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Exploration of Candidate Korean Native Poaceae Plants for Breeding New Varieties as Garden Materials in the New Climate Regime

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Abstract: There are increasing needs for models of public garden with low-maintenance, and environmental stress to plant due to climate change is growing. Therefore, the demand for developing new plant varieties based on native plants as garden materials against climate change has increased fairly. Many plants in the family Poaceae are applied for various purposes such as food crops, fodder grasses, ornamental plants, or medical plants. Also, native plants have some economic and ecological benefits, and the utilization of native plants is positive in a garden. However, there are some difficulties in Poaceae breeding researches and utilization of wild native plants for breeding. To overcome these problems, model plants can be utilized in breeding researches of Poaceae plant species. In this study, to explore the possibility of utilizing Korean native Poaceae plants as model plants and for breeding new cultivars, the candidate species were selected from the Korean Plant Names Index (KPNI). A total of 3 Korean native plants in the family Poaceae including *Brachypodium sylvaticum*, *Setaria viridis*, and *Zoysia japonica* were selected, and their properties and their genome information were compared with the representative model plants, *Arabidopsis thaliana* and *Brachypodium distachyon*. The modern research status of *B. sylvaticum*, *S. viridis* and *Z. japonica* has been summarized, and the genome size, life cycle, and other characteristics of these model plants have been compared and discussed. Application of these newly selected candidate plants in breeding research would build a foundation for breeding of native Poaceae plants in Korea against the new climate regime.

Keywords: garden plants; model plants; molecular breeding; native plants; Poaceae; ornamental plants

1. Introduction

Role of gardens is expanding for biodiversity conservation as rapid urban expansion, and there are increasing needs for models of public garden with low-maintenance [1,2]. Native plants can be used as garden materials for effective maintenance, because they are good materials for gardens, restoration, and erosion control [3,4]. Recently, environmental stress to plant due to climate change is growing, and to cope with its brunt, plant breeding is valuable [5,6]. Therefore, the demand for developing new plant varieties based on native plants as garden materials against climate change has increased fairly.

Many plants in the family Poaceae are applied as food crops, fodder grasses, ornamental plants, or medical plants [7]. Souza et al. [8] described the capability of native Poaceae plants for usage as garden materials. Moreover, Dunster [9] insisted that Poaceae must be used for not solely for ornamental but multi-functions in the age of climate change. However, some plant species in the family Poaceae are polyploid or have large and complicated genomes which make difficulties for breeding researches [10]. To overcome this problem, model plants, which have a lot of advantages such as short lifecycle and small genome size [11,12], can be utilized in breeding researches of Poaceae plant species.

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Model plants are extensively researched in plant science or agriculture [11,13]. *Arabidopsis thaliana* has been widely applied as a model plant from 1980s [14]. However, *Arabidopsis* is a dicotyledon in the family Brassicaceae, which is not advisable in some areas as a model plant of principal plants in the family Poaceae [15,16]. *Brachypodium distachyon*, which is distributed in the Mediterranean region, has been broadly investigated from the late 2000s by researchers and breeders on cereal crops notably wheat and barley which are valuable crops in the tribe Triticeae [17]. However, *B. distachyon* is not native in Korea so that it is not suitable to utilize as garden materials in Korea.

B. sylvaticum and *Setaria viridis* have been lately proposed as model plants in the family Poaceae [18]. *B. sylvaticum* can be utilized as a model plant for perennial grasses [19]. *S. viridis* has a potentiality to be applied as a model plant for C_4 photosynthesis exploration [20]. Both *B. sylvaticum* and *S. viridis* are native in Korea so that they are suitable to utilize as not only model plants but also garden materials in Korea.

Zoysia japonica, which is perennial C_4 grass, is the most popular warm-season turfgrass in Korea [21,22]. The reference genome of *Z. japonica* and *Z. matrella* was assembled and available [23]. Also, transgenic *Z. japonica* accessions were obtained by genetic transformation method [24]. Therefore, *Z. japonica* has not referred as a model plant yet, but it seems that *Z. japonica* can also be used as a model plant for perennial C_4 plants as well as a garden material.

In this study, to explore the possibility of utilizing Korean native Poaceae plants as model plants and for breeding new cultivars, the candidate species were selected from the Korean Plant Names Index (KPNI). The modern research status of *B. sylvaticum*, *S. viridis* and *Z. japonica* has been summarized, and the genome size, life cycle, and other characteristics of these model plants have been compared.

2. Materials and Methods

The list of the Poaceae plant species was download from the KPNI (http://www.nature.go.kr/kpni/). The scientific names of all plant were modified to delete information about authority, subspecies, or variety with leaving only the genus name and the species name. In the 'Classification' column, only 'Species' was selected while 'Variety', 'Subspecies', 'Horticultural cultivar', and 'Cultivar' were unchecked so that the list was filtered (Supplementary Table S1). From the Published Plant Genomes (https://www.plabipd.de/), the plants in which the reference genome was assembled were investigated. Based on the cladogram of the flowering plant menu, the list of the Poaceae plants in which the reference genome was assembled was created, and their genome size were investigated (Supplementary Table S2). Finally, the Poaceae plants in which the reference genome was assembled were selected from the list of the Poaceae plants registered in the KPNI, and the characteristics including life cycle, and photosynthetic type were investigated (Table 1). The life cycles of the selected plants were investigated from the Korean Biodiversity Information System (http://www.nature.go.kr/) and the USDA PLANTS Database (https://plants.usda.gov/). The photosynthetic types of the selected plants were investigated from the previous researches.

Table 1. Characteristics of 38 plant species in the family Poaceae selected from the KPNI.

Plant category	Subfamily	Scientific name	Genome size (Mbps)	Life cycle^z	Photosynthetic Type
Native	Arundinoideae	*Phragmites australis*	1,200	P	C_3 [72]
Native	Chloridoideae	*Leptochloa chinensis*	460	A	C_4 [73]
Native	Chloridoideae	*Eleusine indica*	590	A	C_4 [74]

Native	Chloridoideae	*Cynodon dactylon*	1,020	P	C_4 [75]
Native	Chloridoideae	*Zoysia japonica*	390	P	C_4 [75]
Native	Oryzoideae	*Zizania latifolia*	1,800	P	C_3 [73]
Native	Panicoideae	*Setaria viridis*	400	A	C_4 [76]
Native	Panicoideae	*Echinochloa oryzoides*	1,000	A	C_4 [77]
Native	Panicoideae	*Microstegium vimineum*	1,300	A	C_4 [78]
Native	Panicoideae	*Echinochloa crus-galli*	1,400	A	C_4 [77]
Native	Panicoideae	*Themeda triandra*	840	P	C_4 [79]
Native	Panicoideae	*Miscanthus sinensis*	2,500	P	C_4 [73]
Native	Pooideae	*Poa annua*	1,800	A	C_3 [76]
Native	Pooideae	*Brachypodium sylvaticum*	360	P	C_3 [80]
Cultivated	Bambusoideae	*Phyllostachys edulis*	2,080	P	C_3 [81]
Cultivated	Chloridoideae	*Zoysia matrella*	380	P	C_4 [82]
Cultivated	Chloridoideae	*Zoysia pacifica*	370	P	C_4 [82]
Cultivated	Oryzoideae	*Oryza sativa*	430	A	C_3 [76]
Cultivated	Panicoideae	*Panicum miliaceum*	920	A	C_4 [76]
Cultivated	Panicoideae	*Sorghum bicolor*	820	A	C_4 [76]
Cultivated	Panicoideae	*Coix lacryma-jobi*	1,560	A	C_4 [76]
Cultivated	Panicoideae	*Zea mays*	2,300	A	C_4 [76]
Cultivated	Panicoideae	*Setaria italica*	490	A	C_4 [76]
Cultivated	Pooideae	*Avena sativa*	4,000	A	C_3 [76]
Cultivated	Pooideae	*Triticum aestivum*	17,000	A	C_3 [76]
Cultivated	Pooideae	*Hordeum vulgare*	5,100	A	C_3 [76]
Exotic	Chloridoideae	*Eragrostis curvula*	660	P	C_4 [83]
Exotic	Panicoideae	*Saccharum spontaneum*	3,360	P	C_4 [76]
Exotic	Panicoideae	*Paspalum notatum*	550	P	C_4 [76]
Exotic	Panicoideae	*Eremochloa ophiuroides*	800	P	C_4 [76]
Exotic	Panicoideae	*Panicum virgatum*	1,200	P	C_4 [76]
Exotic	Pooideae	*Lolium rigidum*	2,400	A	C_3 [76]
Exotic	Pooideae	*Poa pratensis*	3,500	P	C_3 [76]
Exotic	Pooideae	*Alopecurus myosuroides*	3,500	A	C_3 [84]
Exotic	Pooideae	*Lolium multiflorum*	600	A	C_3 [76]

Exotic	Pooideae	*Poa trivialis*	1,350	P	C_3 [76]
Exotic	Pooideae	*Bromus tectorum*	2,500	A	C_3 [76]
Exotic	Pooideae	*Lolium perenne*	2,000	P	C_3 [76]

z P: perennial; A: annual.

Small genome size is one of criteria for model plants [11]. The genome sizes of *Brachypodium distachyon*, which is the model plant for monocots but not native in Korea, and rice (*Oryza sativa*), which is the representatively cultivated crop but not native in Korea, are 270 Mbps and 430 Mbps, respectively. In this point, the Korean native plant species with genome size smaller than that of rice (*O. sativa*) were selected for candidate model plants. The current research states of the candidate model species were investigated. The candidate model plants were compared with the representative model plants, *Arabidopsis thaliana* and *Brachypodium distachyon*, and the properties of these plant were analyzed (Table 2). Also, based on the Phytozome 13 (https://phytozome-next.jgi.doe.gov/), the genomes of the 2 representative model plants and the 2 newly suggested model plants were summarized (Table 3). For each plant species, two versions of genomes were selected and compared. Because it had no genome information in the Phytozome 13, it was hard to analyze *Zoysia japonica* directly with the other 4 plants. Therefore, based on other researches [23,25], the genome of *Zoysia japonica* was analyzed separately with those of other species in the genus *Zoysia* such as *Z. matrella* and *Z. pacifica* which are cultivated plants in Korea (Table 4).

Table 2. Basic information about the 2 representative model plants and the 3 candidate model plants.

	Arabidopsis thaliana	***Brachypodium distachyon***	***Brachypodium sylvaticum***	***Setaria viridis***	***Zoysia japonica***
Common name	mouseear cress	purple false brome	slender false brome	green bristlegrass	Korean lawngrass
Cotyledon	Eudicots	Monocots	Monocots	Monocots	Monocots
Order	Brassicales	Poales	Poales	Poales	Poales
Family	Brassicaceae	Poaceae	Poaceae	Poaceae	Poaceae
Tribe	Camelineae	Brachypodieae	Brachypodieae	Paniceae	Zoysieae
Genus	*Arabidopsis*	*Brachypodium*	*Brachypodium*	*Setaria*	*Zoysia*
Life cycle	Annual	Annual	Perennial	Annual	Perennial
Photosynthetic type	C_3	C_3	C_3	C_4	C_4
Chromosome number	2n = 2x = 10	2n = 2x = 10	2n = 2x = 18	2n = 2x = 18	2n = 4x = 40
Native in Korea	Y	N	Y	Y	Y

Table 3. Comparison of the reference genomes data of the 4 model plants from the Phytozome 13.

	Arabidopsis thaliana		***Brachypodium distachyon***		***Brachypodium sylvaticum***		***Setaria viridis***	
Genome version	**TAIR10**	**Araport11**	**v2.1**	v3.2	v1.1	v2.1	v2.1	v4.1
Source	TAIR	TAIR	JGI	JGI	JGI	JGI	JGI	JGI
Accession	Col-0	Col-0	Bd21	Bd21	Ain-1	Ain-1	A10.1	A10
Assembled genome size	119,667,750	119,667,750	271,997,306	271,163,419	358,283,154	360,731,464	395,731,502	397,277,387
No. of contigs	169	169	485	34	1,117	14	75	39

Protein-coding transcripts	35,386	48,456	42,868	56,847	50,263	54,423	52,459	50,526
Protein-coding genes	27,416	27,655	31,694	32,439	36,927	31,643	38,334	29,807
Reference publication	Lamesch et al. [85]	Cheng et al. [86]			Lei et al. [50]		Mamidi et al. [56]	

Table 4. Comparison of the reference genomes data of *Zoysia* species.

	Zoysia japonica		***Zoysia matrella***	***Zoysia pacifica***
Accession	Yaji	Nagirizaki	Wakaba	Zanpa
Estimated genome size	421 Mbps	390 Mbps	380 Mbps	370 Mbps
Genome version	unknown	ZJN_r1.1	ZMW_r1.0	ZPZ_r1.0
Source	unreleased	Zoysia Genome Database	Zoysia Genome Database	Zoysia Genome Database
Number of sequences	1,350	11,786	13,609	11,428
Total length	373,429,196	334,384,427	563,438,595	397,009,957
Average length	276,614	28,371	41,402	34,740
Max. length	17,601,860	8,501,895	1,041,506	1,506,652
Min. length	unknown	500	500	500
N50 length	3,962,554	2,370,062	108,897	111,449
Number of predicted genes	50,140	59,271	95,079	65,252
Reference publication	Yang et al. [25]	Tanaka et al. [23]	Tanaka et al. [23]	Tanaka et al. [23]

3. Results

Of the 494 Poaceae plants registered in the KPNI, the 352 plants were registered as species (Supplementary Table S1), and finally the 38 plants of them were analyzed in this study (Table 1). The number of the Korean native plants were 14, and the number of both the cultivated plants and the exotic plants were 12, respectively. The number of the plants with the genome sizes less than 1 Gbps was 16. The number of the annual plants was 20 whereas the number of the perennial plants was 18. The number of the C_3 plants was 16 whereas the number of the C_4 plants was 22. The plants, whose genome sizes were less than the genome size of rice (*O. sativa*), were selected, and a total of 5 plants were selected. Of them, the 3 plants (*Brachypodium sylvaticum*, *Setaria viridis*, and *Zoysia japonica*) were native plants in Korea, whereas the 2 plants (*Z. matrella* and *Z. pacifica*) were cultivated plants in Korea.

The 3 Korean native plants were selected as the candidate model plants, and the properties of them and the 2 representative model plants (*Arabidopsis thaliana* and *Brachypodium distachyon*) were analyzed (Table 2). *A. thaliana* was eudicots in the family Brassicaceae whereas the others were monocots in the family Poaceae. *A. thaliana*, *B. distachyon*, and *S. viridis* were annual but *B. sylvaticum* and *Z. japonica* were perennial. *A. thaliana*, *B. distachyon*, and *B. sylvaticum* were C_3 plants whereas *S. viridis* and *Z. japonica* were C_4 plants. Both *A. thaliana* and *B. distachyon* were diploids with 10 chromosomes, but both *B. sylvaticum* and *S. viridis* were diploids with 18 chromosomes. Also, *Z.*

japonica was a tetraploid with 40 chromosomes. Except for *B. distachyon*, the others were native plants in Korea.

The Information of the genomes of the 4 plants (*A. thaliana*, *B. distachyon*, *B. sylvaticum*, and *S. viridis*) was obtained from the Phytozome 13 and their reference publications (Table 3). Within the same species, assembled genome sizes sometimes varied depending on the genome version but were approximately same. The genome size of *A. thaliana* was the smallest, followed by *B. distachyon*, *B. sylvaticum*, and *S. viridis*. Compared to *A. thaliana* and *S. viridis*, *B. distachyon* and *B. sylvaticum* showed relatively high differences in the number of contigs between the genome versions. No constant trend was found in the protein-coding transcripts and the protein-coding genes.

The genome of *Z. japonica* was analyzed based on other researches (Table 4). There were large differences of the genomes of *Z. japonica* between Yang et al. [25] and Tanaka et al. [23]. Yang et al. [25] used the PacBio long-read sequencing so that their average length and maximum length were longer than those of Tanaka et al. [23]. Also, Tanaka et al. [23] estimated the genome sizes of *Z. japonica*, *Z. matrella*, and *Z. pacifica* by flow cytometry as 390 Mbps, 380 Mbps, and 370 Mbps, respectively. The obtained genome sizes of *Z. matrella* and *Z. pacifica* were larger than the estimated genome sizes, but the obtained genome size of *Z. japonica* was smaller than the estimated genome size.

4. Discussion

Plants in the family Poaceae can be utilized for various uses [7]. However, most plant breeders focus on cereal crops such as rice, wheat, and maize, and only few researchers perform a breeding program for ornamental purposes [26]. Ornamental grasses in the family Poaceae are utilized in garden formation for landscaping, and gardens are economically important in climate change acclimatization and extenuation [27,28]. Also, native plants have some economic and ecological benefits, and the utilization of native plants is positive in a garden [29,30].

Nowadays, breeders can use genomic resources such as reference genomes for molecular breeding of crop improvement [31]. A lot of species persists uncharted even though thousands of genomes have been explored [32]. Due to the recent technological development, various sequencing methods have developed and their cost have been cheaper than before [33]. However, assembly of the reference genome is still a costly, energy demanding, and protracted task [34]. Furthermore, due to insufficient information, there are difficulties in utilization of wild plants for breeding [35]. Information obtained from model plants can be hypothesized to the target species of breeding, making the researcher easy to conduct research on studies of those plant species [36]. Therefore, building a foundation through researches using model plants may play an important role in the breeding of wild native plants which have not yet been explored.

In this study, to explore the possibility of utilizing Korean native plants in the family Poaceae for breeding new cultivars and as model plants and garden materials, the candidate species were explored from the KPNI. A total of 3 Korean native plants in the family Poaceae including *Brachypodium sylvaticum*, *Setaria viridis*, and *Zoysia japonica* were selected, and their properties and their genome information were compared with the representative model plants, *Arabidopsis thaliana* and *Brachypodium distachyon*.

Brachypodium distachyon was first suggested as a model plant for cereals and forage grasses at 2001 [37]. *B. distachyon* is an annual C_3 grass and distributed in the Mediterranean region (Figure 1A). In Japan, a country geographically close to Korea, *B. distachyon* was first discovered from the Shimizu Port in 1953, and it is classified as a naturalized plant [38,39]. In Korea, *B. distachyon* has been used in researches since the late 2000s [40,41]. However, the discovery of *B. distachyon* in the wilds of Korea has not been reported for over a decade. According to the Köppen-Geiger classification system, *B. distachyon* distributes on Bsh, Csa, Csb/Bsk, and Cfa/Cfb regions [42]. Also, most parts of Japan belong to Cfa [43], so that *B. distachyon* can survive in Japan. However, most of the Korean Peninsula shows Dwa climate, and Cfa is mainly observed in some southern regions including Wando and Jeju [44,45]. Actually, in some island regions of the southern part of the Korean Peninsula mainly Jeju Island, there are some plants not distributed in the Korean Peninsula but distributed in China, Japan, and

Taiwan [46]. Therefore, *B. distachyon* would be able to adapt naturally and survive only to some southern regions of Korea, and it is inevitable to artificially cultivate with cost and effort to utilize *B. distachyon* as a garden material in most regions of Korea.

Unlike *B. distachyon*, *B. sylvaticum* is a perennial C_3 grass and native in Korea (Figure 1B). Both *B. sylvaticum* and *B. distachyon* are plants in the genus *Brachypodium* of the subfamily Pooideae so that they are genetically close to each other [47]. Genetically close species can be utilized for breeding with a hybridization and an introgression [48]. The first version of the reference genome of *B. distachyon* was announced at 2010 [49], by comparison, the reference genome of *B. sylvaticum* was recently reported [50]. Steinwand et al. [19] suggested *B. sylvaticum* as a model plant for perennial grasses. Also, according to Kim [51], *B. sylvaticum* was one of potential candidates for ornamental grasses and it was applied from abroad but not in Korea. Therefore, *B. sylvaticum* can be utilized as not only a model plant for perennial C_3 grasses but also a garden material in Korea.

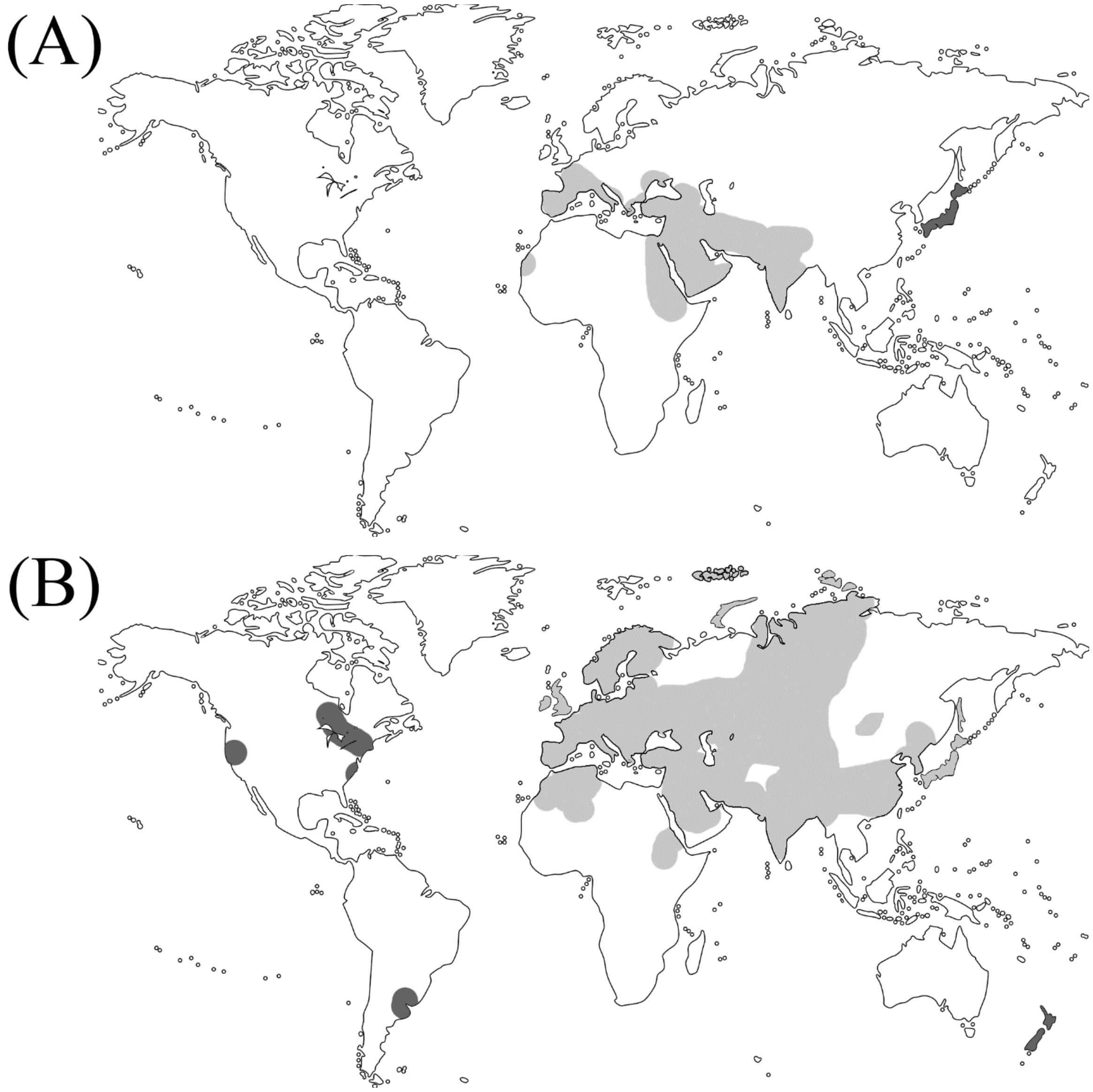

Figure 1. Geographic distributions of *B. distachyon* (A) and *B. sylvaticum* (B). Bright gray indicates native regions, and dark gray indicates introduced regions.

In the genus *Brachypodium* of the subfamily Pooideae, there is no species which is native or cultivated in Korea apart from *B. sylvaticum*. In the subfamily Pooideae, there are many significant C_3 perennial grasses such as bentgrasses (*Agrostis* spp.), bluegrasses (*Poa* spp.), fescues (*Festuca* spp.), and ryegrasses (*Lolium* spp.), applied as turf in temperate zones [52]. Except for annual cereal crops such as wheat, barley, and oat, and their relatives, only few plants for a perennial turf in the subfamily

Pooideae such as *Poa pratensis* and *Lolium perenne* have been studied for the reference genome assembly [53,54]. Therefore, *B. sylvaticum* can be utilized as a model plant for the perennial cool season grasses whose reference genome have not been reported such as bentgrasses (*Agrostis* spp.) and fescues (*Festuca* spp.) in Korea.

S. viridis is an annual C_4 grass in the subfamily Panicoideae, which included many economically valuable C_4 species such as maize, sorghum, and sugarcane [55]. Brutnell et al. [20] suggested *S. viridis* as a model plant for C_4 photosynthesis. The reference genomes of *S. viridis* were first reported at 2020 [56,57]. Therefore, compared to *B. distachyon*, *S. viridis* were received attention relatively later as a model plant. However, *S. viridis* can be transformed with the floral-dip method which has not been reported in *B. distachyon* yet [58]. As a result, *S. viridis* is used for genome editing research such as CRISPR/Cas9 [59]. Additionally, various researches on the C_4 photosynthesis using *S. viridis* as a model plant were conducted [60,61]. Therefore, *S. viridis* is highly valuable to conduct breeding research on the family Poaceae apart from *B. distachyon*.

In the genus *Setaria*, some species were applied as garden materials. *S. italica*, which is cultivated for food or forage in Korea, was planted and analyzed for composition and utilization in garden [62]. Also, according to Frey and Moretti [63], 4 species in the genus *Setaria*, (*S. italica*, *S. pumila*, *S. verticillata*, and *S. viridis*) could be discovered in urban gardens. Additionally, in the subfamily Panicoideae, the genus *Paspalum* and the genus *Axonopus* are applied for lawns [64]. Apart from *S. viridis*, the reference genomes of *S. italica* and *Paspalum notatum* have been reported [65,66], but those of *S. pumila*, *S. verticillata*, and carpet grasses (*Axonopus* spp.) have not been reported yet. Also, *S. viridis* has a smaller genome than *S. italica* [57,67]. Therefore, *S. viridis* can be utilized as a model plant for the annual C_4 grass for garden materials.

Z. japonica is a widely used turfgrass and distributed in East Asia including Korea, Japan, and China [68,69]. The genomes of *Z. japonica* were reported by Tanaka et al. [23] and Yang et al. [25]. However, there were large differences between the two genomes, therefore, further researches should be required to improve an accuracy (Table 4). Also, considering the errors in *Z. japonica*, the estimated genome sizes of the other species, *Z. matrella* and *Z. pacifica*, could be uncertain as well. Therefore, genome assemblies of both *Z. matrella* and *Z. pacifica* using other accessions would be required to estimate more accurate genome sizes of both species. Also, it would be inevitable to artificially cultivate with cost and effort to utilize *Z. matrella* and *Z. pacifica*, which are not native but cultivated in Korea, as garden materials in Korea.

B. distachyon, *B. sylvaticum*, and *S. viridis* were reported as model plants for annual C_3 grasses, perennial C_3 grasses, and annual C_4 grasses, respectively, whereas a model plant for perennial C_4 grasses has not been reported. The genus *Zoysia*, which is consisted of 11 species, is a perennial C_4 grass in the subfamily Chloridoideae and native in the western Pacific Rim and Indian Ocean [69,70]. *Z. japonica*, *Z. matrella*, and *Z. pacifica* have been utilized as turf and ornate grasses [68]. Also, their genome sizes were relatively small [23], so that one species in the genus *Zoysia*, which are perennial C_4 grasses, can be utilized as a model plant for perennial C_4 grasses. However, compared to *B. sylvaticum* and *S. viridis*, plants in the genus *Zoysia* were less studied, probably because they are not native in Europe or America. Additionally, plants in the genus *Zoysia* were allotetraploids but Flavell [71] presented diploid genetics as one of characteristics of model plants. Therefore, *Zoysia* species are suitable as garden materials but can be unsuitable as model plants. For an appearance of a model plant for perennial C_4 grasses, a discovery of a diploid perennial C_4 species with a small genome size would be necessary.

5. Conclusions

In summary, three candidate plants were selected for model plants for breeding garden materials in Korean native Poaceae plants. *Brachypodium sylvaticum* and *Setaria viridis* are used as model plants for perennial C_3 grasses and annual C_4 grasses, respectively, so that they would be also utilized in breeding research for garden materials. *Zoysia japonica* cannot be a model plant for perennial C_4 grasses but it is studied and applied for various horticultural purposes. Application of these newly selected candidate plants in breeding research would build a foundation for breeding of native Poaceae plants in Korea and contribute to garden industry in Korea. Also, further research is required for breeding and utilization of native plants in preparation for the new climate regime.

Supplementary Materials: The following supporting information can be downloaded at the website of this paper posted on Preprints.org.

Author Contributions: For research articles with several authors, a short paragraph specifying their individual contributions must be provided. The following statements should be used "Conceptualization, X.X. and Y.Y.; methodology, X.X.; software, X.X.; validation, X.X., Y.Y. and Z.Z.; formal analysis, X.X.; investigation, X.X.; resources, X.X.; data curation, X.X.; writing—original draft preparation, X.X.; writing—review and editing, X.X.; visualization, X.X.; supervision, X.X.; project administration, X.X.; funding acquisition, Y.Y. All authors have read and agreed to the published version of the manuscript." Please turn to the CRediT taxonomy for the term explanation. Authorship must be limited to those who have contributed substantially to the work reported.

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Data Availability Statement: We encourage all authors of articles published in MDPI journals to share their research data. In this section, please provide details regarding where data supporting reported results can be found, including links to publicly archived datasets analyzed or generated during the study. Where no new data were created, or where data is unavailable due to privacy or ethical restrictions, a statement is still required. Suggested Data Availability Statements are available in section "MDPI Research Data Policies" at https://www.mdpi.com/ethics.

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