

OR397*Foraging gene expression patterns in eusocial sweat bees using qRT-PCR*David Awde, Adonis Skandalis, **Miriam Richards**

The foraging gene (*for*) is associated with variation in foraging behaviour in insects, including honeybees and ants. Variation in foraging behaviour is one of the major hallmarks of caste differentiation in primitively eusocial sweat bees, such as *Lasioglossum laevissimum*. We hypothesize that in *L. laevissimum*, actively foraging individuals have high expression levels of *for*, while non-foragers have low levels. To investigate this hypothesis, we designed a quantitative RT-PCR (qRT-PCR) study ultimately aimed at comparing expression patterns in queens and workers. A critical step in designing qRT-PCR studies that will generate biologically meaningful expression patterns for target genes is to find a set of appropriate control loci, because relative gene expression is measured in terms of ratios of target to control genes (reported as Delta-Delta-Ct values). It is also important to establish whether gene expression varies among tissues, developmental stages, males and females, etc. As a baseline, we evaluated *for* expression in newly eclosed males not yet capable of flight, calculating Delta-Delta-Ct values with respect to eight control genes (actin, arginine kinase, EF-1alpha, GAPDH, Rpl13, Rpl32, PrP2, and RpS5); *for* gene expression levels were similar in heads, thoraces, and abdomens. We then analysed spring queens caught on the wing during the first brood provisioning period; *for* expression levels were highest in thoraces and lowest in abdomens. These preliminary results suggest that increased *for* expression is indeed associated with flight activity in *L. laevissimum*, so comparisons between queens and workers are likely to reveal caste-specific patterns in *for* gene expression. Methodologically, analyses based on multiple versus single control genes demonstrated that robust inferences require comparisons based on multiple control genes. We will present further analyses comparing *for* gene expression levels in queens and workers, specifically, foraging (spring) and nonforaging (summer) queens, foraging and non-foraging workers, and young gynes prior to hibernation.