

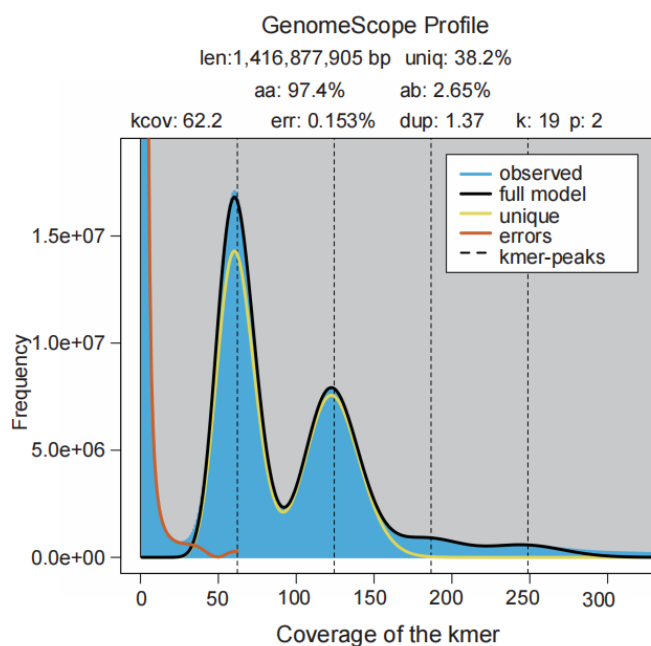


Figure S1. Genome survey based on a frequency distribution map.

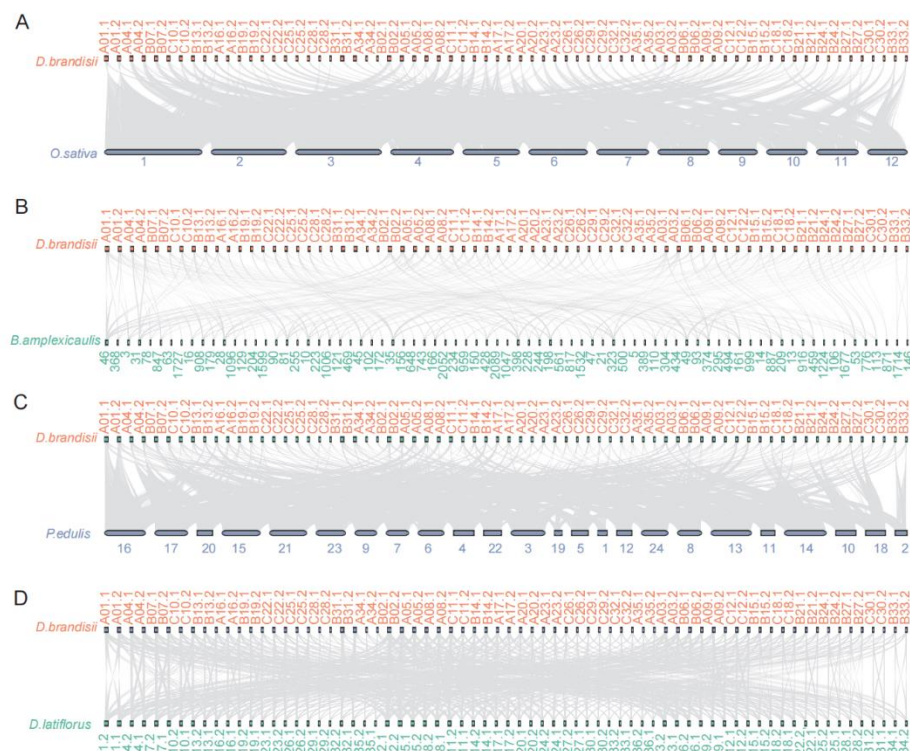


Figure S2. Colinearity relationships of *D. brandisii* with three Gramineae species.

(A) *O. sativa*, (B) *B. amplexicaulis*, (C) *P. edulis*, and (D) *D. latiflorus*.

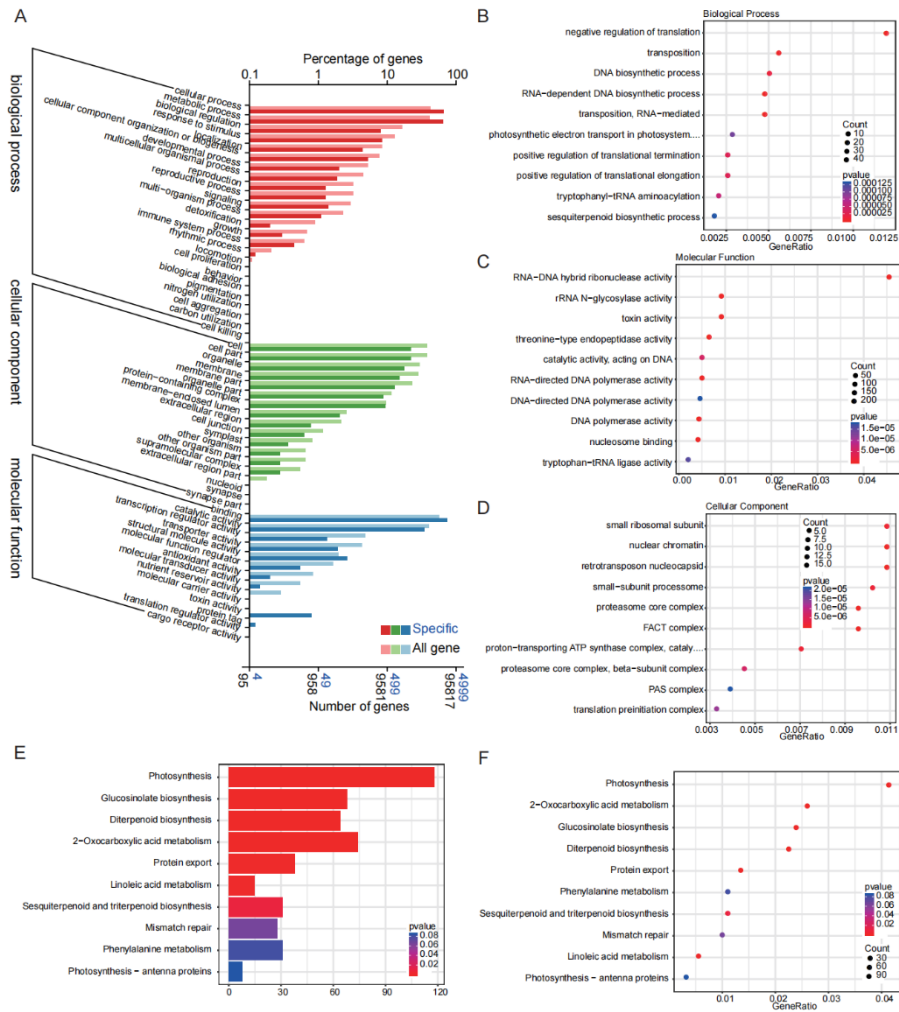


Figure S3. GO term and KEGG pathway enrichment analyses for gene families in *D. brandisii*.

(A) GO analysis for the 2126 gene families specific to *D. brandisii*. The *x*-axis exhibits GO terms categorized into three distinct types, each denoted by a unique color. On the *y*-axis, both the percentage and the number of genes specific to *D. brandisii* are depicted. (B) GO analysis (Biological process) for the gene families specific to *D. brandisii*. (C) GO analysis (Molecular function) for the gene families specific to *D. brandisii*. (D) GO analysis (Cellular component) for the gene families specific to *D. brandisii*. (E) KEGG analysis for the gene families specific to *D. brandisii*.

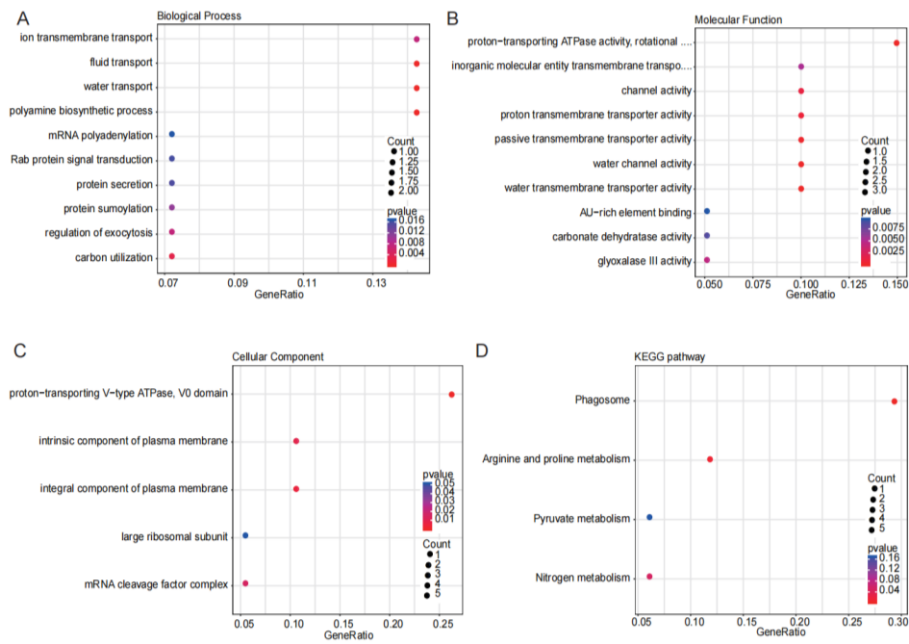


Figure S4. GO term and KEGG pathway enrichment analyses for contracted gene families in *D. brandisii*.

(A) Enriched biological processes among contracted gene families in *D. brandisii*. (B) Enriched molecular functions among contracted gene families in *D. brandisii*. (C) Enriched cellular components among contracted gene families in *D. brandisii*. (D) KEGG pathway analysis among contracted gene families in *D. brandisii*.

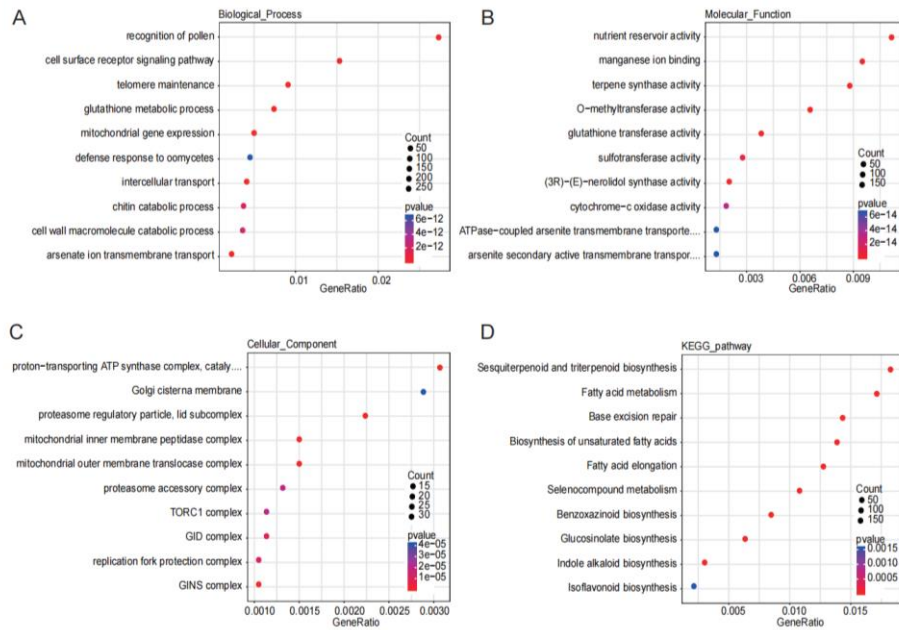


Figure S5. GO term and KEGG pathway enrichment analyses for expanded gene families in *D. brandisii*.

(A) Enriched biological processes among expanded gene families in *D. brandisii*. (B) Enriched molecular functions among expanded gene families in *D. brandisii*. (C) Enriched cellular components among expanded gene families in *D. brandisii*. (D) KEGG pathway analysis among expanded gene families in *D. brandisii*.

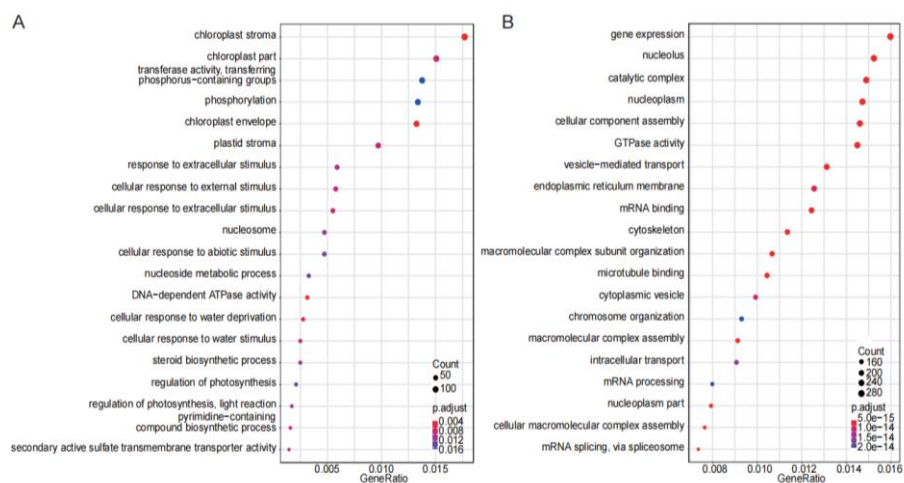


Figure S6. GO term enrichment analysis for APA genes in *D. brandisii*.

(A) Enriched GO terms among genes with only one polyadenylation site in *D. brandisii*.
 (B) Enriched GO terms for genes with more than two polyadenylation sites in *D. brandisii*.

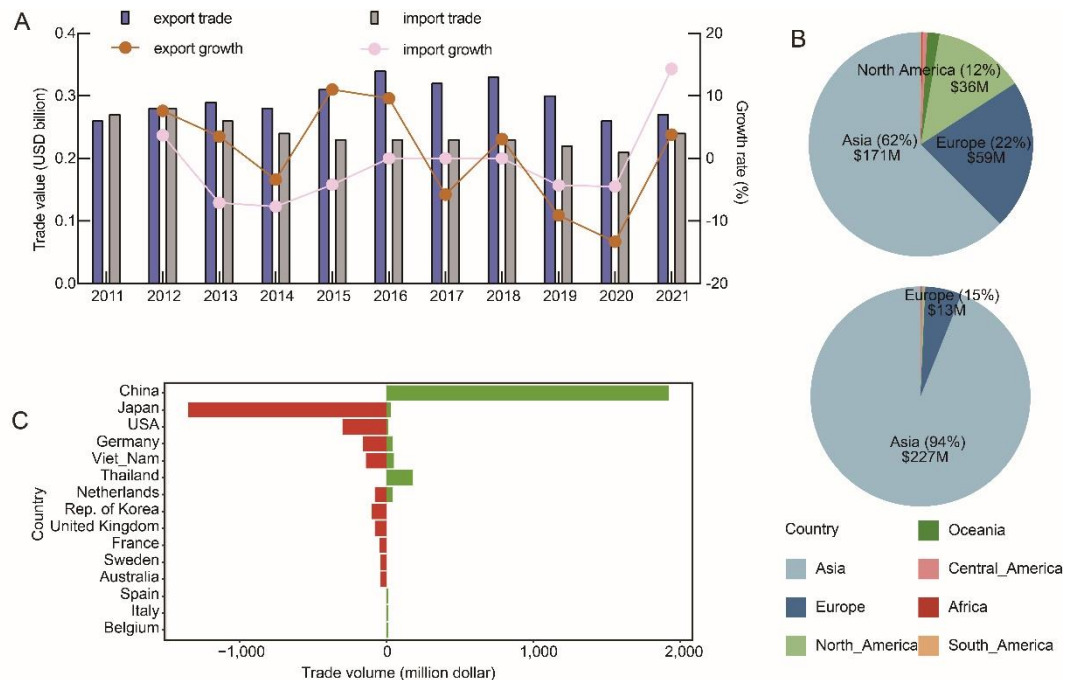


Figure S7. Export and import trade of bamboo shoots in different countries.

(A) Global bamboo shoot import and export trade volume and growth rate from 2011 to 2021. (B) Global bamboo shoot trade inflow and outflow by continent in 2021 (Million US \$). (C) Global bamboo shoot import and export trade flow in 2021 (Unit: Billion US \$).

Table S1. The distribution coordinates of *Dendrocalamus* in the world. The data is sourced from the Global Biodiversity Information Facility, accessible at <https://doi.org/10.15468/DL.879ZRT>. In the decimal latitude, negative numbers represent south latitude, positive numbers indicate north latitude. In the decimal longitude, negative numbers denote west longitude, positive numbers signify east longitude.

Table S2. The distribution coordinates of *Dendrocalamus brandisii* in the world. The data is sourced from the Global Biodiversity Information Facility, accessible at <https://doi.org/10.15468/dl.tp4br7>. In the decimal latitude, negative numbers represent south latitude, positive numbers indicate north latitude. In the decimal longitude, negative numbers denote west longitude, positive numbers signify east longitude.