Supplemental Figure and Table Legends

Sup Figure 1) Simulation of *LHY* mRNA levels using the 3-loop model for WT and *prr7;prr9* mutant plants.
a) Comparison of simulated *LHY* mRNA levels in WT plant under constant light (LL) conditions (dotted line, left axis), with corresponding experimental data extracted from (Farre et al., 2005) (solid line, right axis).
b) Comparison of simulated *LHY* mRNA levels in *prr7;prr9* plant under constant LL conditions (dotted line, left axis), with corresponding experimental data extracted from (Farre et al., 2005) (solid Line, right axis). Translation rate of *PRR7/9* mRNA in simulated mutant is 1/1000 WT value.

Sup Figure 2) Stability analysis of optimal parameter set in the 3-loop model.
The period and amplitude of *LHY* mRNA oscillations over 300h in LL are calculated for a 5% increase and decrease to each parameter in turn. The red circle represents the period and amplitude of the simulation using the optimal parameter values.

Sup Figure 3) Comparison of 3-loop model simulations of *TOC1* mRNA levels for WT, *lhy;cca1*, and *gi;lhy;cca1* plants to data.
a) Simulation of *TOC1* mRNA levels in WT (Black line), *lhy;cca1* (green line) and *gi;lhy;cca1* (red line) in LL conditions.
b) Simulation of *TOC1* mRNA levels in WT (Black line), *lhy;cca1* (green line) and *gi;lhy/cca1* (red line) in DD conditions.
c-f) Experimental data showing *TOC1:LUC* (C,E) and *CCR2:LUC* (D,F) expression patterns in WT (solid black line) *lhy;cca1* double (solid green line) and *gi;lhy;cca1* triple (solid red line) mutants under constant red/blue light (c,d) or constant dark (E,F) conditions. Luminescence values were normalised to the average of counts recorded during the course of the experiment. Time zero corresponds to the onset of the constant conditions (c,d) or to the time of the first subjective dawn (e,f). White and black bars indicate constant light or dark conditions, respectively.

Sup Figure 4) Simulations and experimental data for mean *TOC1* mRNA levels in WT, *lhy;cca1* and *gi;lhy;cca1* mutant plants.
a) Experimental data showing mean expression levels of *TOC1:LUC* in WT, *lhy;cca1* double and *gi;lhy;cca1* triple mutant under constant red/blue light (white bars) or constant dark (black bars). Luminescence counts were recorded at 1-2 hr intervals for five days under the specified light condition. Error bars represent standard error values.
b) Simulated mean expression levels of TOC1 for WT, *lhy;cca1, and gi;lhy;cca1* conditions in LL (white bars) and DD (black bars).

Sup Figure 5) Simulations of effect of change in photoperiod on *TOC1* and *LHY* mRNA levels for one loop LHY/CCA1 – TOC1 network (Locke et al., 2005a).
a) *LHY* mRNA levels and b) *TOC1* mRNA levels under LD8:16. c) *LHY* and d) *TOC1* mRNA levels under LD16:8 conditions.

Sup Figure 6) Simulations of effect of change in photoperiods on *TOC1* and *LHY* mRNA levels for interlocked feedback loop network (Locke et al., 2005b).
a) *LHY* mRNA levels and b) *TOC1* mRNA levels under LD8:16. c) *LHY* and d) *TOC1* mRNA levels under LD16:8.

Sup Figure 7) An *x* mutation can de-couple the two clocks.
Simulation of *LHY* mRNA levels and *TOC1* mRNA levels in an *x* mutant background, shown for an interval of free running rhythm in LL. Translation rate of *X* mRNA in simulated mutant is 1/1000 WT value. Peak levels of *TOC1* and *LHY* mRNA can be seen to go in and out of phase with each other. Data was normalised to the maximum level of expression.

Sup Table 1) Optimal parameter values for the 3-loop model.

References

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