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Predicting the regulation of circadian rhythms by RNA methylation

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Eating behaviour is known to influence our sleep-wake cycle, and the mechanism remains elusive. We have focused on RNA methylation that possibly connect metabolic and circadian systems. Recently, RNA methylation inhibition was found to elongate circadian period by as-yet-unknown mechanism. Since the regulatory network for circadian rhythm has been studied well, modelling can be a powerful tool for predicting the mechanism. Our study aimed at predicting possible mechanisms by which RNA methylation regulates circadian rhythm using a computational model and also a simpler model [1]. To predict the mechanism, we used information from our experimental collaborators: (1) RNA methylation inhibits enzymes, important for circadian rhythms, (2) there are many modification processes presumably activated by the enzymes. Based on experimental data, we predicted the most likely process that is activated by the enzymes and then by RNA methylation inhibition. The prediction was confirmed experimentally by our collaborators.

[1] Kurosawa *et al.* 2017 *PLoS Comp Biol*

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