. van Jaarsveld var. *brachyphylla*	No	Asphodelaceae	M	28	4	P	32,438	33.1	66.2	132.4	377	O	B	Fe
366	*Gasteria decipiens*[l]	No	Asphodelaceae	M	14	2	P	15,582	15.9	31.8	63.6	377	O	B	Fe
367	*Gasteria pulchra*[l]	No	Asphodelaceae	M	14	2	P	15,582	15.9	31.7	63.4	377	O	B	Fe
368	*Gossypioides kirkii* (Mast.) Skovsted	No	Malvaceae	D	24[o]	2	P	588	0.6	1.3	2.5	349	O	G[b2]	FC:PI
369b	*Gossypium harknessii* Brandg.	No	Malvaceae	D	26[o]	2	P	980	1.0	2.1	4.2	349	O	G[b2]	FC:PI
370	*Grammatophyllum scriptum* (L.) Bl.	No	Orchidaceae	M	38, 40[o]	—[p]	P	1,686[t]	1.7	3.4	6.8	307	O	*Gallus*[f]	FC:PI
371	*Guatteria schlechtendaliana* Mart.	Yes	Annonaceae	D	28	4	P	980	1.0	2.0	4.0	341	O	B[c]	Fe
372	*Guatteriopsis hispida* R.E.Fr.	Yes	Annonaceae	D	28	4	P	1,078	1.1	2.2	4.4	341	O	B[c]	Fe
373	*Hedysarum aucheri* Boiss.	Yes	Leguminosae	D	16	2	P	2,744[t]	2.8	5.7	11.3	363	O	B[c]	Fe
374	*Hedysarum nitidum* Willd.	Yes	Leguminosae	D	16	2	P	2,646[t]	2.7	5.4	10.8	363	O	B[c]	Fe
375	*Hedysarum pestalozzae* Boiss.	Yes	Leguminosae	D	16	2	P	2,744[t]	2.8	5.5	11.0	363	O	B[c]	Fe
376	*Hedysarum pycnostachyum* Hedge & Hub. -Mor.	Yes	Leguminosae	D	16	2	P	2,254[t]	2.3	4.7	9.3	363	O	B[c]	Fe
377	*Hedysarum rotundifolium* Boiss. & Noe	Yes	Leguminosae	D	16	2	P	3,332[t]	3.4	6.8	13.5	363	O	B[c]	Fc
378	*Hedysarum varium* Willd.	Yes	Leguminosae	D	16	2	P	2,450[t]	2.5	4.9	9.8	363	O	B[c]	Fe
379	*Helcia sanguinolenta* Lindl.	Yes	Orchidaceae	M	—[n]	—[p]	P	3,724	3.8	7.7	15.3	377	O	F	Fe

380	*Hemiphylacus alatostylus* (L.) Hernandez	Yes	Asparagaceae	M	112	8 or 16	P	4,116	4.2	8.4	16.7	317	O	B	Fe
381	*Hernandia* sp.[y]	Yes	Hernandiaceae	D	40	—[p]	P	1,764	1.8	3.6	7.3	341	O	B[c]	Fe
382	*Hibiscus cannabinus L.*	No	Malvaceae	D	36	—[p]	A	1,470	1.5	3.0	6.1	373	O	G[b2]	FC:PI
383	*Hieracium aurantiacum* L. ssp. *aurantiacum*	Yes	Compositae	D	36[o]	4	P	3,430	3.5	7.0	14.1	352[an]	O	*Gallus*-388[f]	FC:PI
384	*Hieracium bauhini* Schult. ssp. *bauhini*	Yes	Compositae	D	45[o]	5	P	4,410	4.5	8.9	17.9	352[an]	O	*Gallus*-388[f]	FC:PI
385	*Hieracium brachiatum* Bert. ex DC.	Yes	Compositae	D	36[o]	4	P	3,430	3.5	6.9	13.8	352[an]	O	*Gallus*-388[f]	FC:PI
386	*Hieracium brachiatum* Bert. ex DC.	Yes	Compositae	D	54[o]	6	P	4,998	5.1	10.3	20.6	352[an]	O	*Gallus*-388[f]	FC:PI
387	*Hieracium caespitosum* Dumort. ssp. *madarum*	Yes	Compositae	D	45[o]	5	P	4,410	4.5	9.1	18.1	352[an]	O	*Gallus*-388[f]	FC:PI
388	*Hieracium lactucella* Wallr.	Yes	Compositae	D	18[o]	2	P	1,764	1.8	3.7	7.3	352[an]	O	*Gallus*[f]	FC:PI
389	*Hieracium leptophyton* Nageli & Peter	Yes	Compositae	D	63[o]	7	P	5,586	5.7	11.5	23.0	352[an]	O	*Gallus*-388[f]	FC:PI
390b	*Hieracium pilosella* L. ssp. *pilosella*	Yes	Compositae	D	36[o]	4	P	3,038	3.1	6.3	12.6	352[an]	O	*Gallus*-388[f]	FC:PI
391	*Hieracium piloselloides* Vill. ssp. *obscurum*	Yes	Compositae	D	36[o]	4	P	3,626	3.7	7.3	14.7	352[an]	O	*Gallus*-388[f]	FC:PI
392	*Hordeum bogdanii* Wilensky	No	Gramineae[j]	M	14	2	P	4,606	4.7	9.5	19.9	343[al]	O	A[c] & F[c]	FC:PI
393	*Hordeum brachyantherum* Nevski	No	Gramineae[j]	M	14	2	P	4,704	4.8	9.7	19.3	343[al]	O	A[c] & F[c]	FC:PI
394	*Hordeum brevisubulatum-violaceum* (Boise & Hofenacker) Tzvelev	No	Gramineae[j]	M	14	2	P	4,900	5.0	9.9	19.9	343[al]	O	A[c] & F[c]	FC:PI
395b	*Hordeum bulbosum* L.	No	Gramineae[j]	M	14	2	P	4,508	4.6	9.2	18.3	343[al]	O	A[c] & F[c]	FC:PI
396b	*Hordeum bulbosum* L.	No	Gramineae[j]	M	28	4	P	8,722	8.9	17.7	35.5	343[al]	O	A[c] & F[c]	FC:PI
397	*Hordeum californicum* Covas & Stebbins[i]	No	Gramineae[j]	M	14	2	P	4,704	4.8	9.5	19.0	343[al]	O	A[c] & F[c]	FC:PI
398b	*Hordeum chilense* Roemer & Schultes	No	Gramineae[j]	M	14	2	P	4,900	5.0	9.9	19.8	343[al]	O	A[c] & F[c]	FC:PI
399	*Hordeum comosum* K.Presl	No	Gramineae[j]	M	14	2	P	4,508	4.6	9.3	18.5	343[al]	O	A[c] & F[c]	FC:PI
400	*Hordeum flexuosum* Nees cv. Castelar 730	No	Gramineae[j]	M	14	2	P	4,312	4.4	8.9	17.7	343[al]	O	A[c] & F[c]	FC:PI
401	*Hordeum glaucum* Steud.	Yes	Gramineae	M	28	4	A	10,486	10.7	21.3	42.6	375	O	F	Fe
402	*Hordeum haplophilum* Griseb.	No	Gramineae[j]	M	14	2	P	4,312	4.4	8.9	17.7	343[al]	O	A[c] & F[c]	FC:PI
403b	*Hordeum roshevitzii* Bowden	No	Gramineae[j]	M	14	2	P	4,998	5.1	10.1	20.2	343[al]	O	A[c] & F[c]	FC:PI
404	*Hordeum stenostachys* Godron[i]	No	Gramineae[j]	M	14	2	P	4,900	5.0	10.1	20.1	343[al]	O	A[c] & F[c]	FC:PI
405n	*Hordeum vulgare* L. cv. Morex	No	Gramineae	M	14	2	A	5,351	5.5	10.9	21.8	337	O	*Gallus*[f]	FC:PI
405o	*Hordeum vulgare* L. cv. Sultan	No	Gramineae	M	14	2	A	5,361	5.5	10.9	21.9	337	O	*Gallus*[f]	FC:PI
406	*Horsfieldia iriya* (Gaertner) Warb.	Yes	Myristicaceae	D	50	—[p]	P	1,666	1.7	3.4	6.9	341	O	B[c]	Fe
407	*Hyphaene benguelensis* Welw. ex H.Wendl.	Yes	Palmae	M	—[n]	—[p]	P	3,332	3.4	6.8	13.6	377	O	B	Fe

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

Entry number[g]	Species	Voucher	Family	Monocot or dicot	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††
408	*Ilex argentina* Lillo	Yes	Aquifoliaceae	D	80	8	P	2,058	2.1	4.3	8.5	322	O	B	Fe
409	*Ilex paraguariensis* St.Hil.	Yes	Aquifoliaceae	D	40	4	P	1,078	1.1	2.2	4.5	322	O	B	Fe
410	*Imperata cylindrica* Beauv.	Yes	Gramineae	M	—[n]	—[p]	P	5,292	5.4	10.9	21.7	375	O	F	Fe
411	*Ionopsidium savianum*[l]	—[m]	Cruciferae[j]	D	32[o]	4	A	1,372	1.4	2.8	5.6	313	O	C[d]	Fe
412	*Ipomoea aquatica* Forsk.	Yes	Convolvulaceae	D	30	2	A-P	980	1.0	1.9	3.8	375	O	F	Fe
413	*Iris* aff. *maracandica* Vved.	Yes	Iridaceae	M	20	—[p]	P	7,546	7.7	15.4	30.9	377	O	B	Fe
414	*Iris* aff. *orchioides* Carr.	Yes	Iridaceae	M	26+3	—[p]	P	9,114	9.3	18.6	37.2	377	O	B	Fe
415	*Iris albomarginata* R.C.Foster	No	Iridaceae	M	26	—[p]	P	9,996	10.2	20.3	40.7	377	O	B	Fe
416	*Iris albomarginata* R.C.Foster	No	Iridaceae	M	50	—[p]	P	18,424	18.8	37.7	75.3	377	O	B	Fe
417a	*Iris bucharica* Foster	Yes	Iridaceae	M	20	—[p]	P	8,232	8.4	16.9	33.7	377	O	B	Fe
417b	*Iris bucharica* Foster	Yes	Iridaceae	M	22	—[p]	P	8,526	8.7	17.3	34.7	377	O	B	Fe
418	*Iris capnoides*[l]	Yes	Iridaceae	M	28	—[p]	P	9,310	9.5	19.0	38.1	377	O	B	Fe
419a	*Iris graebneriana* Sealy cv. Yellow Fall	Yes	Iridaceae	M	36	—[p]	P	12,446	12.7	25.5	51.0	377	O	B	Fe
419b	*Iris graebneriana* Sealy cv. White Fall	Yes	Iridaceae	M	c.38-40	—[p]	P	13,524	13.8	27.5	55.1	377	O	B	Fe
420	*Iris magnifica* Vved.	Yes	Iridaceae	M	26	—[p]	P	8,918	9.1	18.3	36.6	377	O	B	Fe
421a	*Iris orchioides* Carr.	Yes	Iridaceae	M	26	—[p]	P	9,496	9.7	19.4	38.8	377	O	B	Fe
421b	*Iris orchioides* Carr.	No	Iridaceae	M	30	—[p]	P	10,263	10.5	20.9	41.9	377	O	B	Fe
422	*Iris tubergeniana* Foster	No	Iridaceae	M	20	—[p]	P	9,197	9.4	18.8	37.5	377	O	B	Fe
423	*Iris tubergeniana* Foster	No	Iridaceae	M	30	—[p]	P	10,780	11.0	22.1	44.1	377	O	B	Fe
424	*Iris vicaria* Vved.	No	Iridaceae	M	22	—[p]	P	8,293	8.5	16.9	33.9	377	O	B	Fe
425a	*Iris vicaria* Vved.	Yes	Iridaceae	M	c.46	—[p]	P	14,700	15.0	30.0	60.1	377	O	B	Fe
425b	*Iris vicaria* Vved.	Yes	Iridaceae	M	46	—[p]	P	16,562	16.9	33.8	67.5	377	O	B	Fe
426	*Iris zenaidae*[l]	No	Iridaceae	M	50	—[p]	P	18,228	18.6	37.2	74.5	377	O	B	Fe
427	*Kadsura coccinea*[l]	Yes	Schisandraceae	D	28	—[p]	P	7,252	7.4	14.8	29.6	341	O	B[c]	Fe
428	*Kadsura japonica* (L.) Dunal.	Yes	Schisandraceae	D	28	—[p]	P	7,938	8.1	16.3	32.5	341	O	B[c]	Fe
429	*Kadsura longespicata*[l]	Yes	Schisandraceae	D	28	—[p]	P	8,722	8.9	17.7	35.4	341	O	B[c]	Fe
430	*Kokia drynarioides* Lewton	No	Malvaceae	D	24[o]	2	P	588	0.6	1.3	2.5	349	O	G[b2]	FC:PI
431	*Laelia rubescens* Rolfe	No	Orchidaceae	M	40[o]	—[p]	P	1,200[t]	1.3	2.5	5.0	307	O	*Gallus*[f]	FC:PI
432	*Laelia tenebrosa* Rolfe	No	Orchidaceae	M	—[n]	—[p]	P	1,720[t]	1.8	3.5	7.0	307	O	*Gallus*[f]	FC:PI
433	*Lagurus ovatus* L.	No	Gramineae	M	14	2	A	3,430	3.5	7.0	14.0	373	O	G[b2]	FC:PI
434	*Largarosiphon major* Moss	Yes	Hydrocharitaceae	M	22	—[p]	—[q]	3,234	3.3	6.5	13.0	375	O	F	Fe
435c	*Lathyrus annuus* L.[h]	Yes	Leguminosae	D	14	2	A	6,664	6.8	13.5	27.0	319	O	F & G	FC:PI
435d	*Lathyrus annuus* L.[h]	Yes	Leguminosae	D	14	2	A	7,350	7.5	15.0	30.0	319	O	F & G	FC:PI
436	*Lathyrus basalticus* Rech.f	Yes	Leguminosae	D	14	2	A	4,998	5.1	10.2	20.4	319	O	F & G	FC:PI
437	*Lathyrus belinensis* Maxted & Goyder	Yes	Leguminosae	D	14	2	A	7,546	7.7	15.3	30.6	319	O	F & G	FC:PI
438	*Lathyrus blepharicarpus* Boiss.	Yes	Leguminosae	D	14	2	A	6,566	6.7	13.3	26.6	319	O	F & G	FC:PI

439b	*Lathyrus cassius* Boiss.	Yes	Leguminosae	D	14	2	A	8,428	8.6	17.2	34.4	319	O	F & G	FC:PI
440	*Lathyrus chloranthus* Boiss.	Yes	Leguminosae	D	14	2	A	6,370	6.5	13.0	26.0	319	O	F & G	FC:PI
441b	*Lathyrus chrysanthus* Boiss.	Yes	Leguminosae	D	14	2	A	6,860	7.0	13.9	27.8	319	O	F & G	FC:PI
442e	*Lathyrus cicera* L.	Yes	Leguminosae	D	14	2	A	5,880	6.0	11.9	23.8	319	O	F & G	FC:PI
443b	*Lathyrus ciliolatus* Rech.f[i]	Yes	Leguminosae	D	14	2	A	5,194	5.3	10.6	21.2	319	O	F & G	FC:PI
443c	*Lathyrus ciliolatus* Rech.f[i]	Yes	Leguminosae	D	14	2	A	5,292	5.4	10.7	21.4	319	O	F & G	FC:PI
444	*Lathyrus cirrhosus* Ser.	Yes	Leguminosae	D	14	2	P	10,780	11.0	21.9	43.8	319	O	F & G	FC:PI
445	*Lathyrus giganteus*[l]	Yes	Leguminosae	D	14	2	P	9,898	10.1	20.1	40.2	319	O	F & G	FC:PI
446a	*Lathyrus gorgoni* Parl.[h]	Yes	Leguminosae	D	14	2	A	5,684	5.8	11.5	23.0	319	O	F & G	FC:PI
446b	*Lathyrus gorgoni* Parl.[h]	Yes	Leguminosae	D	14	2	A	6,370	6.5	13.0	26.0	319	O	F & G	FC:PI
447	*Lathyrus grandiflorus* Sibth & Sm.	Yes	Leguminosae	D	14	2	P	9,114	9.3	18.5	37.0	319	O	F & G	FC:PI
448	*Lathyrus heterophyllus* L.	Yes	Leguminosae	D	14	2	P	9,016	9.2	18.4	36.8	319	O	F & G	FC:PI
449	*Lathyrus hierosolymitanus* Boiss.	Yes	Leguminosae	D	14	2	A	6,860	7.0	14.0	28.0	319	O	F & G	FC:PI
450f	*Lathyrus hirsutus* L.[h]	Yes	Leguminosae	D	14	2	A	6,272	6.4	12.7	25.4	319	O	F & G	FC:PI
450g	*Lathyrus hirsutus* L.[h]	Yes	Leguminosae	D	14	2	A	7,154	7.3	14.5	29.0	319	O	F & G	FC:PI
451	*Lathyrus hirticarpus* Mattaia & Heyn	Yes	Leguminosae	D	14	2	A	6,468	6.6	13.1	26.2	319	O	F & G	FC:PI
452d	*Lathyrus latifolius* L.[h]	Yes	Leguminosae	D	14	2	P	9,800	10.0	20.0	40.0	319	O	F & G	FC:PI
452e	*Lathyrus latifolius* L.[h]	Yes	Leguminosae	D	14	2	P	11,858	12.1	24.2	48.4	319	O	F & G	FC:PI
453	*Lathyrus mulkak* Lipsky	Yes	Leguminosae	D	14	2	P	7,644	7.8	15.6	31.2	319	O	F & G	FC:PI
454h	*Lathyrus odoratus* L.	Yes	Leguminosae	D	14	2	A	7,056	7.2	14.3	28.6	319	O	F & G	FC:PI
455	*Lathyrus pseudo-cicera* Pampan.	Yes	Leguminosae	D	14	2	A	5,978	6.1	12.1	24.2	319	O	F & G	FC:PI
456e	*Lathyrus sativus* L.	Yes	Leguminosae	D	14	2	A	6,860	7.0	14.0	28.0	319	O	F & G	FC:PI
457d	*Lathyrus sylvestris* L.[i]	Yes	Leguminosae	D	14	2	P	11,466	11.7	23.3	46.6	319	O	F & G	FC:PI
457e	*Lathyrus sylvestris* L.[i]	Yes	Leguminosae	D	14	2	P	11,564	11.8	23.6	47.2	319	O	F & G	FC:PI
458e	*Lathyrus tingitanus* L.[h]	Yes	Leguminosae	D	14	2	A	7,056	7.2	14.3	28.6	319	O	F & G	FC:PI
458f	*Lathyrus tingitanus* L.[h]	Yes	Leguminosae	D	14	2	A	10,192	10.4	20.7	41.4	319	O	F & G	FC:PI
459	*Lavatera arborea* L.	—[m]	Malvaceae	D	42[o]	6	B	1,666	1.7	3.4	6.7	313	O	C[d]	Fe
460	*Leymus akmolinensis* (Drob.) Tzvelev	No	Gramineae[j]	M	28	4	P	11,074	11.3	22.6	45.2	343[al]	O	A[c] & F[c]	FC:PI
461	*Leymus ambiguus* (Vasey & Schribn.) D.R.Dewey	No	Gramineae[j]	M	—[n]	—[p]	P	10,878	11.1	22.3	44.5	343[al]	O	A[c] & F[c]	FC:PI
462	*Leymus chinensis* (Trin.) Tzvelev[i]	No	Gramineae[j]	M	28	4	P	9,702	9.9	19.7	39.4	343[al]	O	A[c] & F[c]	FC:PI
463	*Leymus flavens* (Scribner & Smith) Pilger	No	Gramineae[j]	M	28	4	P	11,956	12.2	24.4	48.9	343[al]	O	A[c] & F[c]	FC:PI
464	*Leymus racemosus* (Lam.) Tzvelev[i]	No	Gramineae[j]	M	28	4	P	11,172	11.4	22.8	45.6	343[al]	O	A[c] & F[c]	FC:PI
465	*Leymus sabulosus* (M.Bieb.) Tzvelev[i]	No	Gramineae[j]	M	28	4	P	11,270	11.5	23.0	46.0	343[al]	O	A[c] & F[c]	FC:PI
466	*Leymus secalinus* (Georgi) Tzvelev[i]	No	Gramineae[j]	M	28	4	P	10,584	10.8	21.6	43.1	343[al]	O	A[c] & F[c]	FC:PI
467	*Leymus triticoides* (Buckl.) Pilger[i]	No	Gramineae[j]	M	28	4	P	10,976	11.2	22.4	44.8	343[al]	O	A[c] & F[c]	FC:PI
468	*Limonium perezii* (Stapf) Hubb.	No	Plumbaginaceae	D	14	2	P	4,214	4.3	8.7	17.4	316	O	E[v]	FC:PI
469	*Limonium perigrinum* Bergius	No	Plumbaginaceae	D	24	2	P	6,860	7.0	14.0	28.0	315	O	*Avena*[v]	FC:PI
470	*Limonium purpuratum* L.	No	Plumbaginaceae	D	24	2	P	9,506	9.7	19.4	38.7	315	O	*Avena*[v]	FC:PI
471	*Limonium sinuatum* (L.) Mill.	No	Plumbaginaceae	D	16	2	P	3,136	3.2	6.4	12.8	316	O	E[v]	FC:PI

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

Entry number[g]	Species	Voucher	Family	Monocot or dicot	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††
472	*Lockhartia oerstedii* Rchb.f.	Yes	Orchidaceae	M	14[o]	2	P	1,764	1.8	3.6	7.2	377	O	F	Fe
473	*Lonchocarpus acuminatus* (Schldl.) M.Sousa[i]	Yes	Leguminosae	D	22	2	P	644	0.7	1.3	2.6	327	O	F	Fe
474	*Lonchocarpus agyrotrichus* Harms[i]	Yes	Leguminosae	D	22	2	P	615	0.6	1.3	2.5	327	O	F	Fe
475	*Lonchocarpus andrieuxii* M.Sousa	Yes	Leguminosae	D	22	2	P	617	0.6	1.3	2.5	327	O	F	Fe
476	*Lonchocarpus angusticarpus* M.Sousa, ined.	Yes	Leguminosae	D	22	2	P	497	0.5	1.0	2.0	327	O	F	Fe
477	*Lonchocarpus atropurpureus* Benth.	Yes	Leguminosae	D	22	2	P	522	0.5	1.1	2.1	327	O	F	Fe
478	*Lonchocarpus balsensis* M.Sousa & J.C.Soto[i]	Yes	Leguminosae	D	22	2	P	608	0.6	1.2	2.5	327	O	F	Fe
479	*Lonchocarpus castilloi* Standl.	Yes	Leguminosae	D	22	2	P	502	0.5	1.0	2.1	327	O	F	Fe
480	*Lonchocarpus caudatus* Pittier	Yes	Leguminosae	D	22	2	P	652	0.7	1.3	2.7	327	O	F	Fe
481	*Lonchocarpus chavelasii* M.Sousa, ined.	Yes	Leguminosae	D	22	2	P	556	0.6	1.1	2.3	327	O	F	Fe
482	*Lonchocarpus chiangii* M.Sousa	Yes	Leguminosae	D	22	2	P	527	0.5	1.1	2.2	327	O	F	Fe
483	*Lonchocarpus constrictus* Pittier	Yes	Leguminosae	D	22	2	P	568	0.6	1.2	2.3	327	O	F	Fe
484a	*Lonchocarpus cruentus* Lundell ssp. *cruentus*	Yes	Leguminosae	D	22	2	P	593	0.6	1.2	2.4	327	O	F	Fe
484b	*Lonchocarpus cruentus* Lundell ssp. *grandiflorus* M.Sousa, ined.	Yes	Leguminosae	D	22	2	P	610	0.6	1.3	2.5	327	O	F	Fe
485	*Lonchocarpus emarginatus* Pittier	Yes	Leguminosae	D	22	2	P	517	0.5	1.1	2.1	327	O	F	Fe
486	*Lonchocarpus epigaeus* M.Sousa	Yes	Leguminosae	D	22	2	P	666	0.7	1.4	2.7	327	O	F	Fe
487a	*Lonchocarpus eriocarinalis* Micheli[i]	Yes	Leguminosae	D	22	2	P	578	0.6	1.2	2.4	327	O	F	Fe
487b	*Lonchocarpus eriocarinalis* Micheli[i]	Yes	Leguminosae	D	22	2	P	649	0.7	1.3	2.7	327	O	F	Fe
488	*Lonchocarpus eriophyllus* Benth.	Yes	Leguminosae	D	22	2	P	620	0.6	1.3	2.5	327	O	F	Fe
489a	*Lonchocarpus guatemalensis* Benth. var. *guatemalensis*	Yes	Leguminosae	D	22	2	P	593	0.6	1.2	2.4	327	O	F	Fe
489b	*Lonchocarpus guatemalensis* Benth. var. *protantherus* (Pittier) Hermann	Yes	Leguminosae	D	22	2	P	652	0.7	1.3	2.7	327	O	F	Fe
490	*Lonchocarpus hermannii* M.Sousa[i]	Yes	Leguminosae	D	22	2	P	571	0.6	1.2	2.3	327	O	F	Fe
491	*Lonchocarpus hidalgensis* Lundell	Yes	Leguminosae	D	22	2	P	578	0.6	1.2	2.4	327	O	F	Fe
492	*Lonchocarpus hintonii* Sandw.	Yes	Leguminosae	D	22	2	P	647	0.7	1.3	2.6	327	O	F	Fe
493	*Lonchocarpus huetamoensis* M.Sousa & J.C.Soto ssp. *huetamoensis*[i]	Yes	Leguminosae	D	22	2	P	686	0.7	1.4	2.8	327	O	F	Fe

494	*Lonchocarpus hughesii* M.Sousa	Yes	Leguminosae	D	22	2	P	576	0.6	1.2	2.4	327	O	F	Fe
495	*Lonchocarpus lanceolatus* Benth.[i]	Yes	Leguminosae	D	22	2	P	659	0.7	1.4	2.7	327	O	F	Fe
496	*Lonchocarpus longipedunculatus* M.Sousa & J.C.Soto[i]	Yes	Leguminosae	D	22	2	P	676	0.7	1.4	2.8	327	O	F	Fe
497	*Lonchocarpus luteomaculatus* Pittier[i]	Yes	Leguminosae	D	22	2	P	507	0.5	1.0	2.1	327	O	F	Fe
498	*Lonchocarpus macrocarpus* Benth.[i]	Yes	Leguminosae	D	22	2	P	640	0.7	1.3	2.6	327	O	F	Fe
499	*Lonchocarpus martinezii* M.Sousa, ined.	Yes	Leguminosae	D	22	2	P	595	0.6	1.2	2.4	327	O	F	Fe
500	*Lonchocarpus minimiflorus* Donn. Sm.	Yes	Leguminosae	D	22	2	P	559	0.6	1.1	2.3	327	O	F	Fe
501	*Lonchocarpus molinae* Standl. & L.O.Wms.	Yes	Leguminosae	D	22	2	P	532	0.5	1.1	2.2	327	O	F	Fe
502	*Lonchocarpus morenoi* M.Sousa	Yes	Leguminosae	D	22	2	P	637	0.7	1.3	2.6	327	O	F	Fe
503	*Lonchocarpus mutans* M.Sousa	Yes	Leguminosae	D	22	2	P	517	0.5	1.1	2.1	327	O	F	Fe
504	*Lonchocarpus obovatus* Benth.[i]	Yes	Leguminosae	D	22	2	P	505	0.5	1.0	2.1	327	O	F	Fe
505	*Lonchocarpus parviflorus* Benth.	Yes	Leguminosae	D	22	2	P	551	0.6	1.1	2.3	327	O	F	Fe
506	*Lonchocarpus peninsularis* (J.D. Sm.) Pittier	Yes	Leguminosae	D	22	2	P	519	0.5	1.1	2.1	327	O	F	Fe
507	*Lonchocarpus phaseolifolius* Benth.	Yes	Leguminosae	D	22	2	P	556	0.6	1.1	2.3	327	O	F	Fe
508	*Lonchocarpus phlebophyllus* Standl. & Steyerm.	Yes	Leguminosae	D	22	2	P	510	0.5	1.0	2.1	327	O	F	Fe
509a	*Lonchocarpus punctatus* Kunth ssp. *longistylus* M.Sousa, comb. nov., ined.	Yes	Leguminosae	D	22	2	P	532	0.5	1.1	2.2	327	O	F	Fe
509b	*Lonchocarpus punctatus* Kunth ssp. *vittatus* M.Sousa, ined.	Yes	Leguminosae	D	22	2	P	532	0.5	1.1	2.2	327	O	F	Fe
509c	*Lonchocarpus punctatus* Kunth ssp. *berriozabelensis* M.Sousa, ined.	Yes	Leguminosae	D	22	2	P	534	0.6	1.1	2.2	327	O	F	Fe
510a	*Lonchocarpus rugosus* Benth. ssp. *rugosus*[i]	Yes	Leguminosae	D	22	2	P	529	0.5	1.1	2.2	327	O	F	Fe
510b	*Lonchocarpus rugosus* Benth. ssp. *apricus* (Lundell) M.Sousa[i]	Yes	Leguminosae	D	22	2	P	537	0.6	1.1	2.2	327	O	F	Fe
511	*Lonchocarpus salvadorensis* Pittier	Yes	Leguminosae	D	22	2	P	686	0.7	1.4	2.8	327	O	F	Fe
512	*Lonchocarpus sanctuari* Standl. & L.O.Wms.	Yes	Leguminosae	D	22	2	P	696	0.7	1.4	2.8	327	O	F	Fe
513	*Lonchocarpus santarosanus* Donn. Sm[i]	Yes	Leguminosae	D	22	2	P	524	0.5	1.1	2.1	327	O	F	Fe
514	*Lonchocarpus schiedeanus* (Schldl.) Harms[i]	Yes	Leguminosae	D	22	2	P	578	0.6	1.2	2.4	327	O	F	Fe
515	*Lonchocarpus schubertiae* M.Sousa[i]	Yes	Leguminosae	D	22	2	P	652	0.7	1.3	2.7	327	O	F	Fe
516	*Lonchocarpus spectabilis* Hermann	Yes	Leguminosae	D	22	2	P	517	0.5	1.1	2.1	327	O	F	Fe
517	*Lonchocarpus torresiorum* M.Sousa, ined.	Yes	Leguminosae	D	22	2	P	605	0.6	1.2	2.5	327	O	F	Fe

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

Entry number[g]	Species	Voucher	Family	Monocot or dicot	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††
518	*Lonchocarpus xuul* Lundell	Yes	Leguminosae	D	22	2	P	701	0.7	1.4	2.9	327	O	F	Fe
519	*Lupinus anatolicus* W.Swiecicki & W.K.Swiecicki	Yes	Leguminosae[j]	D	c.42	2	A	588	0.6	1.2	2.4	369	O	*Glycine*[e]	FC:PI
520	*Lupinus hispanicus* Boiss. & Reut. ssp. *hispanicus* "Badajoz-2"[i]	Yes	Leguminosae[j]	D	52	2	A	1,078	1.1	2.1	4.2	369	O	*Glycine*[e]	FC:PI
521b	*Lupinus luteus* L. "Palucki"[i]	Yes	Leguminosae[j]	D	52	2	A	1,176	1.2	2.4	4.7	369	O	*Glycine*[e]	FC:PI
522a	*Lupinus pilosus* Murr.[h]	Yes	Leguminosae[j]	D	42	2	A	588	0.6	1.2	2.5	369	O	*Glycine*[e]	FC:PI
522b	*Lupinus pilosus* Murr.[h]	Yes	Leguminosae[j]	D	42	2	A	686	0.7	1.4	2.7	369	O	*Glycine*[e]	FC:PI
523	*Lycianthes asarifolia* Bitter	No	Solanaceae	D	—[n]	—[p]	—[q]	1,568	1.6	3.2	6.3	373	O	G[b2]	FC:PI
524j	*Lycopersicon esculentum* Mill. cv. Moneymaker	No	Solanaceae	D	24	2	A	916	0.9	1.9	3.7	337	O	*Gallus*[f]	FC:PI
525	*Malva sylvestris* L.	—[m]	Malvaceae	D	42[o]	6	P	1,470	1.5	2.9	5.9	313	O	C[d]	Fe
526	*Mammillaria bocasana* Pos.	Yes	Cactaceae	D	22	2	P	4,802[ah]	4.9[ah]	9.7[ah]	19.5[ah]	334	O	B[c]	Fe
527	*Mammillaria boolii* G.Lindsay	Yes	Cactaceae	D	22	2	P	4,508[ah]	4.6[ah]	9.2[ah]	18.4[ah]	334	O	B[c]	Fe
528	*Mammillaria grandiflora* Otto & Pfeiffer	Yes	Cactaceae	D	22	2	P	4,998[ah]	5.1[ah]	10.2[ah]	20.4[ah]	334	O	B[c]	Fe
529	*Mammillaria hahniana* Werd.	Yes	Cactaceae	D	22	2	P	4,802[ah]	4.9[ah]	9.8[ah]	19.6[ah]	334	O	B[c]	Fe
530	*Mammillaria occidentalis* (Br. & R.) Bod.	Yes	Cactaceae	D	22	2	P	5,978[ah]	6.1[ah]	12.2[ah]	24.4[ah]	334	O	B[c]	Fe
531	*Mammillaria plumosa* Web.	Yes	Cactaceae	D	22	2	P	6,468[ah]	6.6[ah]	13.2[ah]	26.5[ah]	334	O	B[c]	Fe
532	*Mammillaria rhodantha* Lk. & O.	Yes	Cactaceae	D	22	2	P	6,860[ah]	7.0[ah]	13.9[ah]	27.8[ah]	334	O	B[c]	Fe
533	*Mammillaria san-angelensis* Sanchez-Mejorada	Yes	Cactaceae	D	22	2	P	1,568	1.6	3.2	6.4	328	O	*Lycopers.*[e]	FC:PI
534	*Mammillaria zeilmanniana* Bod.	Yes	Cactaceae	D	22	2	P	5,684[ah]	5.8[ah]	11.6[ah]	23.1[ah]	334	O	B[c]	Fe
535	*Maranta arundinacea* L. var. *variegatum*	No	Marantaceae	M	48	4	P	392	0.4	0.8	1.5	355	C	J[ao]	Fe
536	*Maranta bicolor* Ker-Gawl	No	Marantaceae	M	52[o]	4	P	490	0.5	1.1	2.1	377	O	J	Fe
537	*Medemia argun* Wuert. ex H.Wendl.	Yes	Palmae	M	—[n]	—[p]	P	3,528	3.6	7.3	14.5	377	O	B	Fe
538	*Microtea scabrida* Urban	Yes	Phytolaccaceae	D	18	2	P	2,058	2.1	4.2	8.3	354	O	B	Fe
539	*Miltonia clowesii* Lindl.	Yes	Orchidaceae	M	—[n]	—[p]	P	3,724	3.8	7.6	15.2	377	O	F	Fe
540	*Miltonia regnellii* Rchb.f.	Yes	Orchidaceae	M	60[o]	—[p]	P	4,606	4.7	9.4	18.8	377	O	F	Fe
541	*Mimosa invisa* Mart	Yes	Leguminosae	D	26	2	B-P	686	0.7	1.4	2.7	375	O	F	Fe
542	*Mimosa pudica*[l]	Yes	Leguminosae	D	52	4	P	588	0.6	1.2	2.4	375	O	F	Fe
543a	*Mollinedia* sp.[y]	Yes	Monimiaceae	D	40	—[p]	P	980	1.0	1.9	3.9	341	O	B[c]	Fe
543b	*Mollinedia* sp.[y]	Yes	Monimiaceae	D	40	—[p]	P	1,176	1.2	2.4	4.7	341	O	B[c]	Fe
544	*Mollinedia* sp.[y]	Yes	Monimiaceae	D	100	—[p]	P	1,078	1.1	2.2	4.4	341	O	B[c]	Fe
545	*Mollinedia* sp.[y]	Yes	Annonaceae	D	16	—[p]	P	1,470	1.5	2.9	5.9	341	O	B[c]	Fe
546c	*Musa acuminata* Colla[h]	No	Musaceae	M	22[o]	2	P	588	0.6	1.1	2.2	335	O	*Citrus*[e]	FC:PI
547b	*Musa balbisiana* Colla	No	Musaceae	M	22[o]	2	P	490	0.5	1.0	2.1	335	O	*Citrus*[e]	FC:PI

548	*Musa schizocarpa* Simmonds	No	Musaceae	M	22[o]	2	P	588	0.6	1.2	2.4	335	O	*Citrus*[e]	FC:PI
549	*Musa textilis* Nee	No	Musaceae	M	20[o]	2	P	588	0.6	1.3	2.5	335	O	*Citrus*[e]	FC:PI
550	*Myristica dactyloides* Gaertner.	Yes	Myristicaceae	D	48	—[p]	P	1,372	1.4	2.9	5.8	341	O	B[c]	Fe
551	*Myristica fragrans* Houtt.	Yes	Myristicaceae	D	48	—[p]	P	1,176	1.2	2.4	4.8	341	O	B[c]	Fe
552	*Neofinetia falcata* (Thunb.) H.H.Hu.	No	Orchidaceae	M	38[o]	—[p]	P	2,317[t]	2.4	4.7	9.4	307	O	*Gallus*[f]	FC:PI
553	*Odontoglossum spectatissimum* Lindl.	Yes	Orchidaceae	M	—[n]	—[p]	P	4,214	4.3	8.6	17.2	377	O	F	Fe
554	*Odontoglossum wyattianum* Gurney Wilson	Yes	Orchidaceae	M	—[n]	—[p]	P	3,920	4.0	7.9	15.8	377	O	F	Fe
555	*Oncidium* aff. *cimiciferum* Rchb.f.	No	Orchidaceae	M	—[n]	—[p]	P	3,332	3.4	6.9	13.7	377	O	F	Fe
556	*Oncidium aloisii* Schltr.	No	Orchidaceae	M	—[n]	—[p]	P	3,038	3.1	6.1	12.2	377	O	F	Fe
557b	*Oncidium ampliatum* Lindl.	Yes	Orchidaceae	M	44[o]	—[p]	P	9,310	9.5	19.1	38.1	377	O	F	Fe
557c	*Oncidium ampliatum* Lindl.	No	Orchidaceae	M	44[o]	—[p]	P	2,342[t]	2.4	4.8	9.6	307	O	*Gallus*[f]	FC:PI
558	*Oncidium ansiferum* Rchb.f.	Yes	Orchidaceae	M	56[o]	—[p]	P	3,038	3.1	6.3	12.6	377	O	F	Fe
559	*Oncidium baueri* Lindl.	Yes	Orchidaceae	M	56[o]	—[p]	P	4,410	4.5	8.9	17.9	377	O	F	Fe
560	*Oncidium bracteatum* Warsz. ex Rchb.f.	Yes	Orchidaceae	M	—[n]	—[p]	P	3,234	3.3	6.6	13.1	377	O	F	Fe
561	*Oncidium caediochilum* Lindl.	Yes	Orchidaceae	M	—[n]	—[p]	P	3,038	3.1	6.2	12.4	377	O	F	Fe
562	*Oncidium crispum* Lodd.	Yes	Orchidaceae	M	56[o]	—[p]	P	1,862	1.9	3.9	7.7	377	O	F	Fe
563	*Oncidium endocharis* Rchb.f.	Yes	Orchidaceae	M	—[n]	—[p]	P	4,508	4.6	9.2	18.4	377	O	F	Fe
564	*Oncidium excavatum* Lindl.	Yes	Orchidaceae	M	c.50	—[p]	P	2,058	2.1	4.3	8.5	377	O	F	Fe
565	*Oncidium floridanum* Ames	Yes	Orchidaceae	M	56[o]	—[p]	P	3,234	3.3	6.6	13.2	377	O	F	Fe
566	*Oncidium globuliferum* H.B.& K.	Yes	Orchidaceae	M	56[o]	—[p]	P	3,136	3.2	6.4	12.8	377	O	F	Fe
567	*Oncidium loxense* Lindl.	Yes	Orchidaceae	M	—[n]	—[p]	P	2,744	2.8	5.6	11.2	377	O	F	Fe
568	*Oncidium marshallianum* Rchb.f.	Yes	Orchidaceae	M	56-58[o]	—[p]	P	1,764	1.8	3.6	7.3	377	O	F	Fe
569	*Oncidium microchilum* Batem. ex Lindl.	Yes	Orchidaceae	M	36-67[o]	—[p]	P	4,802	4.9	9.8	19.5	377	O	F	Fe
570	*Oncidium ochmatochilum* Rchb.f.	Yes	Orchidaceae	M	—[n]	—[p]	P	2,156	2.2	4.4	8.9	377	O	F	Fe
571	*Oncidium onustum* Lindl.	Yes	Orchidaceae	M	56	4	P	2,940	3.0	6.1	12.2	377	O	F	Fe
572	*Oncidium ornithorynchum* H.B.& K.	Yes	Orchidaceae	M	56[o]	2	P	2,842	2.9	5.8	11.5	377	O	F	Fe
573	*Oncidium ovatilabium* C.Schweinf.	Yes	Orchidaceae	M	—[n]	—[p]	P	1,862	1.9	3.9	7.7	377	O	F	Fe
574	*Oncidium phymatochilum* Lindl.	Yes	Orchidaceae	M	56[o]	—[p]	P	5,586	5.7	11.4	22.9	377	O	F	Fe
575	*Oncidium robustissimum* Rchb.f.	Yes	Orchidaceae	M	44[o]	—[p]	P	2,744	2.8	5.7	11.3	377	O	F	Fe
576a	*Oncidium sphacelatum* Lindl.	No	Orchidaceae	M	56[o]	—[p]	P	2,323[t]	2.4	4.7	9.4	307	O	*Gallus*[f]	FC:PI
576b	*Oncidium sphacelatum* Lindl.	Yes	Orchidaceae	M	56[o]	—[p]	P	3,136	3.2	6.4	12.9	377	O	F	Fe
577	*Oncidium stenotis* Rchb.f.	Yes	Orchidaceae	M	56[o]	—[p]	P	2,940	3.0	6.0	12.1	377	O	F	Fe
578	*Oncidium tricostatum* (Kraenzl.) Garay	Yes	Orchidaceae	M	—[n]	—[p]	P	1,960	2.0	4.1	8.1	377	O	F	Fe
579a	*Oncidium trilobum* (Schltr.) Garay & Stacy[i]	Yes	Orchidaceae	M	c.50[o]	c.4	P	3,234	3.3	6.5	13.1	377	O	F	Fe
579b	*Oncidium trilobum* (Schltr.) Garay & Stacy[i]	Yes	Orchidaceae	M	c.50[o]	c.4	P	3,528	3.6	7.3	14.6	377	O	F	Fe
580	*Oncidium varuelum* Moir	No	Orchidaceae	M	63[o]	—[p]	P	1,887[t]	2.0	3.9	7.8	307	O	*Gallus*[f]	FC:PI

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

Entry number[g]	Species	Voucher	Family	Monocot or dicot	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†
581	*Oncidium wentworthianum* Batem. ex Lindl.	Yes	Orchidaceae	M	56[o]	—[p]	P	2,842	2.9	5.9	11.7	377	O	F	Fe
582b	*Origanum vulgare* L.	—[m]	Labiatae[j]	D	32[o]	4	P	784	0.8	1.5	3.0	313	O	C[d]	Fe
583b	*Oryza australiensis* Domin	No	Gramineae	M	24	2	—[q]	980[t]	1.0	2.0	3.9	351	O	*Gallus*[f]	FC:PI
583c	*Oryza australiensis* Domin	No	Gramineae	M	24[o]	2	—[q]	975	1.0	2.0	4.0	365	O	*Gallus*[f]	FC:PI
584	*Oryza brachyantha* A.Chevalier & Roehrich	No	Gramineae	M	24	2	B	392[t]	0.4	0.7	1.4	351	O	*Gallus*[f]	FC:PI
585a	*Oryza eichingeri* Peter	No	Gramineae	M	24[o]	2	—[q]	573	0.6	1.2	2.3	365	O	*Gallus*[f]	FC:PI
585b	*Oryza eichingeri* Peter	No	Gramineae	M	24	2	B-P	686[t]	0.7	1.5	2.9	351	O	*Gallus*[f]	FC:PI
586b	*Oryza glaberrima* Steud.	No	Gramineae	M	24[o]	2	A	372	0.4	0.8	1.5	365	O	*Gallus*[f]	FC:PI
586c	*Oryza glaberrima* Steud.	No	Gramineae	M	24	2	A	392[t]	0.4	0.9	1.7	351	O	*Gallus*[f]	FC:PI
587	*Oryza glumaepatula* Steud.	No	Gramineae	M	24	2	—[q]	490[t]	0.5	1.0	2.0	351	O	*Gallus*[f]	FC:PI
588	*Oryza grandiglumis* Prodoehl	No	Gramineae	M	48[o]	4	—[q]	975	1.0	2.0	4.0	365	O	*Gallus*[f]	FC:PI
589	*Oryza latifolia*[l]	No	Gramineae	M	48[o]	4	—[q]	1,137	1.2	2.3	4.6	365	O	*Gallus*[f]	FC:PI
590c	*Oryza longistaminata* A.Chev. & Rochr.	No	Gramineae	M	24	2	P	392[t]	0.4	0.8	1.6	351	O	*Gallus*[f]	FC:PI
590d	*Oryza longistaminata* A.Chev. & Roehr	No	Gramineae	M	24[o]	2	P	382	0.4	0.8	1.6	365	O	*Gallus*[f]	FC:PI
591	*Oryza meridionalis* N.Q.Ng	No	Gramineae	M	24	2	A-B	490[t]	0.5	1.0	2.0	351	O	*Gallus*[f]	FC:PI
592b	*Oryza minuta* J & C.Presl.	No	Gramineae	M	48[o]	4	—[q]	1,142	1.2	2.3	4.7	365	O	*Gallus*[f]	FC:PI
593b	*Oryza officinalis* Wall & Watt.	No	Gramineae	M	24[o]	2	P	559	0.6	1.1	2.3	365	O	*Gallus*[f]	FC:PI
593c	*Oryza officinalis* Wall. & Watt.	No	Gramineae	M	24	2	P	686[t]	0.7	1.5	2.9	351	O	*Gallus*[f]	FC:PI
594	*Oryza punctata* Kotschy ex Steud.	No	Gramineae	M	24	2	A-B	588[t]	0.6	1.1	2.2	351	O	*Gallus*[f]	FC:PI
595b	*Oryza ridleyi* Hook.[h]	No	Gramineae	M	48[o]	4	—[q]	642	0.7	1.3	2.6	365	O	*Gallus*[f]	FC:PI
595c	*Oryza ridleyi* Hook.[h]	No	Gramineae	M	48[o]	4	—[q]	946	1.0	1.9	3.9	365	O	*Gallus*[f]	FC:PI
596c	*Oryza rufipogon* Griff.	No	Gramineae	M	24	2	A-P	490[t]	0.5	1.0	1.9	351	O	*Gallus*[f]	FC:PI
597n	*Oryza sativa* L. ssp. *indica* cv. IR36	No	Gramineae	M	24	2	A	490[t]	0.5	0.9	1.9	351	O	*Gallus*[f]	FC:PI
597o	*Oryza sativa* L. ssp. *indica* cv. IR36	No	Gramineae	M	24[o]	2	A	441	0.4	0.9	1.8	365	O	*Gallus*[f]	FC:PI
597p	*Oryza sativa* L. ssp. *japonica* cv. Yukihikari	No	Gramineae	M	24[o]	2	A	431	0.4	0.9	1.8	365	O	*Gallus*[f]	FC:PI
597q	*Oryza sativa* L. ssp. *japonica* cv. Nipponbare	No	Gramineae	M	24	2	A	490[t]	0.5	0.9	1.8	351	O	*Gallus*[f]	FC:PI
598	*Oxalis corniculata* L. var. *rubra*	Yes	Oxalidaceae	D	—[n]	—[p]	P	1,470	1.5	2.9	5.8	375	O	F	Fe
599	*Paeonia anomala* L.	Yes	Paeoniaceae	D	10	2	P	18,659	19.0	38.1	76.2	374	O	B	Fe
600	*Paeonia bakeri* Lynch	Yes	Paeoniaceae	D	20	4	P	24,402	24.9	49.8	99.5	374	O	B	Fe
601	*Paeonia californica*[l]	Yes	Paeoniaceae	D	10	2	P	16,366	16.7	33.5	67.0	374	O	B	Fe
602	*Paeonia caucasica* Schipczinsky	Yes	Paeoniaceae	D	10	2	P	15,974	16.3	32.6	65.2	374	O	B	Fe
603	*Paeonia clusii* F.C.Stern & W.T.Stearn	Yes	Paeoniaceae	D	20	4	P	28,374	29.0	57.9	115.8	374	O	B	Fe

604	*Paeonia delavayi*[l]	Yes	Paeoniaceae	D	10	2	P	14,382	14.7	29.4	58.7	374	O	B	Fe
605	*Paeonia hybrida*[l]	Yes	Paeoniaceae	D	10	2	P	17,020	17.4	34.7	69.5	374	O	B	Fe
606	*Paeonia lutea* Delavay ex Franchet	Yes	Paeoniaceae	D	10	2	P	15,680	16.0	32.1	64.2	374	O	B	Fe
607a	*Paeonia mascula* (L.) Mill ssp. *mascula*	Yes	Paeoniaceae	D	10	2	P	17,444	17.8	35.5	71.0	374	O	B	Fe
607b	*Paeonia mascula* (L.) Mill ssp. *triternata*	Yes	Paeoniaceae	D	10	2	P	15,288	15.6	31.2	62.4	374	O	B	Fe
608	*Paeonia mlokosewitschi* Lomakin	Yes	Paeoniaceae	D	10	2	P	15,876	16.2	32.3	64.7	374	O	B	Fe
609	*Paeonia officinalis* ssp. *officinalis*	Yes	Paeoniaceae	D	20	4	P	26,362	26.9	53.8	107.6	374	O	B	Fe
610	*Paeonia peregrina* Miller	Yes	Paeoniaceae	D	20	4	P	25,970	26.5	53.0	105.9	374	O	B	Fe
611	*Paeonia rockii* (Haw & Lauener) Hong Tao & J.J.Li	Yes	Paeoniaceae	D	10	2	P	15,148	15.5	30.9	61.8	374	O	B	Fe
612	*Paeonia tenuifolia* L.	Yes	Paeoniaceae	D	10	2	P	16,268	16.6	33.1	66.2	374	O	B	Fe
613	*Paeonia veitchii* Lynch	Yes	Paeoniaceae	D	10	2	P	17,032	17.4	34.8	69.5	374	O	B	Fe
614	*Panicum dichotomiflorum* Michx.	Yes	Gramineae	M	54	6	A	1,666	1.7	3.4	6.7	375	O	F	Fe
615a	*Panicum virgatum* L. population SWG-24[i & ae]	No	Gramineae	M	36	4	P	1,372	1.4	2.7	5.4	331	O	*Lycopers.*[e] & *Ictal.*[f]	FC:PI
615b	*Panicum virgatum* L. population PMT-279[i & ae]	No	Gramineae	M	36	4	P	1,666	1.7	3.3	6.6	331	O	*Lycopers.*[e] & *Ictal.*[f]	FC:PI
615c	*Panicum virgatum* L.[i]	No	Gramineae	M	36	4	P	1,470	1.5	3.1	5.9	345[am]	O	F[c]	FC:PI
615d	*Panicum virgatum* L.[i]	No	Gramineae	M	36[o]	4	P	1,372	1.4	2.8	5.6	368[at]	O	F[c]	FC:PI
615e	*Panicum virgatum* L.[i]	No	Gramineae	M	36[o]	4	P	1,666	1.7	3.6	6.9	368[at]	O	F[c]	FC:PI
616a	*Panicum virgatum* L. population SWG-1op[i & ae]	No	Gramineae	M	54	6	P	1,960	2.0	3.9	7.8	331	O	*Lycopers.*[e] & *Ictal.*[f]	FC:PI
616b	*Panicum virgatum* L. population SWG-26[i & ae]	No	Gramineae	M	54	6	P	2,058	2.1	4.2	8.4	331	O	*Lycopers.*[e] & *Ictal.*[f]	FC:PI
617a	*Panicum virgatum* L. population SWG-1op[i & ae]	No	Gramineae	M	72	8	P	2,352	2.4	4.7	9.4	331	O	*Lycopers.*[e] & *Ictal.*[f]	FC:PI
617b	*Panicum virgatum* L. population SWG-6[i & ae]	No	Gramineae	M	72	8	P	2,940	3.0	6.0	12.0	331	O	*Lycopers.*[e] & *Ictal.*[f]	FC:PI
617c	*Panicum virgatum* L.[i]	No	Gramineae	M	72	8	P	2,989	3.1	6.1	12.2	345[am]	O	F[c]	FC:PI
617d	*Panicum virgatum* L.[i]	No	Gramineae	M	72[o]	8	P	2,842	2.9	5.7	11.4	368[at]	O	F[c]	FC:PI
617e	*Panicum virgatum* L.[i]	No	Gramineae	M	72[o]	8	P	3,136	3.2	6.5	12.9	368[at]	O	F[c]	FC:PI
618	*Paphiopedilum adductum* J.H.Asher	No	Orchidaceae	M	—[n]	—[p]	P	26,460	27.0	54.0	108.1	377	O	B	Fe
619	*Paphiopedilum armeniacum* S.C.Chen & F.Y.Liu	No	Orchidaceae	M	—[n]	—[p]	P	20,678	21.1	42.2	84.4	377	O	B	Fe
620	*Paphiopedilum bullenianum* Pfitz. var. *celebesense*	Yes	Orchidaceae	M	40	—[p]	P	25,284	25.8	51.7	103.4	377	O	B	Fe
621	*Paphiopedilum ciliolare* Pfitz.	Yes	Orchidaceae	M	32[o]	—[p]	P	29,890	30.5	61.0	122.0	377	O	B	Fe
622	*Paphiopedilum dianthum* T.Tang & F.T.Wang	Yes	Orchidaceae	M	28-30	—[p]	P	35,182	35.9	71.8	143.6	377	O	B	Fe
623	*Paphiopedilum exul* Rolfe	No	Orchidaceae	M	26[o]	—[p]	P	16,170	16.5	33.0	66.0	377	O	B	Fe
624	*Paphiopedilum haynaldianum* (Rchb.f.) Stein	Yes	Orchidaceae	M	26[o]	—[p]	P	22,442	22.9	45.7	91.4	377	O	B	Fe

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

Entry number[g]	Species	Voucher	Family	Monocot or dicot	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††
625	*Paphiopedilum javanicum* Pfitz.	No	Orchidaceae	M	40	—[p]	P	24,794	25.3	50.6	101.2	377	O	B	Fe
626	*Paphiopedilum lawrenceanum* Pfitz.	No	Orchidaceae	M	40	—[p]	P	25,578	26.1	52.3	104.5	377	O	B	Fe
627	*Paphiopedilum lowii* (Lindl.) Stein	Yes	Orchidaceae	M	26	—[p]	P	24,010	24.5	49.1	98.1	377	O	B	Fe
628	*Paphiopedilum purpuratum* (Lindl.) Stein	—[m]	Orchidaceae	M	40	—[p]	P	26,558	27.1	54.3	108.5	377	O	B	Fe
629b	*Pascopyrum smithii* (Rydb.) A.Löve cv. Flintlock (= *Agropyron smithii*)	No	Gramineae[j]	M	56	8	P	17,346	17.7	35.4	70.8	343[al]	O	A[c] & F[c]	FC:PI
630	*Paspalum conjugatum*[l]	Yes	Gramineae	M	—[n]	—[p]	A-P	1,470	1.5	3.1	6.1	375	O	F	Fe
631	*Pennisetum alopecuroides* L.	Yes	Gramineae	M	18	2	—[q]	980	1.0	1.9	3.8	308	O	*Medic.*[e]	FC:EB
632b	*Pennisetum glaucum* R.Br.	Yes	Gramineae	M	14	2	A	2,352	2.4	4.7	9.4	308	O	*Medic.*[e]	FC:EB
633	*Pennisetum hohenackeri* Hochst. ex Steud	Yes	Gramineae	M	18	2	P	882	0.9	1.7	3.4	308	O	*Medic.*[e]	FC:EB
634	*Pennisetum mezianum* Leeke, Abstamm. & Heim.	Yes	Gramineae	M	32	4	P	1,470	1.5	3.0	6.0	308	O	*Medic.*[e]	FC:EB
635	*Pennisetum mollissimum* Hochst.	Yes	Gramineae	M	14	2	A	2,254	2.3	4.5	9.0	308	O	*Medic.*[e]	FC:EB
636	*Pennisetum orientale* L.	Yes	Gramineae	M	36	4	P	1,862	1.9	3.8	7.6	308	O	*Medic.*[e]	FC:EB
637	*Pennisetum pedicellatum* Trin.	Yes	Gramineae	M	36	4	A-P	2,156	2.2	4.4	8.8	375	O	F	Fe
638	*Pennisetum pedicellatum* Trin.	Yes	Gramineae	M	54	6	P	2,744	2.8	5.6	11.2	308	O	*Medic.*[e]	FC:EB
639	*Pennisetum polystachyon* Schult	Yes	Gramineae	M	36	4	A-P	2,058	2.1	4.3	8.5	375	O	F	Fe
640	*Pennisetum polystachyon* Schult	Yes	Gramineae	M	54	6	A	2,842	2.9	5.7	11.4	308	O	*Medic.*[e]	FC:EB
641b	*Pennisetum purpureum* Schum.	Yes	Gramineae	M	28	4	P	2,254	2.3	4.6	9.2	308	O	*Medic.*[e]	FC:EB
642	*Pennisetum ramosum* L.	Yes	Gramineae	M	10	2	A-B	1,960	2.0	4.0	8.0	308	O	*Medic.*[e]	FC:EB
643	*Pennisetum schweinfurthii* Pilg.	Yes	Gramineae	M	14	2	A	2,450	2.5	5.0	10.0	308	O	*Medic.*[e]	FC:EB
644	*Pennisetum setaceum* (Forssk.) Chiov.	Yes	Gramineae	M	27	3	P	1,372	1.4	2.8	5.6	308	O	*Medic.*[e]	FC:EB
645	*Pennisetum setaceum* (Forssk.) Chiov.	Yes	Gramineae	M	54	6	P	2,646	2.7	5.3	10.6	308	O	*Medic.*[e]	FC:EB
646	*Pennisetum squamulatum* Fresen.	Yes	Gramineae	M	54	6	P	4,704	4.8	9.6	19.2	308	O	*Medic.*[e]	FC:EB
647	*Pennisetum villosum* L.	Yes	Gramineae	M	36	4	P	1,764	1.8	3.5	7.0	308	O	*Medic.*[e]	FC:EB
648	*Pennisetum violaceum* Rich.	Yes	Gramineae	M	14	2	A	2,254	2.3	4.5	9.0	308	O	*Medic.*[e]	FC:EB
649	*Peperomia blanda* H.B.& K.	Yes	Piperaceae	D	22	2	P	1,568	1.6	3.1	6.2	341	O	B[c]	Fe
650	*Peperomia fenzlei* Regel.	Yes	Piperaceae	D	44	4	P	1,960	2.0	4.0	8.0	341	O	B[c]	Fe
651	*Peperomia glabella* A.Dieter	Yes	Piperaceae	D	22	2	P	1,666	1.7	3.3	6.7	341	O	B[c]	Fe
652	*Peperomia griseoargantia* Yunker	Yes	Piperaceae	D	22	2	P	588	0.6	1.2	2.5	341	O	B[c]	Fe
653	*Peperomia longespicata* C.DC.	Yes	Piperaceae	D	66	6	P	3,920	4.0	7.9	15.8	341	O	B[c]	Fe
654	*Peperomia magnoliaefolia* A.Dieter	Yes	Piperaceae	D	22	2	P	1,372	1.4	2.7	5.4	341	O	B[c]	Fe
655	*Peperomia metallica* Lind. & Rodrig.	Yes	Piperaceae	D	33	3	P	3,038	3.1	6.2	12.3	341	O	B[c]	Fe

656b	*Peperomia obtusifolia* A.Dieter.	Yes	Piperaceae	D	22	2	P	1,176	1.2	2.4	4.7	341	O	B[c]	Fe
657	*Peristeria elata* Hook.	No	Orchidaceae	M	40°	—[p]	P	4,577[t]	4.7	9.3	18.6	307	O	*Gallus*[f]	FC:PI
658b	*Persea americana* Miller.	Yes	Lauraceae	D	24	2	P	1,176	1.2	2.3	4.6	341	O	B[c]	Fe
659	*Persea indica* (L.) Sprengel.	Yes	Lauraceae	D	24	2	P	1,666	1.7	3.3	6.6	341	O	B[c]	Fe
660c	*Petroselinum crispum* (Mill.) Nym. ex A.W.Hill	Yes	Umbelliferae	D	22°	2	B	2,156	2.2	4.5	8.9	346	O	–[v]	FC:PI
661b	*Phaius tankervilleae* (Banks) Bl.	No	Orchidaceae	M	46°	—[p]	P	5,576[t]	5.7	11.4	22.8	307	O	*Gallus*[f]	FC:PI
662	*Phalaenopsis equestris* (Shauer) Rchb.f.	No	Orchidaceae	M	38°	—[p]	P	2,709[t]	2.8	5.5	11.0	307	O	*Gallus*[f]	FC:PI
663	*Phalaenopsis luedemanniana* Rchb.f.	No	Orchidaceae	M	38°	—[p]	P	4,239[t]	4.4	8.7	17.4	307	O	*Gallus*[f]	FC:PI
664b	*Phoenix dactylifera* L.	—[m]	Palmae	M	36°	2	P	250	0.3	0.5	1.0	340	O	—[w]	—[r]
665	*Phyllostachys nigra* Munro var. *henonis*	No	Gramineae	M	c.50	—[p]	P	2,646	2.7	5.4	10.8	377	O	F	Fe
666	*Phytolacca americana* L.	Yes	Phytolaccaceae	D	36	4	P	1,470	1.5	2.9	5.9	354	O	B	Fe
667	*Phytolacca bogotensis Humb., Bompl. & Kunth*	Yes	Phytolaccaceae	D	36	4	P	1,372	1.4	2.8	5.6	354	O	B	Fe
668	*Phytolacca dioica* L.	Yes	Phytolaccaceae	D	36	4	P	1,274	1.3	2.6	5.2	354	O	B	Fe
669	*Phytolacca rivinoides* Kunth & Bouche	Yes	Phytolaccaceae	D	36	4	P	1,274	1.3	2.6	5.2	354	O	B	Fe
670	*Phytolacca tetramera* Hauman	Yes	Phytolaccaceae	D	72	8	P	2,744	2.8	5.6	11.1	354	O	B	Fe
671	*Prosopis alba* Griseb.	No	Leguminosae[k]	D	28	2	P	392	0.4	0.8	1.7	320	O	*Gallus*[f]	FC:PI
672	*Prosopis chilensis* (Molina) Stuntz.	No	Leguminosae[k]	D	28	2	P	392	0.4	0.9	1.7	320	O	*Gallus*[f]	FC:PI
673a	*Prosopis chilensis* (Molina) Stuntz.[i]	No	Leguminosae[k]	D	56	4	P	882	0.9	1.7	3.4	320	O	*Gallus*[f]	FC:PI
673b	*Prosopis chilensis* (Molina) Stuntz.[i]	No	Leguminosae[k]	D	56	4	P	882	0.9	1.7	3.5	320	O	*Gallus*[f]	FC:PI
674	*Prosopis flexusa* DC.	No	Leguminosae[k]	D	28	2	P	392	0.4	0.8	1.6	320	O	*Gallus*[f]	FC:PI
675	*Prosopis glandulosa* Torr.	No	Leguminosae[k]	D	28	2	P	392	0.4	0.8	1.7	320	O	*Gallus*[f]	FC:PI
676	*Prosopis juliflora* (Swartz) DC.[i]	No	Leguminosae[k]	D	28	2	P	392	0.4	0.9	1.7	320	O	*Gallus*[f]	FC:PI
677	*Prosopis lampa* Willd.	No	Leguminosae[k]	D	28	2	P	392	0.4	0.9	1.7	320	O	*Gallus*[f]	FC:PI
678	*Prosopis pallida* Willd.	No	Leguminosae[k]	D	28	2	P	392	0.4	0.8	1.7	320	O	*Gallus*[f]	FC:PI
679	*Prosopis siliquas* (Willd.)	No	Leguminosae[k]	D	28	2	P	490	0.5	1.0	2.0	320	O	*Gallus*[f]	FC:PI
680c	*Prospero autumnale* s.l. (= *Scilla autumnalis*)[ad]	Yes	Hyacinthaceae	M	12	2	P	5,782	5.9	11.9	23.8	321	O	B	Fe
680d	*Prospero autumnale* s.l. (= *Scilla autumnalis*)[ad]	Yes	Hyacinthaceae	M	12	2	P	6,174	6.3	12.7	25.3	321	O	B	Fe
680e	*Prospero autumnale* s.l. (= *Scilla autumnalis*)[ad]	Yes	Hyacinthaceae	M	14	2	P	4,214	4.3	8.5	17.0	321	O	B	Fe
680f	*Prospero autumnale* s.l. (= *Scilla autumnalis*)[ad]	Yes	Hyacinthaceae	M	14	2	P	7,350	7.5	15.0	30.0	321	O	B	Fe
681	*Prospero obtusifolium* (Poiret) F.Speta (= *Scilla obtusifolia*)	Yes	Hyacinthaceae	M	8	2	P	4,704	4.8	9.7	19.4	321	O	B	Fe
682	*Psathyrostachys fragilis* (Boise) Nevski	No	Gramineae[j]	M	14	2	P	8,232	8.4	16.8	33.6	343[al]	O	A[c] & F[c]	FC:PI

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

Entry number[g]	Species	Voucher	Family	Monocot or dicot	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††
683	*Psathyrostachys juncea* (Fisher) Nevski[i]	No	Gramineae[j]	M	14	2	P	7,644	7.8	15.6	31.2	343[al]	O	A[c] & F[c]	FC:PI
684	*Psathyrostachys stoloniformis* C.Baden[i]	No	Gramineae[j]	M	14	2	P	8,820	9.0	17.9	35.8	343[al]	O	A[c] & F[c]	FC:PI
685	*Pseudoroegneria geniculata* (Trin.) A.Löve[i]	No	Gramineae[j]	M	28	4	P	8,526	8.7	17.5	35.0	343[al]	O	A[c] & F[c]	FC:PI
686	*Pseudoroegneria libanotica* (Hackel) D.R.Dewey	No	Gramineae[j]	M	14	2	P	3,920	4.0	8.0	15.9	343[al]	O	A[c] & F[c]	FC:PI
687a	*Pseudoroegneria spicata* (Pursh.) A.Löve	No	Gramineae[j]	M	14	2	P	4,508	4.6	9.1	18.2	343[al]	O	A[c] & F[c]	FC:PI
687b	*Pseudoroegneria spicata* (Pursh.) A.Löve ssp. *spicata*	No	Gramineae[j]	M	14	2	P	4,606	4.7	9.4	18.9	343[al]	O	A[c] & F[c]	FC:PI
688	*Pseudoroegneria stipifolia* (Czern ex Nevski)	No	Gramineae[j]	M	14	2	P	3,920	4.0	8.0	16.0	343[al]	O	A[c] & F[c]	FC:PI
689a	*Pseudoroegneria strigosa* (M.Bieb) ssp. *aegilopoides*	No	Gramineae[j]	M	14	2	P	4,606	4.7	9.5	18.9	343[al]	O	A[c] & F[c]	FC:PI
689b	*Pseudoroegneria strigosa* (M.Bieb)	No	Gramineae[j]	M	14	2	P	4,802	4.9	9.7	19.4	343[al]	O	A[c] & F[c]	FC:PI
690	*Psilanthus ebracteolatus* Hiern.	No	Rubiaceae	D	22[o]	2	P	588	0.6	1.1	2.3	309	O	*Gallus*[f]	FC:PI
691	*Pueraria lobata* (Willd.) Ohwi	No	Leguminosae	D	22	2	P	1,078	1.1	2.2	4.4	347	O	G & J	FC:PI
692	*Quercus cerris* L.	Yes	Fagaceae	D	24	2	P	980	1.0	1.9	3.8	323	O	*Petunia*[f]	FC:EB
693	*Quercus coccifera* L.	Yes	Fagaceae	D	24	2	P	980	1.0	2.0	4.0	323	O	*Petunia*[f]	FC:EB
694	*Quercus ilex* L.	Yes	Fagaceae	D	24	2	P	980	1.0	2.0	4.0	323	O	*Petunia*[f]	FC:EB
695c	*Quercus petraea* L.[h]	Yes	Fagaceae	D	24	2	P	882	0.9	1.9	3.8	323	O	*Petunia*[f]	FC:EB
695d	*Quercus petraea* L.	—[m]	Fagaceae	D	24	2	P	916[t]	0.9	1.9	3.7	366	O	*Petunia*[f]	FC:EB
696a	*Quercus pubescens* Willd.	—[m]	Fagaceae	D	24	2	P	911[t]	0.9	1.9	3.7	366	O	*Petunia*[f]	FC:EB
696b	*Quercus pubescens* Willd.	Yes	Fagaceae	D	24	2	P	980	1.0	1.9	3.8	323	O	*Petunia*[f]	FC:EB
697a	*Quercus robur* L.	—[m]	Fagaceae	D	24	2	P	902[t]	0.9	1.8	3.7	366	O	*Petunia*[f]	FC:EB
697b	*Quercus robur* L.	Yes	Fagaceae	D	24	2	P	882	0.9	1.9	3.8	323	O	*Petunia*[f]	FC:EB
698	*Quercus suber* L.	Yes	Fagaceae	D	24	2	P	980	1.0	1.9	3.8	323	O	*Petunia*[f]	FC:EB
699	*Reichardia dichotoma* Freyn	Yes	Compositae	D	18	2	P	1,274	1.3	2.6	5.1	356	O	*Lycopers.*[e]	FC:EB
700	*Reichardia gaditana* Cout.	Yes	Compositae	D	16	2	P	784	0.8	1.7	3.3	356	O	*Lycopers.*[e]	FC:EB
701	*Reichardia picroides* Roth	Yes	Compositae	D	14	2	A	686	0.7	1.5	3.0	356	O	*Lycopers.*[e]	FC:EB
702	*Rhynchostele cervantesii* (La Llave & Lex.) Soto, Arenas & Salazar	No	Orchidaceae	M	—[n]	—[p]	P	3,626	3.7	7.4	14.8	377	O	F	Fe
703	*Rhynchostele cordata* (Lindl.) Soto, Arenas & Salazar	Yes	Orchidaceae	M	—[n]	—[p]	P	3,822	3.9	7.8	15.6	377	O	F	Fe
704b	*Rhynchostylis gigantia* (Lindl.) Ridl.	No	Orchidaceae	M	38[o]	—[p]	P	2,950[t]	3.0	6.0	12.0	307	O	*Gallus*[f]	FC:PI
705b	*Rhynchostylis retusa* (L.) Bl.	No	Orchidaceae	M	38[o]	—[p]	P	4,728[t]	4.9	9.7	19.4	307	O	*Gallus*[f]	FC:PI

706	*Rollinia mucosa* (Jacq.) Ball.	Yes	Annonaceae	D	42	—^{p}	P	2,940	3.0	6.0	11.9	341	O	B^{c}	Fe
707a	*Rosa* × *hybrida* cv. 'Ballerina' (Polyantha class)	Yes	Rosaceae	D	14^{o}	2	P	578	0.6	1.2	2.4	346	O	*Petrosel.*^{v}	FC:PI
707b	*Rosa* × *hybrida* cv. 'Felicite et Perpetue' (Hybrid Sempervirens class)	Yes	Rosaceae	D	14^{o}	2	P	632	0.6	1.3	2.6	346	O	*Petrosel.*^{v}	FC:PI
708a	*Rosa* × *hybrida* cv. 'Frensham' (Floribunda class)	Yes	Rosaceae	D	21^{o}	3	P	877	0.9	1.8	3.6	346	O	*Petrosel.*^{v}	FC:PI
708b	*Rosa* × *hybrida* cv. 'New Dawn' (Large-flowered Climber class)	Yes	Rosaceae	D	21^{o}	3	P	862	0.9	1.8	3.5	346	O	*Petrosel.*^{v}	FC:PI
709	*Rosa* × *hybrida* cv. 'Mountbatten' (Floribunda class)	Yes	Rosaceae	D	28^{o}	4	P	1,127	1.2	2.3	4.6	346	O	*Petrosel.*^{v}	FC:PI
710b	*Rosa acicularis* Lindl. var. *engelmannii*	Yes	Rosaceae	D	42^{o}	6	P	1,470	1.5	3.0	6.1	346	O	*Petrosel.*^{v}	FC:PI
711	*Rosa arvensis* Huds.	Yes	Rosaceae	D	14^{o}	2	P	588	0.6	1.1	2.2	346	O	*Petrosel.*^{v}	FC:PI
712	*Rosa banksiae* Ait. var. *lutea*	Yes	Rosaceae	D	14^{o}	2	P	490	0.5	1.0	2.1	346	O	*Petrosel.*^{v}	FC:PI
713	*Rosa bella* Rehd. & Wils.	Yes	Rosaceae	D	28^{o}	4	P	980	1.0	1.9	3.9	346	O	*Petrosel.*^{v}	FC:PI
714	*Rosa bracteata* Wendl.	Yes	Rosaceae	D	14^{o}	2	P	588	0.6	1.2	2.4	346	O	*Petrosel.*^{v}	FC:PI
715b	*Rosa canina* L.	Yes	Rosaceae	D	35^{o}	5	P	1,470	1.5	2.9	5.8	346	O	*Petrosel.*^{v}	FC:PI
716	*Rosa centifolia* L.	Yes	Rosaceae	D	28^{o}	4	P	1,078	1.1	2.2	4.5	346	O	*Petrosel.*^{v}	FC:PI
717	*Rosa chinensis* Jacq.	Yes	Rosaceae	D	14^{o}	2	P	588	0.6	1.2	2.3	346	O	*Petrosel.*^{v}	FC:PI
718	*Rosa damascena* Mill. var. *versicolor*	Yes	Rosaceae	D	28^{o}	4	P	1,078	1.1	2.2	4.3	346	O	*Petrosel.*^{v}	FC:PI
719	*Rosa fedtschenkoana* Reg.	Yes	Rosaceae	D	28^{o}	4	P	980	1.0	1.9	3.9	346	O	*Petrosel.*^{v}	FC:PI
720	*Rosa foetida* Herrm.	Yes	Rosaceae	D	28^{o}	4	P	980	1.0	2.0	3.9	346	O	*Petrosel.*^{v}	FC:PI
721	*Rosa foliolosa* Nutt.	Yes	Rosaceae	D	14^{o}	2	P	490	0.5	0.9	1.9	346	O	*Petrosel.*^{v}	FC:PI
722	*Rosa gallica* L. var. *officinalis*	Yes	Rosaceae	D	28^{o}	4	P	1,078	1.1	2.2	4.4	346	O	*Petrosel.*^{v}	FC:PI
723	*Rosa iliensis* Chrshan	Yes	Rosaceae	D	14^{o}	2	P	490	0.5	1.0	1.9	346	O	*Petrosel.*^{v}	FC:PI
724	*Rosa laevigata* Michx.	Yes	Rosaceae	D	14^{o}	2	P	588	0.6	1.1	2.3	346	O	*Petrosel.*^{v}	FC:PI
725	*Rosa latibracteata* Boulenger	Yes	Rosaceae	D	28^{o}	4	P	980	1.0	1.9	3.8	346	O	*Petrosel.*^{v}	FC:PI
726	*Rosa moyesii* Hemsl. & Wils.	Yes	Rosaceae	D	42^{o}	6	P	1,372	1.4	2.9	5.8	346	O	*Petrosel.*^{v}	FC:PI
727	*Rosa nitida* Willd.	Yes	Rosaceae	D	14^{o}	2	P	490	0.5	1.0	1.9	346	O	*Petrosel.*^{v}	FC:PI
728	*Rosa persica* Michx.	Yes	Rosaceae	D	14^{o}	2	P	392	0.4	0.8	1.7	346	O	*Petrosel.*^{v}	FC:PI
729	*Rosa roxburghii* Tratt. var. *hirtula*	Yes	Rosaceae	D	14^{o}	2	P	490	0.5	1.0	1.9	346	O	*Petrosel.*^{v}	FC:PI
730	*Rosa rugosa* Thunb. var. *alba*	Yes	Rosaceae	D	14^{o}	2	P	490	0.5	1.0	2.0	346	O	*Petrosel.*^{v}	FC:PI
731	*Rosa sempervirens* L.	Yes	Rosaceae	D	14^{o}	2	P	588	0.6	1.1	2.3	346	O	*Petrosel.*^{v}	FC:PI
732	*Rosa sericea* Lindl. f. pteracantha	Yes	Rosaceae	D	14^{o}	2	P	392	0.4	0.8	1.6	346	O	*Petrosel.*^{v}	FC:PI
733	*Rosa spinosissima* L. var. *hispida*	Yes	Rosaceae	D	28^{o}	4	P	882	0.9	1.9	3.7	346	O	*Petrosel.*^{v}	FC:PI
734	*Rosa stellata* Woot. var. *mirifica*	Yes	Rosaceae	D	14^{o}	2	P	392	0.4	0.9	1.7	346	O	*Petrosel.*^{v}	FC:PI
735	*Rosa virginiana* Mill.	Yes	Rosaceae	D	28^{o}	4	P	980	1.0	2.0	3.9	346	O	*Petrosel.*^{v}	FC:PI
736a	*Rosa wichuraiana* Crep.	Yes	Rosaceae	D	14^{o}	2	P	588	0.6	1.1	2.3	346	O	*Petrosel.*^{v}	FC:PI
737	*Rosa willmottiae* Hemsl.	Yes	Rosaceae	D	14^{o}	2	P	490	0.5	0.9	1.8	346	O	*Petrosel.*^{v}	FC:PI
738	*Rosa xanthina* Lindl. cv. 'Canary Bird'	Yes	Rosaceae	D	14^{o}	2	P	392	0.4	0.8	1.6	346	O	*Petrosel.*^{v}	FC:PI

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

Entry number[g]	Species	Voucher	Family	Monocot or dicot	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†
739	*Rossioglossum williamsianum* (Rchb.f.) Garay & G.C.Kennedy	No	Orchidaceae	M	—[n]	—[p]	P	7,546	7.7	15.4	30.8	377	O	F	Fe
740b	*Ruta graveolens* L.	—[m]	Rutaceae	D	72[o]	8	P	686	0.7	1.4	2.8	313	O	C[d]	Fe
741e	*Saccharum officinarum* L.	No	Gramineae	M	80	8	P	3,724	3.8	7.7	15.4	342	O	G[c]	FC:EB
742c	*Saccharum robustum* Brandes & Jesw. ex Grassl	No	Gramineae	M	60	6	P	3,234	3.3	6.5	13.0	342	O	G[c]	FC:EB
743	*Saccharum spontaneum* L.	No	Gramineae	M	64	8	P	3,136	3.2	6.3	12.6	342	O	G[c]	FC:EB
744	*Salacca zalacca* (Gaertn) Voss	Yes	Palmae	M	—[n]	—[p]	P	1,274	1.3	2.6	5.2	377	O	B	Fe
745	*Sarcandra glabra*[l]	Yes	Chloranthaceae	D	30	—[p]	P	4,214	4.3	8.7	17.4	341	O	B[c]	Fe
746	*Sasa veitchii* Rehder	No	Gramineae	M	c.50	—[p]	P	3,528	3.6	7.1	14.3	377	O	F	Fe
747	*Satureja montana* L.	—[m]	Labiatae[j]	D	30[o]	6	P	2,744	2.8	5.5	11.1	313	O	C[d]	Fe
748	*Schomburgkia lyonsii* Lindl.	No	Orchidaceae	M	—[n]	—[p]	P	1,906[t]	2.0	3.9	7.8	307	O	*Gallus*[f]	FC:PI
749	*Semiarundinaria tranquillans* Koidz	No	Gramineae	M	c.50	—[p]	P	3,136	3.2	6.3	12.7	377	O	F	Fe
750	*Sesleria albicans* Kit. ex Schult[h & au]	Yes	Gramineae[j]	M	28	4	P	4,508[t]	4.6	9.3	18.5	370	O	H[c]	FC:PI
751	*Sesleria caerulea* (L.) Ard.	Yes	Gramineae[j]	M	28	4	P	4,508[t]	4.6	9.1	18.2	370	O	H[c]	FC:PI
752	*Sesleria heufleriana* Schur	Yes	Gramineae[j]	M	28	4	P	4,704[t]	4.8	9.6	19.2	370	O	H[c]	FC:PI
753	*Sesleria heufleriana* Schur	Yes	Gramineae[j]	M	56	8	P	9,310[t]	9.5	19.0	37.9	370	O	H[c]-752	FC:PI
754a	*Sesleria sadleriana* Janka "Hainburg"[au]	Yes	Gramineae[j]	M	56	8	P	8,722[t]	8.9	17.7	35.5	370	O	H[c]-752	FC:PI
754b	*Sesleria sadleriana* Janka "Vrsatec"[au]	Yes	Gramineae[j]	M	56	8	P	8,918[t]	9.1	18.3	36.6	370	O	H[c]-752	FC:PI
755	*Sesleria tatrae* (Degen) Deyl	Yes	Gramineae[j]	M	56	8	P	8,918[t]	9.1	18.3	36.6	370	O	H[c]-752	FC:PI
756	*Setaria chevalieri* Stapf	Yes	Gramineae	M	36	4	P	2,156	2.2	4.5	8.9	330	O	*Petunia*[f]	FC:EB
757	*Setaria faberi* Herrm.	Yes	Gramineae	M	36	4	A	1,568	1.6	3.3	6.5	375	O	F	Fe
758	*Setaria glauca*[l]	Yes	Gramineae	M	—[n]	—[p]	A	1,176	1.2	2.5	4.9	375	O	F	Fe
759	*Setaria holstii* Herrm.	Yes	Gramineae	M	18	2	P	882	0.9	1.7	3.4	330	O	*Petunia*[f]	FC:EB
760	*Setaria incrassata* Hack.	Yes	Gramineae	M	36	4	—[q]	2,058	2.1	4.2	8.5	330	O	*Petunia*[f]	FC:EB
761a	*Setaria italica* (L.) Beauv. cv. Little red	No	Gramineae	M	18[o]	2	A	490	0.5	1.1	2.1	372	O	K	Fe
761b	*Setaria italica* (L.) Beauv.[i]	Yes	Gramineae	M	18	2	A	490	0.5	1.0	2.1	330	O	*Petunia*[f]	FC:EB
762	*Setaria leiantha* Hack. ex Stuck.	Yes	Gramineae	M	36	4	—[q]	1,176	1.2	2.4	4.8	330	O	*Petunia*[f]	FC:EB
763	*Setaria macrostachya*[l]	Yes	Gramineae	M	54	6	P	1,764	1.8	3.6	7.2	330	O	*Petunia*[f]	FC:EB
764	*Setaria neglecta*[l]	Yes	Gramineae	M	36	4	—[q]	1,764	1.8	3.5	7.0	330	O	*Lycopers.*[e]	FC:EB
765	*Setaria palmifolia* (Koenig) Stapf	Yes	Gramineae	M	36	4	P	1,862	1.9	3.9	7.8	330	O	*Lycopers.*[e]	FC:EB
766	*Setaria parviflora* (Poiret) M.Kerguelen	Yes	Gramineae	M	36	4	P	2,352	2.4	4.8	9.6	330	O	*Petunia*[f]	FC:EB
767	*Setaria pumila* Nob.[i]	Yes	Gramineae	M	54	6	A	2,548	2.6	5.3	10.5	330	O	*Petunia*[f]	FC:EB
768	*Setaria queenslandica* Domin.	Yes	Gramineae	M	36	4	—[q]	1,372	1.4	2.8	5.5	330	O	*Lycopers.*[e]	FC:EB

769a	*Setaria sphacelata* (Schum.) Stapf & Hubb.[i]	Yes	Gramineae	M	36	4	P	980	1.0	2.1	4.1	330	O	*Lycopers.*[e]	FC:EB
769b	*Setaria sphacelata* (Schum.) Stapf & Hubb.[i]	Yes	Gramineae	M	36	4	P	1,666	1.7	3.3	6.6	330	O	*Lycopers.*[e]	FC:EB
770a	*Setaria viridis* (L.) Beauv.	Yes	Gramineae	M	18	2	E-A	784	0.8	1.6	3.2	375	O	F	Fe
770b	*Setaria viridis* (L.) Beauv.[i]	Yes	Gramineae	M	18	2	E-A	490	0.5	1.0	2.1	330	O	*Petunia*[f]	FC:EB
771	*Setaria woodii* Hack.	Yes	Gramineae	M	18	2	—[q]	784	0.8	1.7	3.3	330	O	*Petunia*[f]	FC:EB
772	*Sida spinosa*[l]	Yes	Malvaceae	D	—[n]	—[p]	A	980	1.0	2.0	3.9	375	O	F	Fe
773	*Smitinandia micrantha* (Lindl.) Holtt.	No	Orchidaceae	M	38[o]	—[p]	P	2,053[t]	2.1	4.2	8.4	307	O	*Gallus*[f]	FC:PI
774b	*Solanum berthaultii* Hawkes	No	Solanaceae	D	24	2	P	784	0.8	1.6	3.2	337	O	*Gallus*[f]	FC:PI
775	*Solanum brevidens* Phil.[h & ak]	No	Solanaceae	D	24	2	P	740	0.1	1.5	3.0	337	O	*Gallus*[f]	FC:PI
776b	*Solanum demissum* Lindl.	No	Solanaceae	D	72	6	P	2,352	2.4	4.9	9.8	337	O	*Gallus*[f]	FC:PI
777	*Solanum etuberosum* Lindl.[h &ak]	No	Solanaceae	D	24	2	P	755	0.8	1.5	3.1	337	O	*Gallus*[f]	FC:PI
778	*Solanum fernandezianum* Phil.[h &ak]	No	Solanaceae	D	24	2	P	799	0.8	1.6	3.3	337	O	*Gallus*[f]	FC:PI
779g	*Solanum tuberosum* L. cv. Pito	No	Solanaceae	D	48	4	P	1,715	1.8	3.5	7.0	337	O	*Gallus*[f]	FC:PI
779h	*Solanum tuberosum* L. cv. Van Gogh	No	Solanaceae	D	48	4	P	1,715	1.8	3.5	7.0	337	O	*Gallus*[f]	FC:PI
779i	*Solanum tuberosum* L. cv. Pentland Crown	No	Solanaceae	D	48	4	P	1,774	1.8	3.6	7.2	337	O	*Gallus*[f]	FC:PI
780	*Spergula arvensis* L.	Yes	Caryophyllaceae	D	18	—[p]	A	1,078	1.1	2.1	4.2	375	O	F	Fe
781	*Stromanthe sanguinea* Sond.	No	Marantaceae	M	44[o]	4	P	686	0.7	1.3	2.7	377	O	J	Fe
782	*Tagetes patula* L.	No	Compositae	D	48[o]	4	A	1,176	1.2	2.4	4.7	373	O	G[b2]	FC:PI
783a	*Tanacetum vulgare* L.[h]	No	Compositae[j]	D	18	2	P	3,822	3.9	7.8	15.7	338	O	F[b2]	FC:PI
783b	*Tanacetum vulgare* L.[h]	No	Compositae[j]	D	18	2	P	4,900	5.0	10.0	19.9	338	O	F[b2]	FC:PI
784	*Thinopyrum bessarabicum* (Savul & Rayass) A.Löve[i]	No	Gramineae[j]	M	14	2	P	7,350	7.5	15.0	29.9	343[al]	O	A[c] & F[c]	FC:PI
785	*Thinopyrum caespitosum* Liu & Wang	No	Gramineae[j]	M	28	4	P	9,702	9.9	19.9	39.8	343[al]	O	A[c] & F[c]	FC:PI
786b	*Thinopyrum elongatum* (Host) D.R.Dewey (= *Agropyron elongatum*)[i]	No	Gramineae[j]	M	14	2	P	5,978	6.1	12.2	24.4	343[al]	O	A[c] & F[c]	FC:PI
787a	*Thinopyrum intermedium* ssp. *barbulatum* (Schur) Barkw. & D.R.Dewey cv. Manska	No	Gramineae[j]	M	42	6	P	12,740	13.0	25.9	51.8	343[al]	O	A[c] & F[c]	FC:PI
787b	*Thinopyrum intermedium* ssp. *intermedium* (Host) Barkw. & D.R.Dewey cv. Slate	No	Gramineae[j]	M	42	6	P	12,838	13.1	26.3	52.5	343[al]	O	A[c] & F[c]	FC:PI
788a	*Thinopyrum junceiforme* (Löve & Löve) A.Löve (= *Agropyron junceum* ssp. *boreoatlanticum*)[h]	No	Gramineae[j]	M	28	4	P	11,564	11.8	23.6	47.2	343[al]	O	A[c] & F[c]	FC:PI
788b	*Thinopyrum junceiforme* (Löve & Löve) A.Löve (= *Agropyron junceum* ssp. *boreoatlanticum*)[h]	No	Gramineae[j]	M	28	4	P	12,740	13.0	26.0	51.9	343[al]	O	A[c] & F[c]	FC:PI

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

Entry number[g]	Species	Voucher	Family	Monocot or dicot	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††
789	*Thinopyrum ponticum* (Podp.) Barkw. & D.R.Dewey cv. Platte (=*Agropyron elongatum* ssp. *ruthenium*)	No	Gramineae[j]	M	70	10	P	22,148	22.6	45.3	90.5	343[al]	O	A[c] & F[c]	FC:PI
790b	*Thymus vulgaris* L.	—[m]	Labiatae[j]	D	30[o]	6	P	2,058	2.1	4.2	8.3	313	O	C[d]	Fe
791	*Trichoceros antennifera* H.B.& K.	No	Orchidaceae	M	—[n]	—[p]	P	4,312	4.4	8.7	17.5	377	O	F	Fe
792	*Trichopilia maculata* Rchb.f.	No	Orchidaceae	M	—[n]	—[p]	P	2,288[t]	2.4	4.7	9.4	307	O	*Gallus*[f]	FC:PI
793e	*Trifolium repens* L. Daeno population[h]	No	Leguminosae	D	32[o]	4	P	1,274	1.3	2.7	5.3	329	O	B & I[c]	Fe
793f	*Trifolium repens* L. Grasslands Kopu population[h]	No	Leguminosae	D	32[o]	4	P	1,078	1.1	2.2	4.4	329	O	B & I[c]	Fe
794	*Vanda lamellata* Lindl.	No	Orchidaceae	M	38[o]	—[p]	P	2,009[t]	2.1	4.1	8.2	307	O	*Gallus*[f]	FC:PI
795	*Vanilla phaeantha* Rchb.f.	No	Orchidaceae	M	32[o]	—[p]	P	7,443[t]	7.6	15.2	30.4	307	O	*Gallus*[f]	FC:PI
796	*Vanilla pompona* Schiede	No	Orchidaceae	M	32[o]	—[p]	P	7,080[t]	7.3	14.5	29.0	307	O	*Gallus*[f]	FC:PI
797	*Vicia amoena* Fisch. ex Ser. var. *sericea*	Yes	Leguminosae	D	12	2	P	6,272	6.4	12.8	25.5	312	O	B	Fe
798a	*Vicia amoena* Fisch. ex Ser.[h]	Yes	Leguminosae	D	24	4	P	8,428	8.6	17.2	34.4	312	O	B	Fe
798b	*Vicia amoena* Fisch. ex Ser.[h]	Yes	Leguminosae	D	24	4	P	9,114	9.3	18.6	37.2	312	O	B	Fe
799b	*Vicia amurensis* Oett.	Yes	Leguminosae	D	12	2	P	6,370	6.5	12.9	25.8	312	O	B	Fe
800c	*Vicia pseudorobus* Fisch & Mey.	Yes	Leguminosae	D	12	2	P	6,958	7.1	14.1	28.2	312	O	B	Fe
801b	*Vicia ramuliflora* (Maxim) Ohwi	Yes	Leguminosae	D	12	2	P	6,958	7.1	14.3	28.5	312	O	B	Fe
802	*Vicia ramuliflora* (Maxim) Ohwi	Yes	Leguminosae	D	24	4	P	12,544	12.8	25.5	51.0	312	O	B	Fe
803b	*Vicia unijuga* A.Br.	Yes	Leguminosae	D	12	2	P	8,428	8.6	17.2	34.4	312	O	B	Fe
804	*Vicia unijuga* A.Br.	Yes	Leguminosae	D	24	4	P	15,876	16.2	32.5	64.9	312	O	B	Fe
805	*Xanthium strumarium*[l]	Yes	Compositae	D	36	—[p]	A	3,136	3.2	6.3	12.6	375	O	F	Fe
806	*Xylopia* sp.[y]	Yes	Annonaceae	D	16	—[p]	P	980	1.0	2.0	4.0	341	O	B[c]	Fe
807a	*Zingiber officinale* Rosc. cv. S-541[h]	Yes	Zingiberaceae	M	22	2	P	5,880	6.0	12.1	24.1	324	O	B[c]	Fe
807b	*Zingiber officinale* Rosc. cv. Z-17[h]	Yes	Zingiberaceae	M	22	2	P	4,802	4.9	9.8	19.7	324	O	B[c]	Fe

‡ 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, cthidium bromide; MI, mithramycin.

standard. As the ratios for *Maranta bicolor* (2·09/0·1734 = 12·053) and *Stromanthe sanguinea* (2·68/0·2254 = 11·889) were both so similar, it is reasonable to assume that plants growing at RBG Kew had the same ploidy levels as those used by Sharma and Mukhopadhyay (loc. cit.).

(ap) 4C DNA amounts for 26 *Carex* species given in Table 1 of Nishikawa *et al.* (1984, Ref. 357) in arbitrary units (a.u.) were converted to absolute units using the conversion factor 1 pg = 98·25 a.u. This factor was obtained as the ratio of the estimates for *Carex ciliatomarginata* (225 a.u.) obtained by Nishikawa *et al.* (loc. cit.) and L. Hanson at RBG, Kew (4C = 2·29 pg). Fixed root-tips of the original material used by Nishikawa *et al.* (1984) were kindly provided by Prof. T. Hoshino (Okayama University of Science, Japan) in 1999, and its 4C DNA amount was estimated as 2·29 pg by Feulgen microdensitometry using *Vigna radiata* 'Berken' (4C = 2·12 pg) as a calibration standard.

Two species listed by Nishikawa *et al.* (loc. cit.) were reported to display aneuploidy (*C. oxyandra*, 2n = 18, 20, 24, 26; and *C. conica*, 2n = 32, 36, 38) but no significant differences in DNA amount were found. Consequently, only the highest DNA amount for each species is given in the Appendix. Nishikawa *et al.* noted 'it seems that these intraspecific aneuploids resulted from simple change of chromosome number caused by fragmentation or fusion, but without deficiency and/or duplication of chromosome segment'. Nishikawa *et al.* (loc. cit.) also reported large intraspecifc variation in DNA content in six species: *C. tristachya* (18 %), *C. capillacea* (13 %), *C. brownii* (15 %), *C. thunbergii* (14 %), *C. paxii* (17 %) and *C. nubigera* (14 %), however, only one DNA value was listed for each of these species in Table 1 of their paper and these are listed in the Appendix.

(aq) Six of the eight species of *Citrus* examined by Ollitrault *et al.* (1994, Ref. 358) showed significant variation in DNA amounts between four or five cultivars of the same species (although this was not greater than 3 %). Table 1 in Ref. 358 gave the mean value for each species, and it is this value that is listed in the Appendix.

(ar) Greilhuber and Obermayer (1998, Ref. 360) investigated genome size variation in eight accessions of *Cajanus cajan* using both flow cytometry and Feulgen microdensitometry. They were however, unable to confirm the 1·29-fold variation in genome size reported for this species by Ohri *et al.* (1994). Only flow cytometry was able to detect statistically significant but minor differences in genome size between different accessions, Feulgen microdensitometry was apparently not sensitive enough. However, the authors noted that '. . . in flow cytometry the preparation and constitution of the material can result in minor systematic deviations from the true value'. Thus the significance of the marginal differences in genome size detected by flow cytometry remains to be determined.

(as) In Ref. 361, Dimitrova *et al.* (1999) estimated the genome sizes of three subspecies of *Crepis foetida* (ssp. *foetida*, ssp. *rhoeadifolia* and ssp. *commutata)* using three techniques: Feulgen microdensitometry, flow cytometry and image analysis. The mean DNA C-values obtained for each subspecies estimated by the first two methods are given in the Appendix. The values for image analysis were found to be somewhat lower. Dimitrova *et al.* (loc. cit.) felt that this bias needed further investigation and so these results have been excluded from the Appendix.

(at) In Ref. 368 (Hultquist *et al.*, 1997), the DNA C-values for 30 germplasm accessions of the switchgrass *Panicum virgatum* from midwestern U.S. prairies were estimated. However, only the highest and lowest DNA amounts for the tetraploid and octoploid populations are listed in the Appendix.

(au) In Ref. 370, Lysák and Doležel (1998) listed DNA amounts for five central European *Sesleria* species. While the mean DNA content of each species given in Table 2 of their paper is listed in the Appendix, the authors noted that intraspecific variation in DNA content for *S. albicans* of 1·84 % was statistically significant. Thus the DNA amount of *S. albicans* given in the Appendix may not be representative of all populations of this species. The cause of the variation was not determined.

Lysák and Doležel (loc. cit.) also reported a statistically significant difference (3·02 %) in DNA amount for two populations of the octoploid *S. sadleriana* ('Vršatec' and 'Hainburg'). Both values were listed in Ref. 370 and are given in the Appendix. The possibility of two distinct origins of the polyploid followed by separate evolution of the populations was suggested to account for these intraspecific differences. Multiple origins of polyploids have been documented in numerous taxa and are not now considered to be rare events (Soltis and Soltis, 1999).

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