Largest-ever study identifies gene regions associated with sleep duration

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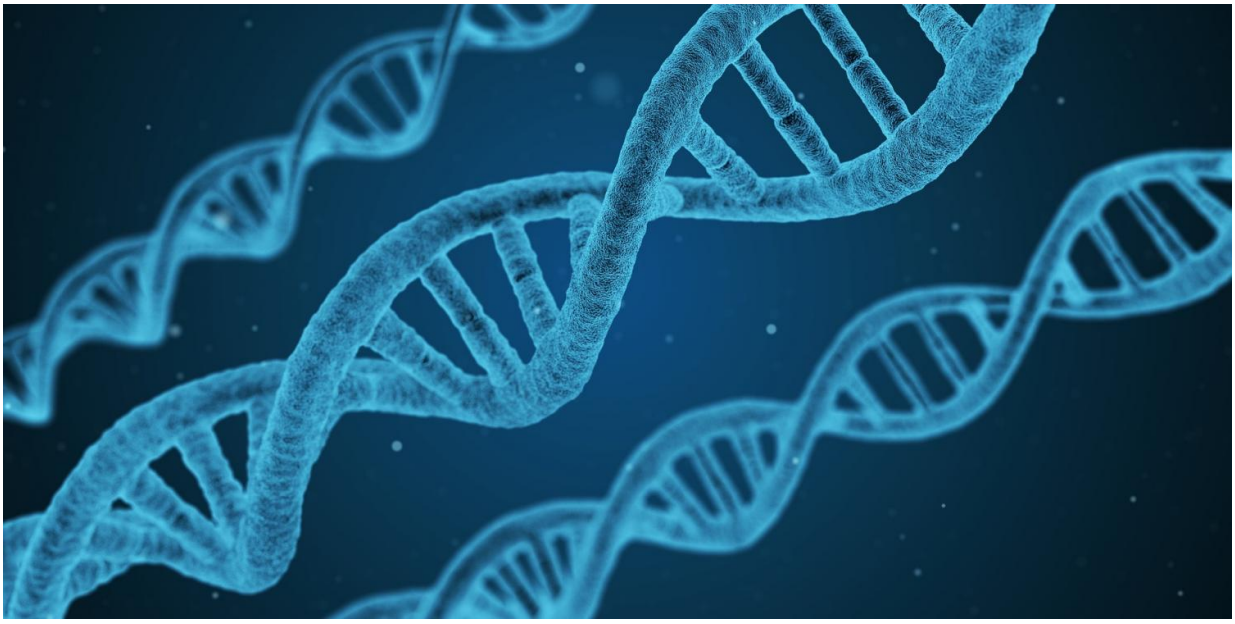

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A study led by investigators from Massachusetts General Hospital (MGH) and the University of Exeter Medical School has identified 76 new gene regions associated with sleep duration. The study by a team that recently reported finding gene sites associated with insomnia risk and chronotype - the tendency to be an early riser or a 'night owl' - has been published in *Nature Communications*.

"While we spend about a third of our life asleep, we have little knowledge of the specific genes and pathways that regulate the amount of sleep people get," says Hassan Saeed Dashti, Ph.D., RD, of the MGH Center for Genomic Medicine, co-lead author of the report. "Our study suggests that many of the genes important for sleep in animal models may also influence sleep in humans and opens the door to better understanding of the function and regulation of sleep."

It is well understood that regularly getting adequate sleep—7 to 8 hours per night—is important to health, and both insufficient sleep—6 or fewer hours—and excessive sleep—9 hours or more—have been linked to significant health problems. Family studies have suggested that from 10 to 40 percent of variation in sleep duration may be inherited, and previous genetic studies have associated variants in two gene regions with sleep duration.

The current study, the largest of its kind to address sleep duration, analyzed genetic data from more than 446,000 participants in the U.K. Biobank who self-reported the amount of sleep they typically received. That genome-wide association study (GWAS) identified 78 gene regions—including the two previously identified—as associated with sleep duration. While carrying a single gene variant influenced the average amount of sleep by only a minute, participants carrying the largest number of duration-increasing variants reported an average of 22 more minutes of sleep, compared with those with the fewest, which is comparable to other well-recognized factors that influence sleep duration.

To confirm the accuracy of findings based on self-reported sleep duration, the researchers tested the 78 duration-associated variants in a subgroup of participants who had worn motion-detecting devices called accelerometers for up to a week. Not only were those gene regions supported by objective measurement of sleep duration, but this analysis

was also able to associate duration-related variants with factors such as sleep efficiency, instances of waking up during the night and daytime inactivity.

Only a few of the gene regions identified in this study overlap with those identified in the group's previous studies of insomnia and chronotype. The sites identified in this study showed consistent effects with a previous GWAS of more than 47,000 adults but limited consistency with another GWAS of sleep duration among more than 10,500 children and adolescents, which supports research suggesting that the genetics of sleep duration may be different in children than in adults.

Since both shorter- and longer-than-average sleep duration have been associated with health problems, the team conducted separate GWASs for participants who reported short or long sleep duration. Those studies identified additional genes not identified in the larger group analysis that contributed to either longer or shorter sleep duration. The researchers also found shared genetic links between both short and long sleep duration and factors such as higher levels of body fat, depression symptoms and fewer years of schooling, implying negative effects from both too little and too much sleep. In addition, short sleep duration was genetically linked with traits such as insomnia and smoking, while long-duration variants were linked with schizophrenia, type 2 diabetes and coronary artery disease.

More information: Hassan S. Dashti et al, Genome-wide association study identifies genetic loci for self-reported habitual sleep duration supported by accelerometer-derived estimates, *Nature Communications* (2019). DOI: 10.1038/s41467-019-08917-4

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