

A mathematical model to understand how the liver tracks meal timing

Aurore Woller, and Marc Lefranc

Laboratoire de Physique des Lasers, Atomes, Molécules
CNRS/Université Lille 1

Aurore Woller, Hélène Duez, Bart Staels

U1011 « Récepteurs nucléaires, maladies cardio-vasculaires et
diabète »

Institut Pasteur de Lille, Université Lille 2, INSERM

CEMPI scientific day,
February 10th, 2017

Lille1-Pasteur collaboration : coupling the clock to metabolism

PhLAM, Université Lille 1



- **Aurore Woller** (PhD student)
 - Marc Lefranc (Univ Lille 1)
- and now
- Katharina Beuke (post-doc)
 - Ambroise de Izarra (Phd student)

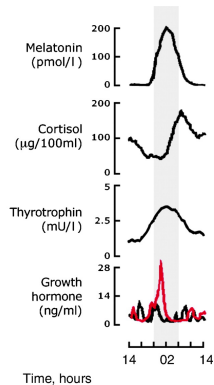
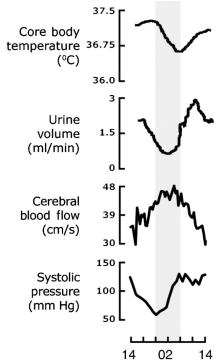
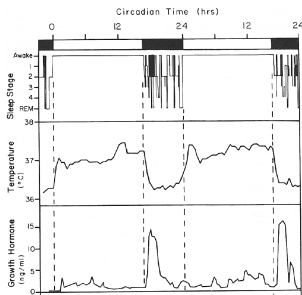
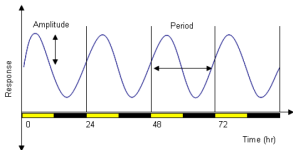
U1011 INSERM, Institut Pasteur Lille



- **Aurore Woller** (PhD student)
- Bart Staels (Univ Lille 2)
- H el ene Duez (INSERM)

Circadian rhythms : adapting to the diurnal cycle

Circadian rhythms are physiological oscillations synchronized to day/night cycle which help organisms to anticipate daily changes in environment.



Circadian rhythms are generated by an internal clock

Circadian rhythms are known since antiquity, however their endogeneous character was evidenced only in 1729 by J.-J. d'Ortous de Mairan, a french physicist and astronomer.

DES SCIENCES. 35

OBSERVATION BOTANIQUE.

ON fait que la Sensitive est *heliotrope*, c'est-à-dire que les rameaux & les feuilles se dirigent toujours vers le côté d'où vient la plus grande lumière; & l'on fait de plus qu'à cette propriété qui lui est commune avec d'autres Plantes, elle en joint une qui lui est plus particulière, elle est Sensitive à l'égard du Soleil ou du jour, ses feuilles & leurs pédicules se replient & se contractent vers le coucher du Soleil, de la même manière dont cela se fait quand on touche la Plante, ou qu'on l'agite. Mais M. de Mairan a observé qu'il n'est point nécessaire pour ce phénomène qu'elle soit au Soleil ou au grand air, il est seulement un peu moins marqué lorsqu'on la tient toujours enfermée dans un lieu obscur, elle s'épanouit encore très-sensiblement pendant le jour, & se replie ou se recroise régulièrement le soir pour toute la nuit. L'expérience a été faite sur la fin de l'Été, & bien répétée. La Sensitive sent donc le Soleil sans le voir et aucune manière; & cela paroît avoir rapport à cette malheureuse délicatesse d'un grand nombre de Malades, qui s'aperçoivent dans leurs Lits de la différence du jour & de la nuit.

Il seroit curieux d'éprouver si d'autres Plantes, dont les feuilles ou les fleurs s'ouvrent le jour, & se ferment la nuit, conserveroient comme la Sensitive cette propriété dans des lieux obscurs; si on pourroit faire par art, par des fourneaux plus ou moins chauds, un jour & une nuit qu'elles sentissent; si on pourroit renverser par là l'ordre des phénomènes du vrai jour & de la vraie nuit, &c. Mais les occupations ordinaires de M. Mairan ne lui ont pas permis de pousser les expériences jusque-là, & il se contente d'une simple invitation aux Botanistes & aux Philosophes, qui pourront eux-mêmes avoir d'autres choses à suivre. La marche de la véritable Philosophie, qui est l'Expérimentale, ne peut être que fort lente.

E ij

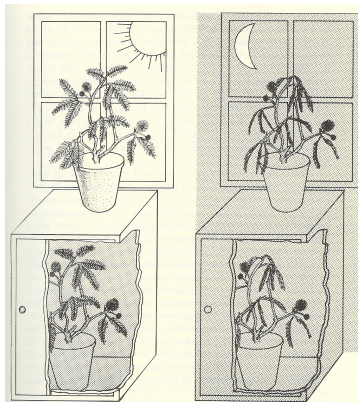


Fig. 14 A representation of de Mairan's original experiment. When exposed to sunlight during the day (upper left), the leaves of the plant were open, and during the night (upper right) the leaves were folded. De Mairan showed that sunlight was not necessary for these leaf movements by placing the plant in total darkness; even under these constant conditions, the leaves opened during the day (lower left) and folded during the night (lower right). (Copyright 1982 by Moore-Ede, Sulzman, and Fuller.)

Leaf oscillations of *Mimosa pudica* persists in the dark.

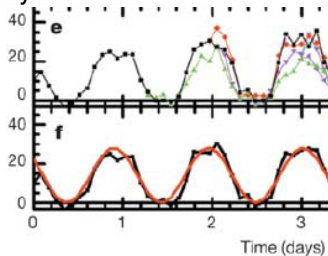
► Circadian oscillations of bean leaves

Circadian clocks are genetic oscillators

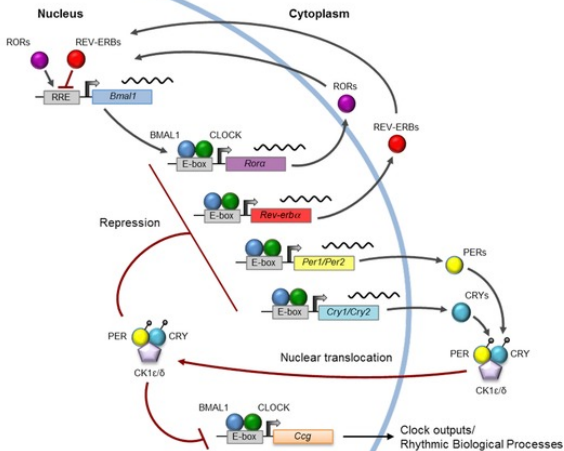
- **Bünning (1935)** Free-running period is an inherited property.
- **Konopka and Benzer (1971)** Mutation of *Per* gene in *Drosophila* induces variations in period or arrhythmia.

Circadian clocks are networks of interacting genes and proteins whose activities oscillate over a 24-hour interval.

Circadian oscillations in gene activity in cyanobacteria



Core mammalian clock network

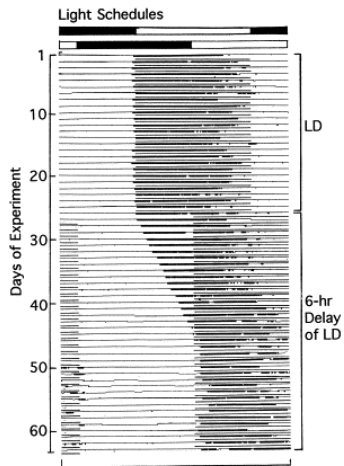


Time keeping requires entrainment by an external cycle

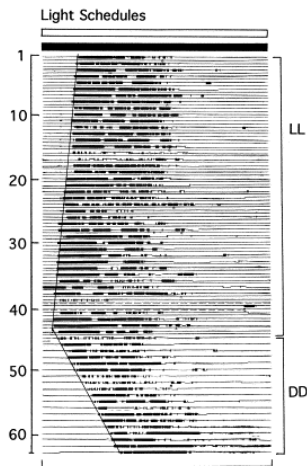


Wheel-running activity of squirrels

A. Photoentrainment



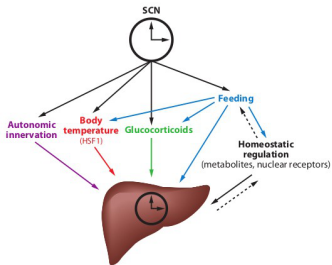
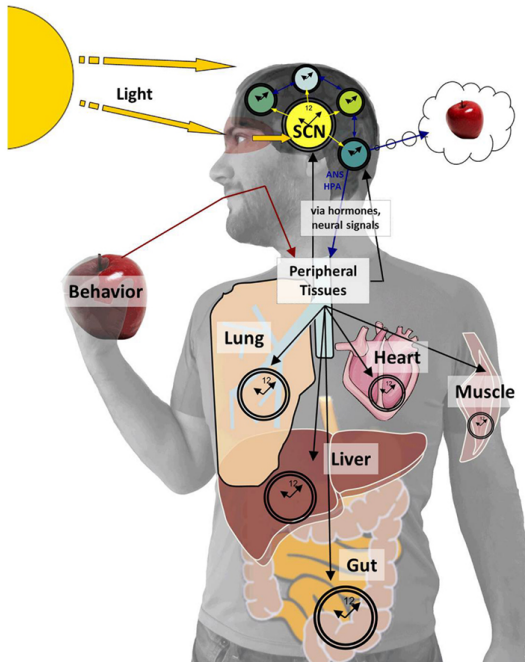
B. Free-Running Rhythms



A network of circadian clocks

Our internal rhythms are governed a network of interconnected clocks in peripheral organs which synchronize to various signals

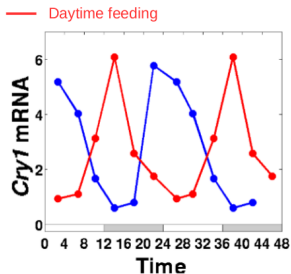
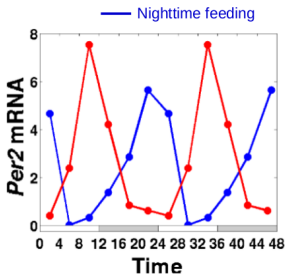
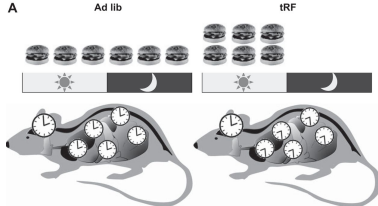
Only the master clock in the brain (SCN) sees the light directly



The liver clock is entrained by feeding/fasting cycles

Feed mice exclusively during the day, which is the normal rest period

Schroder AJP-HCP 2014



Clock gene activity profiles in liver of mice fed during day vs during night

Damiola Genes Dev 2000

Daytime feeding changes the phase of clock gene expression in liver but not in the master clock

Circadian rhythms of metabolism

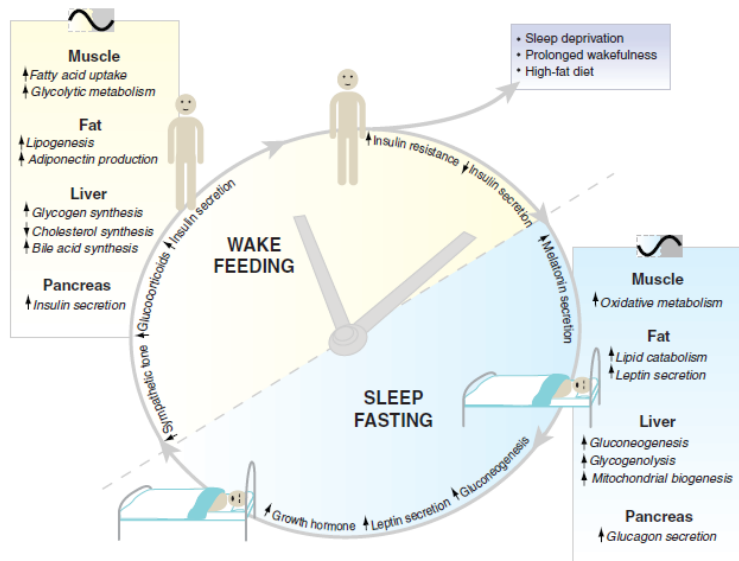


Fig. 3. The clock partitions behavioral and metabolic processes according to time of day. The clock coordinates appropriate metabolic responses within peripheral tissues with the light/dark cycle. For example, the liver clock promotes

Obesity and Metabolic Syndrome in Circadian *Clock* Mutant Mice

Fred W. Turek,^{1,3} Corinne Joshi,^{3,4*} Akira Kohsaka,^{3,4*}
Emily Lin,^{3,4*} Ganka Ivanova,^{2,4} Erin McDearmon,^{3,5}
Aaron Laposky,³ Sue Losee-Olson,³ Amy Easton,³
Dalan R. Jensen,³ Robert H. Eckel,² Joseph S. Takahashi,^{1,3,5}
Joseph Bass^{2,3,4,†}

The *CLOCK* transcription factor is a key component of the molecular circadian clock within pacemaker neurons of the hypothalamic suprachiasmatic nucleus. We found that homozygous *Clock* mutant mice have a greatly attenuated diurnal feeding rhythm, are hyperphagic and obese, and develop a metabolic syndrome of hyperleptinemia, hyperlipidemia, hepatic steatosis, hyperglycemia, and hypoinsulinemia. Expression of transcripts encoding selected hypothalamic peptides associated with energy balance was attenuated in the *Clock* mutant mice. These results suggest that the circadian clock gene network plays an important role in mammalian energy balance.

running rhythm of locomotor activity in heterozygous mice in constant darkness (DD) and a 3- to 4-hour increase (i.e., period = 27 to 28 hours in DD) in circadian period in homozygous mice, which is often followed by a total breakdown of circadian rhythmicity (i.e., arrhythmicity) after a few weeks in DD.

Although previous studies that used running wheel behavior as a marker of locomotor activity did not reveal major differences between homozygous *Clock* mutant and wild-type mice maintained on a light-dark (LD) cycle, use of infrared beam crossing to monitor total activity revealed a significant increase in activity during the light phase and a change in the temporal pattern of total activity during the dark phase (Fig. 1A) (1*d*). In particular, wild-type mice showed two pronounced peaks of activity—one occurring after lights off, the other before lights on—whereas these peaks were atten-

Inactivating the clock leads to severe metabolic diseases

Cell Metabolism
Short Article

Metabolic stress disrupts circadian rhythms

High-Fat Diet Disrupts Behavioral and Molecular Circadian Rhythms in Mice

Akira Kohsaka,^{1,4} Aaron D. Laposky,^{1,2} Kathryn Moynihan Ramsey,^{1,3,4} Carmela Estrada,¹ Corinne Joshi,¹ Yumiko Kobayashi,⁴ Fred W. Turek,^{1,2} and Joseph Bass^{1,2,3,4,*}

¹Department of Neurobiology and Physiology

²Center for Sleep and Circadian Biology

³Department of Medicine, Feinberg School of Medicine

Northwestern University, Evanston, IL 60208, USA

⁴Evanston Northwestern Healthcare Research Institute and Department of Medicine, Evanston Hospital, Evanston, IL 60208, USA

*Correspondence: j-bass@northwestern.edu

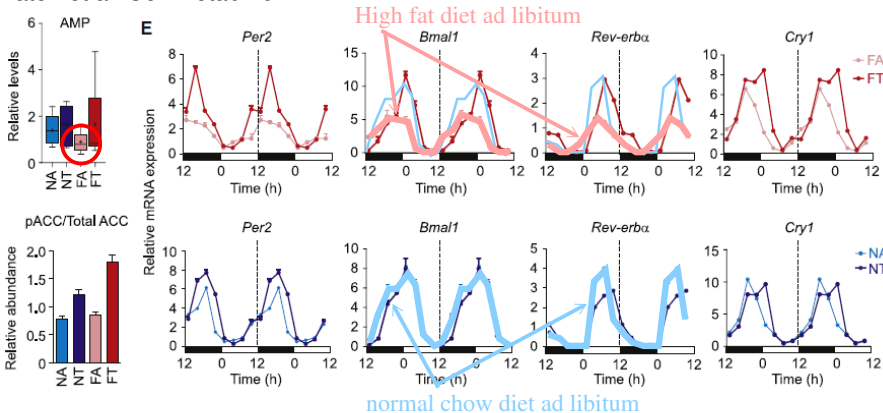
DOI 10.1016/j.cmet.2007.09.006

How to describe mathematically the coupling of clock and metabolism?

High fat diet (HFD) disrupts the clock

In HFD, the feeding/fasting cycles entraining the clock are perturbed and are associated with lower AMP levels

Hatori et al. Cell Metab 2012



Typically, the amplitude of gene activity oscillations is dampened.

How do feeding/fasting cycles entrain the clock ?

What are the metabolic sensors (“nutrireceptors”) ?

Can we build a mathematical model of the clock with these sensors ?

Can it explain how perturbations in feeding/fasting disrupt the clock ?

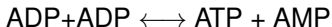
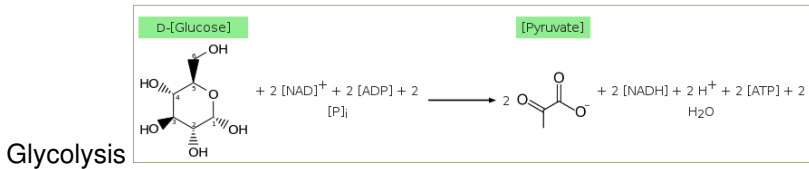
Can we design a pharmacological protocol to restore normal clock profiles ?

How can the cell sense metabolism ?

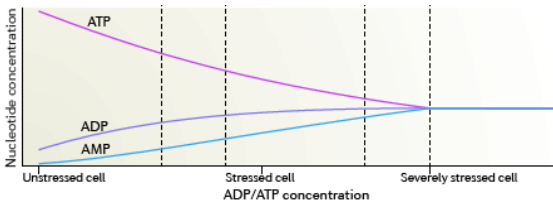
Main gauges of cellular metabolic state : NAD⁺/NADH, AMP/ADP/ATP

ATP is the cell fuel (e.g., muscle contraction)

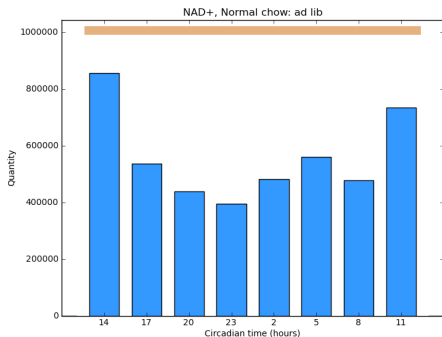
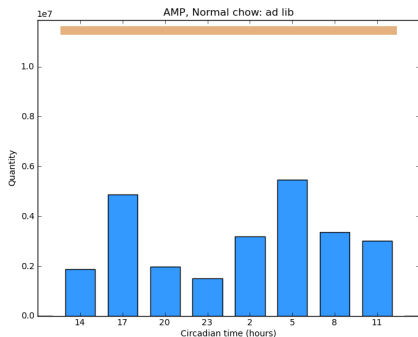
Metabolic reactions consume or produce ATP (ATP ↔ ADP ↔ AMP) and convert NAD⁺ to NADH or vice versa



Low AMP : energy-full
High AMP : energy-deprived



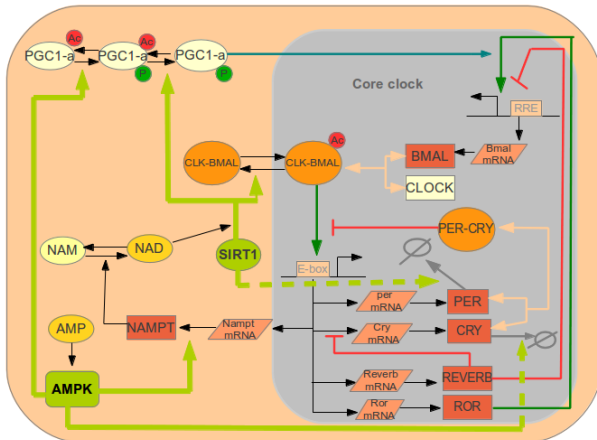
Nad+ and AMP display daily variations



Note the presence of two peaks, including one at ZT5 and another one at ZT14-ZT17

Basic network coupling the clock to metabolism

NAD⁺ and **AMP** are important metabolites characterizing the cell metabolic state, and influence the circadian clock through **SIRT1** (activated by **NAD⁺**), and **AMPK** (activated by **AMP**).



SIRT1 inhibits CLOCK/BMAL1 activity

SIRT1 deacetylates PGC1 α which coactivates Bmal1 with ROR α

SIRT1 deacetylates PER2 and destabilizes it

AMPK destabilizes CRY1 and indirectly PER,

AMPK enables deacetylation of PGC1 α by SIRT1

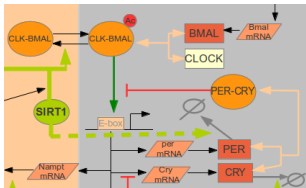
AMPK stabilizes NAMPT

Translating networks into differential equations

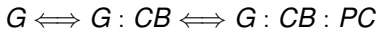
A gene is active when it synthesizes messenger RNA (transcription)

* The *Per* gene can be in 3 states, each with a different mRNA synthesis rate

- 1 bare DNA (low activity)
- 2 BMAL1-CLOCK protein complex bound to DNA (high activity)
- 3 PER-CRY complex bound to BMAL1-CLOCK bound to DNA (reduced activity)



* The fraction of time spent in each state is determined by the chemical equilibrium of



* Affinity of CLOCK/BMAL1 to DNA is reduced by SIRT1

Rate of change of *Per* mRNA

Synthesis

Degradation

$$\frac{d[Per]}{dt} = \left(\frac{V_{max} \cdot \left(1 + \text{fold} \cdot \left(\frac{[CB]}{K_a \cdot (1 + \text{Act_SIRT})} \right)^{\text{hill}_{cb}} \right)}{1 + \left(\frac{[CB]}{K_a \cdot (1 + \text{Act_SIRT})} \right)^{\text{hill}_{cb}} \cdot \left(1 + \left(\frac{[PC]}{K_i} \right)^{\text{hill}_{pc}} \right)} \right) - (d_m \cdot [Per])$$

Mathematical model

$$\begin{aligned} \frac{d([mPer] \cdot V_{\text{compartment}})}{dt} &= -V_{\text{compartment}} \cdot (dmper \cdot [mPer]) \\ &+ V_{\text{compartment}} \cdot \left(\frac{\text{basal_mper} \cdot \left(1 + \text{fold_per} \cdot \left(\frac{[CB]}{\text{thr_perc} \cdot (1 + c_srt \cdot [Sirt1])} \right)^{\text{hill_perc}} \right)}{1 + \left(1 + \left(\frac{[PC]}{\text{thr_perpc}} \right)^{\text{hill_perpc}} \right) \cdot \left(\frac{[CB]}{\text{thr_perc} \cdot (1 + c_srt \cdot [Sirt1])} \right)^{\text{hill_perc}}} \right) \\ \\ \frac{d([mCry] \cdot V_{\text{compartment}})}{dt} &= -V_{\text{compartment}} \cdot (dmcry \cdot [mCry]) \\ &+ V_{\text{compartment}} \cdot \left(\frac{\text{basal_mcry} \cdot \left(1 + \text{fold_cry} \cdot \left(\frac{[CB]}{\text{thr_crycb} \cdot (1 + c_srt \cdot [Sirt1])} \right)^{\text{hill_crycb}} \right)}{1 + \left(1 + \left(\frac{[PC]}{\text{thr_crypc}} \right)^{\text{hill_crypc}} \right) \cdot \left(\frac{[CB]}{\text{thr_crycb} \cdot (1 + c_srt \cdot [Sirt1])} \right)^{\text{hill_crycb}}} \right) \cdot \frac{1}{1 + \left(\frac{[REVERB]}{\text{thr_cryrev}} \right)^{\text{hill_cryrev}}} \\ \\ \frac{d([mRevErb] \cdot V_{\text{compartment}})}{dt} &= -V_{\text{compartment}} \cdot (dmrev \cdot [mRevErb]) \\ &+ V_{\text{compartment}} \cdot \left(\frac{\text{basal_mrev} \cdot \left(1 + \text{fold_rev} \cdot \left(\frac{[CB]}{\text{thr_revcb} \cdot (1 + c_srt \cdot [Sirt1])} \right)^{\text{hill_revcb}} \right)}{1 + \left(1 + \left(\frac{[PC]}{\text{thr_revpc}} \right)^{\text{hill_revpc}} \right) \cdot \left(\frac{[CB]}{\text{thr_revcb} \cdot (1 + c_srt \cdot [Sirt1])} \right)^{\text{hill_revcb}}} \right) \\ \\ \frac{d([mROR] \cdot V_{\text{compartment}})}{dt} &= -V_{\text{compartment}} \cdot (dmror \cdot [mROR]) \\ &+ V_{\text{compartment}} \cdot \left(\frac{\text{basal_mror} \cdot \left(1 + \text{fold_ror} \cdot \left(\frac{[CB]}{\text{thr_rorcb} \cdot (1 + c_srt \cdot [Sirt1])} \right)^{\text{hill_rorcb}} \right)}{1 + \left(1 + \left(\frac{[PC]}{\text{thr_rorpc}} \right)^{\text{hill_rorpc}} \right) \cdot \left(\frac{[CB]}{\text{thr_rorcb} \cdot (1 + c_srt \cdot [Sirt1])} \right)^{\text{hill_rorcb}}} \right) \cdot \frac{1}{1 + \left(\frac{[REVERB]}{\text{thr_rorrev}} \right)^{\text{hill_rorrev}}} \\ \\ \frac{d([mBmal] \cdot V_{\text{compartment}})}{dt} &= -V_{\text{compartment}} \cdot (dmbmal \cdot [mBmal]) \\ &+ V_{\text{compartment}} \cdot \left(\frac{\text{basal_mbmal} \cdot \left(1 + \text{fold_bmal} \cdot (1 + c_pgc \cdot [PGC1]) \cdot \left(\frac{[ROR]}{\text{thr_bmalror}} \right)^{\text{hill_bmalror}} \right)}{1 + \left(\frac{[REVERB]}{\text{thr_bmalrev}} \right)^{\text{hill_bmalrev}} + \left(\frac{[ROR]}{\text{thr_bmalror}} \right)^{\text{hill_bmalror}}} \right) \\ \\ \frac{d([PER] \cdot V_{\text{compartment}})}{dt} &= -V_{\text{compartment}} \cdot (dpper \cdot [PER]) \\ &+ V_{\text{compartment}} \cdot (\text{trans_per} \cdot [mPer]) \\ &- V_{\text{compartment}} \cdot ((k_pc \cdot [CRY] \cdot [PER]) - k_pb \cdot [PC]) \\ \\ \frac{d([CRY] \cdot V_{\text{compartment}})}{dt} &= -V_{\text{compartment}} \cdot (dpcry \cdot [CRY]) \\ &+ V_{\text{compartment}} \cdot (\text{trans_cry} \cdot [mCry]) \end{aligned}$$

16 differential equations describe the time evolution of messenger RNA concentration (=gene activity) and protein concentration.

The model has 96 kinetic constants (mRNA and protein degradation rates, transcription and translation rates, ...) which are mostly unknown and must be estimated from experimental data.

Expression data from mouse livers

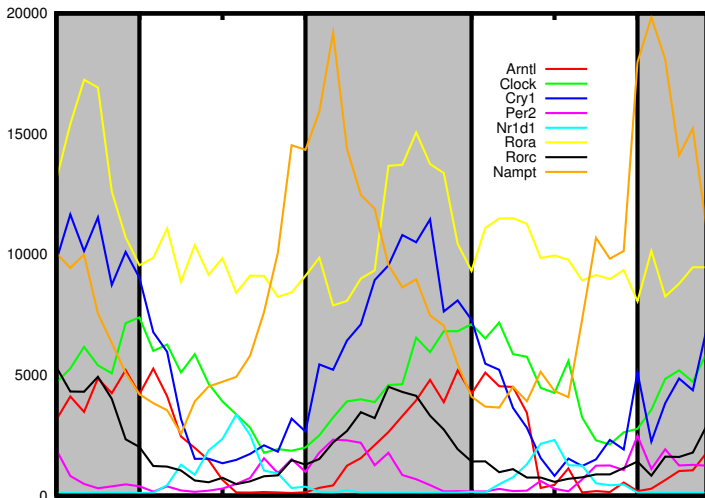
OPEN ACCESS Freely available online

PLOS GENETICS

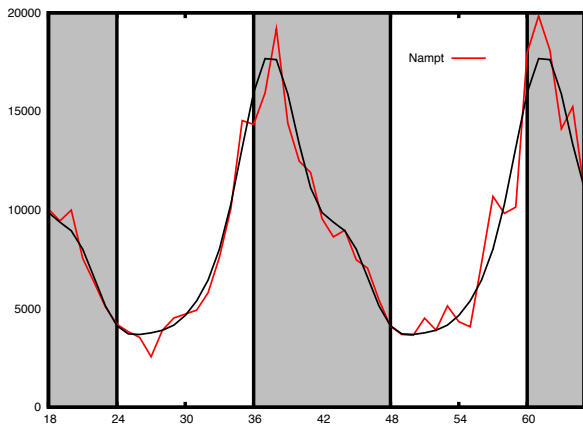
Harmonics of Circadian Gene Transcription in Mammals

Michael E. Hughes^{1*}, Luciano DiTacchio^{2*}, Kevin R. Hayes¹, Christopher Vollmers², S. Pulivarthy², Julie E. Baggs¹, Satchidananda Panda^{2*}, John B. Hogenesch^{1*}

Hughes Plos Genet. 2009



Approximation of exp. data with Fourier Series



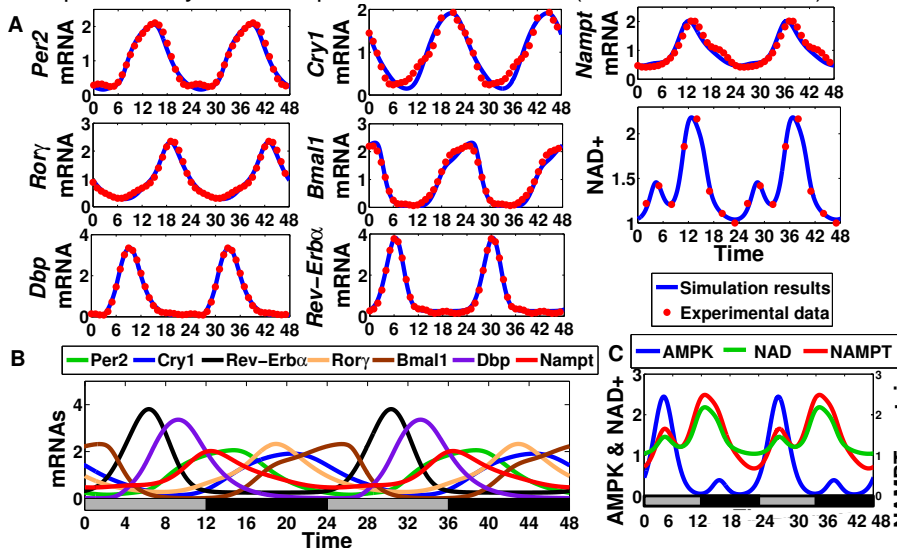
Fourier series and
microarray
expression time
profile

Mice put in DD and fed at libitum.

Even though the data are obtained in vivo, they show a very good reproducibility from one day to the next

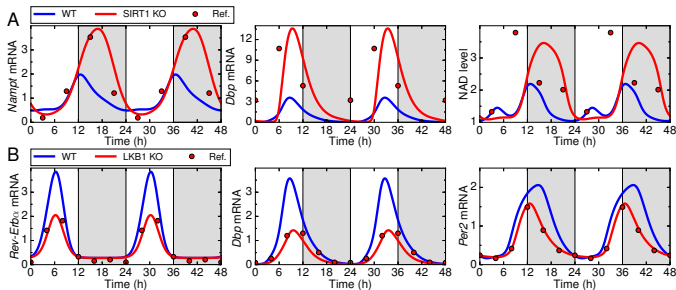
Adjustment of model to experimental data

Computationally intensive parameter estimation (96 kinetic constants)

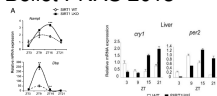


WT clock gene expression data and NAD⁺ profiles well reproduced

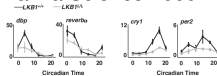
Reproducing Sirt1 and AMPK loss of function



Bellet PNAS 2013



Lamia Science 2009



Mutant phenotypes are well reproduced.

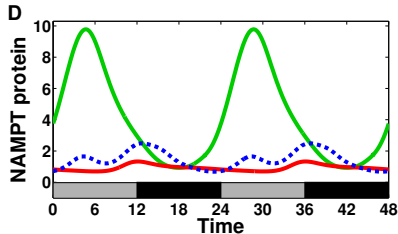
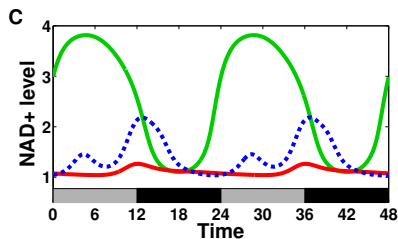
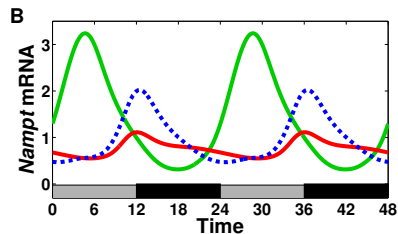
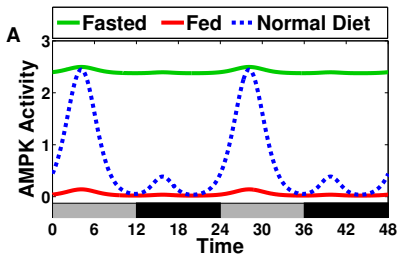
Knocking down Sirt1 generally amplifies oscillations in clock gene expression

Knocking down LKB1, hence disactivating AMPK, generally dampens oscillations in clock gene expression

Understanding the effect of AMPK rhythms

Simulate

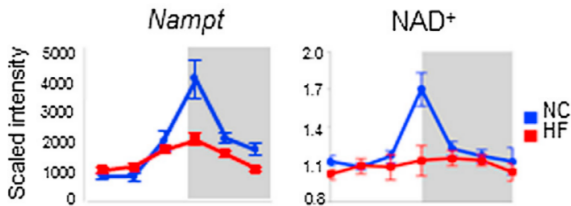
- A constantly fed-like state (AMPK activity constitutively low)
- Alternation of fasting and feeding (oscillating AMPK activity)
- A constantly fasting state (AMPK activity constitutively high)



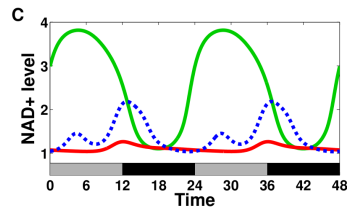
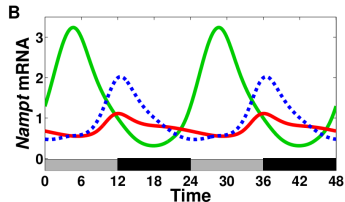
Model reproduces the loss of NAD⁺ oscillations

Loss of NAD⁺ oscillations as observed in a high-fat diet is potentially harmful

Eckel-Mahan et al. Cell 2013



Mathematical model



NAD⁺ peak essential for oxidative metabolism (Peek et al. Science 2013).

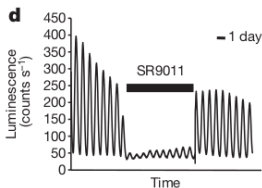
In obesity or type 2 diabetes, AMPK is systematically depressed regardless of the regimen.

A pharmacological approach is needed to restore clock function

Regulation of circadian behaviour and metabolism by synthetic REV-ERB agonists

Laura A. Solt^{1*}, Yongjun Wang^{1*}, Subhashis Banerjee¹, Travis Hughes¹, Douglas J. Kojetin¹, Thomas Lundasen¹, Youseung Shin², Jin Liu¹, Michael D. Cameron², Romain Noel², Seung-Hee Yoo³, Joseph S. Takahashi³, Andrew A. Butler⁴, Theodore M. Kamenecka² & Thomas P. Burris^{1,5}

Drugs that can transiently modulate the activity of the core clock protein REV-ERB α have recently become available.



When a REV-ERB agonist is administered for several days, clock oscillations are abolished due to strong repression by REV-ERB.

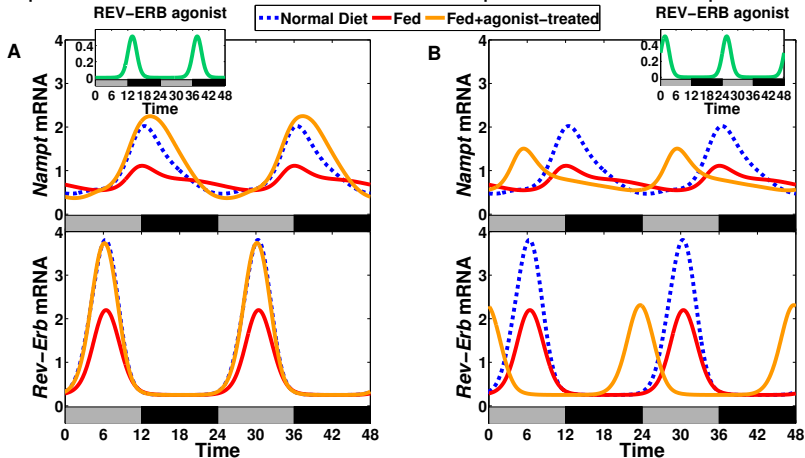
Can we restore normal clock oscillations by administering a short REV-ERB agonist pulse at the right time ?

Rescue of clock gene oscillation amplitude in high-fat diet using a Rev-Erb agonist

Optimal administration time

Not optimal

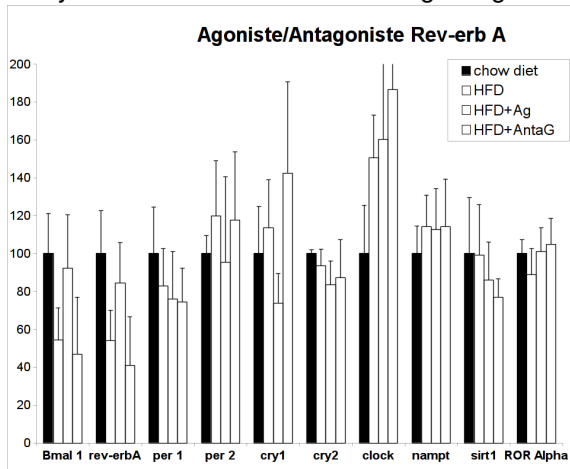
Not optimal



Normal amplitude and phase are restored when the administration time of a REV-ERB agonist (green pulse) is carefully chosen.

First experiment in vivo

Mice at Institut Pasteur de Lille were fed a high fat diet and then administered a Rev-Erb agonist for 2 days before being sacrificed to analyse their livers 2 hours after beginning of the night



Encouraging but still much work is required to make the model more quantitative

Conclusion

- A mathematical model how the liver clock is entrained by feeding/fasting cycles had been designed, incorporating the metabolic sensors SIRT1 and AMPK.
- It agrees well with a number of WT and mutant phenotypes
- The mathematical model explains the daily patterns of NAD⁺ level.
- Adjusting the model to normal chow and high fat diet data may help to understand which actors are perturbed in nutritional stress. It seems important to have a long fasting period during the night to maintain high-amplitude rhythms
- Goal : deliver a drug affecting a clock gene at a precise timing, so as to restore normal clock rhythms.

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A Mathematical Model of the Liver Circadian Clock Linking Feeding and Fasting Cycles to Clock Function

Aurora Woller, H el ene Duez, Bart Staels¹, Marc Lefranc³

³ Lead Contact

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DOI: <http://dx.doi.org/10.1016/j.celrep.2016.09.060> | CrossMark

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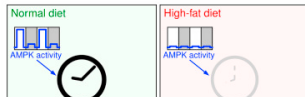
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Summary Full Text Methods Images/Data References Related Articles Comments

Highlights

- We construct a mathematical model of the mammalian liver clock and metabolic sensors
- The model integrates feeding and fasting cycles with the clock
- The model accurately reproduces high-fat-diet-induced loss of NAD⁺ oscillations
- NAD⁺ oscillations are predicted to be rescued by timed delivery of clock modifiers

Graphical Abstract



Mathematical modeling to understand the interplay of proliferation and differentiation in development

Benjamin Pfeuty, *Development* **142**, 477 (2015).

© 2015. Published by The Company of Biologists Ltd | *Development* (2015) 142, 477-485 doi:10.1242/dev.112649

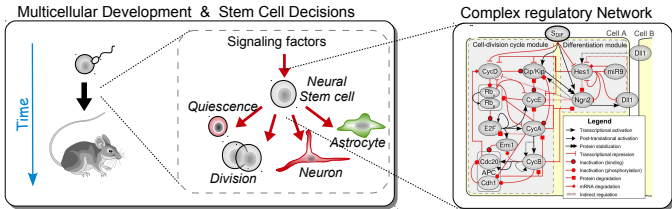


RESEARCH ARTICLE

STEM CELLS AND REGENERATION

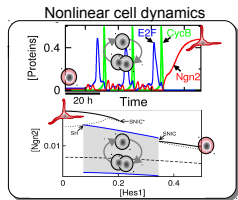
A computational model for the coordination of neural progenitor self-renewal and differentiation through Hes1 dynamics

Benjamin Pfeuty*



REGULATORY PRINCIPLES:

- Diverse and robust decisions driven by intracellular oscillations



MATHEMATICAL MODELLING:

- ODE simulations
- Bifurcation analysis
- Modular analysis

L. Héliot and M. Gonzalez-Pisfil. Characterizing molecular interactions with FRET, FCS, FLIM, etc...

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Compounds Triggering ER Stress Exert Anti-Melanoma Effects and Overcome BRAF Inhibitor Resistance

Michaël Cerezo^{1,4}, Abdelali Lehraiki^{1,4}, Antoine Millet^{1,4}, Florian Rouaud, Magali Plaisant, Emilie Jaune, Thomas Botton, Cyril Ronco, Patricia Abbe, Hella Amdouni, Thierry Passeron, Veronique Hofman, Baharia Mograbi, Anne-Sophie Dabert-Gay, Delphine Debayle, Damien Alcor, Nabil Rabhi, Jean-Sébastien Annicotte, Laurent Héliot, Mariano Gonzalez-Pisfil, Caroline Robert, Solange Moréra, Armelle Vigouroux, Philippe Gual, Maruf M.U. Ali, Corine Bertolotto, Paul Hofman, Robert Ballotti, Rachid Benhida^{1,4}, Stéphane Rochec^{1,4}

^{1,4} Co-first author

DOI: <http://dx.doi.org/10.1016/j.ccell.2016.04.013> CrossMark

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Highlights

- HA15 is a molecule that targets specifically BIP/GRP78/HSPA5
- HA15 induces ER stress leading to cancer cell death in vitro and in vivo
- HA15 overcomes BRAF inhibitor resistance in melanoma cells

Graphical Abstract

The graphical abstract shows the chemical structure of HA15, a small molecule with a benzimidazole core and a sulfonamide group. Below the structure is a diagram illustrating the interaction of HA15 with a protein complex, likely BIP/GRP78/HSPA5, which is involved in the endoplasmic reticulum (ER) stress response. The diagram shows HA15 binding to the protein, leading to ER stress and subsequent cancer cell death.