Dendrocalamus asper and Related Bamboos

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Bamboos represent an emerging forest resource of economic significance and provide an avenue for sustainable development of forest resources. The development of the commercial bamboo industry is founded upon efficient molecular and technical approaches for the selection and rapid multiplication of elite germplasm for its subsequent propagation via commercial agro-forestry business enterprises.

Keywords: bamboo ; Dendrocalamus asper ; micropropagation ; plant tissue culture ; DNA barcoding ; genetic stability

1. Introduction

Bamboo is the fastest-growing flowering perennial grass and considered as one of the world's most important tree species [1]. Bamboos belong to the largest family of grasses, the Poaceae (Gramineae), and constitute the Bambusoideae subfamily [2]. With 121 genera and 1662 species [3], the bamboo population can be divided into three zones geographically: the American zone, the Asian Pacific zone and the African zone [4], and according to reference [5], about 80% of bamboo forest lands and species in the world are distributed across the Asian Pacific region. Bamboo, in general, plays an important role in human life, mainly in terms of meeting the current economic, ecological, and human essential needs [6][7]. Several studies have shown that bamboos cultivated commercially are more renewable and sustainable than other woody plants, as the inefficient harvesting and use of bamboo has become a major focus worldwide [8][9]. A current report by reference [10] stated that the global demand for bamboo is expected to reach a revenue of USD 98.3 billion with a Computed Annual Growth Rate (CAGR) of 5% by 2025. The same study predicted that the biomass energy market will reach USD 98.0 billion by 2027 with a CAGR of 9.2% from 2020 to 2027. Since bamboo is undeniably the most important non-woody forest resource in Malaysia and some Southeast Asian countries, the traditional timber industry needs to develop the use of non-timber bamboo into a value-added material such as floorboards, building materials, composite boards and furniture, as well as biomass products [11].

2. Dendrocalamus asper

Taxonomically, Dendrocalamus belongs to the Bambuseae tribe and comprises about 35 species. In 2017, a study on Dendrocalamus and Bambusa conducted by reference [12] reported a higher similarity between these two genera when compared to other bamboo species. This finding supported the interpretation made by reference [13] that Dendrocalamus belongs to the same tribe as Bambusa. Besides, this similarity can be linked with their chromosome number, as with most species of the tropical bamboo genera, like Bambusa, Cephalostychum, Dendrocalamus, Gigantochloa and Melocanna reported to have a chromosome number of 72 (2n) [14]. D. asper, which is commonly referred to as sweet bamboo, is a multipurpose tropical clumping bamboo with high economic value [15][16]. Known also as rough bamboo, black bamboo or giant bamboo, D. asper grows to a height of 20–30 m, with a diameter of 8–20 cm and 20–45-cm-long internodes, and has relatively thick walls [17]. The origins of D. asper are not definitive, but according to reference [18], they are distributed across India and South East Asia, including Thailand, Vietnam, Malaysia, Indonesia and the Philippines. Recently, D. asper has been introduced in other tropical countries, including Ghana, Benin, DR Congo, Kenya and Madagascar. **Figure 1** shows the distribution map of D. asper based on their endemic origin and subsequent introduction as an exotic species. Within tropical Asia, D. asper grows ideally in humid regions with rich, heavy soils, from lowlands to a 1500-m altitude, with an average annual rainfall of about 2400 mm. It can also survive well in semiarid environments with proper management. The mature stems are used to create furniture, musical instruments, household utensils, handicrafts and paper, while the upper internodes are used to make containers and cooking pots [19]. The tender young shoots are consumed as a vegetable and are thought to be the finest of all tropical Asiatic bamboos [20]. The rhizome, stems and branch cuttings can all be used to propagate D. asper. The propagules are grown in a nursery and then planted out in the field before or during the first half of the monsoon season after the roots have emerged. The best time to harvest stems is during the dry season; it is recommended to harvest mature stems that are 5–7 years old, while retaining some mature tillers in the clump.

Figure 1. Range and distribution of D. asper in its native and introduced habitats.

3. Bamboo Propagation and Diseases

3.1. Traditional Propagation of Bamboos and Tissue Culture

Conventionally, bamboos are propagated through seeds. Short seed viability periods of 3–6 months, long-term gregarious flowering, the monocarpic nature of the plant, poor seed set and large-scale seed consumption by pests are all factors that restrict the use of seeds as a reliable resource of propagation [21][22]. Owing to the segregation of their traits, the genetic homogeneity of seed-based progenies is also in question. As a consequence, vegetative propagation from layering, off-set and rhizome planting, marcotting and branch and culm cuttings are used for propagating the bamboos [17][23][24]. The traditional bamboo propagation methods, on the other hand, are detrimental to mother plants during collection, involving high labor costs, transportation difficulties, bulky materials and seasonal dependence, which is typically limited to a short period of time, and these techniques are only effective for small-scale production [25][26]. The first report on a successful tissue culture of bamboo was done by reference [27], who described the embryo culture of D. strictus on a sucrose-enriched medium. In vitro propagation provides the ability to acquire large progenies from elite genotypes, since it was believed that it could solve most of the problems associated with conventional propagation [28]. In most cases, when designing protocols for in vitro plant propagation, trial-and-error experiments are needed to identify specific conditions for individual species, genotypes and even the donor plant development stages [29]. The aim of bamboo tissue culture regeneration protocols is to achieve the large-scale production of plants for operational planting, to produce disease-free and genetically uniform planting material and to provide material for breeding programs, as well as germplasm conservation [30].

3.2. Bamboo Diseases

Tissue culture has become a platform to confer resistance against specific diseases by manipulating the genetics of the plant systems. Bamboo tissue is composed primarily of Hemicellulose, Cellulose and Lignin [31], and microbes that rely on these as a source of carbon represent potential pathogens. Investigations carried out in China [32] in 148 bamboo species over a 11-year period from 1995 to 2006 recorded 208 potential pathogens, the majority of which were fungi (108). Similar studies carried out in Japan [33] reported 257 fungal strains, of which 75 could be identified using 18S rRNA gene and internal transcribed spacer region (ITS) analyses with Xylariales as the major dominant group. Bamboo died back, which was caused by the fungus Aciculosporium take, reported to predominantly infect Phyllostachys bambusoides, with a lower incidence in Phyllostachys pubescens Western Japan [34], leading to phenotypic changes referred to as the ”witches’ broom” of bamboo. Among the pathogens reported from India [35], Bambusa nutan was found to be infected by Nigrospora oryzae, the causative agent of leaf spot disease, whereas Fusarium oxysporum and F. verticillioides were dominant on Bambusa balcooa and D. asper, respectively. Another extensive study carried out in India across 12 phyla and 46 orders identified the pathogens belonging to the phylum Deuteromycota and Ascomycota as causative agents for foliage-related diseases. Basidiomycota was found to be associated with culm diseases, which is supported by the evidence that white rot fungi belong to this phylum and are involved actively in the degradation of lignin [36] and the utilization of carbohydrate complexes [37] that constitute the structural elements of bamboo. Interestingly, not all microbiota associated with bamboos have been reported to be pathogenic, with reports providing evidence of endophytic bacterial communities [38] associated with the rhizomes of tropical bamboos that share a unique symbiotic relationship and may also serve as a means of host defense [39] and biological control. Recent reports of the new fungal pathogen Arthrinium bambusicola in Thailand [40] and novel techniques such as high-throughput genome sequencing have provided new tools for the discovery and diagnosis of fungal pathogens [41], the early detection of which is critical to their control.

The Bamboo Mosaic Virus (BaMV) is one of the most well-documented and studied among the viruses associated with bamboos [42], although many individuals may be asymptomatic carriers with no physical evidence of viral infection. The mode of transmission of the virus appears to be mechanical injury, either via routine farming operations or insect vectors [43]. Recent reports have emerged of etic recombination events in Indonesia [44], which indicate Taiwan as the origin of the virus. Molecular data has provided evidence of the factors involved in the intracellular movement of the virus, which is mediated by movement proteins [45], and measurements for the containment and eradication of the BaMV have included treatments with abscisic acid [46], which has been reported to induce resistance and improve the host defense, as well as the application of interfering satellite RNA [47] in transgenic bamboo plants. The adoption of pertinent biosecurity measures during import of the germplasm, as well as the monitoring of invasive pathogens in commercial plantations, is currently the best available measure for the control of BaMV and other pathogens.

4. Regeneration of D. asper

In any plant tissue culture, choosing the appropriate propagation method is crucial. Different routes such as direct shoot induction (axillary shoot proliferation), the production of adventitious buds through organogenesis and somatic embryogenesis are pathways of choice for the rapid and large-scale propagation of bamboo using both juvenile and mature explants [48]. Reference [49] stated that callus have three basic developmental ways: somatic embryo development, shoot organ differentiation and a mixed development pathway that includes both somatic embryogenesis and shoot organogenesis. A developed in vitro culture of D. asper was successfully established from various explants. Seeds [50], mature plants of nodal explants [16][19][50][51][52][53][54][55], stem cuttings [56], small branch cuttings [57], nodal and leaf bases [58], inter node segments [59] and clump [60] were successfully used for the mass propagation of D. asper in vitro. Some researchers also used inflorescence explants for establishing protocols for the multiple shoot proliferation in D. asper [61] and in vitro flowering studies [62]. Most of the research available in D. asper used juvenile and mature tissues on enhanced axillary branching, with just a few reports on indirect organogenesis. By using nodal explants, the first regeneration of shoots and roots from D. asper callus was carried out by reference [51]. Moreover, several authors published studies incorporating both in vitro and in vivo multiplications of D. asper to improve the multiplication rate and measure the quality of plantlets in the field. **Table 1** and **Table 2** below respectively show the in vitro regeneration of D. asper through organogenesis and somatic embryogenesis using different explants. According to reference [29], because of the size and diversity of this plant family, establishing the best culture medium, combinations of plant growth regulators and other compounds in promoting the growth of explants will usually take several months. Therefore, to reduce the current gap between demand and supply, cost-effective methods for planting large-scale bamboo propagation in new bamboo forests must be established.

Table 1. Successful micropropagation of D. asper via organogenesis from various explants.

Explant	Basal Medium	PGRs (as Indicated in µM Except Otherwise Mentioned)	Results	Reference(s)
Node (young first three segment)	MS	* BAP (22.0) ** BAP (22.0) + AdS (216.0) *** IBA (4.90)	Shoot multiplication and rooting	[16]
Node	MS	* BAP (15.0) ** BAP (10.0) + AdS (75.0) *** ½ MS + IBA (5.0) + NAA (5.0)	Shoot multiplication and rooting	[19]
Seeds, Nodes	MS	* BAP (13.32) ** BAP(13.32) ***NAA (16.11); IBA (49.0)	Shoot multiplication and rooting	[50]
Node	MS	** BAP (31.08) ***NAA (16.11) + IAA (5.71)	Organogenesis, multiple shoots and rooting	[51]
Nodes	MS	** BAP (13.32) + Ads (270.0) *** IBA (4.90)	Shoot multiplication and rooting	[52]
Node	MS	* BAP (8.86) ** BAP (8.86) + Ads (13.5) + 3% Suc ***IBA (14.76) + NAA (3.67) + 3% Suc # 2,4-D (14.61) ##, ** 2,4-D (14.61) *** IBA (14.76) + NAA (3.67)	Shoot multiplication and rooting	[53][59]
Node	MS	* ¼ MS BAP ** ¾ MS + 3 ppm Kn	Shoot multiplication	[55]

Explant	Basal Medium	PGRs (as Indicated in µM Except Otherwise Mentioned)	Results	Reference(s)
Stem cuttings	MS	* BAP (0–8.88) + CW (0–20.0) ** BAP (22.2) *** NAA (2.68) + AA (283.5) + CA (130) + Cyst (206.25)	Shoot multiplication and rooting	[56]
Small branch cuttings	MS	** BA (3×10^{-5})	Shoot multiplication	[57]
Inter node segments	MS	* BAP (2.22) ** BAP (8.88) # Kin (23.25) + NAA (16.11)	Shoot multiplication, rooting and callusing	[63]
Clump	MS	* BAP (15) ** mT (20)	Shoot multiplication	[60]
Immature and mature inflorescence	MS	* BAP (31.08) ** BAP (13.32) *** IBA (49.0)	Shoot multiplication and rooting	[61]
Seeds	MS	* BAP (22.2) ** BAP(1.332) * IBA (49.0) + NAA (16.11)	Shoot multiplication and rooting	[64]
Seeds	MS	* BAP (22.2) ** BAP (13.32) *** IBA (49.0); NAA (16.11)	Shoot multiplication and rooting	[65]
Seeds	MS	* BA (20.0) ** BA (10.0) *** IBA (40.0)	Shoot multiplication and rooting	[66]
Node	MS	* TDZ (1.135) + NAA (1.34) + AA (283.5) + CA (130.0) + Cyst (206.25) ** TDZ (1.135) + NAA (1.34) + AA (283.5) + CA (130.0) + Cyst (206.25) *** ¼ MS + IBA (9.80)	Shoot multiplication and rooting	[67]
In vitro grown shoots	MS	** BAP (31.08) • NAA (16.11) + IBA (14.70) + 5% Suc	Shoot multiplication and rhizogenesis	[68]
Seeds	MS	* BAP (13.32) ** BAP (13.32) *** IBA (34.30)	Shoot multiplication and rooting	[69]

AA, ascorbic acid; AdS, adenine sulphate; BAP, 6-Benzylaminopurine; CA, citric acid; CW, coconut water (milk); Cyst, cysteine; IAA, indole-3-acetic acid; IBA, indole-3-butyric acid; Kin, kinetin; MS, Murashige & Skoog medium; mT, Meta-topolin 6-(3-hydroxybenzylamino) purine; NAA, α-naphthaleneacetic acid; PGR, plant growth regulator; Suc, sucrose; TDZ, thidiazuron. *, Seed germination/shoot induction; **, Shoot proliferation/multiplication; ***, rooting; •, Rhizogenesis; #, callus initiation; ##, callus proliferation.

Table 2. The successful micropropagation of D. asper through somatic embryogenesis.

Explant	Basal Medium	PGRs (as Indicated in µM Except Otherwise Mentioned)	Results	Reference(s)
Node	MS	# MMS + 2,4-D (30.0) * BAP (20.0) *** NAA (5.0–25.0)	Somatic embryogenesis and germination	[54]
Nodal and leaf bases	MS	# 2,4-D (30.0) ## 2,4-D (9) + IAA (2.85) + BAP (0.88) X BAP (4.4) + GA3 (2.8) ** BAP (13.2) *** NAA (16)	Somatic embryogenesis	[70]
Seeds	MS	#,## 2,4-D (13.59) or 2,4-D (2.265) *,** BAP (8.88) + NAA (2.68) + Kin (4.65) *** ½ MS + IBA (13.32)	Somatic embryogenesis	[71]

2,4-D, 2,4-dichlorophenoxyacetic acid; BAP, 6-Benzylaminopurine; GA, Gibberellic acid; IAA, indole-3-acetic acid; IBA, indole-3-butyric acid; Kin, kinetin; MS, Murashige & Skoog medium; MMS, Modified Murashige & Skoog medium; NAA, α-naphthaleneacetic acid; PGR, plant growth regulator; #, initiation of embryogenic callus; ##, embryogenic callus

proliferation; X, plantlet development from somatic embryos *, Somatic embryo shoot induction; **, somatic embryo shoot proliferation/multiplication; ***, rooting.

5. Bamboo Dormancy and Bud Breaking

5.1. Seed Dormancy

The word “dormancy” refers to the temporary stop of plant growth. It comprises true dormancy, known as (“rest” or “endodormancy”) triggered by internal factors and climatic dormancy (“quiescence” or “ecodormancy”) controlled by external factors [72]. As mentioned by reference [73], dormancy and the breaking of dormancy in buds of bamboos vary with their position on the plant, the season of the year and the species, while seed dormancy is known to occur in many tropical tree species. In seeds, several methods are known to be involved in the induction of dormancy to the germinating state. In this section, the role of plant hormones, various treatments available are discussed for bamboo seed dormancy. Important factors influencing seed germination include the seed quality and their viability. Major causes linked to the loss of seed viability are the endogenous levels of auxins and abscisic acid (ABA) during prolonged storage [74]. Besides, bamboo seeds are short-lived, germinate within 3–7 days and the germination potential is season-dependent [75]. To preserve the viability for a longer period of time, seeds are usually stored at 4 °C in desiccators with anhydrous calcium chloride. Furthermore, reference [76] revealed that prechilling the seeds (4 to 5 °C) for 4 weeks could be the most effective way to extend their life. This process is known as vernalization, and it involves exposing seeds to low temperatures in order to stimulate or to enhance seed development [72]. For instance, reference [65] stored D. asper seeds at 4 °C for 3 months before undergoing surface sterilization. However, degradation can occur during storage. Depending on the predominant causes of dormancy, some authors [77][78][79] have suggested various approaches to break the seed dormancy in order to improve the germination rate and speed up the germination process. Besides, the breaking of seed dormancy varies from species to species. Therefore, it is very important to determine which method and condition are the best for each plant species. Various techniques are available that enhance the vigor of seeds, and these technologies are termed as seed invigoration/seed enhancement techniques [80]. Seed invigoration is a postharvest treatment that enhances seed production by ameliorating the germinability, storability and yield performance of the seeds [74]. Hydropriming, seed hardening, on-farm priming, osmo-priming, osmo-hardening, humidification, priming with plant growth regulators, polyamines, ascorbate, salicylate, ethanol, osmolytes, coating technologies and, more recently, pre-sowing dry heat treatments are some of the treatments used to invigorate seeds [75]. These strategies provide high-value crops with value-added solutions that improve the yield and quality. Generating greater emergence rates, rapid seedling growth and better stand developmental rates are the results of seeds priming [81]. However, no treatments have been applied to D. asper seeds in order to break their dormancy and improve their viability. In terms of plant growth regulators, reference [82] indicated that the major gibberellins formed by the germinating embryo are GA1 and GA3. Furthermore, GA3 and GA7 are thought to activate aleurone cells, and GA1 and GA4 are thought to regulate embryo development. GA2 and GA22 are two other active gibberellins, while others like GA12, GA17 and GA26 show no sign of reaction. The importance of endogenous GAs as a seed germination enhancer has also been earlier emphasized by reference [83]. When the seeds of D. membranaceus Munro were soaked in GA3 solution (50 ppm) overnight, a high percent of seed germination was stimulated, with a corresponding increase in shoot length (2.70 mm) and number of sprouts (7) per explant during culture initiation [84]. Similarly, reference [85] discovered that 0.5-mg/L GA3 supplemented in media promotes the germination of D. giganteus Munro seeds under light better than BAP and Kn. In addition, GA3 at 50 ppm was found to be the best pre-sowing treatment on D. hamiltonii seeds, with a statistically significant improvement in seed viability [75]. Furthermore, seed primed with 1% KNO3 solution increased the germination of D. strictus (Roxb.) by 80.4% at the fastest rate, and no mortality was recorded when transferred to soil [86]. However, reference [87] observed that osmopriming with KCl (10%) resulted in a maximum germination percentage of 83.1% when compared to KNO3 and PEG-6000 on D. strictus seeds. Meanwhile, reference [88] soaked the D. sinicus seeds in 0.5% (v/v) potassium permanganate (KMnO4) for 12 h and resulted in a high germination rate.

5.2. Bud Position on the Bamboo Plants

The position of explants was found to affect the culture initiation and the quality of the shoots formed under in vitro conditions. During in vitro bamboo propagation, the top and bottom portions of the nodal segment in culm bamboo can hardly regenerate. The initiation of the culture is more efficient when nodal segments from a healthy mature mother plant with disinfected lateral branches are used [19]. According to reference [89], the juvenility of lateral shoots, the season of the cultures initiated and the position of axillary bud on the branch highly affect the bud break frequency in D. longispathus. Moreover, reference [90] reported that nodal segments from mature clumps of B. bambos with pre-existing axillary buds were primarily preferred as explants due to their sufficient availability all-year-round to initiate in vitro cultures, while reference [91] reported that explants from young lateral buds showed a bud break in B. tulda. Besides, explants from

healthy mother stock were found to be good for the regeneration of new plants in D. hamiltonii [92], P. stocksii Munro [93], G. angustifolia and D. giganteus [94]. Explants taken from higher branches were found to respond better to a multiplication medium with an early bud break than explants from lower branches [53]. In Arundinaria callosa, the position of the nodal buds in the lateral branches affected the efficiency of the bud breaks, resulting in a higher bud break when nodal explants are taken from the basal and middle nodes compared to the distal part of the secondary branches [95]. Reference [96] illustrated that the 5th–7th positions of B. nutans explants from the mother stock culm were the best for the maximum regeneration in the vitro culture in bud breaking, while reference [97] found the best regeneration for D. strictus taken from the 1st and 2nd positions of the base of the secondary branches. Similar findings have also been reported in D. longispathus [89] and B. vulgaris [98], which mid-culm nodes of secondary branches are in the best position for axillary shoot initiation explants. Furthermore, reference [69] stated that the best explants for axillary shoot proliferation in D. asper were taken from the mid-culm nodes of tertiary branches.

5.3. Season Collection of Explants

The period of explant collection for culture initiation was found to play an important role in reducing the level of contamination, increasing the bud break and increasing the number of shoots per explant [99]. The environmental conditions during different periods of the year varied the maturity status of the explants, hence influencing the response of explants to the culture initiation [69]. D. asper responded best to the culture conditions during the pre-monsoon season (May to June) but with a higher contamination rate [16], while references [19][99] stated that young branches (nodal segments) of D. asper collected in the spring (February–April) gave a better response in terms of lower contamination, early bud break and a higher number of shoots. On the other hand, reference [69] stated that the best time in initiating aseptic cultures for D. asper was in January and February, when the maximum bud break was achieved. In the spring, an increased cell division has been observed in trees as young buds produce auxins, which stimulates cell division in the cambium [100]. Moreover, the months of July–December were discovered to be unsuitable for optimal D. asper bud induction. Reference [19] found that during the rainy season (July–September), almost 50% of the contamination with moderate bud breaks was due to strong fungal and bacterial contaminants remaining underneath the leaf sheaths, while a poor response during the winter (October–December) was primarily due to the plant's dormant and slow development. According to reference [69], the highest rate of contamination was also observed during the time of maximum rainfall (June–August). In a study of B. balcooa by reference [101], the explants collected during the rainy season in India (June–September) resulted in a high presence of contaminated explants. Furthermore, the establishment of B. oldhamii in vitro was a success when reference [102] collected the explant material by the end of the rainy season (June and July) in the Central-West Region of Brazil. Therefore, it is important to understand that bud break responsiveness is normally associated with the rainy season of different locations. Similar seasonal effects on bud breaks were also observed in D. giganteus and B. vulgaris [103], B. nutans [96][104], B. balcoa [105], D. hamiltonii Arn. Ex Munro [99] and B. Bambos [106].

6. Bamboo Genomics

Genome and transcriptome sequencing of commercially important plant species has led to the discovery of novel genes, the elucidation of biosynthetic pathways and the identification of genomic loci linked to quantitative traits. Bamboo occupies an important phylogenetic node in the grass family and the first attempt to compare the genomes of Oryza sativa and Zea mays was made by estimating the genome size of the tetraploid Moso bamboo (Phyllostachys pubescens) which was determined to be 2034 Mb following which, approximately 1000 genome survey sequence for the analysis of synteny [107]. Molecular markers from O. sativa were successfully applied and were able to resolve bamboo species into two major groups which concurred with the morphological classification as rhizome type, runner and clumper [108]. The first high quality of the draft genome of P. heterocycla var. Pubescens provided evidence of genome duplication and led to the identification of 31,967 genes [109]. The Bamboo genome database (Bamboo GDB) which has been developed as a direct result of multiple genome sequencing projects now provides researchers with a library of functionally annotated genes and pathways as well as tools for analysis and graphical representation of data sets [110]. Since then, transcriptome analysis of P. edulis has led to the discovery of genes linked to floral transition and flower development in bamboo, both of which are pertinent to the breeding industry [111]. The cumulative data provides an important resource for the development of molecular markers for the characterization of genome variation in bamboo via genome resequencing [112]. The wealth of information related to microsatellites has facilitated the reconstruction of high-resolution phylogenetic maps of bamboos [113]. The discovery of transposable genetic elements within the bamboo genome, which are responsible for somaclonal variation, has also provided insights into the phylogeny of Asian bamboos [114]. Transcription factors are important for the regulation of genes and their role in growth and development makes them of importance to genetic engineering, the characterization of these transcription factors in P. edulis has provided the foundation for the discovery and application of novel transcription factors for downstream applications in genetic modification [114]. The recent publication of the draft genome sequence of the diploid, herbaceous bamboo Raddia distichophylla (Schrad. ex Nees) Chase, has provide a

clearer understanding of the process of lignification and the genes associated with this biosynthetic pathway [115]. The increase in the availability of both genome sequencing data from multiple projects when integrated with transcriptomic data from different developmental stages [116][117] will provide researchers and commercial breeders with data that can be applied for the improvement of bamboo via the application of Marker Assisted Breeding (MAS) program and genetic engineering of important regulatory pathways.

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