CIRCADIAN GENETICS

Timing is everything

A high-resolution spatiotemporal gene expression atlas that chronicles the 24-hour transcriptional oscillations of thousands of 'rhythmic' genes in mice may help to improve drug efficacy.

Researchers measured gene expression profiles in 12 mouse organs over time by RNA sequencing and DNA arrays to investigate the influence of the circadian clock on he transcriptome. Notably, the expression of almost half (43%) of all protein-coding genes was found to oscillate in at least one organ, although only 10 genes oscillated in all organs tested. In agreement with previous findings, the majority of circadian gene expression seemed to be organspecific, which indicates that the molecular clock regulates biological processes differently throughout the body. In most organs, circadian gene expression peaked in the hours before dusk and dawn, which the authors term transcriptional 'rush hours'.

In addition, oscillating genes were found to be longer, to cluster together and to have more spliceoforms than non-oscillating genes - 46% of the circadian protein-coding genes expressed more than one spliceoform. The splice of orms expressed by the circadian genes tended to differ across organs more than non-oscilating genes, which the authors say is consistent with the hypothesis that circadian genes have more regulatory function than non-circadian genes. More than 1,000 functionally diverse non-coding RNAs were also found to oscillate in expression, which suggests a role for these molecules in mediating clock function.

Notably, many commonly used drugs target the products of circadian genes, highlighting the importance of timing in drug treatment.

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