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The ABCC9 of sleep: A genetic factor that regulates how long we sleep

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A collaborative European study led by LMU researchers has shown that ABCC9, a known genetic factor in heart disease and diabetes, also influences the duration of sleep in humans. This function is evolutionarily conserved as knock-out of the gene reduces the duration of nocturnal sleep in fruit flies.

Legend has it that Napoleon never needed more than four hours of sleep at a stretch. Others only feel fully rested after 10 hours between the sheets. Clearly, individuals vary with respect to how much sleep they need. Indeed, sleep duration is influenced by many factors. Apart from seasonal and other variables, age and sex play a role, as does one's sleep-wake cycle or chronotype, i.e. whether one is a lark (early to bed, early to rise) or the converse, an owl.

An international team of researchers led by LMU chronobiologists Professor Till Roenneberg and Dr. Karla Allebrandt has now identified the first genetic variant that has a significant effect on sleep duration and is found frequently in the general population. The variant was discovered in the course of a so-called genome-wide association study, in which the researchers scanned individual genomes for variations that were correlated with sleep patterns.

More than 4000 people from seven European populations, from countries as diverse as Estonia and Italy, took part in the project, and filled out a questionnaire designed to assess their sleeping habits. Analysis of the genetic and behavioral data revealed that individuals who

had two copies of one common variant of the gene ABCC9 generally slept for a significantly shorter period in an undisturbed environment than did persons with two copies of the other version. The gene ABCC9 codes for the protein SUR2, which forms the regulatory component of a potassium channel in the cell membrane. This ion channel acts a sensor of energy metabolism in the cell.

“It is particularly intriguing that functional studies have shown that the protein plays a role in the pathogenesis of heart disease and diabetes,” says Dr. Karla V. Allebrandt, first author on the new study and a chronogeneticist at LMU Munich. "So apparently the relationships of sleep duration with metabolic syndrome symptoms can be in part explained by an underlying common molecular mechanism".

The ABCC9 gene is evolutionarily ancient, as a similar gene is present in fruitflies. Fruitflies also exhibit sleep-like behavior. In collaboration with scientists from the Leicester University, the team blocked the function of the ABCC9 homolog in the fly nervous system, the duration of nocturnal sleep was shortened. In mammals, the gene is active in various tissues, including the heart, the skeletal muscles and the brain, as well as in parts of the pancreas. “It is very encouraging for us that ABCC9 also affects the nocturnal sleep period in flies,” says Roenneberg. “This tells us that the genetic control of sleep duration may well be based on similar mechanisms in a wide range of highly diverse species.”

More information: A KATP channel gene effect on sleep duration: from genome wide association studies to function in Drosophila
Karla V. Allebrandt et.al. Molecular Psychiatry online, 22. November 2011, Doi: 10.1038/mp.2011.142

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