



Chromosome numbers and polyploidy events in Korean non-commelinids monocots: A contribution to plant systematics

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ABSTRACT: The evolution of chromosome numbers and the karyotype structure is a prominent feature of plant genomes contributing to or at least accompanying plant diversification and eventually leading to speciation. Polyploidy, the multiplication of whole chromosome sets, is widespread and ploidy-level variation is frequent at all taxonomic levels, including species and populations, in angiosperms. Analyses of chromosome numbers and ploidy levels of 252 taxa of Korean non-commelinid monocots indicated that diploids (ca. 44%) and tetraploids (ca. 14%) prevail, with fewer triploids (ca. 6%), pentaploids (ca. 2%), and hexaploids (ca. 4%) being found. The range of genome sizes of the analyzed taxa (0.3–44.5 pg/1C) falls well within that reported in the Plant DNA C-values database (0.061–152.33 pg/1C). Analyses of karyotype features in angiosperm often involve, in addition to chromosome numbers and genome sizes, mapping of selected repetitive DNAs in chromosomes. All of these data when interpreted in a phylogenetic context allow for the addressing of evolutionary questions concerning the large-scale evolution of the genomes as well as the evolution of individual repeat types, especially ribosomal DNAs (5S and 35S rDNAs), and other tandem and dispersed repeats that can be identified in any plant genome at a relatively low cost using next-generation sequencing technologies. The present work investigates chromosome numbers (n or $2n$), base chromosome numbers (x), ploidy levels, rDNA loci numbers, and genome size data to gain insight into the incidence, evolution and significance of polyploidy in Korean monocots.

Keywords: base chromosome number, chromosome number, ploidy level, FISH, hybridization, polyploidization

Chromosome numbers and karyotype structure have always been considered to be an important character in analyses of the phylogenetic relationships and evolutionary processes in angiosperms (Levin and Wilson, 1976; Guerra, 2008; Jang et al., 2013). To date, chromosome numbers have been reported for about 25–30% of flowering plants (Bennett, 1998; Weiss-Schneeweiss and Schneeweiss, 2013). The chromosome numbers in angiosperms vary 160-fold (Weiss-Schneeweiss and Schneeweiss, 2013) ranging from $2n = 4$ (Poaceae, Hyacinthaceae, Asteraceae, Cyperaceae: Vanzela et al., 1996; Roberto, 2005) to $2n = 640$ (Crassulaceae: Uhl, 1978). The haploid chromosome numbers of the majority of angiosperms range between $n = 7$ and $n = 20$ (Grant, 1982; Masterson, 1994). Taxonomic groups display varying degrees of

chromosome number changes both among and within genera (e.g., $2n = 8, 10, 12, 14, 19, 20, 25, 26, 27, 28, 35, 42$ in *Prospero*/Hyacinthaceae: Jang, 2013; $2n = 18, 20, 22, 24, 28, 36, 40, 46, 48, 54, 56, 60, 66$ in *Melampodium*/Asteraceae: Stuessy, 1971; Weiss-Schneeweiss et al., 2009; $2n = 24$ in *Lilium*/Liliaceae: Sultana et al., 2010), and such changes continue to be used in systematics and elucidating evolutionary patterns within these groups of plants (Mayrose et al., 2010; Schubert and Lysak, 2011; Husband et al., 2013; McCann et al., 2016).

Hybridization and polyploidization have been commonly observed in many economically important plant groups (Lim et al., 2007; Mandáková et al., 2013), but recent studies have demonstrated that these processes have also been a major force

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in the diversification and speciation of angiosperms in general (Leitch and Leitch, 2008). Hybrids and polyploids experience numerous chromosomal rearrangements (e.g., inversions, deletions, translocations, centromeric shifts, etc.) and more subtle changes in sequence composition (sequence loss or gain, expansion/reduction of repetitive DNA), and they continue to generate species diversity contributing to speciation events (Soltis and Soltis, 2009; Weiss-Schneeweiss and Schneeweiss, 2013). The propensity for polyploidization appears to be unequally distributed in plant groups with polyploidy in angiosperms being more common in monocots (ca. 58%) than in dicots (ca. 43%) (Soltis and Soltis, 2009; Weiss-Schneeweiss et al., 2013).

There are two general types of polyploidy: autopolyploidy (i.e., multiplication of chromosome sets within a single species or genome) and allopolyploidy (i.e., multiplication of chromosome sets accompanied by merger of genomes of two or more species), both of which arise as a result of a failure of either meiotic or mitotic cell division (Stebbins, 1971; Otto and Whitton, 2000; Ramsey and Schemske, 2002). Although autopolyploidy has historically been considered as less frequent and less important than allopolyploidy (Stebbins, 1971; Soltis et al., 2007), natural autopolyploids are much more common than originally assumed (Ramsey and Schemske, 2002; Parisod et al., 2010), as recent studies continue to demonstrate. Multiple ploidy levels have been demonstrated to exist within many species (autopolyploidy), which often influences the degree of morphological variation in those taxa. Current focus of polyploidy research is on the genetic, epigenetic, chromosomal, and genomic consequences of polyploidization (Bowers et al., 2003; Liu and Wendel, 2003; Osborn et al., 2003; Rapp and Wendel, 2005), mechanisms of polyploid formation and establishment (Ramsey and Schemske, 2002), the ecological effects of polyploidization (Weiss-Schneeweiss et al., 2013; Soltis et al., 2016), and most of all, the impact of polyploidy on plant diversity (Mandáková et al., 2017; Jang et al., 2018).

Modern cytology greatly profits from technical advances especially *in situ* hybridization (e.g., fluorescence *in situ* hybridization [FISH] and genomic *in situ* hybridization [GISH], respectively), large scale screening for polyploidy incidence using flow cytometry, and the advent of next-generation sequencing (NGS) technologies. These allow identification, quantification and localization on the genomes of various repeat types, which contribute to genome size variation and changes of which accompany species diversification and speciation (Weiss-Schneeweiss et al., 2015). Repetitive DNA fraction in plant genomes comprises tandem

repeats (e.g., satellite DNAs, microsatellites, and ribosomal RNA genes [5S and 35S rRNA genes]) and dispersed repeats represented by mobile genetic elements (Weiss-Schneeweiss et al., 2015). The localization and evolution of tandemly repeated genes encoding 35S (18S-5.8S-25S) and 5S rRNAs in plants have been particularly useful for analysing systematic relationships between closely related species (Weiss-Schneeweiss and Schneeweiss, 2013).

The chromosome numbers in Korean non-Commelinids monocots have previously been reported for a number of taxonomically closely related taxa (Rice et al., 2015, references therein), although the incidence of polyploids and its evolutionary aspects have not been addressed in detail. It is therefore timely to summarize the knowledge of chromosome numbers, genome sizes, and polyploidy incidence in the Korean monocots (Rice et al., 2015; Vitales et al., 2017) and to identify the most important taxonomic groups in which questions of chromosomal evolution can be addressed most effectively.

Chromosome numbers and the incidence of polyploidy in non-commelinids monocot species native to Korea

All available chromosome numbers and base chromosome numbers for Korean non-Commelinids monocots were obtained from the Chromosome Counts Database (CCDB, version 1.45; <http://ccdb.tau.ac.il/Angiosperms/>, accessed on 2018 May 22) (Rice et al., 2015) following APG IV classification system (Angiosperm Phylogeny Group IV) (Appendix 1) (The Angiosperm Phylogeny Group, 2016). Due to the scarcity of available data on chromosome numbers and ploidy levels variation in Korean Commelinids including Arecales, Commelinales, Poales, and Zingiberales (The Angiosperm Phylogeny Group, 2016), these were excluded from the current analyses.

The systematic ranking of taxa adopted in this study was mainly based on the recent online resources for monocot plants (<http://e-monocot.org/>), the World Checklist of Selected Plant Families (<http://wcp.science.kew.org>), the Missouri Botanical Garden Tropicos Database (<http://www.tropicos.org/>), and the nomenclature was adopted from the most accepted taxonomic treatment for the species based on the Korean Plant Names Index Committee (<http://www.nature.go.kr/kpni/index.do>) (Appendix 1).

The genome size values and ploidy level inferences in Korean non-Commelinids monocots were retrieved from the Plant DNA C-values database (<http://www.kew.org/cvalues/>, accessed on 2018 May 22) (Bennett and Leitch, 2012). The

data on number and chromosomal localization of rDNA loci (5S and 35S rDNA) in Korean non-Commelinids monocots obtained applying fluorescent *in situ* hybridization were retrieved from the third release of the plant rDNA database (Vitales et al., 2017; <http://www.plantrdnadatabase.com/>, accessed on 2018 May 22).

Chromosome numbers are reported for 252 taxa (232 species, 2 subspecies, and 18 varieties) of Korean monocots, with the exception of Commelinids, due to the scarcity of published chromosome numbers for this very speciose group (Appendix 1). Base chromosome numbers and ploidy levels variation is given for each taxon in Appendix 1. The chromosome numbers reported for Korean non-Commelinids monocots vary between $2n = 2x = 10$ in *Paris verticillata* M. Bieb. and $2n = 40x = 400$ in *Dioscorea japonica* Thunb. (Appendix 1). To date, the documented chromosome numbers in angiosperms vary from $2n = 4$ (e.g., *Ornithogalum tenuifolium* Delarochae in Hyacinthaceae) to $2n = 640$ (*Sedum suaveolens* Kimmach in Crassulaceae), although most species possess between $2n = 14$ and $2n = 40$ chromosomes (Guerra, 2008; Weiss-Schneeweiss and Schneeweiss, 2013). The base chromosome numbers of analyzed Korean species vary from $x = 5$ in the genus *Paris* L. to $x = 30$ in the genus *Hosta* Tratt. (Appendix 1). Not only interspecific base chromosome number variation is found in thirteen genera analyzed here (*Acorus* L., *Arisaema* Mart., *Alisma* L., *Hydrocharis* L., *Potamogeton* L., *Lycoris* Herb., *Asparagus* Tourn. ex L., *Polygonatum* Mill., *Scilla* L., *Iris* Tourn. ex L., *Cephalanthera* Rich., *Gastrodia* R. Br., *Fritillaria* Tourn. ex L.) (Appendix 1) but also intraspecific base chromosome number variation is found within several species ($x = 9, 11, 12$ in *Acorus calmus* L.; $x = 13, 14$ in *Arisaema amurense* Maxim.; $x = 13, 14$ in *Arisaema peninsulae* Nakai; $x = 13, 14$ in most of taxa in the genus *Potamogeton* L.; $x = 9, 10$ in *Polygonatum falcatum* A. Gray; $x = 10, 11$ in *Polygonatum humile* Fisch. ex Maxim.; $x = 9, 10, 11$ in *Polygonatum involucreatum* (Franch. & Sav.) Maxim.; $x = 8, 9$ in *Scilla scilloides* (Lindl.) Druce) (Appendix 1). The incidence of both interspecific ($x = 5, 6, 7$ in *Lotus*/Fabaceae: Grant, 1991; $x = 9, 10, 11, 12, 13, 14$ in *Melampodium*/Asteraceae: Blösch et al., 2009; $x = 3, 4, 5, 6$ in *Crepis*/Asteraceae: Babcock and Jenkins, 1943) and intraspecific base chromosome number variation ($x = 5, 6, 7$: *Prospero autumnale* complex: Jang et al., 2013; $x = 8, 9$: *Scilla scilloides* complex: Choi et al., 2008) have quite frequently been reported in angiosperms (Husband et al., 2003). Due to very low levels of phenotypic variation and thus lack of diagnostic morphological characters for species delimitations in some

taxonomically intricate plant groups (often treated as species complexes), more detailed karyological investigations of the chromosome number variations and karyotype structure are needed for correct interpretation of taxonomic and evolutionary patterns as well as classifications of angiosperms in general, but also specifically of monocot species native in Korea in global world-wide context.

Two general types of polyploids can be distinguished, autopolyploids and allopolyploids. Allopolyploids originate via hybridization of at least two different taxa, thus carrying different multiplied sets of chromosomes, while autopolyploids result from multiplication of entire chromosome sets within one taxon, typically species. Thus, both hybridization and polyploidization may play an important role in creating new species diversity in angiosperms (Guerra, 2008; Soltis and Soltis, 2009; Husband et al., 2013; Weiss-Schneeweiss and Schneeweiss, 2013). In this study, the incidence of polyploidy has frequently been reported in Araceae Juss., Hydrocharitaceae Juss., Juncaginaceae Rich., Amaryllidaceae J. St.-Hil., Asparagaceae Juss., Dioscoreaceae R. Br., Liliaceae Juss., Melanthiaceae Batsch ex Borkh., Smilacaceae Vent. (Appendix 1). Analyses of ploidy levels distribution among these groups indicated that diploids (ca. 44%) and tetraploids (ca. 14%) prevail, with triploids (ca. 6%), pentaploids (ca. 2%), and hexaploids (ca. 4%) being found less frequently (Fig. 1, Appendix 1). Polyploidy is less frequent in Orchidaceae than in other families of Korean non-Commelinids monocots (Appendix 1), in agreement with previous reports for this region (Goldblatt, 1980; Ko et al., 2009; Rice et al., 2015, references therein). Despite the relatively high incidence of polyploidy in Korean non-Commelinids monocot flora and ease of inferring more recent polyploidy events based purely on increase of chromosome numbers, the clear inference of the mode of polyploids origin and inferences of the patterns of their post-polyploidization genome evolution are non-trivial and thus are not attempted here. These require rigorous phylogenetic analyses of the genera harboring polyploids to infer putative parental species and subsequent molecular cytogenetic analyses as well as genome size measurements to infer the patterns of their genome evolution. Such data are available only for a handful of selected monocot taxa (Appendix 1) and thus, more in-depth and group-oriented molecular cytological analyses are required to assist and guide species delimitation and interpretation of phylogenetic relationships and evolutionary patterns among Korean monocots (Choi et al., 2008; Jang et al., 2013; Jang and Weiss-Schneeweiss, 2015).

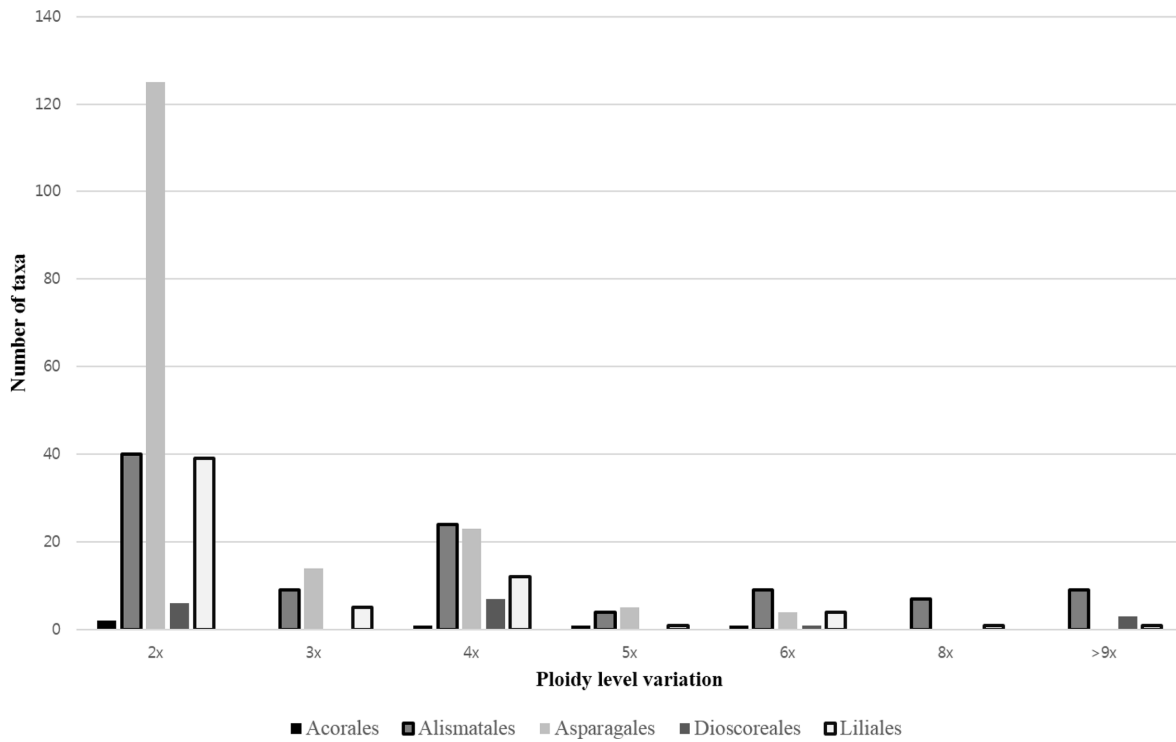


Fig. 1. Distribution of ploidy level variation containing two to eight ploidy levels in non-Commelinids monocot species occurring in Korea (representing their worldwide distribution).

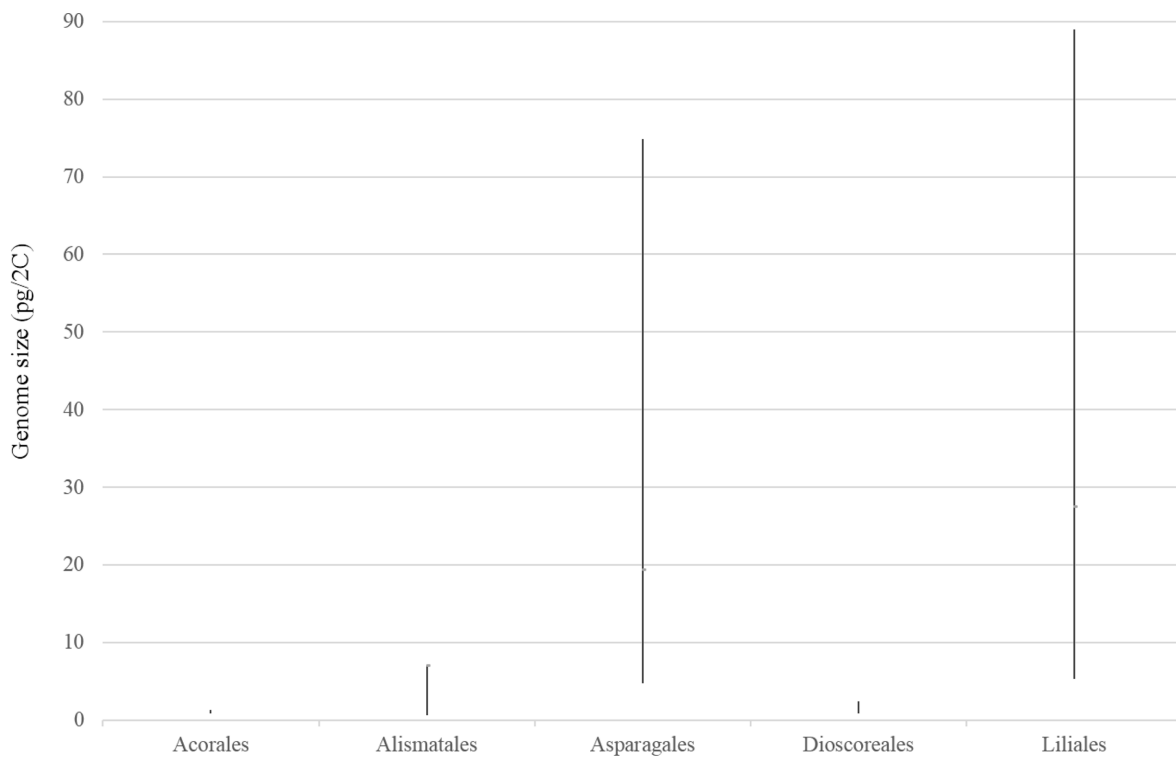


Fig. 2. Distribution of genome size variation in non-Commelinids monocot species occurring in Korea (representing their worldwide distribution).

Genome size variation in non-commelinids monocots species native to Korea (in worldwide context)

The dynamics of genome size variation in a group of related diploid taxa can be very high despite lack of change in chromosome number. Genome size increase is, however, directly correlated to polyploidization, particularly recent one. Genome size changes in the absence of chromosome number changes are attributed to differential accumulation of various types of repetitive DNA elements (Leitch and Leitch, 2013). The range of genome sizes of Korean monocots falls within that reported in the Plant DNA C-values database which ranges from 0.061 pg/1C of DNA in *Genlisea tuberosa* Rivadavia, Gonella & A. Fleischm. (Fleischmann et al., 2014) to 152.33 pg/1C of DNA in *Paris japonica* Franch. (Pellicer et al., 2010). The 1C-values of species studied here differ nearly 150-fold and range from 0.3 pg in *Spirodela polyrrhiza* (L.) Schleid. (Araceae) to 44.5 pg in *Trillium kamschaticum* Pall. ex Pursh (Melanthiaceae) (Fig. 2, Appendix 1). In general, the broad range of variation of genome sizes in flowering plants correlates with the differences of total karyotype length and incidence of polyploidy, but also correlates with other factors, like the life cycle types (annual/perennial) (Bennett, 1972; Chumová et al., 2015).

Patterns of genome evolution: the use of molecular cytogenetics and phylogenetic analyses in Plant Systematics

Extensive studies of chromosome numbers (including polyploidy incidence) and genome sizes in evolutionary context, aiming to elucidate the genome dynamics and often aiding taxonomic classifications have often been carried out in plants of agricultural importance or in model plants (Gong et al., 2012; Renny-Byfield et al., 2013; Novák et al., 2014; Zhang et al., 2014). However, recent advances in the advent of NGS technologies that enable large amounts of DNA sequence data to be generated in a single sequencing run at low cost, wild plants groups are now also amenable for in-depth genomic analyses. Such studies often address the evolution of polyploid complexes and focus on genome evolution in comparative context (e.g., polyploid and its lower-ploidy parental taxa) (Table 1) (Novák et al., 2010; Dodsworth et al., 2015; Weiss-Schneeweiss et al., 2015; McCann et al., 2018). These approaches allow for rapid identification of numerous types of DNA repeats providing new chromosomal markers that can be used in molecular cytological analyses applying *in situ* hybridization (fluorescence and genomic *in situ* hybridization;

FISH and GISH, respectively) and thus, contributing to better understanding of the evolution of plant genomes (Table 1) (Renny-Byfield et al., 2010; Emadzade et al., 2014; Novák et al., 2014; Zhang et al., 2014; Jang and Weiss-Schneeweiss, 2015). Repetitive DNA fraction of plant genomes is composed of tandem repeats encompassing satellite DNAs, microsatellites and rDNAs (5S and 35S ribosomal RNA genes) as well as dispersed repeats represented by mobile genetic elements, known also as transposable elements. The latter comprise class I retroelements and class II DNA transposons (Weiss-Schneeweiss et al., 2015). In-depth analyses of repeatomes have recently been demonstrated to be informative for inferences of phylogenetic relationships in plants (Table 1) (Dodsworth et al., 2015, 2017; McCann et al., 2018).

Molecular cytogenetic mapping of the nuclear ribosomal RNA genes encoding for 35S (18S-5.8S-25S) and 5S rDNAs have proved useful for identifying the patterns and dynamics of chromosomal changes in closely related species groups (Jang et al., 2013, 2016a; Vitales et al., 2017). The distribution of rDNA loci has been reported for some Korean monocots, as summarized in Table 1 (data retrieved from Plant rDNA Database; <http://www.plantrdnadatabase.com/>, 2018 May 22). The number and localization of rDNA loci in diploids and polyploids was intensively studied in selected genera of Alismatales (Wan et al., 2012), Asparagales (Hizume, 1994; Hizume and Araki, 1994; Lee et al., 1999; Do et al., 1999, 2001; Remon-Büttner et al., 1999; Kim et al., 2004; Hayashi et al., 2005; Lim et al., 2007; Deng et al., 2012; Son et al., 2012), and Liliales (Sultana et al., 2010). A survey of rDNA loci numbers reported for Korean monocots indicated that rDNA loci number can vary at the interspecific level in the genera *Allium*, *Lilium*, and *Potamogeton* (between 2 and 6) (Table 1) regardless of chromosome number and ploidy level variation between species, as show for many other plant groups (Table 1, Appendix 1). The rDNA loci number variation within species or among closely related taxa have often been shown to be correlated with geographic and/or populational factors (e.g., Jang et al., 2016a). Thus, the localization of rDNA loci analyzed in comparative context aids not only the analyses of chromosomal structural changes, but when interpreted in phylogenetic context (e.g., Jang et al., 2013, 2016b), it also allows broader conclusions with implications for taxonomy. Monocot genomes are often more dynamically evolving than those of the dicots. Thus, further cytogenetic analyses of selected groups of Korean monocots will be undertaken to shed light into their genome evolution and evolutionary relationships. Such analyses should and will certainly include also populations and relatives from other geographical areas to allow for more robust conclusions to be drawn.

Table 1. Summary of the chromosome numbers, ploidy level variation, and numbers of 5S and 35S rDNA signals in non-Commelinids monocot species occurring in Korea (representing their worldwide distribution)

Taxon	2n	Ploidy levels	5S rDNA	35S rDNA	References
Alismatales R. Br. ex Bercht. & J. Presl					
<i>Potamogeton crispus</i> L.	48	4x	2	2	Wan et al. (2012)
	52	4x	2	2	Wan et al. (2012)
<i>P. distinctus</i> A. Benn.	52	4x	2	2	Wan et al. (2012)
<i>P. malaianus</i> Miq.	52	4x	2	4	Wan et al. (2012)
<i>P. natans</i> L.	52	4x	4	6	Wan et al. (2012)
<i>P. octandrus</i> Poir.	28	2x	2	2	Wan et al. (2012)
<i>P. perfoliatus</i> L.	50	4x	2	4	Wan et al. (2012)
	52	4x	2	2	Wan et al. (2012)
Asparagales Link					
<i>Allium cepa</i> L.	16	2x	4	2	Hizume (1994)
	16	2x	2	2	Do et al. (2001)
	16	2x	4	4	Do et al. (2001)
<i>A. fistulosum</i> L.	16	2x	2	1	Hizume (1994)
	16	2x	2	-	Son et al. (2012)
	16	2x	2	-	Lee et al. (1999)
<i>A. sativum</i> L.	16	2x	2	2	Son et al. (2012)
	16	2x	6	2	Lee et al. (1999)
<i>A. senescens</i> L.	16	2x	2	2	Lee et al. (1999)
	32	4x	6	2	Lee et al. (1999)
<i>A. tuberosum</i> Rottler ex Spreng.	30	4x	8	3	Do et al. (1999)
	32	4x	8	4	Do et al. (1999)
<i>Lycoris radiata</i> (L'Hér.) Herb.	33	3x	4	6	Hayashi et al. (2005)
<i>Anemarrhena asphodeloides</i> Bunge	22	2x	2	4	Kim et al. (2004)
<i>Asparagus officinalis</i> L.	20	2x	2	6	Remon-Büttner et al. (1999)
	20	2x	8	6	Deng et al. (2012)
<i>Scilla scilloides</i> (Lindl.) Druce	16	2x	-	2	Hizume and Araki (1994)
	18	2x	-	2	Hizume and Araki (1994)
	27	3x	-	2	Hizume and Araki (1994)
	34	4x	-	4	Hizume and Araki (1994)
<i>Iris setosa</i> Pall. ex Link	38	2x	4	6	Lim et al. (2007)
Liliales Perleb					
<i>Lilium amabile</i> Palib.	24	2x	2	6	Sultana et al. (2010)
<i>L. callosum</i> Siebold & Zucc.	24	2x	2	10	Sultana et al. (2010)
<i>L. cernuum</i> Kom.	24	2x	2	10	Sultana et al. (2010)
<i>L. concolor</i> Salisb.	24	2x	2	10	Sultana et al. (2010)
<i>L. dauricum</i> K. Gawl.	24	2x	2	8	Sultana et al. (2010)
<i>L. distichum</i> Nakai ex Kamib.	24	2x	2	8	Sultana et al. (2010)
<i>L. hansonii</i> Leichtlin ex D. D. T. Moore	24	2x	2	15	Sultana et al. (2010)
<i>L. lancifolium</i> Thunb.	24	2x	2	10	Sultana et al. (2010)
<i>L. lancifolium</i> Thunb.	36	3x	3	15	Sultana et al. (2010)
<i>L. tsingtauense</i> Gilg	24	2x	2	8	Sultana et al. (2010)
<i>L. tsingtauense</i> Gilg	24	2x	2	8	Sultana et al. (2010)

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Conflict of Interest

The authors declare that there are no conflicts of interest.

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Appendix 1. Information on base chromosome number, ploidy level (if known), and genome size data with emphasis on non-Commelinids monocot species occurring in Korea (representing their worldwide distribution)

Order/Family/Genus/Species	Chromosome number (2n)	Base chromosome number (x)	Ploidy levels	2C-value (pg)	Korean name
Acorales Mart.					
Acoraceae Martinov					
<i>Acorus calamus</i> L.	18, 24, 36, 44, 45, 48, 66	x = 9, 11, 12	2x, 4x, 5x, 6x	1.3	창포
<i>A. gramineus</i> Aiton	18, 22, 24	x = 9, 11, 12	2x	0.8	석창포
Alismatales R. Br. ex Bercht. & J. Presl					
Araceae Juss.					
<i>Arisaema amurense</i> Maxim.	26, 28, 39, 48, 52, 56, 70	x = 13, 14	2x, 3x, 4x, 5x	-	등근잎천남성
<i>A. heterophyllum</i> Blume	28, 56, 84, 140, 168	x = 13, 14	2x, 4x, 10x, 12x	-	두루미천남성
<i>A. negishii</i> Makino	28	x = 14	2x	-	섬천남성
<i>A. peninsulae</i> Nakai	26, 28	x = 13, 14	2x	-	점박이천남성
<i>A. ringens</i> (Thunb.) Schott	28	x = 14	2x	-	큰천남성
<i>A. thunbergii</i> Blume	28	x = 14	2x	-	무늬천남성
<i>Calla palustris</i> L.	36, 60, 72	x = 18	2x, 3x, 4x	2.1	산부채
<i>Lemna perpusilla</i> Torr.	20, 40, 50, 60, 70, 72, 84	x = 10	2x, 4x, 5x, 6x, 7x, 8x	0.8	좁개구리밥
<i>Pinellia ternata</i> (Thunb.) Breitenb.	26, 42, 54, 72, 78, 90, 91, 99, 104, 108, 115, 117	x = 13	2x, 3x, 4x, 5x, 6x, 7x, 8x, 9x	7.0	반하
<i>P. tripartita</i> (Blume) Schott	26, 52	x = 13	2x, 4x	-	대반하
<i>Spirodela polyrrhiza</i> (L.) Schleid.	30, 32, 38, 40, 50, 80	Unknown	Unknown	0.6	개구리밥
<i>Symplocarpus nipponicus</i> Makino	30	x = 15	2x	-	에기얇은부채
<i>S. renifolius</i> Schott ex Tzvelev	60	x = 15	4x	-	얇은부채
Tofieldiaceae Takht.					
<i>Tofieldia coccinea</i> Richardson	30, 32	x = 15, 16	2x	-	속은돌창포
Alismataceae Vent.					
<i>Alisma canaliculatum</i> A. Braun & C. D. Bouché	26, 28, 40, 42	x = 13, 14	2x, 3x	-	택사
<i>A. plantago-aquatica</i> subsp. <i>orientale</i> (Sam.) Sam.	14, 28	x = 7	2x, 4x	-	질경이택사
<i>Sagittaria aginashii</i> Makino	22	x = 11	2x	-	보풀
<i>S. natans</i> Pall.	22	x = 11	2x	-	대택소귀나물
<i>S. pygmaea</i> Miq.	22	x = 11	2x	-	올미
<i>S. trifolia</i> L.	22	x = 11	2x	-	벗풀
Hydrocharitaceae Juss.					
<i>Blyxa aubertii</i> Rich.	24, 32, 40	x = 8, 12	2x, 4x, 5x	-	올챙이자리
<i>B. japonica</i> (Miq.) Maxim. ex Asch. & Gürke	72	x = 12	6x	-	올챙이술
<i>Hydrilla verticillata</i> (L.) Royle	16, 24, 32	x = 8	2x, 3x, 4x	-	검정말
<i>Najas graminea</i> Delile	12, 24, 36, 48, 72	x = 6	2x, 4x, 6x, 8x, 12x	-	나자스말
<i>N. marina</i> L.	12, 24, 48, 60	x = 6	2x, 4x, 8x, 10x	-	민나자스말

Appendix 1. Continued.

Order/Family/Genus/Species	Chromosome number (2n)	Base chromosome number (x)	Ploidy levels	2C-value (pg)	Korean name
<i>N. minor</i> All.	12, 24, 36, 46, 56	x = 6	2x, 4x, 6x, 8x, 9x	-	톱니나자스말
<i>Vallisneria natans</i> (Lour.) H. Hara	20	x = 10	2x	-	나사말
Scheuchzeriaceae F. Rudolphi					
<i>Scheuchzeria palustris</i> L.	22	x = 11	2x	-	장지채
Juncaginaceae Rich.					
<i>Hydrocharis dubia</i> (Blume) Backer	16, 22	x = 8, 11	2x	-	자라풀
<i>Ottelia alismoides</i> (L.) Pers.	22, 44, 66, 88	x = 11	2x, 4x, 6x, 8x	-	물질경이
<i>Triglochin maritima</i> L.	12, 24, 36, 48, 96, 120	x = 6	2x, 4x, 6x, 8x, 16x, 20x	-	지채
<i>T. palustre</i> L.	24, 36	x = 6	2x, 6x	-	물지채
Zosteraceae Dumort.					
<i>Zostera asiatica</i> Miki	12	x = 6	2x	-	왕거머리말
<i>Z. marina</i> L.	12	x = 6	2x	1.2	거머리말
<i>Z. nana</i> Roth	12	x = 6	2x	1.5	애기거머리말
<i>Phyllospadix iwatensis</i> Makino	16, 20	x = 8, 10	2x	-	새우말
Potamogetonaceae Bercht. & J. Presl					
<i>Potamogeton bertholdii</i> Fieber	26	x = 13	2x	-	실말
<i>P. crispus</i> L.	48, 52, 56	x = 13, 14	3x, 4x	1.0	말즘
<i>P. cristatus</i> Regel & Maack	28	x = 14	2x	-	가는가래
<i>P. distinctus</i> A. Benn.	52	x = 13	4x	-	가래
<i>P. fryeri</i> A. Benn.	42, 48	x = 13, 14	3x	-	선가래
<i>P. maackianus</i> A. Benn.	52, 56	x = 13, 14	4x	-	새우가래
<i>P. malaianus</i> Miq.	26, 52	x = 13	2x, 4x	-	대가래
<i>P. natans</i> L.	42, 52, 195	x = 13	3x, 4x, 15x	-	대동가래
<i>P. octandrus</i> Poir.	28	x = 14	2x	-	애기가래
<i>P. oxyphyllus</i> Miq.	26, 28	x = 13, 14	2x	-	말
<i>P. pectinatus</i> L.	42, 78	x = 13	4x, 6x	-	솔잎가래
<i>P. perfoliatus</i> L.	50, 52, 78	x = 13	4x, 6x	-	넓은잎말
<i>Ruppia maritima</i> L.	20, 40	x = 10	2x, 4x	--	줄말
<i>R. rostellata</i> Koch	40	x = 10	4x	-	나사줄말
<i>Zamichellia palustris</i> subsp. <i>pedicellata</i> (Wahlenb. & Rosén) Hook.	24, 36	x = 12	2x, 3x	-	빨말
Dioscoreales Mart.					
Nartheciaceae Fr. ex Bjurzon					
<i>Aletris glabra</i> Bureau & Franch.	52	x = 13	4x	-	여우꼬리풀
<i>A. spicata</i> (Thunb.) Franch.	26, 52	x = 13	2x, 4x	-	취꼬리풀
<i>Metanartheceum luteoviride</i> Maxim.	52	x = 13	4x	-	칠보치마

Appendix 1. Continued.

Order/Family/Genus/Species	Chromosome number (2n)	Base chromosome number (x)	Ploidy levels	2C-value (pg)	Korean name
Dioscoreaceae R. Br.					
<i>Dioscorea batatas</i> Decne.	140	x = 10	14x	-	마
<i>D. bulbifera</i> L.	40, 60, 80	x = 10	2x, 4x, 6x	2.4	등근마
<i>D. japonica</i> Thunb.	100, 400	x = 10	10x, 40x	-	참마
<i>D. nipponica</i> Makino	20, 40	x = 10	2x, 4x	-	부채마
<i>D. septemloba</i> Thunb.	20, 40	x = 10	2x, 4x	-	국화마
<i>D. tenuipes</i> Franch. & Sav.	20, 40	x = 10	2x, 4x	-	각시마
<i>D. tokoro</i> Makino ex Miyabe	20	x = 10	2x	0.8	도꼬로마
Liliales Perleb					
Melanthiaceae Batsch ex Borkh.					
<i>Chionographis japonica</i> (Willd.) Maxim.	24, 42	x = 12	2x, 4x	-	실꽃풀
<i>Heloniopsis orientalis</i> (Thunb.) Tanaka	34	x = 17	2x	5.3	처녀치마
<i>Paris verticillata</i> M. Bieb.	10, 15, 20	x = 5	2x, 3x, 4x	-	삿갓나물
<i>Trillium kamschaticum</i> Pall. ex Pursh	10, 30	x = 5	2x, 6x	89.0	연영초
<i>T. tschonoskii</i> Maxim.	10, 20	x = 5	2x, 4x	-	큰연영초
<i>Veratrum bohnhoffii</i> var. <i>latifolium</i> Nakai	16, 32	x = 8	2x, 4x	-	삼수여로
<i>V. dolichopetalum</i> O. Loes.	32	x = 8	4x	-	푸른박새
<i>V. maackii</i> Regel	16	x = 8	2x	-	긴잎여로
<i>V. maackii</i> var. <i>parviflorum</i> (Maxim.) H. Hara	16, 32	x = 8	2x, 4x	-	파란여로
<i>V. nigrum</i> var. <i>ussuriense</i> Lose. f.	16	x = 8	2x	-	참여로
<i>V. oxyspalum</i> Turcz.	32, 64, 80	x = 8	4x, 8x, 10x	-	박새
<i>V. versicolor</i> Nakai	16	x = 8	2x	-	흰여로
<i>Zygadenus sibiricus</i> (L.) A. Gray	32	x = 8	4x	-	나도여로
Colchiaceae DC.					
<i>Disporum sessile</i> (Thunb.) D. Don ex Schult. & Schult.	16, 24	x = 8	2x, 3x	37.2	윤관나물
<i>D. smilacinum</i> A. Gray	16	x = 8	2x	-	애기나리
<i>D. viridescens</i> (Maxim.) Nakai	16, 17	x = 8	2x	-	큰애기나리
Smilacaceae Vent.					
<i>Smilax china</i> L.	32, 64, 96	x = 16	2x, 4x, 6x	-	청미래덩굴
<i>S. nipponica</i> Miq.	32	x = 16	2x	-	선밀나물
<i>S. riparia</i> var. <i>ussuriensis</i> (Regel) Hara & T. Koyama	32	x = 16	2x	-	밀나물
<i>S. sieboldii</i> Miq.	32	x = 16	2x	-	청가시덩굴
Liliaceae Juss.					
<i>Clintonia udensis</i> Trautv. & C. A. Mey.	14, 28, 38	x = 7	2x, 4x, 5x	-	나도옥잠화
<i>Erythronium japonicum</i> (Balrer) Decne.	24	x = 12	2x	-	얼레지
<i>Fritillaria usuriensis</i> Maxim.	22, 24	x = 11, 12	2x	-	패모

Appendix 1. Continued.

Order/Family/Genus/Species	Chromosome number (2n)	Base chromosome number (x)	Ploidy levels	2C-value (pg)	Korean name
<i>Gagea lutea</i> (L.) K. Gawl.	36, 48, 72, 96, 132	x = 16, 18	2x, 3x, 4x, 6x, 8x	39.5	중의무릇
<i>Lilium amabile</i> Palib.	24	x = 12	2x	27.4	털중나리
<i>L. callosum</i> Siebold & Zucc.	24	x = 12	2x	-	땅나리
<i>L. cernuum</i> Kom.	24	x = 12	2x	-	솔나리
<i>L. concolor</i> Salisb.	24	x = 12	2x	-	하늘나리
<i>L. dauricum</i> K. Gawl.	24	x = 12	2x	-	날개하늘나리
<i>L. distichum</i> Nakai ex Kamib.	24	x = 12	2x	-	말나리
<i>L. hansonii</i> Leichtlin ex D. D. T. Moore	24	x = 12	2x	-	섬말나리
<i>L. lancifolium</i> Thunb.	24, 36	x = 12	2x, 3x	-	참나리
<i>L. leichtlinii</i> var. <i>maximowiczii</i> (Regel) Baker	26	x = 12	2x	-	중나리
<i>L. tenuifolium</i> Fisch.	24	x = 12	2x	-	큰솔나리
<i>L. tsingtauense</i> Gilg	24	x = 12	2x	-	하늘말나리
<i>Lloydia serotina</i> (L.) Rchb.	24	x = 12	2x	-	개감채
<i>L. triflora</i> (Ledeb.) Baker	24	x = 12	2x	-	나도개감채
<i>Streptopus amplexifolius</i> (L.) DC.	16, 32	x = 8	2x, 4x	13.0	죽대아재비
<i>S. koreanus</i> (Kom.) Ohwi	24, 48	x = 8	3x, 6x	-	왕죽대아재비
<i>S. ovalis</i> (Ohwi) F. T. Wang & Y. C. Tang	16	x = 8	2x	-	진부애기나리
<i>Tricyrtis macropoda</i> Miq.	26	x = 13	2x	8.5	빼꼭나리
<i>Tulipa edulis</i> (Miq.) Baker	24	x = 12	2x	-	산자고
<i>T. heterophylla</i> (Regel) Baker	24	x = 12	2x	37.5	금대산자고
Asparagales Link					
Orchidaceae Juss.					
<i>Amitostigma gracile</i> (Blume) Schltr.	42	x = 21	2x	-	병아리난초
<i>Bletilla striata</i> (Thunb.) Rchb.	32, 76	x = 16, 19	2x, 4x	5.9	자란
<i>Bulbophyllum drymoglossum</i> Maxim.	40	x = 20	2x	-	콩짜개난
<i>B. inconspicuum</i> Maxim.	38	x = 19	2x	-	흑난초
<i>Calanthe discolor</i> Lindl.	40	x = 20	2x	-	새우난초
<i>C. reflexa</i> Maxim.	40	x = 20	2x	-	여름새우난
<i>C. striata</i> R. Br. ex Lindl.	40	x = 20	2x	-	금새우난
<i>Calypso bulbosa</i> (L.) Oakes	28	x = 14	2x	-	풍선난초
<i>Cephalanthera erecta</i> (Thunb.) Blume	34	x = 17	2x	-	은난초
<i>C. falcata</i> (Thunb.) Blume	34	x = 17	2x	-	금난초
<i>C. longibracteata</i> Blume	32	x = 16	2x	-	은대난초
<i>Coeloglossum viride</i> var. <i>bracteatum</i> (Willd.) Rich.	40	x = 20	2x	-	개재비난
<i>Corallorhiza trifida</i> Châtel.	42	x = 21	2x	-	산호란

Appendix 1. Continued.

Order/Family/Genus/Species	Chromosome number (2n)	Base chromosome number (x)	Ploidy levels	2C-value (pg)	Korean name
<i>Cremastra appendiculata</i> (D. Don) Makino	48	x = 24	2x	-	약난초
<i>C. unguiculata</i> (Finet) Finet	48	x = 24	2x	-	두잎약난초
<i>Cymbidium goeringii</i> (Rchb.) Rchb.	40	x = 20	2x	-	보춘화
<i>C. kanran</i> Makino	40	x = 20	2x	-	한란
<i>C. macrorhizon</i> Lindl.	38	x = 19	2x	-	대홍란
<i>Cypripedium calceolus</i> L.	20	x = 10	2x	64.7	노랑복주머니란
<i>C. guttatum</i> var. <i>koreanum</i> Nakai	20	x = 10	2x	-	털복주머니란
<i>C. japonicum</i> Thunb.	20	x = 10	2x	64.0	광릉요강꽃
<i>C. macranthos</i> Sw.	20, 21, 22	x = 10	2x	74.8	복주머니란
<i>Dendrobium moniliforme</i> (L.) Sw.	38, 57	x = 19	2x, 3x	-	석곡
<i>Epipactis papillosa</i> Franch. & Sav.	40	x = 20	2x	-	청닭의난초
<i>E. thunbergii</i> A. Gray	40	x = 20	2x	-	닭의난초
<i>Epipogium aphyllum</i> Sw.	68	x = 17	4x	-	유령란
<i>Galeola septentrionalis</i> Rchb.	28	x = 14	2x	-	으름난초
<i>Gastrodia elata</i> Blume	36	x = 18	2x	-	천마
<i>Goodyera macrantha</i> Maxim.	30	x = 15	2x	-	붉은사철란
<i>G. maximowicziana</i> Makino	28, 56	x = 14	2x, 4x	-	섬사철란
<i>G. repens</i> (L.) R. Br.	30	x = 15	2x	9.7	애기사철란
<i>G. schlechtendaliana</i> Rchb.	30	x = 15	2x	-	사철란
<i>G. velutina</i> Maxim. ex Regel	30	x = 15	2x	-	털사철란
<i>Gymnadenia conopsea</i> (L.) R. Br.	40, 80, 100	x = 20	2x, 4x, 5x	11.0	손바닥난초
<i>Habenaria flagellifera</i> Makino	42, 46, 88	x = 21, 22, 23	2x, 4x	-	방울난초
<i>H. linearifolia</i> Maxim.	28	x = 14	2x	-	잠자리난초
<i>H. radiata</i> (Thunb.) Spreng.	32, 64	x = 16	2x, 4x	-	해오라비난초
<i>Herminium lanceum</i> var. <i>longicrure</i> (C. Wright) H. Hara	38, 76	x = 19	2x, 4x	-	씨눈난초
<i>H. monorchis</i> (L.) R. Br.	38, 40	x = 19, 20	2x	-	나도씨눈난
<i>Hetaeria sikokiana</i> (Makino & F. Maek.) Tuyama	42	x = 21	2x	-	애기천마
<i>Lecanorchis japonica</i> Blume	36	x = 18	2x	-	무엽란
<i>Liparis japonica</i> (Miq.) Maxim.	30	x = 15	2x	-	키다리난초
<i>L. koreana</i> (Nakai) Nakai	30	x = 15	2x	-	참나리난초
<i>L. krameri</i> Franch. & Sav.	30	x = 15	2x	-	나나별이난초
<i>L. kumokiri</i> F. Maek.	26, 30	x = 13, 15	2x	-	옥잠난초
<i>L. makinoana</i> Schltr.	30	x = 15	2x	-	나리난초
<i>Listera nipponica</i> Makino	38	x = 19	2x	-	털쌍잎난초
<i>L. pinetorum</i> Lindl.	40	x = 20	2x	-	쌍잎난초
<i>Microstylis monophyllos</i> (L.) Lindl.	30	x = 15	2x	-	이삭단엽란

Appendix 1. Continued.

Order/Family/Genus/Species	Chromosome number (2n)	Base chromosome number (x)	Ploidy levels	2C-value (pg)	Korean name
<i>Myrmechis japonica</i> (Rchb.) Rolfe	56	x = 14	4x	-	개미난초
<i>Neofinetia falcata</i> (Thunb.) Hu	38	x = 19	2x	4.7	풍란
<i>Neottia acuminata</i> Schltr.	18	x = 9	2x	-	애기무엽란
<i>N. nidus-avis</i> var. <i>manshurica</i> Kom.	36	x = 9	4x	-	새둥지란
<i>Oberonia japonica</i> (Maxim.) Makino	30	x = 15	2x	-	차걸이난
<i>Orchis cyclochila</i> (Franch. & Sav.) Maxim.	42	x = 21	2x	-	나도제비란
<i>O. graminifolia</i> (Rchb.) Tang & F. T. Wang	42	x = 21	2x	-	나비난초
<i>O. jooiokiana</i> Makino	42	x = 21	2x	-	너도제비난
<i>Oreorchis patens</i> (Lindl.) Lindl.	48	x = 24	2x	-	감자난
<i>Platanthera hologlottis</i> Maxim.	42	x = 21	2x	-	흰제비난
<i>P. japonica</i> (Thunb.) Lindl.	42	x = 21	2x	-	갈매기난초
<i>P. mandarinorum</i> Rchb.	42	x = 21	2x	-	산제비난
<i>P. minor</i> (Miq.) Rchb.	42	x = 21	2x	-	한라잠자리난
<i>P. ophrydioides</i> F. Schmidt	42	x = 21	2x	-	구름제비난
<i>P. sachalinensis</i> F. Schmidt	42	x = 21	2x	-	큰제비난
<i>Pogonia japonica</i> Rchb.	20	x = 10	2x	-	큰방울새난
<i>P. minor</i> (Makino) Makino	18	x = 9	2x	-	방울새난
<i>Sedirea japonica</i> (Rchb. f.) Garay & Sweet	38	x = 19	2x	-	나도풍란
<i>Spiranthes sinensis</i> (Pers.) Ames	30	x = 15	2x	-	타래난초
<i>Taeniophyllum glandulosum</i> Blume	38	x = 19	2x	-	거미난
<i>Tipularia ussuriensis</i> (Regel) H. Hara	42	x = 21	2x	-	나도잠자리난
<i>Vexillabium yakushimense</i> (Yamam.) F. Maek.	26	x = 13	2x	-	백운란
Iridaceae Juss.					
<i>Belamcanda chinensis</i> (L.) DC.	32	x = 16	2x	-	범부채
<i>Iris dichotoma</i> Pall.	34	x = 17	2x	-	대청부채
<i>I. ensata</i> var. <i>spontanea</i> (Makino) Nakai	24	x = 12	2x	-	꽃창포
<i>I. koreana</i> Nakai	50	x = 25	2x	-	노랑붓꽃
<i>I. lactea</i> var. <i>chinensis</i> (Fisch.) Koidz.	32, 40	x = 16, 20	2x	-	타래붓꽃
<i>I. laevigata</i> Fisch.	28, 32, 34	x = 14, 16, 17	2x	-	제비붓꽃
<i>I. minutoaurea</i> Makino	22	x = 11	2x	-	금붓꽃
<i>I. rossii</i> Baker	32	x = 16	2x	-	각시붓꽃
<i>I. ruthenica</i> K. Gawl.	32, 40, 84	x = 16, 20, 21	2x, 4x	-	솔붓꽃
<i>I. sanguinea</i> Donn ex Hornem.	26, 28	x = 13, 14	2x	-	붓꽃
<i>I. setosa</i> Pall. ex Link	40	x = 20	2x	-	부채붓꽃
<i>I. uniflora</i> var. <i>caricina</i> Kitag.	42	x = 21	2x	-	난장이붓꽃

Appendix 1. Continued.

Order/Family/Genus/Species	Chromosome number (2n)	Base chromosome number (x)	Ploidy levels	2C-value (pg)	Korean name
Asphodelaceae Juss.					
<i>Hemerocallis dumortieri</i> E. Morren	22	x = 11	2x	-	각시원추리
<i>H. fulva</i> (L.) L.	22, 33	x = 11	2x, 3x	-	원추리
<i>H. lilioasphodelus</i> L.	22	x = 11	2x	-	골잎원추리
<i>H. littorea</i> Makino	22	x = 11	2x	-	홍도원추리
<i>H. middendorffii</i> Trautv. & C. A. Mey.	22	x = 11	2x	-	큰원추리
<i>H. minor</i> Mill.	22	x = 11	2x	-	애기원추리
<i>H. thunbergii</i> Barr	22	x = 11	2x	-	노랑원추리
Amaryllidaceae J. St.-Hil.					
<i>Allium condensatum</i> Turcz.	16	x = 8	2x	-	노랑부추
<i>A. longistylum</i> Baker	16	x = 8	2x	-	강부추
<i>A. linearifolium</i> H. J. Choi & B. U. Oh	16	x = 8	2x	-	선부추
<i>A. macrostemon</i> Bunge	32, 40, 48	x = 8	4x, 5x, 6x	43.2	산달래
<i>A. maximowiczii</i> Regel	16	x = 8	2x	-	산파
<i>A. microdictyon</i> Prokh.	16	x = 8	2x	-	산마늘
<i>A. monanthum</i> Maxim.	16, 24, 32	x = 8	2x, 3x, 4x	-	달래
<i>A. ochotense</i> Prokh.	16, 32	x = 8	2x, 4x	-	울릉산마늘
<i>A. sacculiferum</i> Maxim.	16, 32, 42	x = 8	2x, 4x, 5x	-	참산부추
<i>A. senescens</i> L.	16, 32	x = 8	2x, 4x	-	두메부추
<i>A. taquetii</i> H. Lév. & Vaniot	16	x = 8	2x	-	한라부추
<i>A. thunbergii</i> G. Don	16, 32	x = 8	2x, 4x	-	산부추
<i>A. thunbergii</i> var. <i>deltoides</i> (S.Yu, W. Lee & S. Lee) H. J. Choi & B. U. Oh	16	x = 8	2x	-	세모산부추
<i>A. thunbergii</i> var. <i>teretifolium</i> H. J. Choi & B. U. Oh	16	x = 8	2x	-	둥근산부추
<i>Crinum asiaticum</i> var. <i>japonicum</i> Baker	22	x = 11	2x	-	문주란
<i>Lycoris albiflora</i> Koidz.	17, 18, 19	x = 9	2x	-	환상사화
<i>L. radiata</i> (L'Hér.) Herb.	33	x = 11	3x	-	석산
<i>L. sanguinea</i> var. <i>koreana</i> (Nakai) T. Koyama	21, 22, 33, 45	x = 11	2x, 3x, 4x	-	백양꽃
Asparagaceae Juss.					
<i>Anemarrhena asphodeloides</i> Bunge	22	x = 11	2x	5.7	지모
<i>Asparagus cochinchinensis</i> (Lour.) Merr.	20	x = 10	2x	-	천문동
<i>A. oligoclonos</i> Maxim.	20, 40	x = 10	2x, 4x	-	방울비짜루
<i>A. schoberioides</i> Kunth	20, 40	x = 10	2x, 4x	-	비짜루
<i>Convallaria keiskei</i> Miq.	38	x = 19	2x	-	은방울꽃
<i>Hosta capitata</i> (Koidz.) Nakai	60	x = 30	2x, 3x	19.3	일월비비추
<i>H. clausa</i> Nakai	60, 90, 96	x = 30	2x, 3x	28.5	참비비추

Appendix 1. Continued.

Order/Family/Genus/Species	Chromosome number (2n)	Base chromosome number (x)	Ploidy levels	2C-value (pg)	Korean name
<i>H. clausa</i> var. <i>normalis</i> F. Maek.	48, 60, 90	x = 30	2x, 3x	19.3	주걱비비추
<i>H. longipes</i> (Franch. & Sav.) Matsum.	60	x = 30	2x	26.3	비비추
<i>H. longissima</i> F. Maek.	60	x = 30	2x	19.3	산옥잠화
<i>H. minor</i> (Baker) Nakai	60	x = 30	2x	-	좁비비추
<i>Liriope platyphylla</i> F. T. Wang & T. Tang	36, 72, 108, 112	x = 18	2x, 4x, 6x	21.1	맥문동
<i>L. spicata</i> Lour.	36, 72, 108	x = 18	2x, 4x, 6x	25.6	개맥문동
<i>Maianthemum bifolium</i> (L.) F. W. Schmidt	36, 54	x = 18	2x, 3x	30.6	두루미꽃
<i>M. dilatatum</i> (A. Wood) A. Nelson & J. F. Macbr.	36, 54	x = 18	2x, 3x	33.4	큰두루미꽃
<i>Ophiopogon jaburan</i> (Siebold) Lodd.	36	x = 18	2x	-	맥문아재비
<i>O. japonicus</i> (Thunb.) K. Gawl.	36, 67, 68, 70, 72	x = 18	2x, 4x	21.6	소엽맥문동
<i>Polygonatum falcatum</i> A. Gray	18, 20	x = 9, 10	2x	-	진황정
<i>P. humile</i> Fisch. ex Maxim.	20, 22, 30	x = 10, 11	2x, 3x	-	각시등굴레
<i>P. inflatum</i> Kom.	22	x = 11	2x	-	통등굴레
<i>P. involucratum</i> (Franch. & Sav.) Maxim.	18, 20, 22	x = 9, 10, 11	2x	-	용등굴레
<i>P. lasianthum</i> Maxim.	20	x = 10	2x	-	죽대
<i>P. odoratum</i> var. <i>pluriflorum</i> (Miq.) Ohwi	20, 30	x = 10	2x, 3x	-	등굴레
<i>P. stenophyllum</i> Maxim.	20, 24, 30	x = 10, 12	2x, 3x	-	층층등굴레
<i>Scilla scilloides</i> (Lindl.) Druce	16, 18, 26, 27, 34, 36, 38, 44, 53, 70	x = 8, 9	2x, 3x, 4x, 5x, 6x	-	무릇
<i>Smilacina dahurica</i> Turcz. ex Fisch. & C. A. Mey.	36	x = 18	2x	-	민숨대
<i>S. japonica</i> A. Gary	36	x = 18	2x	-	풀숨대
<i>S. trifolium</i> (L.) Desf.	36	x = 18	2x	22.2	세잎숨대

The table is arranged alphabetically by order, family, and genus recognized by APG IV classification system (The Angiosperm Phylogeny Group, 2016).

Note: All chromosome number information was taken from Rice et al. (2015).