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Human Genetics Patterns: Bond for Day and Night Sleep Performance

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Abstract

Sleep remains one of the supreme mysteries in science. In the history few years, great advances have been made to healthier realize this happening. Human genetics has contributed appreciably to this faction, as many features of sleep have been found to be inborn. Discoveries about these genetic variations that affect human sleep will assist us in understanding the underlying mechanism of sleep. Here we recapitulate latest discoveries about the genetic variations affecting the timing and duration of sleep, EEG patterns. To wrap up, Author also discusses some of the sleep-related neurological disorders such as Autism Spectrum Disorder and Alzheimer's disease. The potential challenges and future directions of human genetics in sleep research.

Keywords: Alzheimer's disease; Autism spectrum disorder; Circadian clock; Genetic; Sleep

Introduction

Human genetics field began to grow momentum as a dominant approach for defining the causes of diseases start in the 80s. After three decades still this approach continues to be fruitful. Over the past thirty years, human genetics has revolutionized the area of biomedical research and medicine in common. The identification of genetic causes for diseases generated a striking pattern swing in the process of learning disease pathophysiology.

The great optimism is that understanding of genetics and biology of specific diseases will lead to a more coherent approach to devising better treatments. Sleep is known to have a large impact on human health but remains a great mystery today. Studies of human behaviors, including sleep, are more challenging than studies of diseases because behavioral phenotypes are typically more multifaceted and are generally subject to many environmental factors.

An opportunity arose in the late 90s with identification of the first familial circadian phenotype (familial advanced sleep phase syndrome-FASP) that made it possible to begin genetic mapping and cloning of genes/mutations that have strong effects on human circadian timing. Less than 20 years after the recognition of these families, great strides into understanding regulatory mechanisms of human sleep behaviour [1]. Growing evidence has accumulated over the last 2 decades and revealed that a number of sleep traits in humans are heritable, such as timing of sleep, total daily sleep requirement, response to sleep deprivation, and various EEG measurements/patterns.

Mendelian sleep phenotypes, fussy mutations of large effect were shown to be causative for different phenotypes. Therefore, mutations identified using genetics in human families have led to new insights into the detailed molecular mechanisms regulating sleep behavior. We summarize latest discoveries in the field of human genetics implicating genes in sleep regulation. We will focus primarily on natural variations in sleep traits including the timing, duration and the EEG characteristics of sleep (Figure 1).

Sleep timing

Timing of sleep is dogged by the circadian clock, which is entrained to the environment primarily by illumination. At a molecular level, periodicity of biological clocks is generated by transcriptional translational feedback loops [2-5]. Mounting lists of core clock genes have been discovered that encode proteins engaging in this criticism loop. Components of the molecular clock are highly conserved in vertebrates [3,4]. Theoretically, mutations that alter the molecular clock feedback loops may result in altered circadian timing. Indeed, researchers has identified several genetic mutations including casein kinase 1 delta (CK1d) T44A and H46R, period2 (PER2) S662G, period3 (PER3) P415A/H417R and cryptochrome2 (CRY2) [6-11]. Sleep onset and offset times are significantly advanced in individuals with familial advance sleep phase (FASP) (Figure 2).

Most of the mutations identified to date pick up the pace of clock and shorten the period, which leads to the advanced phase phenomena. In addition, the importance of clock protein post translation modifications was elucidated by mutations found in PER2 and CK1d [7,8]. Reality that control of clock protein turnover and stability is critical for sleep regulation is demonstrated repeatedly by studies of PER2, PER3, and CRY2 mutations. Each of the mutations found by this approach contributed to a better overall picture of regulatory clock mechanisms.

Notably, some individuals have the physically powerful sleep phase advance phenotype do not carry any mutation in known clock genes. Altered phase in the setting of a normal core clock may result from altering the connection between the environment and the clock system in the body or the coupling of the core clock to physiological outputs. For example, the light entrainment pathway from retina to Suprachiasmatic nucleus may be affected by the potential genetic mutation. Reliable with this hypothesis, circadian and photo transduction genes and pathways were enriched in the recent genome-wide association analysis of self-reported morningness [12,13]. Therefore, invention and cram of such fresh genes with more concentrated genetic tools promise to be rewarding.

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Human genetics in sleep studies perspectives view

Authors have paying attention here on normal variants of human circadian timing and total sleep requirement. Some individuals find it troublesome to wake up in the early morning hours while others feel honest for getting up early. Separate from this, there are many primary sleep disorders like restless leg syndrome, obstructive sleep apnea or narcolepsy. In addition, sleep problems also are seen in many disorders that lead to abnormal brain development or degeneration of normal brain. For instance, autism spectrum disorder (ASD) is a neurodevelopment disorder with evidence for strong genetic susceptibility and a high frequency of insomnia [14]. Defects in synaptic pruning during the development of neural circuits disrupt the excitatory/inhibitory balance of synapses, which may underlie the atypical neurodevelopment in ASD [15]. Thus, it is intriguing to consider whether sleep problems exacerbate atypical synaptic pruning or if severe neurodevelopmental problem leads to sleep disorders in ASD.





Figure 1: Genes that affect the timing, duration, or EEG characteristics of sleep.

Discussion

Patients with AD have severe sleep problems but recent evidence suggests that sleep disruption is a major contributing factor to AD. Amyloid- β plaques, the hallmark of AD, are formed by Amyloid- β plaques accumulation. The height of Amyloid- β in brain interstitial space is high while awake and buck upon awakening from a night of sleep [16,17]. Importantly, sleep disruption abolishes this Amyloid- β reduction, suggesting a neurotoxin clearance function for sleep [18].

These examples highlight the importance of understanding the regulatory mechanisms of sleep and sleep functions. Although much remains to be learned about sleep abnormalities in people with brain disorders, likely the case that in general, brain dysfunction leads to alterations in sleep. At the same time, chronic sleep deprivation or desynchrony of the clock from the solar day contributes to development or progression of brain disorders. One issue for many sleep studies conducted in humans is the use of self-reported phenotypes like sleep duration, timing, etc. Several environmental factors such as drugs, seasonal cycle, modern lifestyle and even lunar cycle may affect human sleep [19-21]. Such factors are not easily controlled and can confound phenotyping. Usually, genetic association studies only provide suggestions that the disease could result from an interaction of environmental factors on a susceptible genetic setting. Thus, introducing the genetic mutations into laboratory housed animals is a powerful approach to test the contribution of a gene to a phenotype. Moreover, in contrast to many well-established model organisms, the human population is genetically more heterogeneous, which adds another layer of complexity.

In recent years, researchers mainly focused on single-gene phenotypes, especially those where mutations have dominant effects. However, mutant alleles that segregate as autosomal dominant traits must have a large enough effect to arise on a heterogeneous genetic background. This family with FASP is in the 'tails' of the normal distributions in general human populations.

Conclusion

Here Authors have published genetic mutations discovered to affect the timing, duration and EEG features of human sleep behaviors. Genetic tools in these systems have allowed researchers to undertake large-scale screens to identify new genes for regulation of sleep-like behavior. Such progress has further provided opportunities to probe sleep circuitry and sleep function on a molecular level. Nonetheless, due to the large variation of sleep characteristics among different species and the unique features of human sleep, human genetics will continue to be an indispensable and invaluable source of insight providing critical information on this mysterious phenomenon-sleep.

Conflict of Interest

None

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References

- Jones CR, Campbell SS, Zone SE, Cooper F, De Sano A, et al. (1999) Familial advanced sleep-phase syndrome: A short-period circadian rhythm variant in humans. Nat Med 5: 1062-1065.
- Gustafson CL, Partch CL (2015) Emerging models for the molecular basis of mammalian circadian timing. Biochem 54: 134-149.

- Partch CL, Green CB, Takahashi JS (2014) Molecular architecture of the mammalian circadian clock. Trends Cell Biol 24: 90-99.
- Lowrey PL, Takahashi JS (2011) Genetics of circadian rhythms in mammalian model organisms. Adv Genet 74: 175-230.
- Shearman LP, Sriram S, Weaver DR, Maywood ES, Chaves I, et al. (2000) Interacting molecular loops in the mammalian circadian clock. Science 288: 1013-1019.
- Toh KL, Jones CR, He Y, Eide EJ, Hinz WA, et al. (2001) An hper2 phosphorylation site mutation in familial advanced sleep phase syndrome. Science 291: 1040-1043.
- Xu Y, Toh KL, Jones CR, Shin JY, Fu YH, et al. (2007) Modeling of a human circadian mutation yields insights into clock regulation by per2. Cell 128: 59-70.
- Xu Y, Padiath QS, Shapiro RE, Jones CR, Wu SC, et al. (2005) Functional consequences of a ckidelta mutation causing familial advanced sleep phase syndrome. Nature 434: 640-644.
- Zhang L, Hirano A, Hsu PK, Jones CR, Sakai N, et al. (2016) A period3 variant causes a circadian phenotype and is associated with a seasonal mood trait. Proc Natl Acad Sci USA 113: E1536-E1544.
- Hirano A, Shi G, Jones CR, Lipzen A, Pennacchio LA, et al. (2016) A cryptochrome 2 mutation yields advanced sleep phase in human. eLife 5: e16695.
- Brennan KC, Bates EA, Shapiro RE, Zyuzin J, Hallows WC, et al. (2013) Casein kinase idelta mutations in familial migraine and advanced sleep phase. Sci Transl Med 5: 183ra56.
- 12. Hu Y, Shmygelska A, Tran D, Eriksson N, Tung JY, et al. (2016) Gwas of

89,283 individuals identifies genetic variants associated with self-reporting of being a morning person. Nat Commun 7: 10448.

- Jones SE, Tyrrell J, Wood AR, Beaumont RN, Ruth KS, et al. (2016) Genomewide association analyses in 128,266 individuals identifies new morningness and sleep duration loci. PLoS Genet 12: e1006125.
- 14. Veatch OJ, Maxwell-Horn AC, Malow BA (2015) Sleep in autism spectrum disorders. Curr Sleep Med Rep 1: 131-140.
- Thomas MS, Davis R, Karmiloff-Smith A, Knowland VC, Charman T (2016) The over-pruning hypothesis of autism. Dev Sci 19: 284-305.
- 16. Roh JH, Huang Y, Bero AW, Kasten T, Stewart FR, et al. (2012) Disruption of the sleep-wake cycle and diurnal fluctuation of beta-amyloid in mice with Alzheimer's disease pathology. Sci Trans Med 4: 150ra122.
- Huang Y, Potter R, Sigurdson W, Santacruz A, Shih S, et al. (2012) Effects of age and amyloid deposition on abeta dynamics in the human central nervous system. Arch Neurol 69: 51-58.
- Rothman SM, Herdener N, Frankola KA, Mughal MR, Mattson MP (2013) Chronic mild sleep restriction accentuates contextual memory impairments, and accumulations of cortical abeta and ptau in a mouse model of Alzheimer's disease. Brain Res 1529: 200-208.
- Cajochen C, Altanay-Ekici S, Munch M, Frey S, Knoblauch V, et al. (2013) Evidence that the lunar cycle influences human sleep. Curr Biol 23: 1485-1488.
- Yetish G, Kaplan H, Gurven M, Wood B, Pontzer H, et al. (2015) Natural sleep and its seasonal variations in three pre-industrial societies. Curr Biol 25: 2862-2868.
- Allebrandt KV, Teder-Laving M, Kantermann T, Peters A, Campbell H, et al. (2014) Chronotype and sleep duration: The influence of season of assessment. Chronobiol Int 31: 731-740.

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