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Sexual selection is considered as a potent evolutionary force that has been shown to vary in strength and direction depending on demographic factors such as density and sex ratio. However, the effect of other environmental factors on the mode of sexual selection remains largely unexplored. Here we tested experimentally how food restriction affects the potential for sexual selection in the male and female sex function of the simultaneously hermaphroditic freshwater snail Physa acuta. We manipulated food availability and compared Bateman's metrics of sexual selection between groups of five well-fed and five food-restricted snails. Our results indicate that food-restricted snails had a reduced female reproductive output suggesting that we successfully manipulated the reproductive resources. Importantly, food restriction reduced the male opportunity for sexual selection (in terms of a lowered variance in male mating success) and lead to diminishing returns of mating in both sexes (in terms of non-significant Bateman gradients). Furthermore, we observed significant changes in the relative contribution of different fitness components suggesting stronger post-copulatory selection in the male and stronger fecundity selection in the female sex role under restricted food conditions. This study highlights the need to incorporate ecological factors to better understand how sexual selection operates in the wild.

Poster session A - POL 300

Searching for signatures of selection in Iberian honey bee (Apis mellifera iberiensis) using whole genome sequences (52236)

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The Iberian Peninsula comprises a diverse set of habitats. It was an important glacial refugium during the Pleistocene and has served as a bridge for populations migrating between Africa and Europe, resulting in a complex mix of ancestry and diversity. The Iberian honey bee (A. m. iberiensis) is no exception and has been the subject of numerous incongruent population genetic surveys. Recent mtDNA and SNP analyses indicate a steep northeastern-southwestern cline of African ancestry along the peninsula, which has been explained by selection. Advances in DNA sequencing technology and computational tools provide unprecedented opportunities to study demography, search for signatures of selection across the genome and illuminate its role in shaping genomic diversity. We used Illumina technology to sequence the whole genomes of 86 Iberian honeybees, collected across three longitudinal transects in the Iberian Peninsula and spanning semi-arid climates in the southeastern peninsula to oceanic in the North-West. The dataset was first analyzed for FST-outliers, CLR (composite-likelihood ratio) and EHH (Extended Haplotype Homozygosity) methods were further deployed to evaluate polymorphisms implicated in local adaptation and possibly in the response to human-mediated environmental changes, including known and novel variants in genes related to behavior, vision, xenobiotic detoxification and immune response.