Distinct mechanisms underlie two types of Caenorhabditis elegans sleep

Nicholas F Trojanowski^{1,2,3}, Matthew D. Nelson^{1,4}, Steven W. Flavell⁵, Christopher Fang-Yen^{2, 3}, David M. Raizen¹

¹Department of Neurology, Perelman School of Medicine, University of Pennsylvania, Philadelphia, Pennsylvania; ²Department of Bioengineering, School of Engineering and Applied Science, University of Pennsylvania, Philadelphia, Pennsylvania; ³Department of Neuroscience, Perelman School of Medicine, University of Pennsylvania, Philadelphia, Pennsylvania; ⁴Current address: Department of Biology, Saint Joseph's University, Philadelphia, Pennsylvania; ⁵Howard Hughes Medical Institute, Lulu and Anthony Wang Laboratory of Neural Circuits and Behavior, The Rockefeller University, New York, NY



Electrophysiological recordings have enabled identification of physiologically distinct yet behaviorally similar states of mammalian sleep. In contrast, sleep states in non-mammalian animals are typically described behaviorally, and therefore non-mammalian sleep is often regarded as a homogenous state characterized by guiescence of feeding and locomotion, reduced responsiveness, and rapid reversibility. In the nematode *C*.elegans, behavioral sleep has been described under two conditions: developmentally timed sleep (DTS or lethargus) occurs during transitions between larval stages, just before the molt (Raizen et al, Nature 2008), while stress-induced sleep (SIS) occurs following exposure to cellular stress during any stage of life (Hill et al, Curr. Biol. 2014). Behaviorally, DTS and SIS appear identical, as during both states feeding and locomotion cease and arousal threshold is increased. Based on genetic analysis, DTS is similar to circadian-timed sleep in Drosophila (Singh et al, Sleep 2014) whereas SIS is similar to sleep induced by cellular stress in Drosophila (Lenz et al, Brain Behav. Immun. 2015). We used optogenetic manipulations of neuronal and muscular activity, pharmacology, and genetic perturbations to uncover circuit and molecular mechanisms of DTS and SIS. We find that locomotion guiescence induced by DTS- and SIS-associated neuropeptides (NLP-22 and FLP-13, respectively) occurs via their action on the nervous system. However, in mutants with activated signaling through the Gs/cAMP pathway, overexpression of NLP-22 causes locomotion phenotypes distinct from those seen after overexpression of FLP-13, suggesting that their neuronal target(s) and/or molecular mechanisms differ. We also find that while feeding quiescence feeding quiescence during SIS results from a loss of excitability in the nervous system, during DTS feeding is inhibited due to loss of pharyngeal muscle excitability. Together these results indicate that, as in mammals, distinct types of sleep in *C. elegans* are subserved by different mechanisms. Thus, our data uncover a previously unappreciated heterogeneity in non-mammalian sleep.