# Supplemenatary Materials

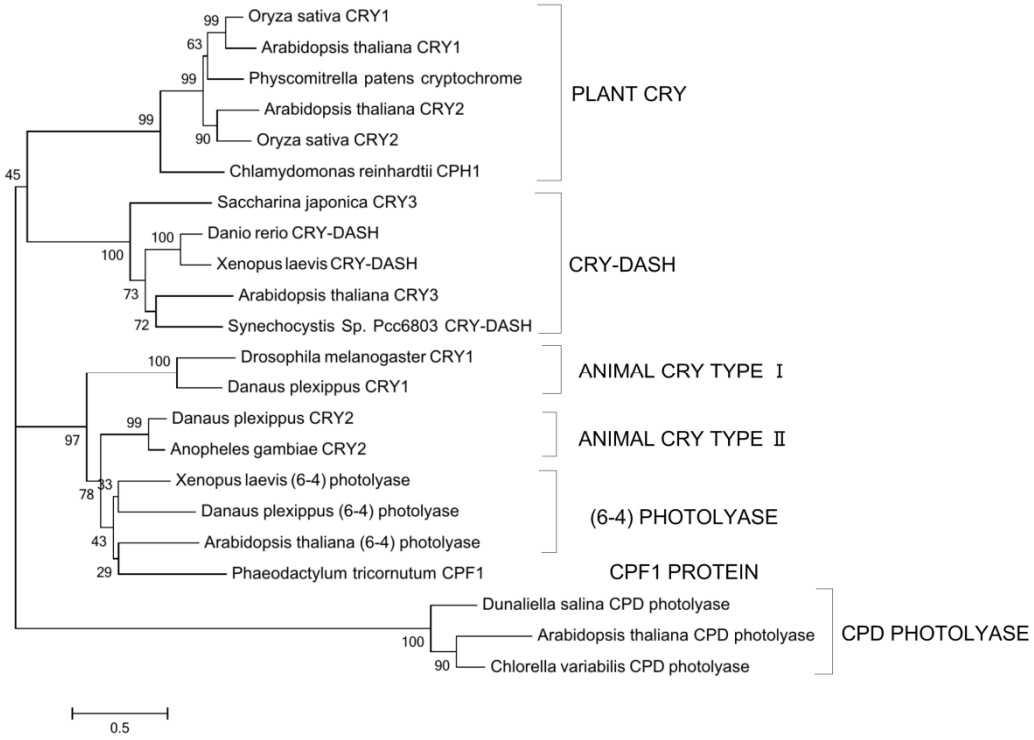


**Figure S1.** Phylogenetic analysis of CRY-DASHs. In total, 22 protein sequences were used to perform phylogeny analysis using the MEGA 6.0 platform with the neighbor-joining method. Bootstraps of 1000 replicates are expressed in percentage.

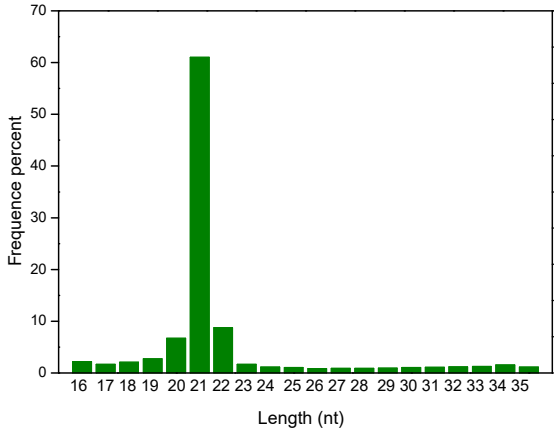


**Figure S2.** Length distributions of small RNAs in *S. japonica*.

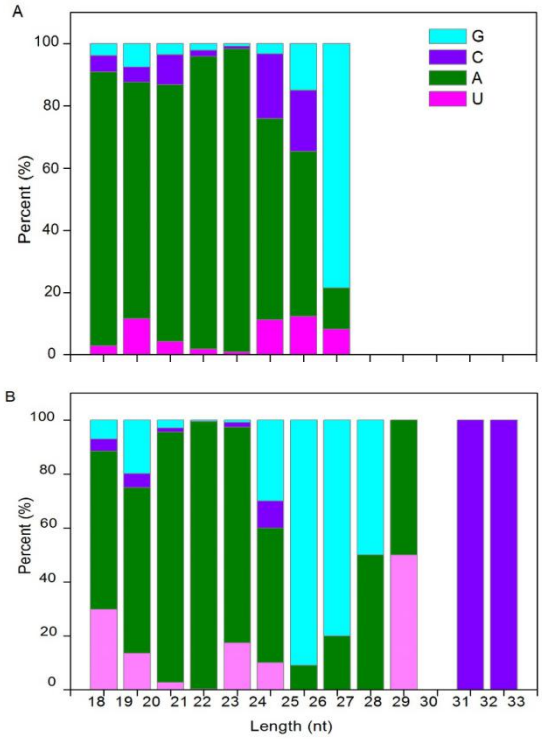


**Figure S3.** Base bias on the first site of novel (**A**) and known (**B**) miRNAs with specific lengths.

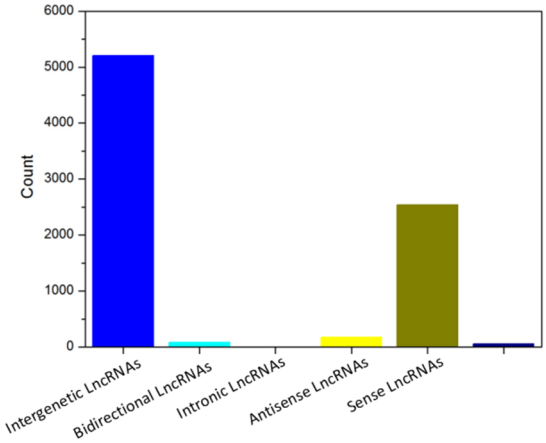


**Figure S4.** Classification of lncRNA based on their position.

**Table S1.** Summary of small-RNA seq reads mapping to *S. japonica* reference genome. The suffixes -1, -2 indicate biological replicates for each sample.

| Sample | Total Reads | Match Reads | Ratio |
|---|---|---|---|
| sjDR-1 | 17021748 | 12137953 | 71.31% |
| sjDR-2 | 14696034 | 10186706 | 69.32% |
| sjBL-1 | 13404621 | 9518639 | 71.01% |
| sjBL-2 | 13674165 | 9969389 | 72.91% |
| sjWL-1 | 13199760 | 9539465 | 72.27% |
| sjWL-2 | 9352909 | 6478724 | 69.27% |

**Table S2.** Summary of lncRNA library reads mapping to the reference genome of *S. japonica* in strand-specific RNA-seq library. The suffixes-1, -2 indicate biological replicates for each sample.

| Sample | Total reads | Match reads | Ratio |
|---|---|---|---|
| sjDR-1 | 86003128 | 77156097 | 89.71% |
| sjDR-2 | 93901340 | 80952915 | 86.21% |
| sjBL-1 | 104039374 | 95201422 | 91.51% |
| sjBL-2 | 86321882 | 80310174 | 93.04% |
| sjWL-1 | 113955214 | 104651692 | 91.84% |
| sjWL-2 | 78715228 | 71700462 | 91.09% |

**Table S3.** List of primers used in the study.

| Primer | Sequence (5′ to 3′) | Description |
|---|---|---|
| CRY-DASH-5O | CCCCAAGTGGAATATGGAGTTGCCATTC | 5′ RACE |
| CRY-DASH-5I | CCCGCCGTCTCGCCCCCCTTGAA | 5′ RACE |
| CRY-DASH-3O | CAAGGAGGTCTGGGGCAATG | 3′ RACE |
| CRY-DASH-3I | CTGCCTTCCGACTTGCCGTT | 3′ RACE |
| CRY-DASH-F | CATATGATGGCGAGCTTTTCATCTGA | ORF amplification |
| CRY-DASH-R | GAATTCCTAGGAAAACTGCCGAAACG | ORF amplification |
| qCRY-DASH-F | AATGGAGGTCGGGAAGTAC | qRT-PCR for *SjCRY-DASH* |
| qCRY-DASH-R | CCCCCAAGTGGAATATGG | qRT-PCR for *SjCRY-DASH* |
| Actin-F | GACGGGTAAGGAAGAACGG | qRT-PCR for *β-actin* |
| Actin-R | GGGACAACCAAAACAAGGGCAGGAT | qRT-PCR for *β-actin* |
| U6-F | TCGGGGACATCCGATAAAATTGGAA | qRT-PCR for *U6* |
| U6-R | GGACCATTT-CTCGATTTATGCGTGTCA | qRT-PCR for *U6* |
| novel-m3234-5p | CTCAACTGGTGTCGTGGAGTCGGCAATT CAGTTGAGCCGGTAG | RT-primer |
| novel-m3234-5p-F | GCCGAGTCCAGCCCGGCGTT | qRT-PCR for novel-m3234-5p |
| novel-m3234-5p-R | CTCAACTGGTGTCGTGGA | qRT-PCR for novel-m3234-5p |
| TCONS_00001280-F | TAGTGCATTCGGTCCCCCTT | qRT-PCR for TCONS_00001280 |
| TCONS_00001280-R | ACCAAGCCCGTACCAACTCT | qRT-PCR for TCONS_00001280 |
| TCONS_00002718-F | AGCGCACTGCTGTAACTAACTGC | qRT-PCR for TCONS_00002718 |
| TCONS_00002718-R | TCACTTGTTCGCGTCCACGTTG | qRT-PCR for TCONS_00002718 |
| TCONS_00006247-F | AGCTCCACGCACGTTATTCTTCAG | qRT-PCR for TCONS_00006247 |
| TCONS_00006247-R | AATGACACAGCAGTACCACGACAG | qRT-PCR for TCONS_00006247 |
| TCONS_00008286-F | CGTGACGACTCCACATTCCA | qRT-PCR for TCONS_00008286 |
| TCONS_00008286-R | GGCGTGGTAATCGGGTTGAA | qRT-PCR for TCONS_00008286 |
| TCONS_00017519-F | TGCTGCGATGACCTGAACTAACTG | qRT-PCR for TCONS_00017519 |
| TCONS_00017519-R | TGGTGCAGTTGGTGTAACAGGTAC | qRT-PCR for TCONS_00017519 |
| TCONS_00009907-F | GACGACGACGTATGGATTGGAACC | qRT-PCR for TCONS_00009907 |
| TCONS_00009907-R | TAGCTCTGCCGCCGAACATCTAG | qRT-PCR for TCONS_00009907 |
| TCONS_00043396-F | ACGATTACAAGGTGGCACGG | qRT-PCR for TCONS_00043396 |
| TCONS_00043396-R | CTGTTTGCTCGGCTGGCAT | qRT-PCR for TCONS_00043396 |
| TCONS_00043393-F | TCAGAGAGTGACAGCAAGGCGG | qRT-PCR forTCONS_00043393 |
| TCONS_00043393-R | CGGCCCGGGTTGAGCTTTAC | qRT-PCR forTCONS_00043393 |
| TCONS_00008371-F | GGCTGACGCCGCTCGCTA | qRT-PCR forTCONS_00008371 |
| TCONS_00008371-R | GCATCCCGAGCATGTTTTGCA | qRT-PCR forTCONS_00008371 |

**Phylogenetic Analysis**

Alignments of cryptochrome and photolyase protein sequences were performed with the ClustalW algorithm using the following parameters: for pairwise alignments, a gap opening penalty of 10 and a gap extension penalty of 0.1. For multiple alignments, a gap opening penalty of 10 and a

gap extension penalty of 0.2 were used. A Gonnet weight matrix was used with residue-specific penalties ON, hydrophilic penalties ON, a gap separation distance of 4, end gap separation OFF, negative matrix OFF, and a delay divergent cutoff of 30%. A phylogenetic tree was constructed by the neighbour-joining method [1], and a bootstrap consensus tree was obtained after 1000 replications. Parameters were set as follows: Poisson correction model, complete deletion of gaps/missing data, and uniform rates among sites.

**Reference**

1. Saitou N, and Nei M. The neighbor-joining method: A new method for reconstructing phylogenetic trees. *Mol. Biol Evol*. 1987; 4:406-425.