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Dynamical Modelling of the Heat Shock Response in Chlamydomonas reinhardtii

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1995-2004 Mean Temperatures

Image from http://mapsof.net

Introduction

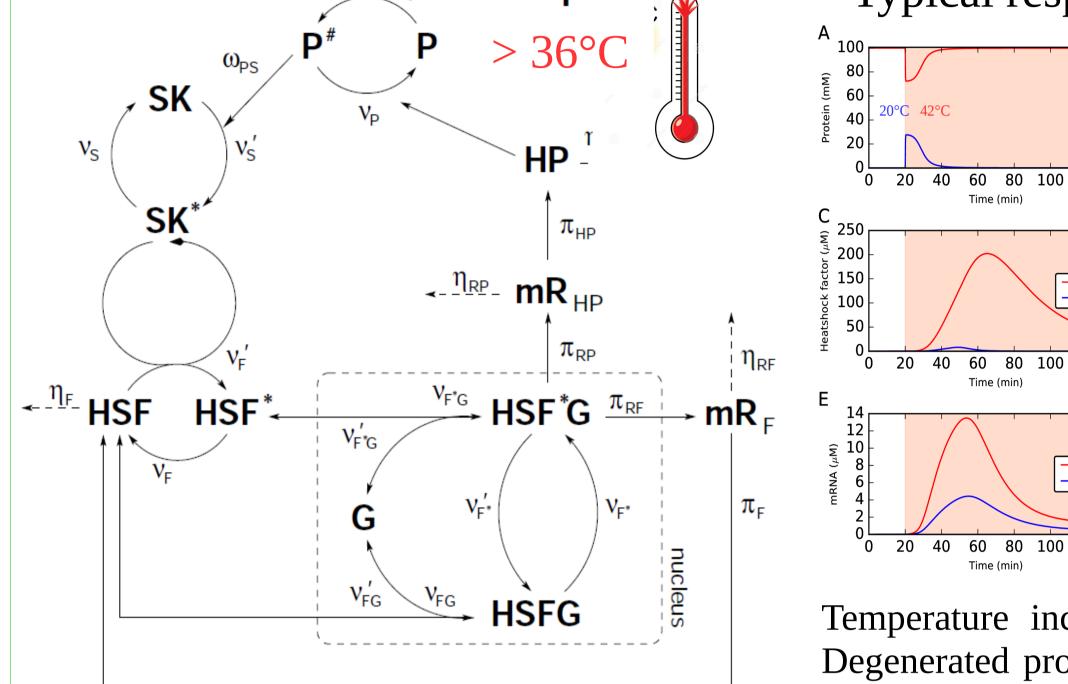
Organisms exposed to temperatures higher than usual can activate a heat shock response (HSR) allowing them to react to the new conditions. Due to global warming, crop plants will encounter more frequent heat waves which might reduce their crop yield [1]. We focus on *Chlamydomonas reinhartii*, a well known model organism for green algae. Processes involved in the HSR are highly conserved among species, thus similar mechanisms might be at work in crop plants. Here we present the implementation of a data driven mathematical model for the HSR in *C. reinhartii*, originally proposed by Ebenhöh and Skupin. The signalling network structure is based on the experimental results of [2], also used in addition to those of [3] for validation of the model. The model aims at capturing general features of the mechanism and allows to reproduce the qualitative behaviour of the above mentioned data. In *C. reinhardtii* the HSR can be elicited also by light, via a regulatory pathway independent from the one activated by temperature. We thus propose an extension of our model to include the description of this activation mechanism.

The dynamical model of the heat shock response (HSR)

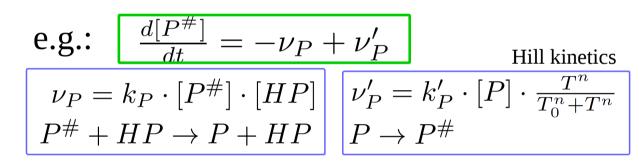


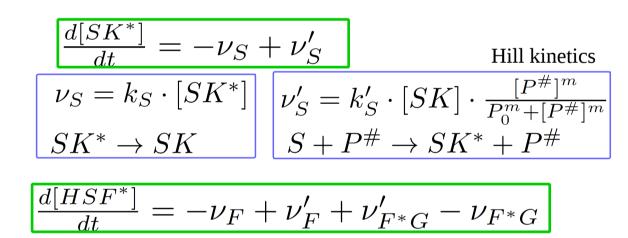
Typical response to heat shock

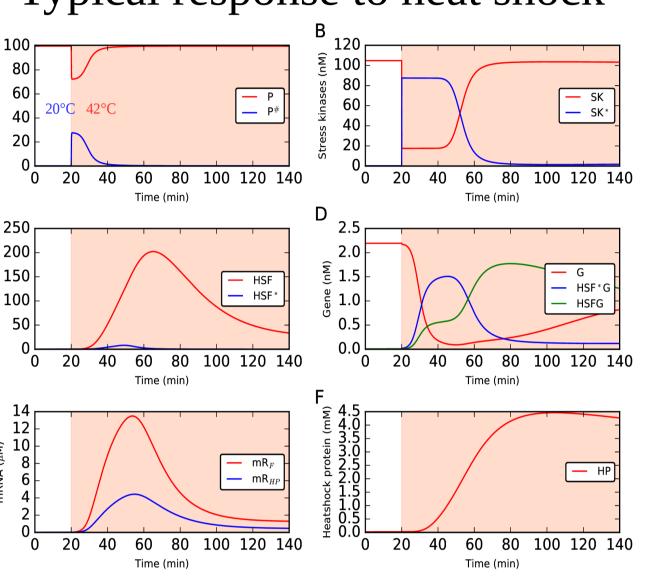
Comparison with experimental data: determination of the parameters' values and validation of the model



ODEs, mainly mass action kinetics





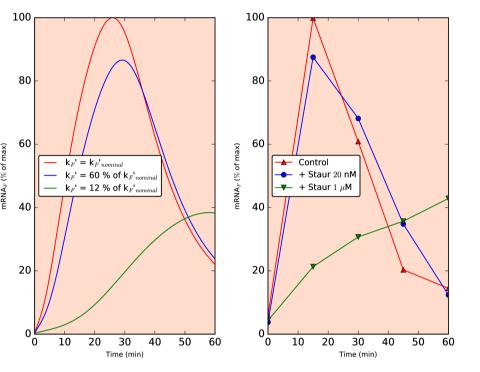


Temperature increase unfolds proteins P. Degenerated proteins P[#] (concentrations in panel A) trigger the HSR. The stress kinesis SK are activated, SK^{*} (B), and in turn phosporilate the heat shock factor HSF into HSF^{*} (C). This binds to free gene loci G (D), activating the production of $mRNA_{T}$ and $mRNA_{_{HP}}$ (E), which are translated into HSF and heat shock protein HP (F). The chaperone HP helps refolding P[#], switching off the response. ODEs are used to describe the time-evolution of concentrations. The reactions are modelled using mass action kinetics, a part from SK activation (Michaelis-Menten), HSF activation and the action of Temperature (Hill kinetics).

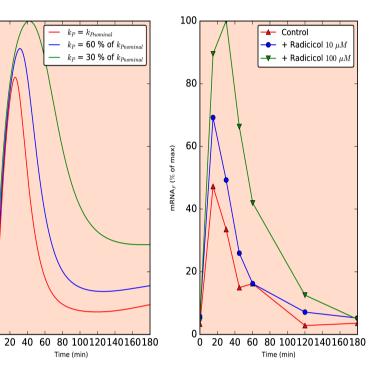
With a biologically reasonable, rough estimate of the parameters, the model is able to reproduce the qualitative behaviour of the heat shock responses observed in experiments. We next would like to split the data in two subsets, use one to obtain the parameters set which minimizes the least square distance from the data, and the other to validate the model.

Experiments on feeding with pharmaceuticals (data from [2])

In [2] cells are fed with different concentrations of pharmaceuticals to study HSR changes.

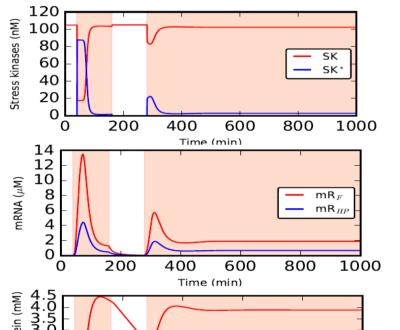


We simulate the feeding with Staurosporine (a protein kinesis inhibitor) by lowering the rate of HSF activation. We simulate the feeding with Radicicol (an inhibitor of HSP90 activity) by lowering the rate of the refolding of $P^{\#}$ by the HP.

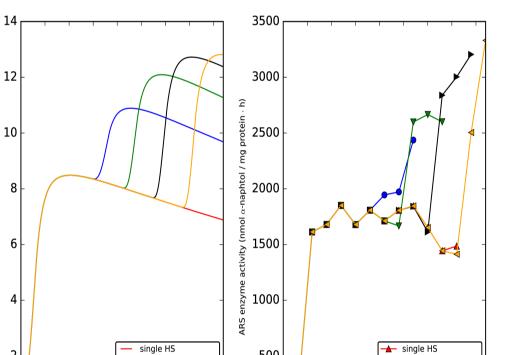


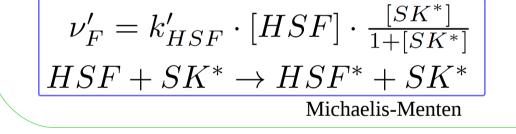
Experiments on double heat shock (data from [3])

Which is the minimum time between two subsequent HS necessary to have two full HSR?



In the experiments of [3], as in our simulations, a full response is obtained after about 5h, while the second response is less intense then the first one for smaller times. This because HSF, mRNAs and HSP

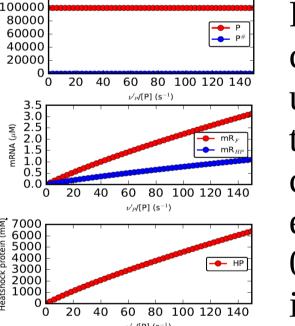




remain available for some time after the first HS. 200 600 800 1000 400 Time (min

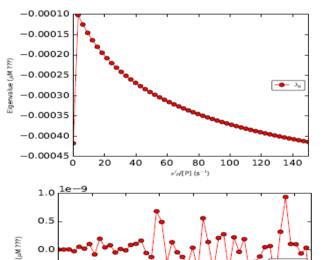
2nd HS 2 h after 1st 2nd HS 2 h after 1s 2nd HS 3 h after 1st 2nd HS 3 h after 1st 2nd HS 4 h after 1st → 2nd HS 4 h after 1st 2nd HS 5 h after 1st 2nd HS 5 h after 1s .00 150 200 250 300 350 40 150 200 250 300 350 400

Studying the steady state of the system and its stability



For variations in the unfolding rate, the steady state concentrations evolve in such a way to maintain the unfolded proteins close to zero at steady state. All the eigenvalues of the Jacobian of the system computed at steady state have negative real part, except for two which numerically oscillates around 0 (two equations in the system are not linearly independent from the others).

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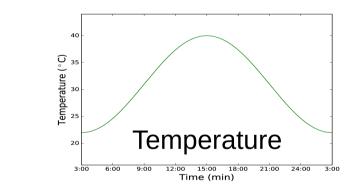


60 80

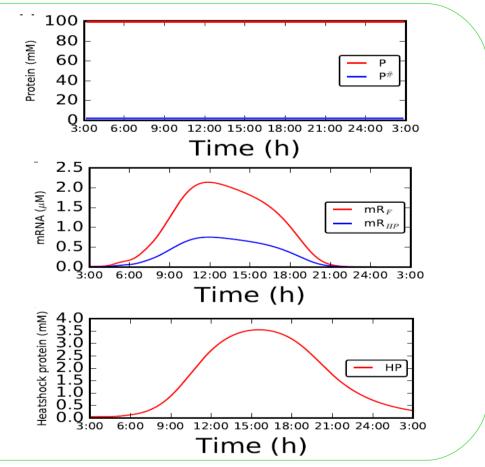
100 120 140

The heat shock response in a hot day

We simulate the HSR elicited by the variation of T of a hot day. Concentrations of mRNAs and HSF are not timesymmetric as the variation of T.



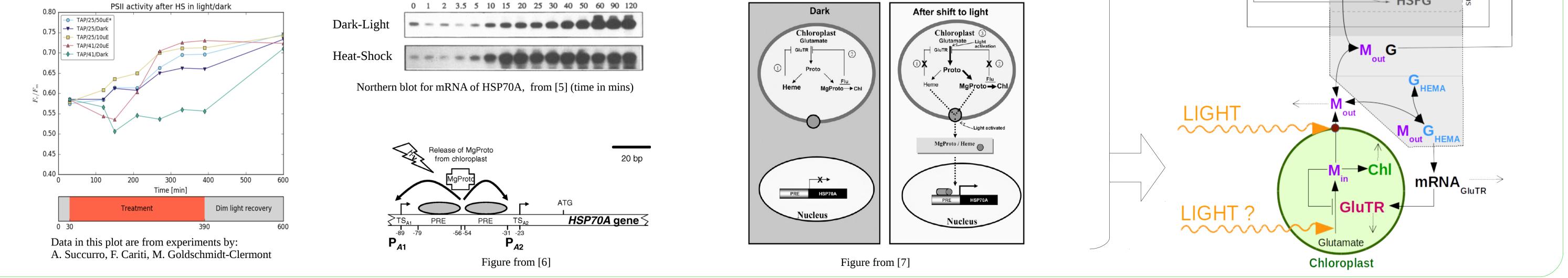
The mechanism seems to be tuned the concentration of keep to unfolded proteins $P^{\#}$, undesired by the cell, close to zero.

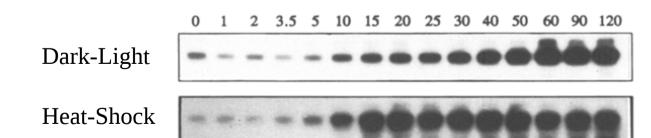


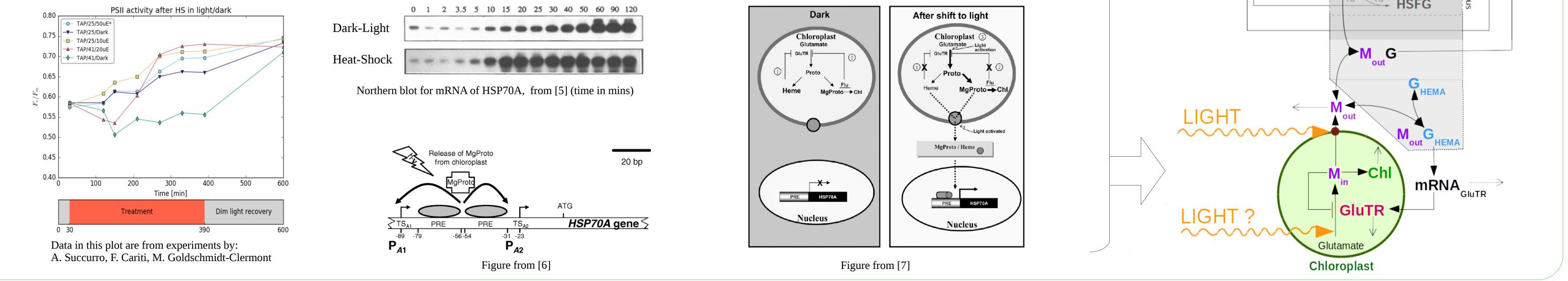
Proposing to extend the model to include activation of a heat shock response by shift from dark to light

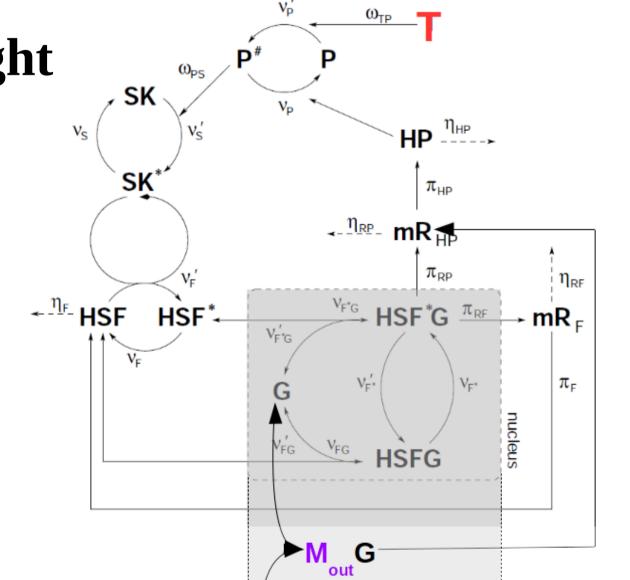
Question: how does light control the activation of the HSP genes in Chlamydomonas reinhardtii?

- Preliminary Experiments: recovery from photo inhibition after different treatments.[§]
- Observation I: shift from dark to light can induce the expression of certain HSP genes [4].
- Observation II: the pathways regulating T induction and light induction of HSP70A gene are independent [5].
- Observation III: the HSP70A promoter region has transcription sites activated by HSF and MgProto [6].
- Observation IV: MgProto mediates the activation by light of the gene HSP70A [7].
- Observation V: MgProto is an intermediate in the biosynthesis of Chlorophyll.
- Observation VI: also the HEMA gene, necessary for the synthesis of Chlorophyll is activated by MgProto [8].









Bibliography

Acknowledgements

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