Sup Figure 1: Network diagram for the single-loop *LHY/CCA1-TOC1* network. TOC1 protein in the nucleus and light mediated by protein P (not shown) activate transcription of mRNA of *LHY*, which represents both *LHY* and *CCA1*. When LHY protein reaches the nucleus it represses *TOC1* mRNA transcription. Symbol convention as in Figure 1.

Sup Figure 2: Simulations of the *LHY/CCA1-TOC1-X* network. Left panel: simulated TOC1 protein levels (dashed line), data from (Mas et al. 2003) (solid line). Maxima have been normalised to 1 for each trace. Right panel: Prediction of *X* mRNA (dotted line) and X protein levels (black line). In this and other supplementary figures, filled box above panel, dark interval; open or no box, light interval.

Sup Figure 3: Stability analysis of optimal parameter set in the interlocked feedback loop model. The period and amplitude of *TOC1* mRNA oscillations over 300h in LL are calculated for a 5% increase and decrease to each parameter value in turn. The circle represents the period and amplitude of the optimal parameter values.

Sup Figure 4: Simulations of the interlocked feedback loop network in LD12:12 and LL. Left panel: mRNA levels for WT in LD12:12 then LL. *LHY* mRNA level peaks at dawn (dotted line) and *TOC1* mRNA level (solid line) at dusk in LD cycles. Period is 25h in LL. Right panel: mRNA levels for *cca1;lhy* double mutant in LD12:12 then LL. *TOC1* mRNA peaks in the middle of the day and oscillates with an 18h period in LL, as seen experimentally in Fig 2.

Sup Figure 5: Effects of altered photoperiod on circadian rhythms. Simulations using the interlocked feedback network (dashed line), compared to data (solid line), under LD16:8 (upper panels) and LD8:16 (lower panels). *CCR2* mRNA data from (Roden et al. 2002) is used as a late evening marker to compare to simulations of *TOC1* mRNA (left-hand panels). *LHY* mRNA levels are from (Yanovsky & Kay 2002), highest value of data and simulation is set to 1 (right-hand panels).

Sup Figure 6: Effects of partial *y* loss-of-function in the interlocked feedback network. Simulation of *LHY* mRNA in WT (dashed line) and simulated *gi* mutant (solid line), simulated by halving the *Y* mRNA translation rate compared to WT.

Sup Table 1: Optimal parameter values for *LHY/CCA1-TOC1-X* network

Sup. Table 2: Comparison of models: period estimates of the 3 models developed for the Arabidopsis circadian clock network are compared to experimental data. The simulation estimates are the average period over 300h in DD, for WT, *cca1* single mutant, and *cca1;lhy* double mutant. Experimental data for WT and *cca1* mutant periods from (Alabadi et al. 2002), *cca1;lhy* data from Fig 2.

Sup Table 3: Optimal parameter values for interlocked feedback loop network

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