

Abstract

After influenza infection, C57BL/6J mice develop increased slow-wave sleep (SWS) during the dark phase of the circadian cycle, whereas BALB/cByJ mice develop decreased SWS during the light phase. An analysis of CXB recombinant inbred mice revealed a quantitative trait locus (QTL) that was related to expression of the BALB/cByJ phenotype. This QTL, designated *Srilp* (sleep response to influenza, light phase), is located on Chr 6 in a 10-12 cM region between *D6Mit74* and *D6Mit188*. *Temt* (thioether S-methyltransferase), which is located at region B3 of Chr 6, is a potential candidate gene for *Srilp*. We evaluated *temt* expression in hypothalamus and basal forebrain of healthy and influenza-infected C57BL/6J and BALB/cByJ mice. We report here that *temt* expression varies significantly in both brain regions. During influenza infection, BALB/cByJ mice show reduced expression in hypothalamus and basal forebrain at 30 hours post-inoculation time point, whereas C57BL/6J mice do not. Our data suggest the possibility that strain- and infection-related alterations in sleep may be influenced by *temt* and the metabolism of selenium.