

Article



# An Exploration of Candidate Korean Native Poaceae Plants for Breeding New Varieties as Garden Materials in the New Climate Regime Based on Existing Data

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Abstract: There is an increasing demand for low-maintenance public garden models, and environmental stress on plants due to climate change is growing. As a result, the demand for developing new plant varieties based on native species for use in gardens in response to climate change has increased significantly. Many plants in the Poaceae family are applied for various purposes, including food crops, fodder grasses, ornamental plants, and medicinal plants. Additionally, native plants provide economic and ecological benefits, making them advantageous for use in gardens. However, there are some difficulties in Poaceae breeding studies and the utilization of wild native plants for breeding. Model plants can be utilized in breeding studies of Poaceae plant species. In this study, to identify Korean native Poaceae species with the potential for use not only as garden materials but also as model plants for breeding research in response to climate change, candidate species were selected from the Korean Plant Names Index (KPNI). A total of three Korean native plants in the Poaceae family, including Brachypodium sylvaticum, Setaria viridis, and Zoysia japonica, were selected, and their properties and genome information were compared with the existing representative model plants, Arabidopsis thaliana and Brachypodium distachyon. The current research status of B. sylvaticum, S. viridis, and Z. japonica has been summarized, and the genome size and other characteristics of these model plants have been compared and discussed. As a result, both A. thaliana (2n = 2x = 10) and *B. distachyon* (2n = 2x = 10) are annual C<sub>3</sub> plants, but *B. sylvaticum* (2n = 2x = 18) is a perennial  $C_3$  plant, and S. viridis (2n = 2x = 18) is an annual  $C_4$  plant. Thus, B. sylvaticum and S. viridis can be utilized as model plants for perennial C<sub>3</sub> plants and annual C<sub>4</sub> plants, respectively. Z. japonica (2n = 4x = 40) is a perennial C<sub>4</sub> plant, but it can be unsuitable as a model plant because it is an allotetraploid. The application of these newly selected candidate plants in breeding research can build a foundation for breeding native Poaceae plants in Korea in the new climate regime.

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

## 1. Introduction

The role of gardens in biodiversity conservation is expanding due to rapid urban growth, which has increased the need for low-maintenance public garden models [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 on plants 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.

Many plants in the Poaceae family are used as food crops, fodder grasses, ornamental plants, and medicinal plants [7]. Souza et al. [8] described the capability of native Poaceae plants for usage as garden materials. Moreover, Dunster [9] argued that Poaceae should be used not only for ornamental purposes but also for a variety of functions in the age of



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**Copyright:** © 2024 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/). climate change. However, some Poaceae species are polyploid or have large and complex genomes, which pose challenges for breeding studies [10]. To overcome this problem, model plants, which have many advantages, such as short life cycles and small genome sizes [11,12], can be utilized in breeding studies of Poaceae plant species.

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

*B. sylvaticum* and *Setaria viridis* have been recently proposed for use as model plants in the Poaceae family [18]. *B. sylvaticum* can be utilized as a model plant for perennial grasses [19]. *S. viridis* has the potential to be applied as a model plant for C<sub>4</sub> photosynthesis exploration [20]. Both *B. sylvaticum* and *S. viridis* are native to Korea, so they are suitable for use as not only model plants but also garden materials in Korea.

*Zoysia japonica*, which is a 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 using the genetic transformation method [24]. Therefore, *Z. japonica* has not yet been referred to as a model plant, but it seems that it can be used as a model plant for both perennial  $C_4$  plants and garden materials.

In this study, to identify Korean native Poaceae species with the potential to be used not only as garden materials but also as model plants for breeding research on abiotic stress tolerance in response to climate change, candidate species were selected from the Korean Plant Names Index (KPNI) based solely on previous research. The current research status of *B. sylvaticum*, *S. viridis*, and *Z. japonica*, which were finally selected from the KPNI, has been summarized, and their genome size, life cycle, and other characteristics have been compared with those of *A. thaliana* and *B. distachyon*, existing representative model plants, to evaluate their applicability. The main goals of this study are to establish criteria for selecting suitable candidate species for full-scale breeding research without incurring costs from expensive experiments and to review their applicability.

### 2. Materials and Methods

The list of Poaceae plant species was downloaded from the KPNI (http://www.nature. go.kr/kpni/, accessed on 11 July 2024). The scientific names of all plants were modified to remove information about authority, subspecies, or variety, leaving only the genus and species names. Since reference genomes are usually provided on a species basis, in the 'Classification' column, only 'Species' was selected, whereas 'Variety', 'Subspecies', 'Horticultural cultivar', and 'Cultivar' were deselected to filter the list (Supplementary Table S1). Furthermore, plant species with assembled reference genomes were investigated from the Published Plant Genomes database (https://www.plabipd.de/, accessed on 11 July 2024). A list of Poaceae plant species with assembled reference genomes was created based on the flowering plant cladogram, and their genome sizes were examined (Supplementary Table S2). Poaceae plant species with available reference genomes were selected from the KPNI list, and their characteristics, including life cycle and photosynthetic type, were investigated (Table 1). Since securing, cultivating directly, and evaluating all of the selected species take time and labor and is expensive, the analysis was conducted preferentially based on existing data. The life cycles of the selected plant species were investigated by the Korean Biodiversity Information System (http://www.nature.go.kr/, accessed on 12 July 2024) and the USDA PLANTS Database (https://plants.usda.gov/, accessed on 12 July 2024), and they were classified as annual or perennial. The photosynthetic types of the selected plants were investigated from previous studies, and they were classified as C<sub>3</sub> or C<sub>4</sub>.

Plant Category	Subfamily	Scientific Name	Genome Size (Mbps)	Life Cycle <sup>z</sup>	Photosynthetic Type	
Native	Arundinoideae	Phragmites australis	1200	Р	C <sub>3</sub> [25]	
Native	Chloridoideae	Leptochloa chinensis	460	А	C <sub>4</sub> [26]	
Native	Chloridoideae	Eleusine indica	590	А	C <sub>4</sub> [27]	
Native	Chloridoideae	Cynodon dactylon	1020	Р	C <sub>4</sub> [28]	
Native	Chloridoideae	Žoysia japonica	390	Р	C <sub>4</sub> [28]	
Native	Oryzoideae	Zizania latifolia	1800	Р	C <sub>3</sub> [26]	
Native	Panicoideae	Setaria viridis	400	А	C <sub>4</sub> [29]	
Native	Panicoideae	Echinochloa oryzoides	1000	А	C <sub>4</sub> [30]	
Native	Panicoideae	Microstegium vimineum	1300	А	C <sub>4</sub> [31]	
Native	Panicoideae	Echinochloa crus-galli	1400	А	C <sub>4</sub> [30]	
Native	Panicoideae	Themeda triandra	840	Р	C <sub>4</sub> [32]	
Native	Panicoideae	Miscanthus sinensis	2500	Р	C <sub>4</sub> [26]	
Native	Pooideae	Poa annua	1800	А	C <sub>3</sub> [29]	
Native	Pooideae	Brachypodium sylvaticum	360	Р	C <sub>3</sub> [33]	
Cultivated	Bambusoideae	Phyllostachys edulis	2080	Р	C <sub>3</sub> [34]	
Cultivated	Chloridoideae	Žoysia matrella	380	Р	C <sub>4</sub> [35]	
Cultivated	Chloridoideae	Zoysia pacifica	370	Р	C <sub>4</sub> [35]	
Cultivated	Oryzoideae	Oryza sativa	430	А	C <sub>3</sub> [29]	
Cultivated	Panicoideae	Panicum miliaceum	920	А	C <sub>4</sub> [29]	
Cultivated	Panicoideae	Sorghum bicolor	820	А	C <sub>4</sub> [29]	
Cultivated	Panicoideae	Coix lacryma-jobi	1560	А	C <sub>4</sub> [29]	
Cultivated	Panicoideae	Zea mays	2300	А	C <sub>4</sub> [29]	
Cultivated	Panicoideae	Setaria italica	490	А	C <sub>4</sub> [29]	
Cultivated	Pooideae	Avena sativa	4000	А	C <sub>3</sub> [29]	
Cultivated	Pooideae	Triticum aestivum	17,000	А	C <sub>3</sub> [29]	
Cultivated	Pooideae	Hordeum vulgare	5100	А	C <sub>3</sub> [29]	
Exotic	Chloridoideae	Eragrostis curvula	660	Р	C <sub>4</sub> [36]	
Exotic	Panicoideae	Saccharum spontaneum	3360	Р	C <sub>4</sub> [29]	
Exotic	Panicoideae	Paspalum notatum	550	Р	C <sub>4</sub> [29]	
Exotic	Panicoideae	Eremochloa ophiuroides	800	Р	C <sub>4</sub> [29]	
Exotic	Panicoideae	Panicum virgatum	1200	Р	C <sub>4</sub> [29]	
Exotic	Pooideae	Lolium rigidum	2400	А	C <sub>3</sub> [29]	
Exotic	Pooideae	Poa pratensis	3500	Р	C <sub>3</sub> [29]	
Exotic	Pooideae	Alopecurus myosuroides	3500	А	C <sub>3</sub> [37]	
Exotic	Pooideae	Lolium multiflorum	600	А	C <sub>3</sub> [29]	
Exotic	Pooideae	Poa trivialis	1350	Р	C <sub>3</sub> [29]	
Exotic	Pooideae	Bromus tectorum	2500	А	C <sub>3</sub> [29]	
Exotic	Pooideae	Lolium perenne	2000	Р	C <sub>3</sub> [29]	

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

<sup>z</sup> P: perennial; A: annual.

Small genome size is one of the criteria for model plants [11]. The genome sizes of *Brachypodium distachyon*, 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. Rice is one of the major food crops in the world, and many studies have already been conducted. Some researchers have suggested the use of rice as a model plant for monocots due to its relatively small genome size. Thus, if the genome size of a candidate species is larger than rice, the species is not worth being used as a model plant. To add to this point, Korean native plant species with genome sizes smaller than that of rice were selected as 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 plants were compared and analyzed (Table 2). Also, based on Phytozome 13 (https://phytozome-next.jgi.doe.gov/, accessed on 18 July 2024), the genomes of the 2 existing representative model plants species, two versions of genomes were

selected and compared. Because it had no genome information in Phytozome 13, it was hard to analyze *Zoysia japonica* directly with the other 4 plants. Therefore, based on other studies [23,38], the genome of *Zoysia japonica* was analyzed separately from those of other species in the *Zoysia* genus, 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
Örder	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 <sub>3</sub>	C <sub>3</sub>	C <sub>3</sub>	$C_4$	$C_4$
Chromosome number	2n = 2x = 10	2n = 2x = 10	2n = 2x = 18	2n = 2x = 18	2n = 4x = 40
Native in Korea	Y	Ν	Y	Y	Y

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

	Arabidopsis	s thaliana	Brachypodiu	m distachyon	Brachypodiur	n sylvaticum	Setaria vir	idis
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	1117	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 Reference publication	27,416 Lamesch et al. [39]	27,655 Cheng et al. [40]	31,694	32,439	36,927 Lei et al. [41]	31,643	38,334 Mamidi et al. [42]	29,807

Table 4. Comparison of the reference genome data of Zoysia species.

	Zoysi	Zoysia japonica		Zoysia pacifica
Accession Estimated genome size Genome version Source Number of sequences Total length Average length Max. length Min. length NS0 length Number of predicted genes	Yaji' 421 Mbps unknown unreleased 1350 373,429,196 276,614 17,601,860 unknown 3,962,554 50,140	'Nagirizaki' 390 Mbps ZJN_r1.1 Zoysia Genome Database 11,786 334,384,427 28,371 8,501,895 500 2,370,062 59,271	Wakaba' 380 Mbps ZMW_r1.0 Zoysia Genome Database 13,609 563,438,595 41,402 1,041,506 500 108,897 95,079	'Zanpa' 370 Mbps ZPZ_r1.0 Zoysia Genome Database 11,428 397,009,957 34,740 1,506,652 500 1111,449 65,252
Reference publication	Yang et al. [38]	Tanaka et al. [23]	Tanaka et al. [23]	Tanaka et al. [23]

## 3. Results

Of the 494 Poaceae plants listed in the KPNI, 352 were registered as species (Supplementary Table S1), and 38 were selected for analysis in this study (Table 1). The number of Korean native plants was 14, the number of cultivated plants was 12, and the number of exotic plants was 12, respectively. The number of plants with genome sizes less than 1 Gbps was 16. The number of annual plants was 20, whereas the number of perennial plants was 18. The number of the C<sub>3</sub> plants was 16, whereas the number of the C<sub>4</sub> plants was 22. Plants with genome sizes smaller than that of rice (*O. sativa*) were selected, resulting in five species chosen for analysis. Of them, three plants (*Brachypodium sylvaticum, Setaria viridis*, and *Zoysia japonica*) were native to Korea, whereas two plants (*Z. matrella* and *Z. pacifica*) were cultivated in Korea.

Thus, three Korean native plants were selected as the candidate model plants, and their properties and the two representative model plants (*Arabidopsis thaliana* and *Brachypodium distachyon*) were analyzed (Table 2). *A. thaliana* was determined to be eudicots in the Brassicaceae family, whereas the others were monocots in the Poaceae family. *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 on the genomes of the four plants (*A. thaliana, B. distachyon, B. sylvaticum,* and *S. viridis*) was obtained from 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 the 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. As the genome versions were updated, the number of contigs decreased, indicating increased genome completeness through gap-filling. No constant trend was found in either the protein-coding transcripts or the protein-coding genes. As the genome versions were updated, the protein-coding transcripts of *A. thaliana, B. distachyon,* and *B. sylvaticum* increased, whereas those of *S. viridis* decreased. As the genome versions were updated, the protein-coding genes of *A. thaliana* and *B. distachyon* and *B. sylvaticum* increased, whereas those of *S. viridis* decreased. As the genome versions were updated, the protein-coding genes of *A. thaliana* and *B. distachyon* increased, whereas those of *B. sylvaticum* and *S. viridis* decreased.

The genome of *Z. japonica* was analyzed based on other studies (Table 4). There were large differences in the genomes of *Z. japonica* between Yang et al. [38] and Tanaka et al. [23]. Yang et al. [38] used the PacBio long-read sequencing, so the average length and maximum length they found were longer than those found by Tanaka et al. [23]. Also, Tanaka et al. [23] estimated the genome sizes of *Z. japonica*, *Z. matrella*, and *Z. pacifica* using 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, whereas the obtained genome size of *Z. japonica* was smaller than the estimated genome size.

#### 4. Discussion

Plants in the Poaceae family can be utilized in various ways [7]. However, most plant breeders focus on cereal crops such as rice, wheat, and maize, and only a few researchers have performed breeding programs for ornamental purposes [43]. Ornamental grasses in the Poaceae family are utilized in garden design and landscaping; these gardens are economically important in climate change acclimatization and extenuation [44,45]. Also, native plants have some economic and ecological benefits, and the utilization of native plants is advantageous in gardens [46,47]. Thus, although there is a need to study more diverse Korean native Poaceae species for garden plant breeding in response to increasingly severe and frequent abnormal climate damage by climate change, basic breeding studies on wild native plants in Korea are relatively scarce compared to cultivated crops.

Nowadays, breeders can utilize genomic resources such as reference genomes for molecular breeding for crop improvement [48]. Many species persist uncharted even though thousands of genomes have been explored [49]. Due to recent technological developments, various sequencing methods have been developed, and their cost is cheaper than before [50]. However, assembling the reference genome is still a costly, energy-demanding, and protracted task [51]. Furthermore, due to insufficient information, there are difficulties in utilizing wild plants for breeding [52]. Information obtained from model plants can be hypothesized for application to the target species of breeding, making it easier for researchers to conduct studies on those plant species [53]. Thus, building a foundation through research using model plants may play an important role in the breeding of wild native plants, which has not yet been explored. Additionally, if the model plant itself can be used as a garden material, it would be economically beneficial because it could be developed for a cultivar, not only for research purposes but also for practical use as a garden material.

Conducting experiments with actual plants requires significant time and money, and it is not feasible to include all plant species native to Korea. Therefore, it is crucial to select plant species for study using reasonable criteria before starting a full-scale experiment. In this study, to identify some Korean native Poaceae species with the potential to be used not only as garden materials but also as model plants for breeding research on abiotic stress tolerance in response to climate change, candidate species were explored from the KPNI based solely on previous research. A total of three native Korean Poaceae plants, including *Brachypodium sylvaticum, Setaria viridis*, and *Zoysia japonica*, were ultimately selected, and their characteristics and genome information were compared with those of representative model plants *Arabidopsis thaliana* and *Brachypodium distachyon*. Additionally, based on previous studies and existing data, the potential for using these plant species as garden materials in Korea will be discussed.

Brachypodium distachyon was first suggested as a model plant for cereals and forage grasses in 2001 [54]. B. distachyon is an annual  $C_3$  grass and is primarily distributed in the Mediterranean region (Figure 1A). Meanwhile, in Japan, a country geographically close to Korea, B. distachyon was first discovered at the Shimizu Port in 1953, and it is classified as a naturalized plant [55,56]. In Korea, however, although *B. distachyon* has been used in studies since the late 2000s [57,58], the discovery of *B. distachyon* in the wilds of Korea has not yet been reported. According to the Köppen–Geiger climate classification system, B. distachyon mainly distributes in Bsh, Csa, Csb/Bsk, and Cfa/Cfb regions [59]. Also, most parts of Japan belong to the Cfa region [60], so *B. distachyon* can survive there. However, most of the Korean Peninsula is composed of the Dwa climate, and Cfa is mainly observed in some southern regions, including Wando and Jeju [61,62]. Actually, in some island regions of the southern part of the Korean Peninsula, mainly Jeju Island, there are some plant species that are not distributed in the Korean Peninsula but are instead distributed in China, Japan, and Taiwan [63]. Therefore, it is reasonable to judge that B. distachyon would be able to adapt naturally and survive only in some southern regions of Korea, and it is inevitable that it will require significant effort and high costs to artificially cultivate B. distachyon as a garden material in most regions of Korea. For this reason, even though B. distachyon is a model plant for Poaceae plants, it is inefficient to use it for breeding purposes as a garden material in Korea.

Unlike *B. distachyon*, *B. sylvaticum* is a perennial  $C_3$  grass native to Korea (Figure 1B). Both *B. sylvaticum* and *B. distachyon* are plants in the *Brachypodium* genus of the Pooideae subfamily, so they are genetically close to each other [64]. Genetically close species can be utilized for breeding with hybridization and introgression [65]. The first version of the reference genome of *B. distachyon* was announced in 2010 [66]; by comparison, the reference genome of *B. sylvaticum* was recently reported [41]. Steinwand et al. [19] suggested *B. sylvaticum* for use as a model plant for perennial grasses. Also, according to Kim [67], *B. sylvaticum* was one of the potential candidates for ornamental grasses, and it was applied abroad but not in Korea. Therefore, *B. sylvaticum* can be utilized not only as a model plant for perennial  $C_3$  grasses but also as a garden material in Korea.

In the *Brachypodium* genus of the Pooideae subfamily, there is no species that is native or cultivated in Korea apart from *B. sylvaticum*. In the Pooideae subfamily, there are many significant C<sub>3</sub> perennial grasses, such as bentgrasses (*Agrostis* spp.), bluegrasses (*Poa* spp.), fescues (*Festuca* spp.), and ryegrasses (*Lolium* spp.), applied as turf in temperate zones [68]. Except for annual cereal crops such as wheat, barley, and oat, and their relatives, only a few plants for a perennial turf in the Pooideae subfamily, such as *Poa pratensis* and *Lolium perenne*, have been studied for reference genome assembly [69,70]. Therefore, *B. sylvaticum* can be utilized as a model plant for perennial cool-season grasses whose reference genomes have not been reported, such as bentgrasses (*Agrostis* spp.) and fescues (*Festuca* spp.) 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.

*S. viridis* is an annual  $C_4$  grass in the Panicoideae subfamily, which includes many economically valuable  $C_4$  species such as maize, sorghum, and sugarcane [71]. Brutnell et al. [20] suggested the use of *S. viridis* as a model plant for  $C_4$  photosynthesis. The reference genomes of *S. viridis* were first reported in 2020 [42,72]. Therefore, compared to *B. distachyon*, *S. viridis* received attention relatively late as a model plant. However, *S. viridis* can be transformed using the floral-dip method, which has not yet been reported in *B. distachyon* [73]. As a result, *S. viridis* is used for genome editing research, such as CRISPR/Cas9 [74]. Additionally, various studies on  $C_4$  photosynthesis using *S. viridis* as a model plant were conducted [75,76]. Therefore, *S. viridis* is highly valuable for breeding research within the Poaceae family alongside *B. distachyon*.

In the *Setaria* genus, 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 settings [77]. Also, according to Frey and Moretti [78], four species in the *Setaria* genus (*S. italica, S. pumila, S. verticillata,* and *S. viridis*) were discovered in urban gardens. Additionally, in the Panicoideae subfamily, the *Paspalum* genus and the *Axonopus* genus have been applied for lawns [79]. Apart from *S. viridis*, the reference genomes of *S. italica* and *Paspalum notatum* have been reported [80,81], but those of *S. pumila, S. verticillata,* and carpet grasses (*Axonopus* spp.) have not yet been reported. Also, *S. viridis* has a

smaller genome than *S. italica* [72,82]. Therefore, *S. viridis* can be utilized as a model plant for annual  $C_4$  grass for garden materials.

*Z. japonica* is a widely used turfgrass that is distributed in East Asia, including in Korea, Japan, and China [83,84]. 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 studies should be conducted to improve 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. Additionally, utilizing *Z. matrella* and *Z. pacifica* as garden materials in Korea will inevitably require significant cost and effort, as these species are not native but cultivated in the country.

*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 *Zoysia* genus, which consists of 11 species, is a perennial  $C_4$  grass in the Chloridoideae subfamily and is native to the western Pacific Rim and Indian Ocean [84,85]. *Z. japonica, Z. matrella*, and *Z. pacifica* have been utilized as turf and ornate grasses [83]. Also, their genome sizes were relatively small [23], so one species in the *Zoysia* genus, 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 *Zoysia* genus were less studied, probably because they are not native to Europe or America. Additionally, plants in the *Zoysia* genus were allotetraploids, but Flavell [86] presented diploid genetics as one of the characteristics of model plants. Therefore, *Zoysia* species are suitable as garden materials but can be unsuitable as model plants. For the appearance of a model plant for perennial  $C_4$  grasses, the discovery of a diploid perennial  $C_4$  species with a small genome size is necessary.

#### 5. Conclusions

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

**Supplementary Materials:** The following supporting information can be downloaded at https: //www.mdpi.com/article/10.3390/horticulturae10111158/s1. Table S1: The list of 352 species registered as 'species' of the 494 Poaceae plants listed in the Korean Plant Names Index (KPNI); Table S2: The list of Poaceae plant species with assembled reference genomes based on the flowering plant cladogram from the Published Plant Genomes database.

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# References

- 1. Goddard, M.A.; Dougill, A.J.; Benton, T.G. Scaling up from gardens: Biodiversity conservation in urban environments. *Trends Ecol. Evol.* **2010**, *25*, 90–98. [CrossRef]
- 2. Yang, L.; Ye, W. Landscape design of garden plants based on green and low-carbon energy under the background of big data. *Energy Rep.* **2022**, *8*, 13399–13408. [CrossRef]
- Basey, A.C.; Fant, J.B.; Kramer, A.T. Producing native plant materials for restoration: 10 rules to collect and maintain genetic diversity. *Nativ. Plants J.* 2015, 16, 37–53. [CrossRef]
- 4. Kruckeberg, A.R.; Chalker-Scott, L. *Gardening with Native Plants of the Pacific Northwest*, 3rd ed.; University of Washington Press: Seattle, WA, USA, 2019.
- 5. Mareri, L.; Parrotta, L.; Cai, G. Environmental Stress and Plants. Int. J. Mol. Sci. 2022, 23, 5416. [CrossRef]
- 6. Xiong, W.; Reynolds, M.; Xu, Y. Climate change challenges plant breeding. Curr. Opin. Plant Biol. 2022, 70, 102308. [CrossRef]
- Gupta, A.; Ranjan, R. Grasses as an Immense Source of Pharmacologically Active Medicinal Properties: An Overview. Proc. Indian Natl. Sci. Acad. 2020, 86, 1323–1329. [CrossRef]
- 8. Souza, F.H.D.D.; Gusmão, M.R.; Cavallari, M.M.; Barioni, W., Jr. Characterization of the potential of native grasses for use as lawns. *Ornam. Hortic.* 2020, 26, 109–120. [CrossRef]
- 9. Dunster, K. Beyond Turf and Lawn: Poaceae in This Age of Climate Change. In *Grasses-Benefits, Diversities and Functional Roles;* Almusaed, A., Al-Samaraee, S.M.S., Eds.; IntechOpen: London, UK, 2017; pp. 87–118.
- 10. Aitken, K.S.; McNeil, M.D.; Berkman, P.J.; Hermann, S.; Kilian, A.; Bundock, P.C.; Li, J. Comparative mapping in the Poaceae family reveals translocations in the complex polyploid genome of sugarcane. *BMC Plant Biol.* **2014**, *14*, 190. [CrossRef]
- 11. Ray, S.; Satya, P.; Sharma, L.; Roy, S.; Bera, A.; Santra, S.; Ghosh, S. Model Plants in Genomics. In *Plant Genomics for Sustainable Agriculture*; Singh, R.L., Mondal, S., Parihar, A., Singh, P.K., Eds.; Springer Nature: Singapore, 2022; pp. 241–264.
- 12. Gaut, B.S. Evolutionary dynamics of grass genomes. New Phytol. 2002, 154, 15–28. [CrossRef]
- 13. Zhdanov, O.; Blatt, M.R.; Cammarano, A.; Zare-Behtash, H.; Busse, A. A new perspective on mechanical characterisation of *Arabidopsis* stems through vibration tests. *J. Mech. Behav. Biomed. Mater.* **2020**, *112*, 104041. [CrossRef] [PubMed]
- 14. Meinke, D.W.; Cherry, J.M.; Dean, C.; Rounsley, S.D.; Koornneef, M. *Arabidopsis thaliana*: A Model Plant for Genome Analysis. *Science* **1998**, 282, 662–682. [CrossRef]
- 15. Kellogg, E.A. Evolutionary History of the Grasses. Plant Physiol. 2001, 125, 1198–1205. [CrossRef]
- Raissig, M.T.; Woods, D.P. The Wild Grass Brachypodium Distachyon as a Developmental Model System. In *Current Topics in Developmental Biology*; Goldstein, B., Srivastava, M., Eds.; Academic Press: Cambridge, MA, USA, 2022; Chapter Two; Volume 147, pp. 33–71.
- 17. Scholthof, K.-B.G.; Irigoyen, S.; Catalan, P.; Mandadi, K.K. *Brachypodium*: A Monocot Grass Model Genus for Plant Biology. *Plant Cell* **2018**, *30*, 1673–1694. [CrossRef]
- 18. Brutnell, T.P.; Bennetzen, J.L.; Vogel, J.P. *Brachypodium distachyon* and *Setaria viridis*: Model Genetic Systems for the Grasses. *Annu. Rev. Plant Biol.* **2015**, *66*, 465–485. [CrossRef]
- 19. Steinwand, M.A.; Young, H.A.; Bragg, J.N.; Tobias, C.M.; Vogel, J.P. *Brachypodium sylvaticum*, a Model for Perennial Grasses: Transformation and Inbred Line Development. *PLoS ONE* **2013**, *8*, e75180. [CrossRef]
- Brutnell, T.P.; Wang, L.; Swartwood, K.; Goldschmidt, A.; Jackson, D.; Zhu, X.-G.; Kellogg, E.; Van Eck, J. Setaria viridis: A Model for C<sub>4</sub> Photosynthesis. *Plant Cell* 2010, 22, 2537–2544. [CrossRef]
- 21. Cai, H.-w.; Inoue, M.; Yuyama, N.; Takahashi, W.; Hirata, M.; Sasaki, T. Isolation, characterization and mapping of simple sequence repeat markers in zoysiagrass (*Zoysia* spp.). *Theor. Appl. Genet.* **2005**, *112*, 158–166. [CrossRef]
- 22. Sun, H.-J.; Song, I.-J.; Bae, T.-W.; Lee, H.-Y. Recent developments in biotechnological improvement of *Zoysia japonica* Steud. *J. Plant Biotechnol.* **2010**, *37*, 400–407. [CrossRef]
- 23. Tanaka, H.; Hirakawa, H.; Kosugi, S.; Nakayama, S.; Ono, A.; Watanabe, A.; Hashiguchi, M.; Gondo, T.; Ishigaki, G.; Muguerza, M. Sequencing and comparative analyses of the genomes of zoysiagrasses. *DNA Res.* **2016**, *23*, 171–180. [CrossRef]
- 24. Muguerza, M.B.; Gondo, T.; Ishigaki, G.; Shimamoto, Y.; Umami, N.; Nitthaisong, P.; Rahman, M.M.; Akashi, R. Tissue Culture and Somatic Embryogenesis in Warm-Season Grasses—Current Status and Its Applications: A Review. *Plants* **2022**, *11*, 1263. [CrossRef]
- 25. Antonielli, M.; Pasqualini, S.; Batini, P.; Ederli, L.; Massacci, A.; Loreto, F. Physiological and anatomical characterisation of *Phragmites australis* leaves. *Aquat. Bot.* **2002**, *72*, 55–66. [CrossRef]
- 26. Yang, H.; Li, X.; Yu, D.; Liu, G.; Luo, L. Anatomical Characteristics of C<sub>4</sub> and C<sub>3</sub> Photosynthetic-pathway Poaceae Plants in Hainan. *Chin. Bull. Bot.* **2011**, *46*, 456–469. [CrossRef]
- 27. Kobayashi, T.; Okamoto, K.; Hori, Y. Differences in Field Gas Exchange and Water Relations Between a C<sub>3</sub> Dicot (*Plantago asiatica*) and a C<sub>4</sub> Monocot (*Eleusine indica*). *Photosynthetica* **1999**, *37*, 123–130. [CrossRef]
- Carmo-Silva, A.E.; Soares, A.S.; Marques da Silva, J.; Bernardes da Silva, A.; Keys, A.J.; Arrabaça, M.C. Photosynthetic responses of three C<sub>4</sub> grasses of different metabolic subtypes to water deficit. *Funct. Plant Biol.* 2007, 34, 204–213. [CrossRef]
- 29. Waller, S.; Lewis, J. Occurrence of C<sub>3</sub> and C<sub>4</sub> Photosynthetic Pathways in North American Grasses. *J. Range Manag.* **1979**, *32*, 12–28. [CrossRef]

- Covshoff, S.; Szecowka, M.; Hughes, T.E.; Smith-Unna, R.; Kelly, S.; Bailey, K.J.; Sage, T.L.; Pachebat, J.A.; Leegood, R.; Hibberd, J.M. C<sub>4</sub> Photosynthesis in the Rice Paddy: Insights from the Noxious Weed *Echinochloa glabrescens*. *Plant Physiol.* 2015, 170, 57–73. [CrossRef]
- Barden, L.S. Invasion of Microstegium vimineum (Poaceae), An Exotic, Annual, Shade-Tolerant, C<sub>4</sub> Grass, into a North Carolina Floodplain. *Am. Midl. Nat.* 1987, 118, 40–45. [CrossRef]
- 32. Hodgson, R.J.; Liddicoat, C.; Cando-Dumancela, C.; Fickling, N.W.; Peddle, S.D.; Ramesh, S.; Breed, M.F. Increasing aridity strengthens the core bacterial rhizosphere associations in the pan-palaeotropical C<sub>4</sub> grass, *Themeda triandra. Appl. Soil Ecol.* **2024**, 201, 105514. [CrossRef]
- Hager, H.A.; Ryan, G.D.; Kovacs, H.M.; Newman, J.A. Effects of elevated CO<sub>2</sub> on photosynthetic traits of native and invasive C<sub>3</sub> and C<sub>4</sub> grasses. *BMC Ecol.* 2016, 16, 28. [CrossRef] [PubMed]
- Bianconi, M.E.; Hackel, J.; Vorontsova, M.S.; Alberti, A.; Arthan, W.; Burke, S.V.; Duvall, M.R.; Kellogg, E.A.; Lavergne, S.; McKain, M.R.; et al. Continued Adaptation of C<sub>4</sub> Photosynthesis After an Initial Burst of Changes in the Andropogoneae Grasses. *Syst. Biol.* 2019, 69, 445–461. [CrossRef] [PubMed]
- 35. Beard, J.B. Origin, Biogeographical Migrations and Diversifications of Turfgrasses; Michigan State University Press: East Lansing, MI, USA, 2012.
- 36. Prendergast, H.D.V.; Hattersley, P.W.; Stone, N.E.; Lazarides, M. C<sub>4</sub> acid decarboxylation type in *Eragrostis* (Poaceae) patterns of variation in chloroplast position, ultrastructure and geographical distribution. *Plant Cell Environ*. **1986**, *9*, 333–344. [CrossRef]
- 37. Chauvel, B.; Munier-Jolain, N.; Letouzé, A.; Grandgirard, D. Developmental patterns of leaves and tillers in a black-grass population (*Alopecurus myosuroides* Huds.). *Agronomie* **2000**, 20, 247–257. [CrossRef]
- Yang, D.-H.; Jeong, O.-C.; Sun, H.-J.; Kang, H.-G.; Lee, H.-Y. Genome analysis of Zoysia japonica 'Yaji' cultivar using PacBio long-read sequencing. *Plant Biotechnol. Rep.* 2023, 17, 275–283. [CrossRef]
- Lamesch, P.; Berardini, T.Z.; Li, D.; Swarbreck, D.; Wilks, C.; Sasidharan, R.; Muller, R.; Dreher, K.; Alexander, D.L.; Garcia-Hernandez, M.; et al. The Arabidopsis Information Resource (TAIR): Improved gene annotation and new tools. *Nucleic Acids Res.* 2011, 40, D1202–D1210. [CrossRef]
- Cheng, C.-Y.; Krishnakumar, V.; Chan, A.P.; Thibaud-Nissen, F.; Schobel, S.; Town, C.D. Araport11: A complete reannotation of the *Arabidopsis thaliana* reference genome. *Plant J.* 2017, *89*, 789–804. [CrossRef]
- Lei, L.; Gordon, S.P.; Liu, L.; Sade, N.; Lovell, J.T.; Rubio Wilhelmi, M.D.M.; Singan, V.; Sreedasyam, A.; Hestrin, R.; Phillips, J. The reference genome and abiotic stress responses of the model perennial grass *Brachypodium sylvaticum*. *G3 Genes Genomes Genet*. 2024, 14, jkad245. [CrossRef]
- Mamidi, S.; Healey, A.; Huang, P.; Grimwood, J.; Jenkins, J.; Barry, K.; Sreedasyam, A.; Shu, S.; Lovell, J.T.; Feldman, M. A genome resource for green millet *Setaria viridis* enables discovery of agronomically valuable loci. *Nat. Biotechnol.* 2020, *38*, 1203–1210. [CrossRef]
- 43. Baenziger, P.S. Plant breeding training in the US. HortScience 2006, 41, 40. [CrossRef]
- 44. Tomaškin, J.; Tomaškinová, J.; Kizeková, M. Ornamental grasses as part of public green, their ecosystem services and use in vegetative arrangements in urban environment. *Thaiszia. J. Bot. Košice* **2015**, *25*, 1–13.
- 45. Pamukcu-Albers, P.; Ugolini, F.; La Rosa, D.; Grădinaru, S.R.; Azevedo, J.C.; Wu, J. Building green infrastructure to enhance urban resilience to climate change and pandemics. *Landsc. Ecol.* **2021**, *36*, 665–673. [CrossRef]
- 46. Helfand, G.E.; Park, J.S.; Nassauer, J.I.; Kosek, S. The economics of native plants in residential landscape designs. *Landsc. Urban Plan.* **2006**, *78*, 229–240. [CrossRef]
- 47. Gillis, A.J.; Swim, J.K. Adding native plants to home landscapes: The roles of attitudes, social norms, and situational strength. *J. Environ. Psychol.* **2020**, *72*, 101519. [CrossRef]
- 48. Ribaut, J.-M.; de Vicente, M.; Delannay, X. Molecular breeding in developing countries: Challenges and perspectives. *Curr. Opin. Plant Biol.* **2010**, *13*, 213–218. [CrossRef]
- 49. Kersey, P.J. Plant genome sequences: Past, present, future. Curr. Opin. Plant Biol. 2019, 48, 1-8. [CrossRef]
- 50. Van Dijk, E.L.; Auger, H.; Jaszczyszyn, Y.; Thermes, C. Ten years of next-generation sequencing technology. *Trends Genet.* **2014**, 30, 418–426. [CrossRef]
- 51. Rice, E.S.; Green, R.E. New Approaches for Genome Assembly and Scaffolding. Annu. Rev. Anim. Biosci. 2019, 7, 17–40. [CrossRef]
- 52. Sano, Y. Constraints in Using Wild Relatives in Breeding: Lack of Basic Knowledge on Crop Gene Pools. In *International Crop Science I*; Crop Science Society of America: Madison, WI, USA, 1993; pp. 437–443.
- Cesarino, I.; Dello Ioio, R.; Kirschner, G.K.; Ogden, M.S.; Picard, K.L.; Rast-Somssich, M.I.; Somssich, M. Plant science's next top models. Ann. Bot. 2020, 126, 1–23. [CrossRef]
- 54. Draper, J.; Mur, L.A.; Jenkins, G.; Ghosh-Biswas, G.C.; Bablak, P.; Hasterok, R.; Routledge, A.P. *Brachypodium distachyon*. A New Model System for Functional Genomics in Grasses. *Plant Physiol.* **2001**, *127*, 1539–1555. [CrossRef]
- 55. Osada, T. Nihon Kika Shokubutsu Zukan: Illustrated Japanese Alien Plants; Hokuryukan: Nagano, Japan, 1972.
- 56. Makino, T.; Ohashi, H.; Murata, J.; Iwatsuki, K. *Shin Makino Nihon Shokubutsu Zukan: New Makino's Illustrated Flora of Japan;* Hokuryukan: Nagano, Japan, 2008.
- 57. Jeon, W.B.; Lee, M.B.; Kim, D.Y.; Hong, M.J.; Lee, Y.J.; Seo, Y.W. Efficient Phosphinothricin Mediated Selection of Callus Derived from *Brachypodium* Mature Seed. *Korean J. Breed. Sci.* **2010**, *42*, 351–356.

- 58. Hong, S.-Y.; Seo, P.J.; Yang, M.-S.; Xiang, F.; Park, C.-M. Exploring valid reference genes for gene expression studies in *Brachypodium distachyon* by real-time PCR. *BMC Plant Biol.* **2008**, *8*, 112. [CrossRef]
- 59. Mayer, B.F.; Bertrand, A.; Charron, J.-B. Treatment Analogous to Seasonal Change Demonstrates the Integration of Cold Responses in *Brachypodium distachyon*. *Plant Physiol*. **2020**, *182*, 1022–1038. [CrossRef]
- Takada, A.; Kodera, S.; Suzuki, K.; Nemoto, M.; Egawa, R.; Takizawa, H.; Hirata, A. Estimation of the number of heat illness patients in eight metropolitan prefectures of Japan: Correlation with ambient temperature and computed thermophysiological responses. *Front. Public Health* 2023, *11*, 1061135. [CrossRef]
- 61. Lee, J.; Lim, J.; Lee, J.; Park, J.; Won, M. Ground-Based NDVI Network: Early Validation Practice with Sentinel-2 in South Korea. Sensors 2024, 24, 1892. [CrossRef]
- 62. Park, I.-K.; Shin, Y.; Baek, H.-J.; Kim, J.; Kim, D.-I.; Seok, M.; Oh, Y.; Park, D. Establishment potential across South Korea for two gecko species, *Gekko japonicus* and *G. swinhonis*, adapted to different climates. *NeoBiota* **2024**, *93*, 39–62. [CrossRef]
- 63. Im, H.T. Plant geographical study for the plant of Cheju. Korean J. Plant Taxon. 1992, 22, 219–234. [CrossRef]
- 64. Catalan, P.; López-Álvarez, D.; Díaz-Pérez, A.; Sancho, R.; López-Herránz, M.L. Phylogeny and Evolution of the Genus *Brachypodium*. In *Genetics and Genomics of Brachypodium*; Springer: Berlin/Heidelberg, Germany, 2016; pp. 9–38. [CrossRef]
- Felber, F.; Kozlowski, G.; Arrigo, N.; Guadagnuolo, R. Genetic and Ecological Consequences of Transgene Flow to the Wild Flora. In *Green Gene Technology: Research in an Area of Social Conflict;* Fiechter, A., Sautter, C., Eds.; Springer: Berlin/Heidelberg, Germany, 2007; pp. 173–205.
- 66. The\_International\_Brachypodium\_Initiative. Genome sequencing and analysis of the model grass *Brachypodium distachyon*. *Nature* **2010**, *463*, 763–768. [CrossRef]
- 67. Kim, J. The Current State and Characteristics of Ornamental Grasses in South Korea. J. Korean Inst. Landsc. Archit. 2021, 49, 151–162. [CrossRef]
- 68. Moser, L.E.; Hoveland, C.S. Cool-Season Grass Overview. In Cool-Season Forage Grasses; Wiley: Hoboken, NJ, USA, 1996; pp. 1–14.
- 69. Phillips, A.R.; Seetharam, A.S.; Albert, P.S.; AuBuchon-Elder, T.; Birchler, J.A.; Buckler, E.S.; Gillespie, L.J.; Hufford, M.B.; Llaca, V.; Romay, M.C. A happy accident: A novel turfgrass reference genome. *G3 Genes Genomes Genet.* **2023**, *13*, jkad073. [CrossRef]
- Frei, D.; Veekman, E.; Grogg, D.; Stoffel-Studer, I.; Morishima, A.; Shimizu-Inatsugi, R.; Yates, S.; Shimizu, K.K.; Frey, J.E.; Studer, B.; et al. Ultralong Oxford Nanopore Reads Enable the Development of a Reference-Grade Perennial Ryegrass Genome Assembly. *Genome Biol. Evol.* 2021, 13, evab159. [CrossRef]
- Li, P.; Brutnell, T.P. Setaria viridis and Setaria italica, model genetic systems for the Panicoid grasses. J. Exp. Bot. 2011, 62, 3031–3037. [CrossRef] [PubMed]
- 72. Thielen, P.M.; Pendleton, A.L.; Player, R.A.; Bowden, K.V.; Lawton, T.J.; Wisecaver, J.H. Reference Genome for the Highly Transformable *Setaria viridis* ME034V. *G3 Genes Genomes Genet.* **2020**, *10*, 3467–3478. [CrossRef]
- Martins, P.K.; Nakayama, T.J.; Ribeiro, A.P.; da Cunha, B.A.D.B.; Nepomuceno, A.L.; Harmon, F.G.; Kobayashi, A.K.; Molinari, H.B.C. *Setaria viridis* floral-dip: A simple and rapid *Agrobacterium*-mediated transformation method. *Biotechnol. Rep.* 2015, 6, 61–63. [CrossRef]
- 74. Weiss, T.; Wang, C.; Kang, X.; Zhao, H.; Elena Gamo, M.; Starker, C.G.; Crisp, P.A.; Zhou, P.; Springer, N.M.; Voytas, D.F. Optimization of multiplexed CRISPR/Cas9 system for highly efficient genome editing in *Setaria viridis*. *Plant J.* 2020, 104, 828–838. [CrossRef]
- Anderson, C.M.; Mattoon, E.M.; Zhang, N.; Becker, E.; McHargue, W.; Yang, J.; Patel, D.; Dautermann, O.; McAdam, S.A.; Tarin, T. High light and temperature reduce photosynthetic efficiency through different mechanisms in the C<sub>4</sub> model *Setaria viridis*. *Commun. Biol.* 2021, 4, 1092. [CrossRef]
- 76. Danila, F.R.; Thakur, V.; Chatterjee, J.; Bala, S.; Coe, R.A.; Acebron, K.; Furbank, R.T.; von Caemmerer, S.; Quick, W.P. Bundle sheath suberisation is required for C<sub>4</sub> photosynthesis in a *Setaria viridis* mutant. *Commun. Biol.* **2021**, *4*, 254. [CrossRef]
- 77. Hong, I.K.; Yun, H.K.; Lee, S.M.; Jung, Y.B.; Lee, M.R. Composition and Utilization of Urban Garden Space Using the Planting System Design Process. J. People Plants Environ. 2020, 23, 615–624. [CrossRef]
- Frey, D.; Moretti, M. A comprehensive dataset on cultivated and spontaneously growing vascular plants in urban gardens. *Data Brief* 2019, 25, 103982. [CrossRef]
- 79. de Oliveira Maximino, J.V.; Machado, M.A.S.; Mittelmann, A.; da Cunha Pinheiro, E.; da Silva Pires, E.; Longaray, M.B.; de Souza, F.H.D.; Stumpf, E.R.T. Potential of grass seed production for new lawns. *Ornam. Hortic.* **2017**, *23*, 200–206. [CrossRef]
- 80. Zhang, G.; Liu, X.; Quan, Z.; Cheng, S.; Xu, X.; Pan, S.; Xie, M.; Zeng, P.; Yue, Z.; Wang, W. Genome sequence of foxtail millet (*Setaria italica*) provides insights into grass evolution and biofuel potential. *Nat. Biotechnol.* **2012**, *30*, 549–554. [CrossRef] [PubMed]
- 81. Yan, Z.; Liu, H.; Chen, Y.; Sun, J.; Ma, L.; Wang, A.; Miao, F.; Cong, L.; Song, H.; Yin, X. High-quality chromosome-scale de novo assembly of the *Paspalum notatum* 'Flugge' genome. *BMC Genom.* **2022**, *23*, 293. [CrossRef] [PubMed]
- Doust, A.N.; Kellogg, E.A.; Devos, K.M.; Bennetzen, J.L. Foxtail millet: A Sequence-Driven Grass Model System. *Plant Physiol.* 2009, 149, 137–141. [CrossRef]
- 83. Loch, D.S.; Ebina, M.; Choi, J.S.; Han, L. Ecological Implications of *Zoysia* Species, Distribution, and Adaptation for Management and Use of Zoysiagrasses. *Int. Turfgrass Soc. Res. J.* 2017, 13, 11–25. [CrossRef]
- 84. Tsuruta, S.-I.; Kobayashi, M.; Ebina, Z.M. *Wild Crop Relatives: Genomic and Breeding Resources: Millets and Grasses*; Kole, C., Ed.; Springer: Berlin/Heidelberg, Germany, 2011; pp. 297–309.

- 85. Magni, S.; Pompeiano, A.; Gaetani, M.; Caturegli, L.; Grossi, N.; Minelli, A.; Volterrani, M. Zoysiagrass (*Zoysia* spp. Willd.) for European lawns: A review. *Ital. J. Agron.* **2017**, *12*, 44. [CrossRef]
- 86. Flavell, R. Role of Model Plant Species. In *Plant Genomics: Methods and Protocols*; Gustafson, J.P., Langridge, P., Somers, D.J., Eds.; Humana Press: Totowa, NJ, USA, 2009; pp. 1–18.

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