

Supplementary Materials for

Temporal gene expression patterns in the coral *Euphyllia paradivisa* reveal the complexity of biological clocks in the cnidarian-algal symbiosis

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Sci. Adv. **8**, eabo6467 (2022)
DOI: 10.1126/sciadv.abo6467

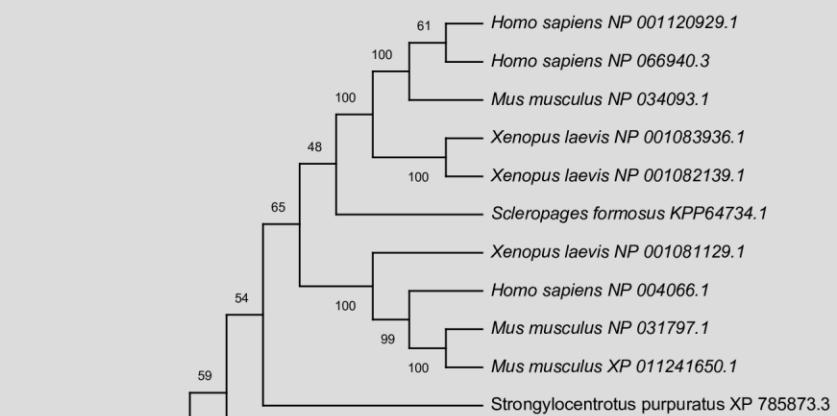
The PDF file includes:

Figs. S1 and S2
Table S1
Legend for table S2
Legends for data S1 to S3

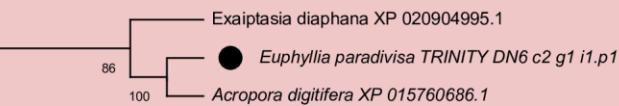
Other Supplementary Material for this manuscript includes the following:

Table S2
Data S1 to S3

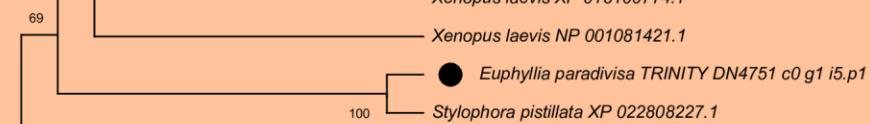
Animal CRY-IIIs



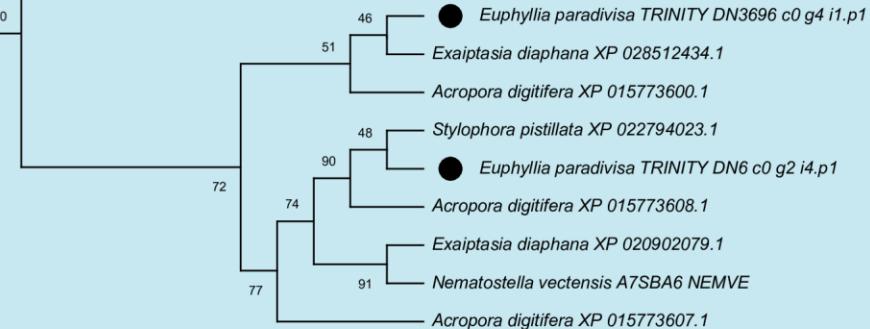
Anthozoan CRY-IIIs



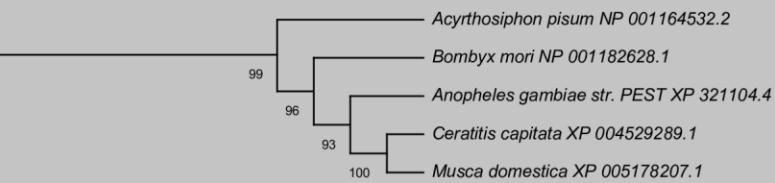
(6-4) PLs



AnthoCRYs



CRY-Is



CRY-DASHs

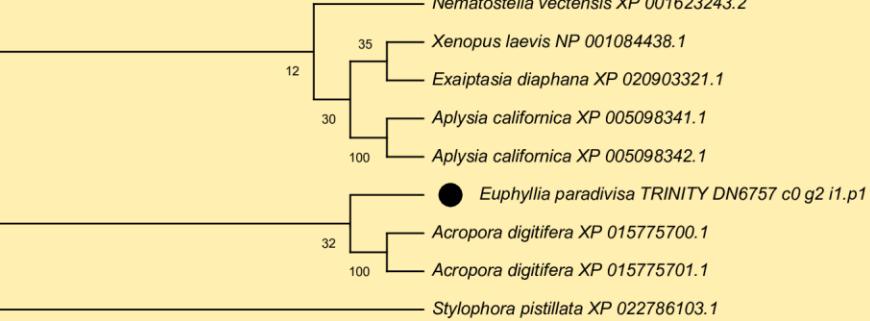


Fig. S1. Phylogenetic analysis of *Cry* genes. Maximum Parsimony tree, bootstrap method with 1,000 iterations, aligned by MUSCLE codons generated using the MEGA X software version 10.0.5. Reference sequences were chosen based on Supplementary Figure 5 in Gornik et al. 2021 (27). *Euphyllia paradvisa* proteins are marked with a solid circle.

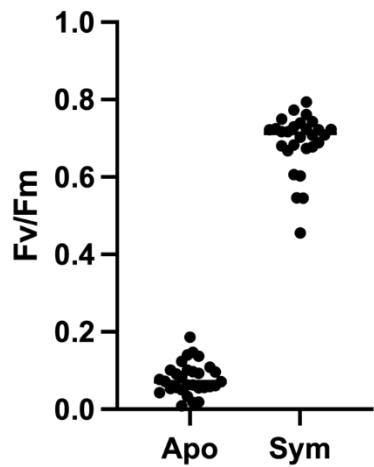


Fig. S2. Photosynthetic quantum yield (F_v/F_m) of *Euphyllia paradvisa* symbionts.
Measurements of representative symbiotic (Sym) and aposymbiotic (Apo) *E. paradvisa* polyps ($n = 80$) were taken prior to the experiment using a diving PAM (pulse amplitude modulator) fluorometer (Walz).

| Gene name | Subgroup | Period (hour) | RAIN P-value |
|------------------------|--------------|------------------|--------------|
| <i>Cry1</i> | LDsym | 24*** | 1.97E-16 |
| | DDsym | 24*** | 2.62E-05 |
| | LDapo | 24*** | 7.40E-14 |
| | DDapo | 24*** | 5.29E-05 |
| <i>Cipc-like</i> | LDsym | 24*** | 3.8E-17 |
| | DDsym | 24*** | 0.000000711 |
| | LDapo | 24*** | 1.88E-13 |
| | DDapo | 24** | 0.001187469 |
| <i>Hlf</i> | LDsym | 24*** | 1.05E-22 |
| | DDsym | 24*** | 2.99E-06 |
| | LDapo | 24*** | 8.10E-21 |
| | DDapo | 24*** | 0.000129121 |
| <i>Tef</i> | LDsym | 24*** | 1.93E-15 |
| | DDsym | 24** | 0.002730665 |
| | LDapo | 24*** | 3.70E-16 |
| | DDapo | 24*** | 0.00012925 |
| <i>Hebp2</i> | LDsym | 24*** | 3.89E-10 |
| | DDsym | 24*** | 9.40E-05 |
| | LDapo | 24*** | 1.79E-17 |
| | DDapo | 24*** | 0.00084787 |
| <i>Clock</i> | LDsym | 24*** | 6.93E-17 |
| | DDsym | 24* | 0.033 |
| | LDapo | 24*** | 3.77E-14 |
| | DDapo | 24 ^{ns} | 0.349 |
| <i>Cry2</i> | LDsym | 24*** | 2.52E-08 |
| | DDsym | 24 ^{ns} | 0.056 |
| | LDapo | 24*** | 6.85E-11 |
| | DDapo | 24 ^{ns} | 0.602 |
| <i>Casein kinase 1</i> | LDsym | 24*** | 4.05E-08 |
| | DDsym | 24 ^{ns} | 0.085 |
| | LDapo | 24*** | 6.47E-07 |
| | DDapo | 24 ^{ns} | 0.186 |
| <i>Cry-DASH</i> | LDsym | 24*** | 4.98E-09 |
| | DDsym | 24 ^{ns} | 0.339 |
| | LDapo | 24*** | 4.98E-09 |
| | DDapo | 24* | 0.011 |

Table S1. RAIN results for candidate circadian clock genes of *E. paradoxa* subgroups.

*Asterisks indicate the power of significance: * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$; ^{ns}not significant.

†Exact Benjamini-Hochberg corrected RAIN P-values.

Table S2. 24-h to 12-h period alternations.

List of 59 *E. paradvisa* annotated transcripts showing 24-h to 12-h period alternations between symbiotic and aposymbiotic morphs.

Data S1. Annotation and expression patterns of rhythmic transcripts in each subgroup.

Each subgroup: **A**) LDsym24, **B**) DDsym24, **C**) LDapo24, **D**) DDapo24, **E**) LDsym12, **F**) Dsym12, **G**) LDapo12, **H**) DDapo12.

Data S1I. Eight-way Venn diagram analysis.

Data S2. Gaussian mixture models (GMM) clustering results.

Data S2A. Results for rhythmic transcripts of the LDapo24, LDsym24, and DDsym24 subgroups.

Data S2B. Results for rhythmic transcripts of the LDapo12, LDsym12, and DDsym12 subgroups.

Data S3. Functional enrichment analysis.

Data S3A. Analysis of the rhythmic genes with a precise 24-h period of each *E. paradvisa* subgroup found in Cluster 1.

Data S3B. Analysis of the rhythmic genes with a precise 24-h period of each *E. paradvisa* subgroup found in Cluster 2.

Data S3C. Analysis of the rhythmic genes with a precise 24-h period of each *E. paradvisa* subgroup found in Cluster 3.

Data S3D. Analysis of the rhythmic genes with a precise 24-h period of each *E. paradvisa* subgroup found in Cluster 4.

Data S3E. Analysis of the rhythmic genes with a precise 12-h period of each *E. paradvisa* subgroup found in Cluster 1.

Data S3F. Analysis of the rhythmic genes with a precise 12-h period of each *E. paradvisa* subgroup found in Cluster 2.

Data S3G. GO analysis of rhythmic genes showing 12-h to 24-h period alternations between sym to apo *E. paradvisa*

Data S3H. GO analysis of rhythmic genes showing 24-h to 12-h period alternations between sym to apo *E. paradvisa*