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# Comparative Metabolic Physiology in the 'omics' Era: A Call to Arms, Paws, Flippers, and Claws[1–3]

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**ABSTRACT**

In nutrition, medicine, and animal science, metabolism research is often focused on solving questions using a single organism. Outcomes are most often linked to translational outcomes, understanding or treating a disease, optimizing nutritional status, improving select qualities of production animals, which have tremendous value to human and animal health as well as economic benefit. There is also value in clarifying basic biological principles and integrative systems that determine how organisms function and deal with their environment. Relevant to both translational and basic research questions, comparative metabolic physiology provides a context by which new "omics" technologies and other approaches can be coupled to multi-species metabolic phenotype diversity. These principles were highlighted at the "Adipose and Lipid Biology: Crossing Taxonomic Boundaries" symposium held at the 2013 Experimental Biology meeting in Boston, MA. By considering differences and shared physiology across a spectrum of phenotypes (especially when considering "extremes" that have emerged from evolutionary processes or breeding selection), one may unmask subtle processes and learn from natural adaptations. *Adv. Nutr. 4: 568–569, 2013.*

## Introduction

A strong case can be made that consideration of multi-species metabolic physiology enhances our depth of understanding of processes relevant to nutritional and biomedical scientists, animal and comparative physiologists, and biochemists alike. In addition to fostering cross-fertilization of knowledge among disparate scientific groups, the study of comparative metabolic physiology allows one to benefit from the natural experiments emanating from adaptive evolutionary processes and from the directed selection resulting from animal breeding for desirable traits. Such studies are complementary to experimental manipulation of genes to understand function (knockout or transgenic animal models, e.g.). Variance, normally the bane of statisticians and experimentalists, is considered a blessing to comparative physiologists when considered in light of phenotypic divergence across strains, breeds, and species. Phenotype extremes and model-specific metabolic nuances can and should be leveraged to better understand the fundamental physiological and biochemical principles of nature. In addition, a comparative viewpoint fosters iconoclastic thinking and reduces the intellectual rigidity that can result from group-think within a specific research field.

These principles were highlighted by the 4 speakers at the "Adipose and Lipid Biology: Crossing Taxonomic Boundaries" symposium held at the 2013 Experimental Biology meeting in Boston, MA. Building upon the informative contrasts and similarities among divergent biologic systems, this symposium was designed to provide a forum in which lipid biology and adipose physiology could be discussed in a comparative context. With a variety of species in mind, speakers addressed diverse topics relevant to human physiology and biomedicine, companion animal health and comparative medicine, animal production, and wild animal adaptation. Talks focused on mechanisms underlying hepatic lipid trafficking using rodent and cell models (Douglas Mashek, University of Minnesota), adipokine biology and obesity-associated disease in domestic cats (Claudia Kirk, University of Tennessee), the impact of hyperphagia and adiposity on ovarian function in hens (Rosemary Walzem, Texas A&M University), and shifts in intermediary metabolism and oxidation of fuels in animals that undergo a long-term natural

[1] This article is a summary of the symposium "Adipose and Lipid Biology: Crossing Taxonomic Boundaries" held April 19, 2013 at ASN Scientific Sessions and Annual Meeting at Experimental Biology 2013 in Boson, MA. The symposium was sponsored by the American Society for Nutrition and was supported in part by Proctor & Gamble Pet Care, Nutreco, the North Central Regional Association of Agricultural Experiment Station Directors (NCCC-210 Multi-State Project), the USDA-Agricultural Research Service Western Human Nutrition Research Center, and Human Nutrition National Program NP-107.

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fast such as the northern elephant seal (Daniel Crocker, Sonoma State University). By considering lipid and adipose biology across taxa, symposium participants and attendees had the opportunity to formulate a synthesis of shared metabolic events and biological principles. The intent was to forge a perspective that would promote advancements in nutrition across disciplines and encourage unique collaboration opportunities.

Rapid developments in "omics" technologies have revolutionized metabolic research and, looking to the future, will provide powerful new tools that promise to unleash a resurgence of comparative physiology. Prior experimental constraints such as the dearth of cross-taxa gene sequence knowledge have fallen away with the advent of rapid whole-genome, metagenomic, and total transcriptome sequence analyses. Furthermore, improvements in detection methods have provided insights into chemical modification of the genome (e.g., epigenetics) and changes in the gut microbial ecology that help regulate host phenotype in response to environment and diet. In addition, metabolomics technologies that comprehensively measure hundreds to thousands of metabolites in blood, tissues, and biofluids are by definition species independent and thus directly applicable to comparative metabolic physiology studies. Because many biochemical and molecular events that underlie physiological processes can be subtle, to find the proverbial needle in the haystack, "omics" technologies are most successfully applied under conditions that maximize signal-to-noise. Again, comparative physiology is a field perfectly positioned to take advantage of this. Animal models that span a broad spectrum of phenotypes or that display large dynamic ranges of metabolism in response to experimental or natural challenges provide stark contrasts to study: e.g., disparate species- or breed-specific responses to natural fasting and feeding cycles, metabolic adaptations to ambient temperature and season, physiological shifts during migration or physical activity bouts, etc. Application of species-independent "omics" technologies to discover and compare the biology of varied animal models should prove valuable in better understanding basic biological principles important to nutrition, biomedicine, physiology and biochemistry, and animal and veterinary sciences.

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