Geographic variation in biological rhythms and clock gene polymorphisms in *Nasonia vitripennis*

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Timing of biological behavior occurs in many organisms ranging from bacteria to insects, rodents and primates. Three types of rhythm can be distinguished depending on their period duration: seasonal (yearly), circadian (daily) and ultradian (few minutes to few seconds). Examples of such behavior are: diapause, locomotor activity and courtship, respectively.

Nasonia vitripennis is a parasitic wasp presenting those three behaviors. Therefore, it is commonly used as a model in chronobiology to study these rhythms. In this insect, the circadian clock comprises four main genes: period, cryptochrome-2, clock and cycle, that give an endogenous period to the clock (observable under constant darkness condition), called the free running period. Measurement of external stimuli (light, temperature, food availability) enable the organism to synchronize with the natural environment. It is hypothesized that the circadian clock is the driver of both seasonal and ultradian behavior but the involvement and role of each of the clock genes is still to be determined. Two splicing-isoforms of period have been identified and their expression is sex-dependent but their function is still unknown. The first part of the project will be to investigate the role of those isoforms. RNA modifications tools will be used to knock down the isoform transcripts and to study the impact on insect behavior such as locomotor activity and courtship. Other clock genes will also be investigated for isoforms using bioinformatic analysis of NCBI databases and by Reverse-transcriptase PCR.

Another interesting fact about *Nasonia vitripennis* is that its rhythmic behavior varies with latitudinal origin. Allelic variations have been found in period that are correlated with variation in seasonal behavior, but the other clocks genes have not been studied yet in detail. The second part of the project will be to screen cryptochrome-2, clock and/or cycle for such polymorphisms, using northern and southern lines collected and maintained in the laboratory. For functional analysis, RNA modification tools as well as behavior monitoring might be used.

Methods: Trikinetics locomotor activity monitoring, courtship behavior observation, molecular biology tools (RNAi, CRISPR/Cas9, RT PCR), bioinformatics analysis using NCBI database, *Nasonia vitripennis* breeding.

Starting date: Spring 2019 or later