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Seasonal Energetics of Ice-Dependent Arctic Seals Reveal the Metabolic Consequences of Different Molting Strategies

Ice-dependent Arctic seals, including bearded (*Erignathus barbatus*), ringed (*Pusa hispida*), and spotted (*Phoca largha*) seals, are uniquely affected by sea ice loss. These species use sea ice as a substrate for various critical functions, including rest, giving birth, nursing, predator avoidance, and foraging. They also rely on sea ice during the annual molt, when they shed several layers of epidermis and fur and grow a new coat. To facilitate this process, seals haul out for extended periods, increase blood flow to the skin, and maintain elevated skin temperatures. Molting is assumed to have a significant metabolic cost, which would increase if appropriate haul-out substrate were unavailable; however, molting costs have only been quantified for a few species. Working with trained seals, we tracked changes in coat condition and seasonal energetic demands to identify key periods when the loss of sea ice may have the greatest impact. We documented the timing, progression, and duration of the visible molt for bearded (n=2), ringed (n=3), and spotted (n=4) seals. In addition, we used open-flow respirometry to track fine-scale changes in the resting metabolic rate (RMR) of six seals for a minimum of one year. We observed clear patterns in seasonal costs that related to the distinct molting strategies of each species. For species that molted over a short interval (spotted: 36±4.6 days, ringed: 29±2.5 days), RMR increased on average 26-47% across the molting period. In contrast, molting over a longer interval (bearded: 107±14.8 days) appeared to limit the cost of molting as indicated by a stable annual RMR. This study highlights the relationship between molting strategy and seasonal energetic requirements and provides quantitative data that can be used to assess species-specific vulnerabilities to changing conditions.

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Is Daytime Mass Management and Pre-Roost Hyperphagia Common in Hummingbirds?

Several studies assume hummingbirds fill their crop prior to roosting, and have included crop filling in nighttime metabolism protocols. To test the validity of this assumption, we examined daytime mass management in both males and females of three SE Arizona hummingbird species that differ in size and ecological role: the black-chinned hummingbird (*Archilochus Alexandria,* 3.0g; opportunistic forager), the Rivoli's hummingbird (*Eugenes fulgens,* 7.5g; trap-liner), and blue-throated hummingbird (*Lampornis clemenciae,* 8.0g; territorialist). Male Rivoli's and black chinned hummingbirds maintained mass throughout the day, but appeared to crop load prior to roosting. Blue-throated hummingbirds maintained mass but did not crop load, and fed infrequently during the last 30 minutes of activity, possibly due to unlimited access to resources. Female black-chinned hummingbirds exhibited high variation in mass and no crop-loading even though they were numerically dominant at the feeders during the last 30 minutes of activity. In contrast, female blue-throated and Rivoli's hummingbirds had higher activity in the beginning and end of the day, but were infrequent visitors to feeders mid-day when temperature was high. These data suggest that daytime mass management and pre-roost crop loading is likely influenced by social interaction and to some degree thermal tolerance. Additionally, since this study was conducted during the breeding season, females were likely influenced by egg production, and all phases of nest construction and attendance.

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The Ontogeny of Static Allometry is Not So Simple for Grasshoppers: Genetic Variation for Nutrient Sensitive Plasticity is Masked by Size-Dependent Compensatory Growth

Grasshoppers develop larger head width and shorter leg length, relative to body size, when fed low nutrient, silica rich grasses compared to sibs fed a diet of high nutrient grasses. To elucidate how underlying genetic variation and plasticity of growth generate static allometry in *Melanoplus sanguinipes* (Orthoptera; Acrididae), I measured head and leg size of three nymphal instars and adults raised on either a low or high nutrient diet within a half-sib quantitative genetic experiment. A doubly-multivariate MANOVA of head growth, leg growth, and growth period per instar was used to analyze how these variables and additive genetic variation for plasticity (G x E interaction) contribute to scaling of functional allometry (trait x instar x G x E). Genetic variation for diet-induced plasticity of head and leg size varied through ontogeny, as did genetic variation for plasticity of growth in 3rd and 4th instar nymphs. Despite extensive genetic variation in plasticity of head width and leg length in the 4th instar, the static allometry between head and leg was stable within each diet because the patterns of G x E were concordant for head width, leg length and their coordinated growth. However, genetic variation for 4th instar morphological plasticity was suppressed in adults by negatively size-dependent compensatory growth in the last period of ontogeny. Bivariate reaction norms of adult head and leg size were parallel with diet specific scaling but no G x E. Thus, the hemimetabolous ontogeny of seemingly simple allometry between functional body parts comprised qualitatively different patterns of nutrient sensitive growth rates and periods and compensatory or targeted growth, all relevant to understanding development and evolution.

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Evidence of Plant-encoded miRNAs in Green Peach Aphid (Myzus persicae) Gut

The aphid/*Buchnera* symbiosis was the first insect nutritional endosymbiosis for which the genome of both the insect and its symbiont were known. In this model, *Buchnera* are housed intracellularly in bacteriocytes within bacteriomes where they work to provide essential amino acids to the host aphid. Recently, we worked to characterize miRNAs that are implicated in regulation of the symbiosis in the green peach aphid, *Myzus persicae*. To do this we generated small RNA-seq datasets from aphid gut and bacteriome tissue. Remarkably, we found that 45% of reads in gut samples failed to map to the aphid and/or *Buchnera* genomes. In contrast, only 5% of reads from bacteriome samples failed to map to the aphid and/or *Buchnera* genomes. Here we report our interrogation of the 45% of small RNA-seq reads in gut samples that failed to map to the insect and/or symbiont genome. We found that viruses and possible secondary symbionts were not likely sources of these reads. Rather, 67% of these unknown reads mapped to the genome of the host plant, *Brassica oleracea*. *B. oleracea* reads represented 31% of all reads from gut tissue samples. A subset of these *B. oleracea*-mapped small RNAs were annotated as plant miRNAs with putative targets in the both the *B. oleracea* and *M. persicae* genomes. Our results provide foundational evidence for the regulation of aphid gene expression by plant-encoded miRNAs. This knowledge both advances understanding of cross-kingdom gene regulation in plants and insects, and expands understanding of the regulatory interactions surrounding aphid feeding.