

Table S1 The primers used in this study.

Primer name	Seq (5'-3')
Hosta_10332-F	CACCGCCACGCCGAAGAAC
Hosta_10332-R	ATCGGTCATGTGCTCGCTGTTG
Hosta_55404-F	TCTTCGAGGTGTTTCATGCTCAA
Hosta_55404-R	CAGCAAGAGTGTCGTCCAGT
Hosta_287192-F	CAACCTGTGGAGGGTGCTTTTCG
Hosta_28719-R	TGCTTGGTGATCCGCGTTCTTG
Hosta_15837-F	TCTCAAGCAGCAGCACCTTAGC
Hosta_15837-R	GAAGCCAGAGCCGAAGCATCC
Hosta_28334-F	GTGGAGATGATGCACGCTGGAG
Hosta_28334-R	GGTCAAAGTCCCGGCCACAATC
Hosta_19733-F	CCACCTCCTCCTGCTCCTCTTC
Hosta_19733-R	GCTTCTGCTGCTGCGTTTTGC
Hosta_34831-F	AGTCCAGGTCAAGGGCTGATGC
Hosta_34831-R	TCAGGGTCCAACACCTCCTCAG
Hosta_9177-F	AGTCCAGGTCAAGGGCTGATGC
Hosta_9177-R	TCAGGGTCCAACACCTCCTCAG
Hosta_53559-F	GCTAGCTAGCCCTTTAGTAAATG
Hosta_53559-R	TGACGTAGGTAGCATGCCCA
HvActin-F	TCAAGCTGTGTTGTCCCTATAC
HvActin -R	GGAAGGGCGTAACCTTCATAA

Table S2 Mapping statistics of clean reads against full-length transcript references using Bowtie2

Sample	Total Reads	Mapped Reads(ratio)	Uniq mapped Reads(ratio)	Multi mapped Reads(ratio)
MS-1	47260134	32357896(68.47%)	4846816(14.98%)	27511080(85.02%)
MS-2	43521974	30804920(70.78%)	4119704(13.37%)	26685216(86.63%)
MS-3	48817996	33976508(69.60%)	4762810(14.02%)	29213698(85.98%)
FS-1	57848020	38184098(66.01%)	5984030(15.67%)	32200068(84.33%)
FS-2	44510762	30323738(68.13%)	4310378(14.21%)	26013360(85.79%)
FS-3	47488518	32036468(67.46%)	4708468(14.70%)	27328000(85.30%)
DS-1	43765572	29405696(67.19%)	4142466(14.09%)	25263230(85.91%)
DS-2	51461352	31283108(60.79%)	5778586(18.47%)	25504522(81.53%)
DS-3	50596606	33421994(66.06%)	5212560(15.60%)	28209434(84.40%)

Total Reads: Total clean reads after quality filtering;

Uniquely mapped reads (ratio): Uniquely mapped read count (mapping ratio);

Multiply mapped reads (ratio): Multiply mapped read count (mapping ratio).

Table S3 Differentially Expressed Genes in Deep Shade (DS) versus Moderate Shade (MS) by Functional Category

Metabolic Process Category	Up-regulated in Deep Shade (ZQY > ZBG)	Down-regulated in Deep Shade (ZQY < ZBG)
Photosynthesis	Hosta_21452, Hosta_24170, Hosta_24421, Hosta_41286, Hosta_43833, Hosta_11978, Hosta_230, Hosta_8434, Hosta_1193, Hosta_33789, Hosta_22418, Hosta_30404, Hosta_18060, Hosta_4762, Hosta_14288	Hosta_20786, Hosta_5515, Hosta_510
Plant hormone signal transduction	Hosta_37835, Hosta_41295, Hosta_11500, Hosta_53417, Hosta_19405, Hosta_50844, Hosta_24562	Hosta_11888, Hosta_8799, Hosta_19024, Hosta_22819, Hosta_43104, Hosta_25634
Plant secondary metabolites	Hosta_18326, Hosta_28824	Hosta_15166, Hosta_24677, Hosta_28092, Hosta_32959, Hosta_3887, Hosta_29623, Hosta_19928, Hosta_19449

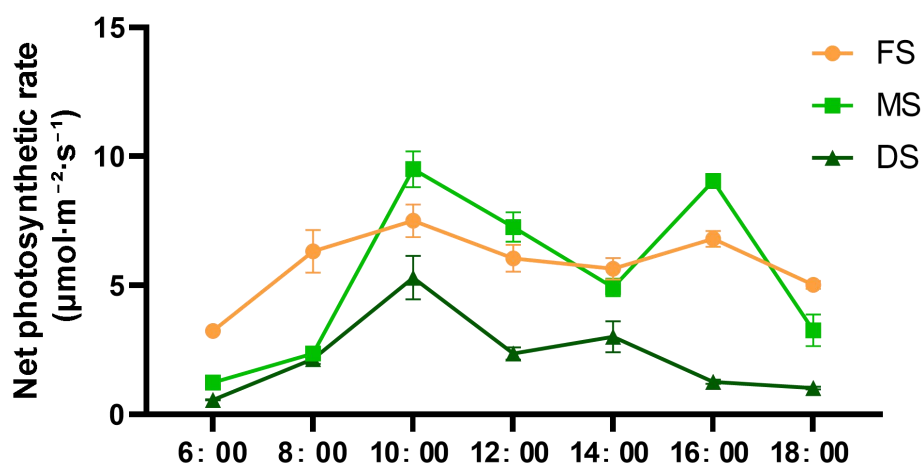


Figure S1 Net photosynthetic rate of *H. ventricosa* at FS, MS and DS treatments, at 2 h intervals from 6:00 to 18:00. Orange circles, green squares, and dark green triangles represent the FS (full sunlight treatment), MS (moderate shade treatment), and DS (deep shade treatment) groups, respectively. Vertical error bars indicate the standard error of the mean (SEM) of biological replicates.

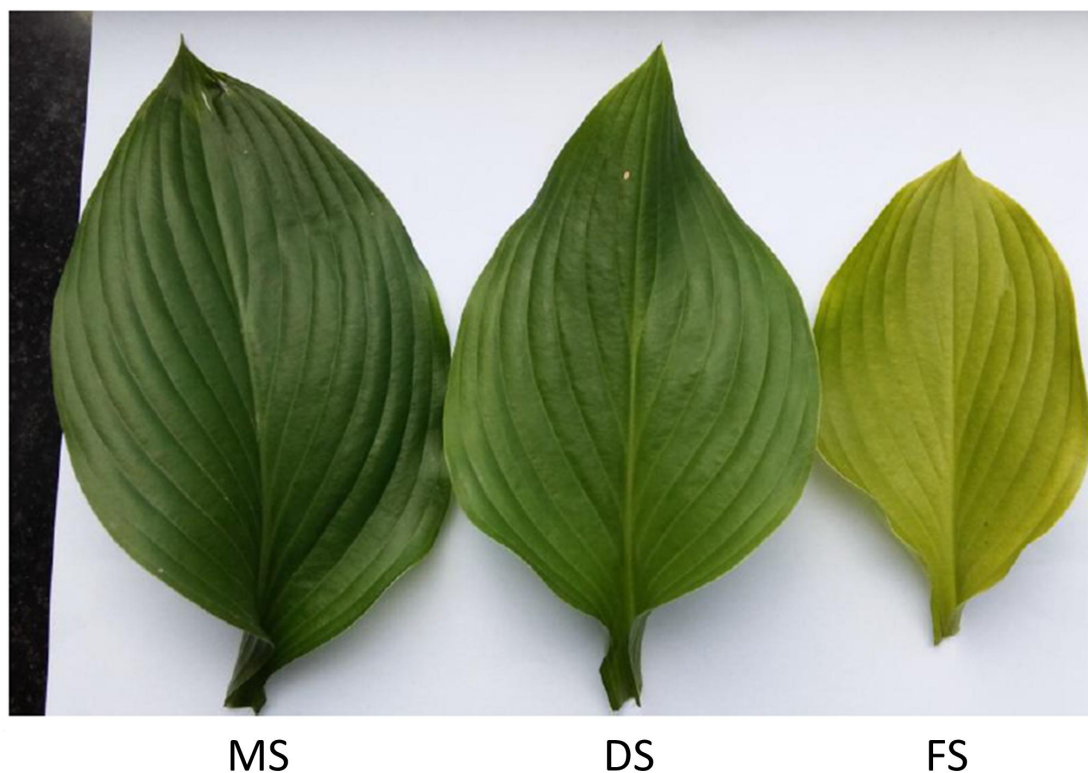


Figure S2 Leaf phenotype of *H. ventricosa* at FS, MS and DS groups
Representative leaves showing yellow-green color change induced by strong light. FS: full sunlight group, MS: moderate shade group, DS: deep shade groups.