**Circadian clock-dependent and -independent rhythmic proteomes implement distinct diurnal functions in mouse liver**

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Diurnal oscillations of gene expression controlled by the circadian clock underlie rhythmic physiology across most living organisms. While such rhythms have been extensively studied at the level of transcription and mRNA accumulation, little is known on the accumulation patterns of proteins. Here, we quantified temporal profiles in the murine hepatic proteome under physiological light-dark conditions using SILAC quantitative mass spectrometry (MS). Our analysis identified over five thousand proteins of which several hundred showed robust diurnal oscillations with peak phases enriched in the morning and during the night and related to core hepatic physiological functions. Combined mathematical modeling of temporal protein and mRNA profiles indicated that proteins accumulate with reduced amplitudes and significant delays, consistent with protein half-live data. Moreover, a group comprising about half of the rhythmic proteins showed no corresponding rhythmic mRNAs, indicating significant translational or post-translational diurnal control. Such rhythms were highly enriched in secreted proteins accumulating tightly during the night. Also, these rhythms persisted in clock deficient animals, suggesting that food related entrainment signals influence rhythms in circulating plasma factors.