Published in final edited form as:

N Engl J Med. 2021 May 20; 384(20): e76. doi:10.1056/NEJMc2104154.

## **Circadian Mechanisms in Medicine**

Hugo Y.-H. Lin, M.D., Ph.D.,

Kaohsiung Medical University Hospital, Kaohsiung, Taiwan

Ming-Yu Yang, Ph.D.,

Chang Gung University, Tao-Yuan, Taiwan

Sheng-Fung Lin, M.D.

E-Da Hospital, Kaohsiung, Taiwan

To the Editor:

Allada and Bass (Feb. 11 issue)<sup>1</sup> provide a comprehensive review of circadian mechanisms in medicine, focusing on physiology, molecular circuitry, and the contribution of circadian processes to disease. Although circadian misalignment causes disease, epigenetic modifications of circadian gene expression are also influential and usually involve DNA methylation at CpG sites (locations in DNA at which a cytosine precedes a guanosine in the 5′ to 3′ sequence).<sup>2–4</sup> DNA methylation plays a crucial role in embryonic development and across the human lifespan, including the recovery of persons with circadian disorders.<sup>4</sup> However, according to our previous research,<sup>5</sup> methylation is not temporary. Methylated CpG sites are prominent in patients with chronic myeloid leukemia (CML). The treatment of patients with CML could reactivate JUNB, an activating protein 1 transcription factor that is important in the control of cell growth and differentiation and neoplastic transformation. Epigenetic modifications of circadian genes should be viewed as central to certain disease processes.

## References

- Allada R, Bass J. Circadian mechanisms in medicine. N Engl J Med 2021; 384: 550–61. [PubMed: 33567194]
- Schultz MD, He Y, Whitaker JW, et al. Human body epigenome maps reveal noncanonical DNA methylation variation. Nature 2015; 523: 212–6. [PubMed: 26030523]
- 3. Feil R, Fraga MF. Epigenetics and the environment: emerging patterns and implications. Nat Rev Genet 2012; 13: 97–109. [PubMed: 22215131]
- 4. Lahtinen A, Häkkinen A, Puttonen S, et al. Differential DNA methylation in recovery from shift work disorder. Sci Rep 2021; 11: 2895. [PubMed: 33536559]
- 5. Yang MY, Liu TC, Chang JG, Lin PM, Lin SF. JunB gene expression is inactivated by methylation in chronic myeloid leukemia. Blood 2003; 101: 3205–11. [PubMed: 12506033]

hugoyl@kmu.edu.tw .