

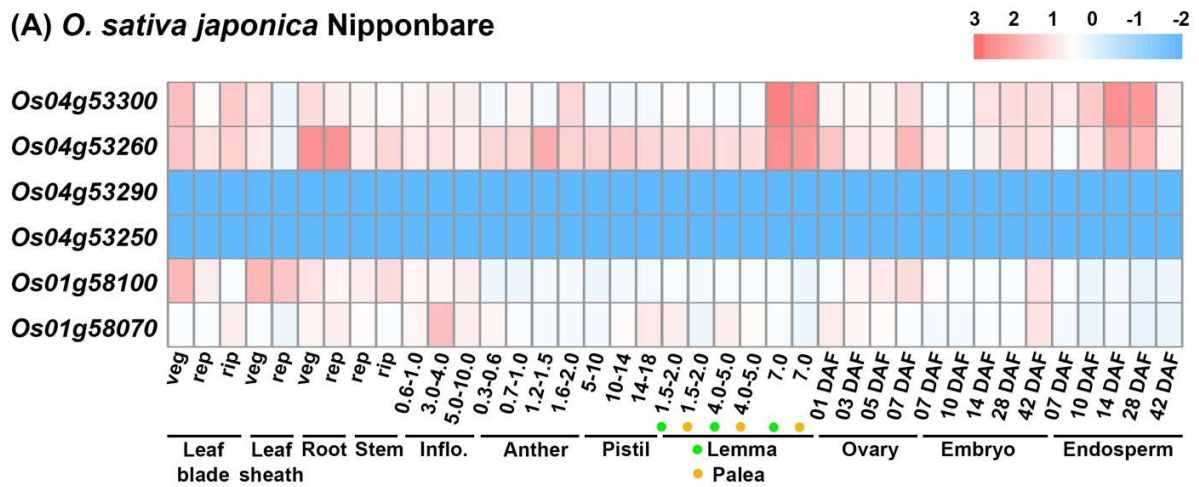
Supplementary Table S1. Sources and accession numbers for the species investigated in this study. Genomic and protein sequence data were obtained from CNCB (<https://ngdc.cncb.ac.cn/>), Ensembl Plants (<https://plants.ensembl.org/>), NCBI (<https://www.ncbi.nlm.nih.gov/>), and RGAP (<https://rice.uga.edu/>).

Species	Genome	ploidy	Database	Accession number
<i>Oryza sativa japonica</i> cv. Nipponbare	AA	Diploid	RGAP	GCA_001433935.1
<i>Oryza rufipogon</i>	AA	Diploid	NCBI	GCA_037997075.1
<i>Oryza sativa indica</i> cv. 9311	AA	Diploid	CNCB	GWHFLAP000000000.1
<i>Oryza nivara</i>	AA	Diploid	NCBI	GCA_000576065.2
<i>Oryza barthii</i>	AA	Diploid	NCBI	GCA_000182155.4
<i>Oryza glaberrima</i>	AA	Diploid	NCBI	GCF_000147395.1
<i>Oryza meridionalis</i>	AA	Diploid	NCBI	GCA_047496205.1
<i>Oryza glumipatula</i>	AA	Diploid	NCBI	GCA_000576495.2
<i>Oryza punctata</i>	BB	Diploid	NCBI	GCA_000573905.2
<i>Oryza malampuzhaensis</i>	BBCC	Tetraploid	NCBI	GCA_048564985.1
<i>Oryza minuta</i>	BBCC	Tetraploid	NCBI	GCA_048166525.1
<i>Oryza officinalis</i>	CC	Diploid	NCBI	GCA_008326285.1
<i>Oryza alta</i>	CCDD	Tetraploid	NCBI	GCA_047899615.1
<i>Oryza latifolia</i>	CCDD	Tetraploid	NCBI	GCA_048174585.1
<i>Oryza australiensis</i>	EE	Diploid	CNCB	GWHFIGT000000000.1
<i>Oryza meyeriana</i>	KK	Diploid	NCBI	GCA_047899645.1
<i>Oryza coarctata</i>	KKLL	Tetraploid	NCBI	GCA_030770085.1
<i>Oryza schlechteri</i>	HHKK	Tetraploid	NCBI	GCA_048320915.1
<i>Oryza rideyi</i>	HHJJ	Tetraploid	NCBI	GCA_047772315.1
<i>Oryza longiglumis</i>	HHJJ	Tetraploid	NCBI	GCA_048014755.1
<i>Oryza brachyantha</i>	FF	Diploid	NCBI	GCA_000231095.3
<i>Oryza granulata</i>	GG	Diploid	NCBI	GCA_005223365.2
<i>Leersia perrieri</i>	--	Diploid	NCBI	GCA_000325765.3
<i>Hordeum vulgare</i>	--	Diploid	Ensembl	GCA_904849725.1
<i>Brachypodium distachyon</i>	--	Diploid	NCBI	GCA_000005505.4

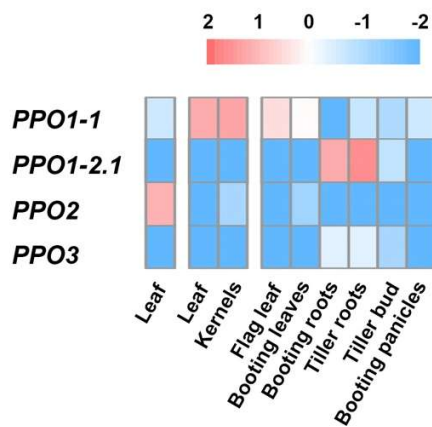
Supplementary Table S3. *PPO1* alleles in eight *Oryza glaberrima* cultivars. All genome assemblies were downloaded from NCBI (<https://www.ncbi.nlm.nih.gov/>). The assembly accession numbers and assembly names correspond to GenBank genome assembly identifiers. The IRGC accession and country of collection were searched from IRRI or web. *PPO1* alleles carrying the one–base-pair deletion are denoted as “-1,” whereas those without the mutation are indicated as “WT.”

Assembly Accession	Assembly Name	IRGC Accession	Country	Genotype
GCA_000147395.3	OglaRS2	96717	Senegal	-1
GCA_965117855.1	Og132_Mg12_LD	103544	Mali	WT
GCA_965117915.1	Og172_TOG7291_EH	104589	Burkina Faso	-1
GCA_965117845.1	Og20_TOG5438_LS	96751	Nigeria	WT
GCA_965117905.1	TOG5681	96793	Nigeria	WT
GCA_965117875.1	Og182_TOG7455_HR	None	Burkina Faso	-1
GCA_965117805.1	Og103_TOG6698_LF	None	Liberia	-1
GCA_965117825.1	Og44_TOG5672_MH	None	Nigeria	WT

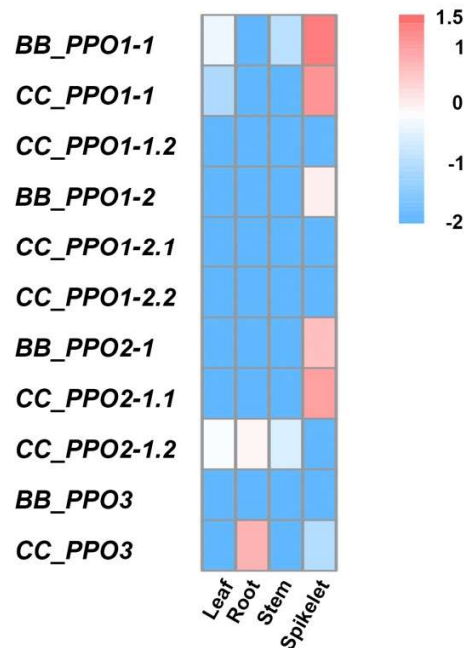
(A) *O. sativa japonica* Nipponbare



(B) *O. sativa indica* 9311



(C) *O. minuta*



Supplementary Figure S1. Transcript levels of PPO genes in *Oryza sativa japonica* Nipponbare, *O. sativa indica* 9311, and *O. minuta* across various tissues. (A) Transcript levels of *O. sativa japonica* (Nipponbare) in 11 tissues. Expression data were obtained from the Rice Annotation Project Database (RAP-DB, <https://rapdb.dna.affrc.go.jp>). Each tissue includes two to five developmental stages with three biological replicates. Average expression values were log₁₀-transformed after adding 0.01. “Inflo” indicates inflorescence; “Vet,” “Rep,” and “Rip” represent

vegetative, reproductive, and ripening stages, respectively. For inflorescence, anther, and lemma/palea, the unit is millimeters (mm); for pistil, the unit is centimeters (cm). DAF indicates days after fertilization. (B) Transcript levels of PPO genes in eight tissues of *O. sativa indica* 9311. Expression data were obtained from the Plant Public RNA-seq Database (PlantRNAdb, <https://plantrnadb.com/>). Each sample was analyzed in two biological replicates, and average values were log₁₀-transformed after adding 0.01. (C) Transcript levels of PPO genes in four tissues of *O. minuta*. Raw RNA-seq data were downloaded from the NCBI SRA archive (accessions: CRR1299413–CRR1299426) and processed using the HISAT2 pipeline for alignment and expression quantification. Each tissue was analyzed in three biological replicates, and average values were log₁₀-transformed after adding 0.01. Tissue names are indicated below each panel.