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A developmental cycle masks output from the circadian oscillator under conditions of choline deficiency in *Neurospora*

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In *Neurospora*, metabolic oscillators coexist with the circadian transcriptional/translational feedback loop governed by the FRQ (Frequency) and WC (White Collar) proteins. One of these, a choline deficiency oscillator (CDO) observed in *chol-1* mutants grown under choline starvation, drives an uncompensated long-period developmental cycle (≈ 60 – 120 h). To assess possible contributions of this metabolic oscillator to the circadian system, molecular and physiological rhythms were followed in liquid culture under choline starvation, but these only confirmed that an oscillator with a normal circadian period length can run under choline starvation. This finding suggested that long-period developmental cycles elicited by nutritional stress could be masking output from the circadian system, although a caveat was that the CDO sometimes requires several days to become consolidated. To circumvent this and observe both oscillators simultaneously, we used an assay using a codon-optimized luciferase to follow the circadian oscillator. Under conditions where the long-period, uncompensated, CDO-driven developmental rhythm was expressed for weeks in growth tubes, the luciferase rhythm in the same cultures continued in a typical compensated manner with a circadian period length dependent on the allelic state of *frq*. Periodograms revealed no influence of the CDO on the circadian oscillator. Instead, the CDO appears as a cryptic metabolic oscillator that can, under appropriate conditions, assume control of growth and development, thereby masking output from the circadian system. *frq*-driven luciferase as a reporter of the circadian oscillator may in this way provide a means for assessing prospective role(s) of metabolic and/or ancillary oscillators within cellular circadian systems.

Frequency-less oscillator | clock

Most organisms on Earth, from cyanobacteria to humans, use an endogenous circadian clock to adapt to daily oscillations of environmental cues (e.g., light, temperature). A functional clock provides adaptive advantages during evolution (1), and many metabolic and developmental processes appropriate for a certain time of day are under control of the endogenous clock. The circadian biological clock displays close to the same period length across a physiological temperature range (2). Temperature compensation in particular sets the circadian biological clock apart from other more typical chemical and biological reactions that run faster when temperature goes up.

The filamentous fungus *Neurospora crassa* has become a salient model system in circadian biology research since a mutant strain (*bd⁻*) was identified in the 1960s (3). The distinct spore bands formed in a rhythmic pattern in strains containing *bd* during growth on an agar surface have made *Neurospora* a tractable system in which to genetically screen for clock components. Historically, two rationales have been used: One was to identify new mutants that changed only clock properties and no other processes. The other route, based on the idea that the clock might arise from metabolic processes, was to screen already known metabolic mutants for clock phenotypes (4, 5).

Genetic screens with the first rationale identified the gene *frequency* (*frq*) (6), whose subsequent cloning opened up molecular analyses of a circadian feedback loop (7, 8). The

FRQ-WCC (Frequency–White Collar Complex) oscillator (FWO) forms a central aspect of the *Neurospora* circadian system (9–12). In this oscillator, White Collar-1 (WC-1) and White Collar-2 (WC-2), two GATA-family transcriptional factors, drive *frq* expression beginning in the late subjective night (13). *frq* RNA levels peak in the subjective morning when FRQ protein, in complex with the FRQ-interacting RNA helicase (FRH), enters into the nucleus and acts as a negative element to inhibit WCC activity (7, 14–17). This causes *frq* levels to decline to a trough in the subjective evening. Mature and phosphorylated FRQ is then ubiquitinated and degraded by the proteasome pathway (18–20).

Strains lacking *frq*, *wc-1*, or *wc-2* have defects in the clock and lose circadian regulation of conidiation under most conditions (21–23). Intriguingly, however, rhythms of conidiation, metabolic regulation, and gene expression can still be observed under certain conditions in the absence of the FWO (reviewed in refs. 11, 24, and 25). Those rhythms, regulated by cryptic FRQ-less oscillators (FLOs) (26), provide a new layer of complexity to clock research and are frequently mentioned as having potential roles within the circadian system (e.g., refs. 24 and 27). Although these FLOs when analyzed on their own have generally lost some or all circadian characteristics, the possibility remains that they may interact with the known intracellular cellular circadian feedback loop, contribute to robustness, or provide driven oscillations with important roles in output. The relative position(s) and importance of these metabolic oscillators within the clockwork have emerged with recent years as a salient question in the study of cellular circadian systems, of which *Neurospora* is a prime example.

Among the fruits of the second genetic approach to identify clock mutants, two lipid biosynthesis mutants were found to affect sporulation rhythmicity. One is *cel*, a mutant in fatty acid synthesis displaying an ≈ 40 -h period rhythm of conidiation on solid medium supplemented with unsaturated fatty acids (28). The other is *chol-1*, whose product catalyzes the first methylation step in the conversion of phosphatidylethanolamine to phosphatidylcholine (29). The mutant shows a conidiation rhythm, controlled by a choline deficiency oscillator (CDO), with a period > 50 h under choline starvation (30) that can be entrained by light to periods near its intrinsic length but not to periods within the circadian range. The rhythm is pH-compensated but not temperature-compensated (30–32). The period length of the

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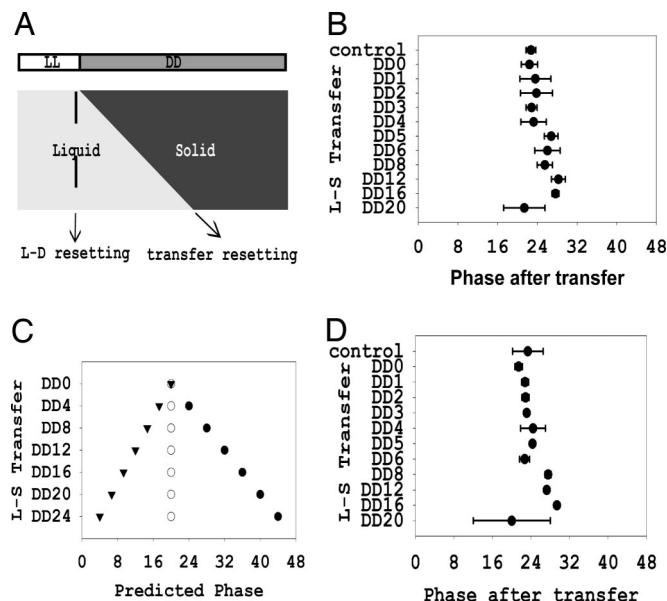


Fig. 2. Normal circadian rhythms in liquid cultures not supplemented with choline. (A) Diagram of the conidia transfer assay (see *Materials and Methods*). If the clock is not reset by conidia transfer from liquid culture to race tube media, phases should be similar in all samples (light to dark reset). See *Results* for details. (B) Phase in WT conidia transfer assay. Phases of all WT cultures are similar regardless of the time of conidia transfer, indicating that liquid-to-solid medium transfer does not reset clock (error bars = 1 SD; $n = 6$). (C) Predicted phase differences in strains with longer (filled circles, period = 66 h), equal (open circles, period = 22 h), or shorter (solid inverted triangles, period = 11 h) period lengths in liquid culture compared with solid culture (see *Results* for details). (D) Conidia transfer assay of *chol-1*. Phase is reported from *chol-1* cultured in liquid with no choline and inoculated onto race tubes supplemented with 100 μ M choline (error bars = 1 SD; $n = 6$). Lack of significant phase differences among cultures transferred at different times suggests that the period under choline deficiency conditions is similar to that of fully choline-supplemented cultures.

This suggests that the circadian clock under choline starvation conditions runs with close to the same period as it does under choline supplementation on solid medium. Thus, the rhythm of the *chol-1* strain in liquid medium with choline starvation appears to be regulated by the FWO instead of the CDO.

Normal Circadian Rhythmicity Under Conditions of Choline Starvation in a Race Tube Assay. Although the results to this point had failed to shed light on any potential impact of choline starvation on the circadian system, there remained several strong caveats. First, it is difficult to know whether choline starvation in liquid culture is reached to the same degree as it is in cultures grown on solid medium lacking choline and expressing the CDO rhythm. Second, the CDO can sometimes take several days to become apparent. Third, and most importantly, we had not actually observed the FWO under conditions when we could also clearly follow the CDO. Because operation of the CDO is manifest only through its output in regulating growth and conidial development, we needed another assay for the FWO besides conidiation. To achieve this, we implemented a luciferase-based assay of WCC activity and circadian clock function. An optimized firefly luciferase reporter gene (36) under control of the *frq* promoter (*frqP-luc*) was used to follow the molecular rhythm of *frq* expression on solid medium in real time (see *Materials and Methods*). *chol-1; csp-1, frqP-luc* strains showed a long-period conidiation rhythm (≈ 78 h) on unsupplemented race tubes (Fig. 3A), consistent with previously published results for *chol-1; csp-1*

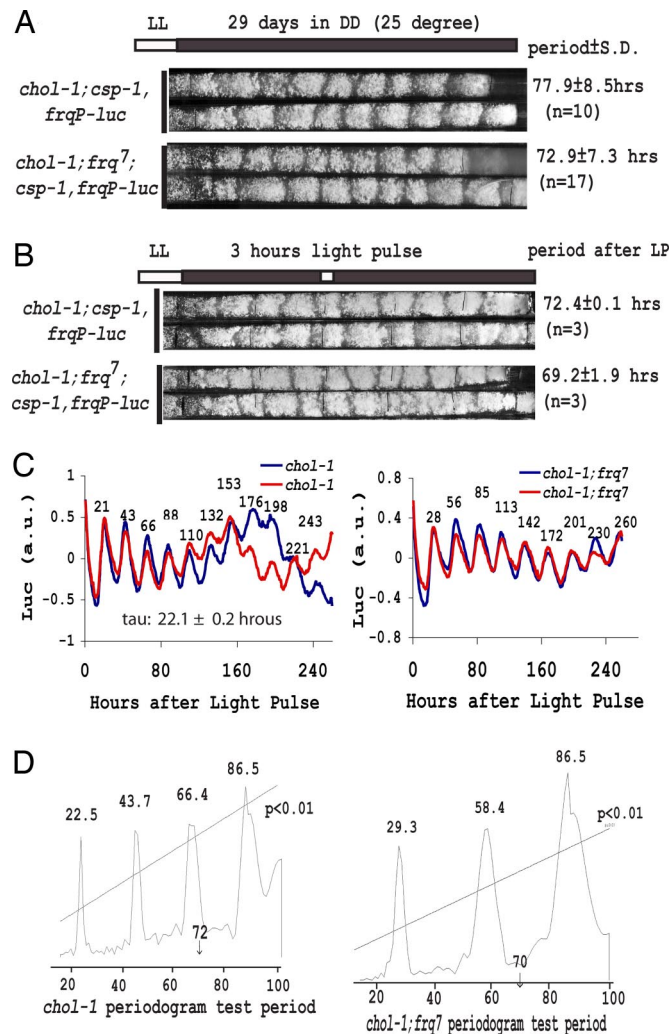


Fig. 3. *frq* allele-dependent luciferase rhythms with normal period lengths in a race tube assay under choline starvation conditions. (A) Characteristically elongated conidiation rhythms in *chol-1; csp-1, frqP-luc* and *chol-1; csp-1, frqP-luc; frq7* strains. (B) Race tube assay containing 12.5 μ M luciferin. Black lines were marked as reference points on the tube before strain growth. The 3 h of saturating light given after 292 h of growth (white bar) did not change the conidiation banding pattern but served to synchronize the FWOs in the culture. (C) Bioluminescence data collected from each of the whole race tubes and detrended to remove background reveals rhythms of ≈ 22 -h period in WT strains and ≈ 29 -h period in *frq7* strains. The rhythms were sustained for >10 days under choline starvation whereas ≈ 70 -h conidiation rhythms were still observed on the race tubes (B). Time values are marked on individual peaks of the detrended luciferase rhythms that show similar period and phase. (D) Periodogram analysis of the luciferase data using a window of 14–100 h shows a strong 22.5-h component in WT strain and a 29.3-h component in *frq7* with their multiples but no appreciable contribution of rhythms with periods near 70 h.

strains on minimal medium (30) and indicating that the strain was in full choline starvation and expressing the CDO.

The FWO was followed in the culture expressing the long-period CDO through the luciferase assay. To synchronize all of the FWO clocks, a 3-h light pulse was given to the race tube cultures after 292 h of growth, about halfway down to the tube (Fig. 3B). The long-period conidiation banding rhythm reflecting the CDO was not affected by the light pulse (compare Fig. 3A and B) as predicted based on previous results (30). Initially, luciferase activity arising from the whole race tube was followed and is plotted in Fig. 3C. Consistent with normal FRQ oscillations in liquid culture without choline (Fig. 1B), *frq* promoter-

the FWO and CDO coexist under choline deficiency conditions on solid media and that the FWO still maintains its circadian properties under these conditions. But we were unable to find evidence suggesting an influence of the CDO on the circadian properties of the FWO.

Discussion

Metabolic oscillators that do not require the transcription/translation-based FWO (FLOs) have been observed in *Neurospora* to influence many developmental and metabolic processes. The first FLO was identified two decades ago in *frq*-null strains where sometimes rhythmic banding would develop after several days' growth on race tubes (21, 25). Later, oscillations of gene expression, diacylglycerol levels, development, or nitrate reductase activity were found in either *frq*-null or *wc-1*-null strains (43–45). Recently, a FLO rhythm was discovered that requires WC-1 but not FRQ (46). In some cases the appearance of the FLO requires a specific genetic background (e.g., refs. 47–49) and in other cases specific nutritional supplements or the lack thereof (50–52). In all, at least nine different FLOs with periods that either are or can be in the circadian range are distinguishable based on some characteristic; although none of these has been shown to possess the full complement of circadian characteristics, most possess one or more of them, and nearly all FLOs have been suggested as possibly influencing the circadian system. The rationale for this is indeed attractive, because it seems plausible that metabolic oscillators operating in the same cytoplasm could or would in some way interact. Mechanisms of how those FLOs operate are still elusive, and the relationships between FLOs and the circadian FWO remain unknown, but the need for new tools and paradigms that can begin to bring order to and to describe a hierarchical relationship among this oscillatory menagerie has become apparent. The ability to directly monitor the circadian FWO in the absence of any of its outputs may be useful in this context.

The FLO revealed under choline deficiency conditions provided a manageable system in which to test this tool and approach, because this CDO is known to maintain its oscillation in the absence and presence of the FWO (31, 33). Here, we confirmed many of the basic characters of the CDO: It has a long period that is not influenced by the allelic state of *frq* in *frq*⁺ versus *frq*⁷, its phase is not consistent from culture to culture, it is not influenced by a short light treatment, and its period is not compensated between 20°C and 25°C.

We asked whether there was a connection between the CDO and the FWO and whether we could discover a role for the CDO in the circadian system. We began by following biochemical and physiological rhythms in liquid cultures starved for choline and found that under these conditions the FWO showed no apparent influence from the CDO. However, because little is known about the events associated with mutations leading to expression of the CDO, or how quickly CDO control is established after the start of choline starvation, there were clear caveats to these studies. The FWO, CDO, and most of the FLOs in *Neurospora* have been detected and observed only when one of these oscillators controls a rhythm in growth and development on race tubes. This precludes the observation of two or more rhythms at the same time. To circumvent this problem, we adopted a luciferase based assay of the FWO function. Using this assay we found that the circadian FWO functions without apparent alteration under conditions of obvious choline starvation. The FWO operates in parallel with the CDO in the same tissue at the same time but is apparently unaffected by the CDO (Fig. 3 and SI Movie 1). Although these studies identified no apparent role for the CDO in the circadian system, it is possible that additional work could detect such a role.

We have not, of course, determined whether there is any physiological relevance to the noncircadian control by the CDO.

The extreme variability of its period and phase, and the lack of correspondence between CDO periods and known environmental periodicities, hamper efforts to define significance. The highly episodic nature of CDO-controlled growth (reviewed in refs. 4, 10, and 24) distinguishes it from growth controlled by the circadian FWO and is suggestive of a relaxation oscillator perhaps timed by the slow accumulation of the metabolites that allow growth of the leaky *chol-1* auxotroph. Even the signals eliciting conidiation (by the circadian FWO) or temporarily overcoming a limitation (by the CDO) would be different; the nature of the signals promoting conidiation may be subtle and complex (53). At present, however, the most straightforward interpretation of the data presented here is that the CDO represents an alternative oscillatory state that can bypass circadian control of conidiation but appears in no way connected to the circadian system.

More generally, this study shows that, by using the luc rhythms as a reporter of the FWO circadian feedback loop, it will be possible to extend these studies to other noncircadian oscillators or even FLOs in *Neurospora* and thereby to dissect the hierarchy of controls and interacting oscillators within the circadian system.

Materials and Methods

Strains. All strains used carry the *ras-1*^{bd} mutation, which promotes expression of the conidiation rhythm (53). PL32-54 (*bd; csp-1; chol-1*) was a kind gift of P. L. Lakin-Thomas (York University, Toronto). In *frqP-luc* strains, a codon-optimized firefly luciferase gene under the control of the *frq* promoter was integrated into the *his-3* locus (36). The strain *chol-1; csp-1; frqP-luc* was a progeny from a cross between *frqP-luc* and PL32-54. The strain *chol-1; csp-1; frqP-luc; frq*⁷ was a progeny from a cross between *chol-1; csp-1; frqP-luc* and *frq*⁷. Strains *chol-1; csp-1*⁺ were cross-progeny from PL32-54 and WT strains.

Culture Conditions. All studies were performed at 25°C, except the specified 20°C or 28°C assays. Vogel's medium (pH 4.5) with 0.4% sucrose and 1.5% agar was used for race tube assays. Choline chloride from Sigma was used as a choline supplement. Period and phase values from race tube assays were measured by using the Chrono program (54) in choline-supplemented cultures. In *chol-1* mutant strains not supplemented with choline, growth rate and distance between conidiation bands were measured and period was calculated by dividing the banding distance by the growth rate.

Vogel's salts and 2% glucose were used for liquid culture (55). For time-course experiments, mycelial discs (8 mm in diameter for choline supplement growth and 20 mm in diameter for no choline supplementation) were inoculated into flasks containing liquid media.

For measurement of luciferase activity, solid race tube medium was supplemented with 12.5 μM luciferin. Light arising from *in vivo* luciferase activity was collected for 10 min every hour with a VersArray 1300 B/LN liquid nitrogen-cooled CCD camera from Princeton Instruments, controlled by a WinView/32 software from Roper Scientific. A Percival incubator was modified to fit the lens of the VersArray system. All luciferase rhythm data were analyzed by BRASS (Biological Rhythm Analysis Software System; www.amillar.org), in which estimates of periodicity are determined by FFT-NLLS (fast Fourier transform–nonlinear least squares) (56). The detrended rhythms as plotted were processed by using the “detrend” function in the Matlab software package. The periodograms were processed by using the Chrono program (54).

Protein Assays. Mycelial tissues were harvested from cultures in flasks and frozen in liquid nitrogen. The frozen tissues were ground in liquid nitrogen by using a mortar and pestle and

