© 2026. Published by The Company of Biologists | Journal of Experimental Biology (2026) 229, jeb251497. doi:10.1242/jeb.251497

REVIEW

SPECIAL ISSUE
THE INTEGRATIVE BIOLOGY OF EXERCISE

Mechanisms and trade-offs of fat-powered endurance flight in migratory animals

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ABSTRACT

Seasonal migration is one of the most physiologically demanding life history events in the animal kingdom, requiring tightly integrated solutions across molecular, organ and whole-animal scales. While three core metabolic 'gears' are broadly conserved across taxa to meet most locomotion demands, a rare 'fourth gear' of fat-fueled high-intensity endurance has evolved as a solution to the physiological problem of how to achieve long-distance migratory powered flight. We synthesize the current understanding of how birds, bats and insects perform such sustained high aerobic power output and how this capacity depends on seasonal phenotypic flexibility: reversible changes in lipid stores and composition, muscle biochemistry, cardiovascular capacity, and antioxidant defenses. Long-distance high-intensity endurance exercise involves increases in total fat stores and the remodeling of fatty acid composition, as well as key changes in fuel mobilization, enzyme kinetics and enhanced antioxidant capacity, and selective dietary intake of protective compounds to avoid oxidative damage. Finally, we outline future research priorities that connect mechanistic insights into lipid biochemistry, oxidative stress management and phenotypic flexibility with the ecological realities of a changing world.

KEY WORDS: Exercise physiology, Phenotypic flexibility, Flight, Fatty acid, Antioxidants

Introduction: phenotypic flexibility in animal migration

Animals living in seasonal environments can, in the most general sense, stay put and contend with the seasonal changes in weather and productivity, or move and thereby reduce the extent of seasonal change encountered each year. Given the inevitable costs of moving, long-distance seasonal animal migration has evolved in relatively few species but in a wide range of animal lineages, including birds, mammals, fish and insects (Newton, 2008; Dingle, 2014). However, the locomotory modes these migrating animals use (running, swimming or flying) impose very different demands on physiology, especially with respect to fuel type, energy cost and heat production. Among these modes, powered flight is uniquely demanding due to its high energetic cost and the inability of most animals to eat or drink while airborne. Consequently, long-distance migratory flight has evolved in only a few taxa, most notably birds. Even in birds, <20% of the ≈10,000 species on earth migrate on a regular basis (Kirby et al., 2008), although close to half of bird species that breed at higher latitudes (above 35° north or south) migrate between breeding and wintering areas (Newton, 2008).

The physiological feat of bird migration has been equated to such athletic feats in mammals as running 130 consecutive marathons (the semipalmated sandpiper *Calidris pusilla* migrates ≈5000–7000 km non-stop; Anderson et al., 2019) and completing three trips to the moon and back in a lifetime (the arctic tern *Sterna paradisaea* migrates ≈80,000 km a year over a 30 year lifespan; Egevang et al., 2010). While comparable distances may be covered by migrating caribou, whales or salmon, those animals use locomotor modes (running or swimming) that operate at lower intensities and also allow for intermittent feeding. In contrast, migratory flight demands sustained high intensity endurance powered almost exclusively by internal fuel stores (primarily fat) and poses a distinct set of physiological demands. In this Review, we explore how animals meet these demands, with a special focus on the unique challenges of migratory flight. Some of the most notable challenges volant migratory animals face is how to: (1) fuel the cost of movement (e.g. store fat or glycogen; Bishop and Guglielmo, 2022); (2) contend with the physiological costs of movement and the associated increase in metabolism (e.g. lipid peroxides, which are unstable molecules with the potential to cause cellular damage and are produced during fat metabolism; McWilliams et al., 2021) often while eating and drinking less (e.g. most birds fast while flying, which reduces gut size and function (Karasov et al., 2025); (3) avoid becoming too hot (heat gained from metabolism and the environment (Bishop and Guglielmo, 2022; McKechnie, 2022); and (4) meet these challenges under a seasonal time constraint (McWilliams et al., 2022).

A key solution to such physiological challenges is the evolution of flexible phenotypes that allow migrants to physiologically, morphologically and biochemically prepare for and respond to the challenges of migration in a dynamic seasonal environment (Piersma and van Gils, 2011; McWilliams and Karasov, 2014; Stager et al., 2024). Indeed, a pervasive theme in migration physiology is phenotypic flexibility across levels of biological organization, from the molecular to whole-organism scale. Phenotypic flexibility and plasticity are too often used interchangeably but are worth distinguishing here. As succinctly outlined by Piersma and van Gils (2011) and recently reviewed by Stager et al. (2024), phenotypic plasticity refers to the general phenomenon where genotype–environment interactions produce different phenotypes; however, this general definition does not specify when during the life of the organism the plasticity occurs and, most important for our discussion here, whether the phenotypic change is reversible. Developmental plasticity refers to the oft-documented changes in phenotype that occur during development into the adult form (Pigliucci, 1996; Schlichting and Pigliucci, 1998), which are then fixed thereafter. In contrast, phenotypic flexibility is defined as rapid reversible changes in phenotypes (Piersma and van Gils, 2011) and it is this type of phenotypic flexibility that pervades the examples in this Review.

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Glossary

Basal metabolic rate
The metabolic rate of organisms in their thermoneutral zone and in a post-absorptive, resting, non-growing, non-reproductive state.

Fuel hypothesis
Fatty acids may be preferentially mobilized and metabolized more quickly and so be advantageous for exercise performance.

Master antioxidant response
The major cellular pathway for regulating the antioxidant response of metazoans against oxidative imbalance within cells that involves the transcription factor NF-E2-related factor 2 (NRF2) and the Kelch-like ECH-associated protein (KEAP1), which negatively regulates NRF2 activity.

Membrane hypothesis
Fatty acids may affect composition and key functions of lipid-rich cell membranes and so be advantageous for exercise performance.

Peak metabolic rate
Maximum 'instantaneous' metabolic rate achieved during short-term intense exercise.

Reactive oxygen species
Pro-oxidant molecules produced primarily in the mitochondria during respiration in metabolic reactions with oxygen that can readily react with and damage cellular lipids, proteins and DNA.

Signal hypothesis
Fatty acids may stimulate key facets of aerobic metabolism, such as stimulating expression of genes involved in fatty acid oxidation, and so be advantageous for exercise performance.

We begin by outlining three core metabolic 'gears' that are broadly conserved across animals and that describe how animals shift between fuel sources (mainly carbohydrates and fats), depending on the intensity and duration of locomotion. We then focus on a rarer, more-specialized 'fourth gear': a set of adaptations that allow fat to power sustained, high-intensity movement, as seen in the extreme endurance of migratory flight, especially in birds. We also explore the evolutionary trade-offs and physiological constraints that make this fat-fueled endurance strategy so rare. We then continue with a discussion about how the body composition of migratory animals changes remarkably in preparation for and during migration, and what the comparison across taxa tells us about the different fuels used by different organisms. Given that fat is the main fuel for volant migratory animals, for good reasons that we describe, we then discuss phenotypic flexibility in fat 'quality' or the fatty acid composition of fat stores (and cell membranes), the mechanisms involved in producing changes in composition, and its consequences for the energetic costs and oxidative balance during migration, especially in birds. We ignore the remarkable phenotypic flexibility of the digestive system in migratory birds and its nutritional implications, because this has already been discussed numerous times (e.g. McWilliams and Karasov, 2001, 2005; Bauchinger and McWilliams, 2010), including more recently (Karasov et al., 2025). The conclusion that emerges is that the integrative biology of high-intensity endurance exercise in animals, exemplified by the super-athlete capabilities of migratory birds, depends on substantial phenotypic flexibility across molecular, cellular and whole-organism levels.

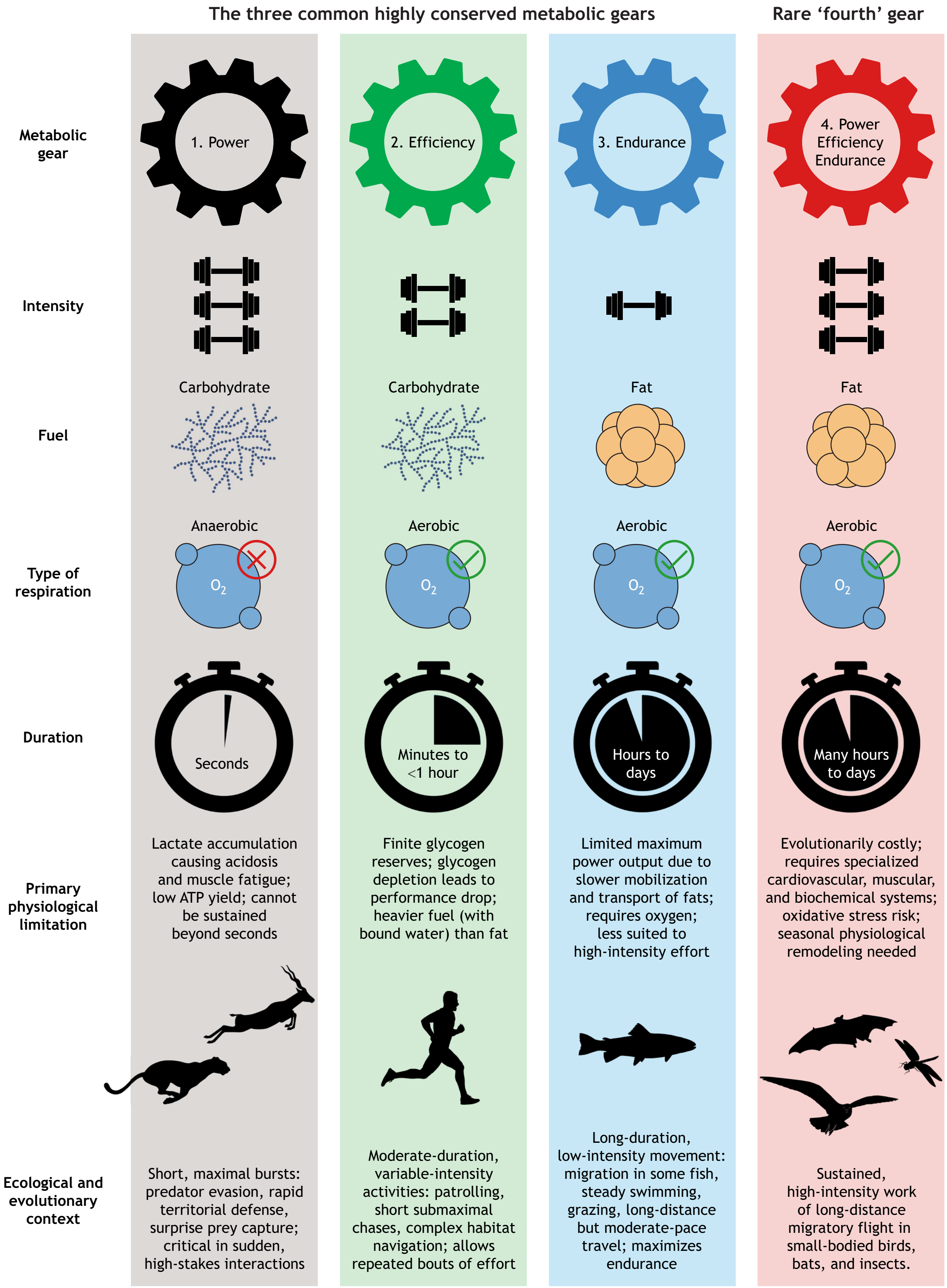
Three conserved metabolic gears and a rare fourth gear for extreme fat-fueled endurance

Locomotion is among the most energetically demanding activities animals perform, and the strategies used to fuel it vary widely across taxa (Weber, 2011; Moyes et al., 1990), yet some universal patterns hold. Across all animals, short, high-intensity bursts of activity, used in sudden predator evasion, territorial fights or surprise attacks on prey, are powered by carbohydrates via anaerobic glycolysis (Gleeson, 1991; Bennett, 1991). This pathway generates ATP extremely rapidly and does not require oxygen, making it ideal for sudden, maximal effort. However, it yields very little ATP per carbohydrate molecule and quickly leads to fatigue due to lactate accumulation (Bennett, 1991). Moderate-duration or variable-intensity activities, such as patrolling territory, shorter distance pursuit of prey, or navigating complex habitats while foraging, are typically fueled by aerobic carbohydrate metabolism (Brooks and Mercier, 1994; Pi et al., 2023). Although this pathway produces ATP more slowly than anaerobic glycolysis, it is much more efficient, supporting repeated or moderately prolonged effort without the rapid fatigue that accompanies anaerobic bursts (Weber, 2011). However, this mode still relies on finite glycogen reserves within muscle tissue that gradually deplete with continued exertion and ultimately limit endurance (McClelland et al., 2017; Bennett, 1991). At the other extreme, long-duration low-intensity movement, such as grazing, slow long-distance travel or steady swimming in open water, is typically fueled by fats (e.g. McClelland and Lyons, 2025; Kooyman et al., 1981). While fat oxidation proceeds more slowly than carbohydrate metabolism, it yields more ATP per gram and draws on vastly larger energy reserves, making it the dominant fuel for prolonged moderate-intensity activity (Weber, 2011, 1988).

These three fueling strategies can be thought of as metabolic 'gears' that animals shift between depending on the task at hand (Fig. 1), in which they prioritize power, efficiency or endurance (Weber, 2011). These gears are broadly conserved across taxa; however, the extent to which species rely on each, and the physiological machinery they invest in to support them, varies widely (Brooks and Mercier, 1994; Weber and Haman, 2004). These species differences emerge from the tight coupling between ecological demands and the physiological traits shaped by evolution: how far, how fast and how often animals need to move influences how they fuel it, and vice versa (Weber, 2011; McClelland et al., 2017; Bennett, 1991).

Here, we focus on a rare 'fourth gear' (Fig. 1) that enables sustained, high-intensity activity powered primarily by fat (Guglielmo, 2018; McWilliams et al., 2022). This evolved in response to a fundamental physiological challenge: how to sustain high aerobic power output for a long time without quickly depleting energy reserves, especially when opportunities to refuel are scarce. Glycogen stores are limited and are rapidly exhausted during intense activity, leading to sharp declines in performance well before the task is complete (Pernow, 1971). Moreover, glycogen is a bulky fuel: it provides only ∼4 kcal g^{-1} and binds approximately 3 g of water per gram, significantly increasing its effective weight (Fernández-Elías et al., 2015). The evolutionary solution, reached independently in several flying lineages, was to shift away from carbohydrate toward fat as a primary fuel source (Rogers et al., 2019; Moyes et al., 1990; Guglielmo, 2018). Fat stores are both more abundant and more energy-dense, yielding ≈9 kcal g^{-1}, and are stored nearly anhydrously, making them a far more compact and lightweight energy reserve (Dixit et al., 2022). Fat oxidation also yields more metabolic water per gram than carbohydrate or protein, a critical benefit during long-distance flights (e.g. Gerson and Guglielmo, 2011) – especially those over deserts or oceans where dehydration is a serious risk (Biebach, 1990). However, burning fat at high intensities requires a suite of specialized physiological adaptations for rapid mobilization, transport and oxidation (Bishop and Guglielmo, 2022; Guglielmo, 2018; McWilliams et al., 2022; Weber, 2009).

In the remainder of this section, we provide an overview of the species and ecological contexts in which fat-fueled, high-intensity endurance capacity evolved, highlighting how a few disparate taxa



	The three common highly conserved metabolic gears			Rare 'fourth' gear
Metabolic gear	1. Power	2. Efficiency	3. Endurance	4. Power Efficiency Endurance
Intensity				
Fuel	Carbohydrate	Carbohydrate	Fat	Fat
Type of respiration	Anaerobic O_2 ✗	Aerobic O_2 ✓	Aerobic O_2 ✓	Aerobic O_2 ✓
Duration	Seconds	Minutes to <1 hour	Hours to days	Many hours to days
Primary physiological limitation	Lactate accumulation causing acidosis and muscle fatigue; low ATP yield; cannot be sustained beyond seconds	Finite glycogen reserves; glycogen depletion leads to performance drop; heavier fuel (with bound water) than fat	Limited maximum power output due to slower mobilization and transport of fats; requires oxygen; less suited to high-intensity effort	Evolutionarily costly; requires specialized cardiovascular, muscular, and biochemical systems; oxidative stress risk; seasonal physiological remodeling needed
Ecological and evolutionary context	Short, maximal bursts: predator evasion, rapid territorial defense, surprise prey capture; critical in sudden, high-stakes interactions	Moderate-duration, variable-intensity activities: patrolling, short submaximal chases, complex habitat navigation; allows repeated bouts of effort	Long-duration, low-intensity movement: migration in some fish, steady swimming, grazing, long-distance but moderate-pace travel; maximizes endurance	Sustained, high-intensity work of long-distance migratory flight in small-bodied birds, bats, and insects.

Fig. 1. Metabolic 'gears' for locomotion across animals. Animals shift between distinct metabolic 'gears' to match fuel supply with locomotor demands that vary with ecological context and carry different physiological limitations.

converged on this strategy. In some species, individuals can shift fuel-use strategies and reconfigure physiological systems in response to training, environmental cues or seasonal demands (Rogers et al., 2019; Joyner, 2008; Husak et al., 2015; McWilliams et al., 2022, 2004). These cases reveal how movement demands have repeatedly driven both evolutionary innovation and phenotypic flexibility, expanding the upper limits of animal performance. We admittedly ignore protein in the context of this Review because it is generally not a core fuel for locomotion. In most animals, protein oxidation contributes minimally to aerobic ATP production, and its use typically increases only under extreme or prolonged energy deficits, such as during late-stage migration, fasting or starvation, when glycogen and fat stores are depleted. Protein oxidation is important when animals must avoid dehydration (Biebach, 1990; Gerson and Guglielmo, 2011) and oxidative damage associated with elevated metabolism (i.e. uric acid, a potent antioxidant) is an end-product of protein metabolism (see section ‘Oxidative costs of high-intensity exercise and the responses of the antioxidant system’).

The evolution of high-intensity, fat-fueled endurance in birds, bats and insects

Powered flight evolved independently in birds, bats and insects (Hunter, 2007; Gordon et al., 2017; Alexander, 2015), yet in each lineage it imposed the same fundamental problem: the need to sustain high aerobic power output for extended periods without access to external fuel. Long-distance migration and wide-ranging foraging in volant animals demand continuous, high-intensity effort, well beyond what carbohydrate-based systems could support alone. The limited availability and low energy density of glycogen, combined with the inability to feed during flight – especially when crossing ecological barriers such as oceans, deserts or mountain ranges – created strong selection pressure for a more-efficient and longer-lasting fuel strategy. In response, birds, bats and insects converged on a rare metabolic solution, which is the capacity to oxidize fat at unusually high rates to sustain powered flight. This transition required a coordinated suite of physiological adaptations, including rapid lipid mobilization, specialized transport proteins, dense mitochondrial networks and flight muscles optimized for sustained aerobic output (Maina, 2000; Guglielmo, 2018; Weber, 2009; McWilliams et al., 2022).

Among vertebrates, fat-fueled high intensity endurance appears to have evolved most fully in migratory birds, where the demands of long-distance flight impose uniquely severe challenges. Sustained powered flight is among the most energetically costly forms of locomotion (Gordon et al., 2017), and many migrating birds maintain it for hours or even days without feeding or drinking, often crossing ecological barriers that offer no opportunity for rest or refueling (Bishop and Guglielmo, 2022). Once in flight, birds rely on fat for up to 95% of their energy needs, preserving most muscle protein and minimizing tissue catabolism (McWilliams et al., 2020; Jenni and Jenni-Eiermann, 1998). Such fat-fueled high-intensity endurance flights require coordinated changes in behavior, morphology and metabolism before migration begins, including hyperphagia, selective fat deposition, reversible changes in organ size, and upregulation of lipid transport and oxidative pathways (Price et al., 2011; McWilliams et al., 2004, 2022). Many species accumulate fat loads exceeding 100% of lean body mass, yet still maintain the mechanical efficiency and lift needed for long-distance flight (Bairlein and Gwinner, 1994; Guglielmo, 2018). In addition, the types of fatty acids that compose the stored fat change during migration (Pierce et al., 2004; McWilliams et al., 2022) and can increase fuel efficiency during long-duration flights (McWilliams et al., 2020, 2022; Bishop and Guglielmo, 2022). Migratory birds also exhibit some of the highest fatty acid oxidation rates recorded in vertebrates (Guglielmo, 2018; Bishop and Guglielmo, 2022), enabling them to maintain high aerobic performance while conserving limited glycogen stores for short high-intensity bursts, such as takeoff, landing or evasive maneuvers. These high fatty acid oxidation rates require fatty acid transport proteins in the flight muscles and heart to facilitate uptake across membranes, along with fatty acid-binding proteins that shuttle lipids within cells (Guglielmo, 2010, 2018). At the cellular level, their flight muscles show exceptionally high capillarity and mitochondrial density, packed with enzymes specialized for fatty acid oxidation. Oxidative enzymes within the mitochondria are also upregulated, accelerating fat breakdown at rates fast enough to support vigorous aerobic activity (Mesquita et al., 2024; Coulson et al., 2024). These metabolic upgrades are supported by structural changes: enlarged flight muscles, heart and lungs increase aerobic capacity, while liver and intestinal tissues often shrink to reduce weight and make space for fat reserves (Maggini et al., 2022; Guglielmo, 2018; McWilliams et al., 2021, 2022).

Bats are the only mammals to have evolved true powered flight and, like birds and insects, they face intense performance demands that have driven high-endurance aerobic capacity (Gordon et al., 2017). In bats, these demands come from the need for extensive nocturnal foraging and, in some cases, seasonal migrations spanning hundreds to thousands of kilometers (Rogers et al., 2019; McGuire et al., 2013). Although some bats may opportunistically forage during migration, many species rely primarily on stored lipids as their dominant fuel source (Guglielmo, 2018). As in birds, bats capable of long-distance flight rely heavily on fat stores and have evolved convergent physiological mechanisms to mobilize and oxidize lipids at high rates. For example, Hoary bats (*Lasiurus cinereus*) accumulate substantial endogenous fat reserves to support prolonged flights (McGuire et al., 2013). Unlike birds, bats rely more heavily on fat stored within their flight muscles, likely to circumvent the slower mobilization of lipids from peripheral adipose tissue, which is a constraint that reflects differences in mammalian lipid transport physiology (Voigt et al., 2010; Guglielmo, 2018). Bats also exhibit elevated activity of mitochondrial enzymes involved in lipid oxidation, along with compositional shifts in muscle membranes and adipose stores toward polyunsaturated fatty acids (PUFAs), which enhance metabolic efficiency and lipid mobilization (Rogers et al., 2019; McGuire et al., 2013; Guglielmo, 2018). Bats also enhance this capacity with dense mitochondrial networks and abundant fatty acid-binding proteins in their flight muscles, allowing them to oxidize fat at high rates (Rogers et al., 2019; Guglielmo, 2018; McGuire et al., 2013). In addition, bats exploit a behavioral adaptation less available to birds (Wojciechowski and Pinshow, 2009): the use of torpor during stopovers (McGuire et al., 2015). By temporarily lowering body temperature and metabolic rate, bats significantly reduce energy expenditure between flight bouts, conserving fat stores and minimizing the need for refueling (McGuire et al., 2015). This strategy enhances migratory efficiency, especially in species with smaller body sizes and lower fat-carrying capacity.

Insects represent a third major lineage to evolve fat-fueled endurance flight, converging on this solution through their own unique physiological architecture (Beenakkers et al., 1984). In migratory species such as monarch butterflies, locusts, hawkmoths and dragonflies, sustained high-intensity flight depends on switching from carbohydrate to lipid metabolism (O’Brien, 1999; Minter et al., 2018; Li et al., 2023; Brown and Chippendale, 1974). Carbohydrates, especially trehalose (the dominant insect blood sugar), power initial takeoff and short bursts (Arrese and Soulages, 2010). However, during prolonged flight, insects transition to oxidizing lipids, drawing on their superior energy density to fuel long-distance travel (Arrese and Soulages, 2010). This shift is supported by a specialized system for lipid mobilization and delivery (Li et al., 2023). Adipokinetic hormone triggers the release of diacylglycerol (DAG) from stored triacylglycerols in the fat body (Chown and Nicolson, 2004). DAG circulates in the hemolymph bound to lipophorin, a reusable lipoprotein that ferries lipid fuel to the flight muscles (Chown and Nicolson, 2004; Canavoso et al., 2003). There, DAG is hydrolyzed and fatty acids enter mitochondria for aerobic metabolism (Li et al., 2023; Canavoso et al., 2003). This recycling shuttle system maintains a steady fuel supply during long flights, enabling insects to bypass the usual rate limitations of fat metabolism. Like birds and bats, insects enhance this capacity with dense mitochondrial networks and abundant fatty acid-binding proteins in their flight muscles, allowing them to oxidize fat at high rates (Beenakkers, 1969). These adaptations allow insects to track shifting resources, escape deteriorating habitats and colonize distant environments. Despite vast anatomical differences, insects, birds and bats have all arrived at the same rare solution: using fat to power high-intensity aerobic endurance in the air.

Evolutionary trade-offs and constraints of fat-fueled high-intensity endurance

While high-intensity long-duration locomotion fueled by fat has evolved in some birds, bats and insects, it remains the exception rather than the rule (Guglielmo, 2018). This rarity is not due to energy inefficiency, as fat is the most energy-dense fuel available (Maggini et al., 2022), but due to the difficulty of building metabolic systems that can burn it fast and reliably enough for locomotion, without incurring physiological costs or trade-offs that jeopardize survival or reproduction (Weber, 2011; Guglielmo, 2018; McWilliams et al., 2022). Oxidizing fat at high rates requires a tightly integrated suite of physiological adaptations, including dense muscle mitochondria, enhanced fatty acid transport, efficient lipid mobilization and delivery, specialized muscle architecture, and ample oxygen supply (Li et al., 2023; Guglielmo, 2018; McWilliams et al., 2022, 2004). Building, maintaining and regulating this machinery is not only energetically costly, but also demands significant metabolic bandwidth, cellular space and regulatory coordination, which are limiting resources that could otherwise support growth, reproduction, immune function or other physiological priorities (Guglielmo, 2010). Investments in this machinery can also compromise other aspects of performance: for example, packing muscles with mitochondria to enhance fat oxidation may reduce contractile strength or power output, creating trade-offs between endurance and burst performance (Weber, 2011; McClelland et al., 2017; Hoppeler and Weibel, 1998).

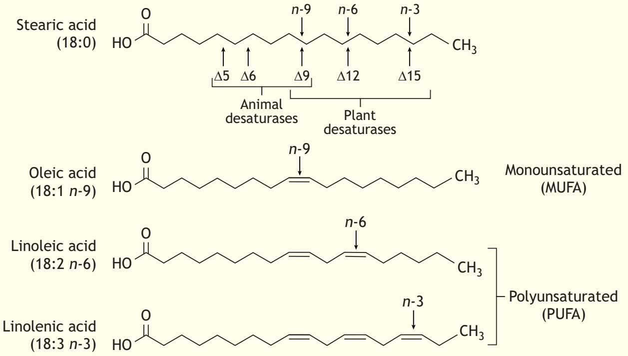
Seasonal changes in fatty acid composition of fat stores and cell membranes, and their implications for the energetic costs of migration

Seasonal migration demands precise timing of how much fat is stored and its fatty acid composition so that animals can optimize the speed, efficiency and thermal performance of fat oxidation during long flights. The seasonal remodeling of fatty acid profiles, evident in both energy stores and cell membranes, represents another layer of metabolic specialization that shapes the endurance capacity of migratory birds, bats and even insects.

Seasonal changes in fatty acid composition in migrating animals

The primary reliance on fat to fuel long-duration endurance exercise in some organisms involves substantial seasonal changes in the amount of fat stores but also in the fatty acids that compose these fat stores – the ‘fuel blend’ so to speak – and this, in turn, can affect how efficiently and quickly it can be burned during sustained activity (Price, 2010; McWilliams et al., 2004; Guglielmo, 2018). Box 1 provides a primer on fatty acid biochemistry (Klasing, 1998). As outlined in a recent review of empirical studies (McWilliams et al., 2022), there are several principle patterns related to seasonal changes in fatty acid composition associated with migration in birds. (1) For fat stores, the observed changes include the proportion of unsaturated fatty acids either remaining the same or increasing during migration, and in particular, the relative amounts of the n-6 and n-3 PUFAs increasing during migration. For muscle membrane phospholipids, reciprocal changes between primarily n-6 and n-3 PUFAs during migration seem the most common pattern. (2) These seasonal changes in fatty acid composition of fat stores and muscle phospholipids seem primarily driven by seasonal changes in diet, and the extent to which diet affects membrane composition is more modest than that of fat stores. In practical terms, migrants are not only loading more ‘fuel’ before departure, they are fine-tuning the molecular structure of that fuel to match the operating requirements of their migratory engines (and engine maintenance), optimizing for rapid mobilization, efficient oxidation and performance under the thermal and metabolic conditions of long-distance flight. Interestingly, similar seasonal changes in fat quantity and quality have been observed in migrating bats (McGuire et al., 2013; Voigt et al., 2019; Guglielmo, 2018) and migrating insects (Anaparasan et al., 2023; Levin et al., 2017). However, unlike migratory birds, there were specific sex-related differences in fatty acid composition that may be associated

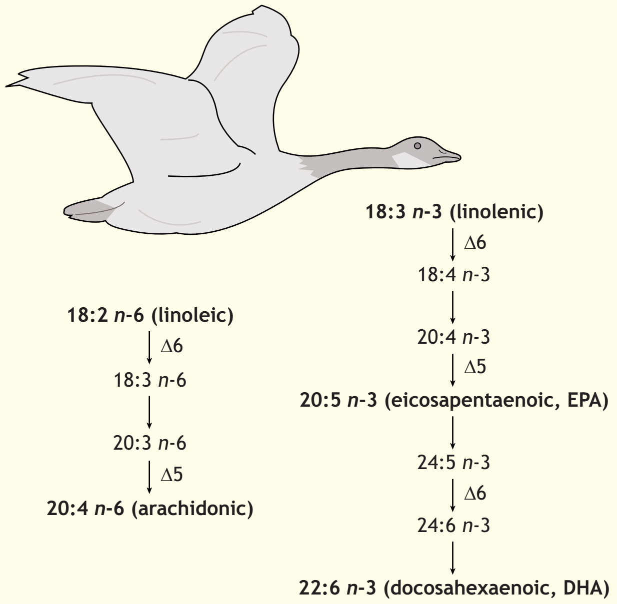
Box 1. Structure of fatty acids and their nomenclature



Conventional fatty acid nomenclature denotes saturated (e.g. stearic acid, no double bonds in the carbon backbone) and unsaturated fatty acids (with double bonds) with a shorthand that describes the number of carbons in the backbone (e.g. 18 carbons for oleic acid) and the number of double bonds (e.g. one for oleic acid), i.e. 18:1 for oleic acid. For unsaturated fatty acids, there is an additional reference to the position of the double bonds relative to the methyl end (CH_3) of the molecule, e.g. 18:2 n-6 for linoleic acid denotes the first double bond at the 6th carbon from this end (n-6 is also referred to as omega-6 or ω-6). The methyl end is typically chosen as the reference end because it is not subject to elongation and desaturation, and it determines nutritional essentiality (Klasing, 1998). For completeness, double bonds can also be referenced to the carboxyl end (-OH), e.g. 18:1 n-9 equals 18:1 Δ9 and 18:2 n-6 equals 18:2 Δ5. In addition, unsaturated fatty acids with a single double bond are nicknamed monounsaturated (i.e. MUFAs) and those with more than one double bond are nicknamed polyunsaturated (i.e. PUFAs).

with reproduction during or soon after migration and, at least for migratory bats, the use of torpor may promote different fatty acid composition (McGuire and Guglielmo, 2009; Guglielmo, 2018).

Box 2. Conversion of fatty acids and their nutritional significance



The pathways of fatty acid elongation and desaturation are limited for animals because they lack the enzymatic capacity to introduce double bonds beyond the ninth carbon from the carboxyl end (as shown for the stearic acid structure in Box 1). Animals can synthesize saturated fatty acids *de novo*, e.g. palmitic acid (16:0) can be produced from acetate and malonate, and then converted to stearic acid (18:0). Animals can then further convert these saturated fatty acids to specific monounsaturated fatty acids by adding double bonds up to the ninth carbon (e.g. 16:1 *n*-7 or 18:1 *n*-9). Only plants have the enzymatic capacity to introduce double bonds into longer-chain (18-carbon or longer) unsaturated fatty acids beyond the ninth carbon from the carboxyl end. Thus, linoleic (18:2 *n*-6) and linolenic acid (18:3 *n*-3) are considered the two ‘essential’ fatty acids for most animals because they must be acquired in their diet (Klasing, 1998), although very few animal studies have determined dietary requirements for other longer-chain unsaturated fatty acids. A notable example is that arachidonic acid (20:4 *n*-6) is required in the diet of carnivorous mammals and fish (Klasing, 1998).

Animals, including long-distance fat-fueled migrants such as geese, can acquire these essential fatty acids (e.g. 18:2 *n*-6 and 18:3 *n*-3) in their diet (Pierce et al., 2004; Price, 2010; Arnold et al., 2014; Guglielmo, 2018; McWilliams et al., 2022) and then use: (1) desaturase enzymes to add double bonds up to the ninth carbon from the carboxyl end (the delta notation in the figure shows which carbon is involved); and (2) elongase enzymes to add more (or fewer) carbons to the backbone of the fatty acid to produce longer-chain polyunsaturated fatty acids (LCPUFAs). The most common LCPUFAs found in migrating animals are indicated in bold in the figure (McWilliams et al., 2004, 2022; Price, 2010; Pierce and McWilliams, 2014; Guglielmo, 2018). Some of these LCPUFAs can also be acquired by animals that consume other animals that have carried out these conversions themselves. A notable pattern in the conversion pathways of fatty acids within animals is that the *n*-3 and *n*-6 families of fatty acids are metabolically independent and not interconvertible, because animals lack the enzymatic capacity to introduce double bonds beyond the ninth carbon from the carboxyl end. The other implication of this within-family pattern of conversion is that the dietary requirement for linoleic (18:2 *n*-6) and linolenic (18:3 *n*-3) acid is decreased by the consumption of other *n*-6 and *n*-3 LCPUFAs, respectively (Klasing, 1998).

Seasonal changes in the fatty acid composition of fat stores in free-living migratory birds and bats suggest that only a few fatty acids may be ecologically relevant (Guglielmo, 2018; Pierce and McWilliams, 2014; McWilliams et al., 2022; Voigt et al., 2019; McGuire et al., 2013). In general, the 16- and 18-carbon fatty acids predominate (usually >75% of lipid stores), and the most common forms are usually 16:0 and 18:1n-9. During migration, 16:0 and 18:1n-9 still predominate, although 16:1n-7 and two PUFAs considered essential for birds and other animals (Box 2) – mostly linoleic acid (18:2n-6) and small amounts of alpha-linolenic acid (18:3n-3) – are often moderately abundant (up to 40%, but usually <20%) in the fat stores of landbirds. The fatty acid composition of fat stores of marine birds, mostly shorebirds (Egeler and Williams, 2000; Maillet and Weber, 2006; Napolitano and Ackman, 1990; Guglielmo, 2018) and waterfowl (Thomas and George, 1975; Heitmeyer and Fredrickson, 1990) studied to date, also includes much 16:0 and 18:1n-9 but can include up to ≈20% of longer-chain 18:2n-6 and smaller amounts of 18:3n-3 PUFA (reviewed by McWilliams et al., 2022). Much the same general patterns have been observed in migrating bats (Clerc, 2015; Voigt et al., 2019; McGuire et al., 2013; Guglielmo, 2018).

In contrast to the composition of fat stores, the fatty acid composition of muscle and mitochondrial membranes is less affected by diet (Abbott et al., 2012). However, the apparently more consistent membrane composition conceals the fact that 95% of relevant membrane-bound fatty acids (i.e. 16:0, 18:2n-6) turn over every 10-17 days, on average, in volant birds, and at a faster rate than fatty acids in fat stores (Carter et al., 2019). Muscle membrane phospholipids usually comprise more saturated fatty acids (notably 16:0 and 18:0), fewer long-chain MUFAs (notably 18:1n-9) and more longer-chain PUFAs (notably 18:2n-6, 20:4n-6 and 20:5n-3, 22:6n-3) compared to the fatty acid composition of fat stores [e.g. western sandpipers (*Calidris mauri*; Egeler and Williams, 2000; Guglielmo et al., 2002), white-throated sparrows (Klaiman et al., 2009) and semipalmated sandpipers (Maillet and Weber, 2006)]. Fatty acid composition of muscle membrane phospholipids changes seasonally in the two species studied to date, with n-3 PUFAs (mostly 22:6n-3) decreasing and n-6 PUFAs (mostly 20:4n-6) coincidentally increasing in white-throated sparrows (Klaiman et al., 2009), whereas, in western sandpipers, the n-3 PUFAs (mostly 22:5n-3 and 22:6n-3) increased and n-6 PUFAs (mostly 20:4n-6) coincidentally decreased (Guglielmo et al., 2002), and there was a modest increase in 18:0 during migration in both species. This suggests that this difference between species in the reciprocal change in long-chain n-3 and n-6 fatty acids in muscle phospholipids during migration were because of diet changes (to more enriched n-3 marine prey for sandpipers, to more enriched n-6 seeds for sparrows). Clearly, more such studies are needed to determine if the general pattern of reciprocal change in long-chain n-3 and n-6 PUFAs in flight muscle membrane phospholipids is robust across bird species with different migration strategies that inhabit terrestrial and/or marine ecosystems.

The fatty acid composition of natural foods eaten by birds and bats in migration can be very variable (Pierce and McWilliams, 2014; Quinn et al., 2017; Krüger et al., 2014): migratory birds discriminate between foods based on fatty acid composition (Pierce and McWilliams, 2014; Bairlein, 1991; Zurovchak, 1997; Boyles, 2011; Rios et al., 2014; McWilliams et al., 2002) and the fatty acid composition of diet primarily determines that of stored fat, at least for the mid-chain length fatty acids (e.g. 16:1 and 18:1) and the essential fatty acids (e.g. 18:2n-6 and 18:3n-3, along with their dominate elongation products, 20:4n-6 and 22:6n-3, respectively), with selective metabolism of some fatty acids playing a possibly important but minor role (Pierce et al., 2005; Price and Guglielmo, 2009; Price, 2010; Blem, 1976). The implication is that migratory birds and bats can select diets in order to achieve a specific fatty acid composition of their stored fat and muscle membranes, and thereby satisfy the changing energy and nutritional demands across seasons, including those associated with endurance exercise during migration (Bairlein, 1996; Conway et al., 1994; Heitmeyer and Fredrickson, 1990; Maillet and Weber, 2006; Weber, 2009; Krüger et al., 2014; McGuire et al., 2013; Voigt et al., 2010). Interestingly, behavioral preferences for some dietary fatty acids (i.e. 18:1 and 18:2 over 18:0) are consistent across migration and non-migration periods of the annual cycle (Pierce et al., 2004) and more recent studies suggest that migratory birds consistently prefer a 2:1 ratio of 18:1 to 18:2 (Pierce and McWilliams, 2014; Boyles, 2011). In summary, any observed seasonal changes in fatty acid composition of migratory birds and bats are likely due primarily to diet and not to some endogenous seasonal change in diet preference for some fatty acids or selective metabolism, although many more such studies are clearly needed.

Fatty acid composition and exercise performance

Seasonal changes in fatty acid composition are a way of tuning the metabolic engine for the specific challenges of long-distance flight and thus have measurable impacts on efficiency and flight performance (Price, 2010; Carter et al., 2018; Guglielmo, 2018; McWilliams et al., 2020) as well as levels of oxidative damage (McWilliams et al., 2021), as outlined in the section 'Oxidative costs of high-intensity exercise and the responses of the antioxidant system'. In theory, selectively eating, and hence storing, specific long-chain unsaturated fatty acids may be advantageous for exercise performance because: (1) such fatty acids may be preferentially mobilized and metabolized more quickly (fuel hypothesis; see Glossary); (2) such fatty acids may affect the composition and key functions of lipid-rich cell membranes (membrane hypothesis; see Glossary); and (3) such fatty acids may stimulate key facets of aerobic metabolism, such as stimulating expression of genes involved in fatty acid oxidation (signal hypothesis; see Glossary). Other reviews should be consulted for more-thorough discussions of these not mutually exclusive hypotheses and their evidence (Guglielmo, 2010; 2018; Pierce and McWilliams, 2014; Price, 2010; Weber, 2009; McWilliams et al., 2022). Our emphasis here is to demonstrate that the seasonal changes in fatty acid composition during migration in birds has consequences for the energy costs of migration and for the oxidative costs associated with long-duration endurance exercise (see section 'Oxidative costs of high-intensity exercise and the responses of the antioxidant system').

Empirical evidence somewhat supports all these alternative hypotheses, although the weight of evidence to date seems to favor the fuel or signal hypotheses. The fuel hypothesis has been invoked to explain how fatty acid composition affects performance in rats, lizards, fish and, more recently, migratory birds (Geiser and Learmonth, 1994; Leyton et al., 1987; McKenzie et al., 1998; Petersson et al., 2010; Pierce et al., 2005; Price and Guglielmo, 2009; Price et al., 2008; Raclot and Groscolas, 1995; Wagner et al., 2004). For example, songbirds with stored fat composed of more n-6 PUFA had improved exercise performance during short-term intense exercise (Price and Guglielmo, 2009; Price, 2010; Pierce et al., 2005) as well as long-duration flights (McWilliams et al., 2020). Birds may optimize energy efficiency during long-duration flights (i.e. flying a specific distance while expending less energy) rather than maximizing metabolic rate and so may not need to maximize the rate of fatty acid supply, as is often assumed. A possible mechanism for such enhanced efficiency that is consistent with the fuel hypothesis includes the documented higher transport rates of unsaturated fatty acids reducing the energy needed for transport of fatty acids (Price, 2010). European starlings (*Sturnus vulgaris*) from a migratory population in southern Germany that were composed of more n-6 (and n-3) PUFA used substantially less energy (≈11%) to fly the same distance (260 km) and duration (6 h) than those composed of more monounsaturated fatty acids (McWilliams and Pierce, 2006; McWilliams et al., 2020). As discussed in the section 'Oxidative costs of high-intensity exercise and the responses of the antioxidant system', the energy savings gained during a long flight by starlings composed of more n-6 PUFA came at the long-term cost of higher oxidative damage in the n-6 PUFA-fed birds (McWilliams et al., 2020). This may explain why migratory birds seasonally shift their diet to increase consumption of n-3 and/or n-6 PUFAs during migration, but then reduce their consumption of long-chain PUFAs during non-migration periods.

Several lines of evidence suggest a link between the n-3 and/or n-6 PUFA content in membrane phospholipids and exercise performance. For example, maximal running speed in 36 species of mammal was strongly related to the n-6 PUFA content of their muscle membrane phospholipids (Ruf et al., 2006), n-6 PUFA in muscle membranes of rats was positively associated with their exercise performance (Ayre and Hulbert, 1997) and regular exercise increased PUFA content of muscle membranes in humans (Andersson et al., 2000). Also, PUFA-rich membranes have been found in various muscle types that have high aerobic capacity, such as the pectoralis muscle in hummingbirds and the shaker muscle in rattlesnakes (Infante et al., 2001). Along with high levels of n-3 PUFAs, these muscle membranes had increased Ca^{2+}-ATPase activity, which may play a significant role in metabolism during exercise (Infante et al., 2001; Ruf et al., 2006). Furthermore, the activity of Na^+/K^+-ATPase enzyme in the tissue membranes of birds and mammals has been correlated with the amount of 22:6n-3 in the membrane, suggesting a causal link between some types of PUFA and metabolic rate (Turner et al., 2003; Wu et al., 2004, 2001).

Studies of migratory birds provide some evidence in support of the membrane hypothesis in terms of effects of diet composition on membrane composition and, in turn, on cellular-level fat metabolism, although the evidence is not consistent (e.g. Maillet and Weber, 2007; Nagahuedi et al., 2009; Guglielmo, 2010; Dick and Guglielmo, 2019). Most studies to date that related membrane composition to whole-animal performance refute the membrane hypothesis. For example, when Price and Guglielmo (2009) used a sequence of feeding and fasting protocols to produce white-throated sparrows with fat stores and muscle membranes composed of different fatty acids, they found that the enhanced performance (i.e. peak metabolic rate; see Glossary) was associated with the fatty acid composition of fat stores rather than muscle membranes. Dick and Guglielmo (2019) used diet manipulations to produce groups of yellow-rumped warblers (*Setophaga coronata*) that differed in the MUFA, n-3 and n-6 composition of flight muscle membranes. They found that membrane composition had an effect on the activity of several flight muscle oxidative enzymes in warblers but diet manipulation had no effect on multiple whole-animal performance measures, including basal metabolic rate (BMR; see Glossary), peak metabolic rate, energy expenditure during wind tunnel flights or the duration of the flights. Carter et al. (2020) fed European starlings one of two diets that differed primarily in 18:2n-6 (reciprocally replaced with 16:0) and this, in turn, produced starlings with corresponding differences in fatty acid composition of fat stores and muscle membranes. They found effects of membrane composition on activity of flight muscle oxidative enzymes (Carter et al., 2021) as well as on multiple whole-animal performance measures (Carter et al., 2020). Specifically, birds with higher concentrations of 18:2n-6 in their membranes and fat stores had a higher BMR and peak metabolic rate, although this pattern was evident early, but not later, during the 4-month experiment. The change through time in performance measures but not membrane composition led Carter et al. (2020) to conclude that their results were most consistent with the signal hypothesis rather than the membrane hypothesis. Thus, evidence to date supports the membrane hypothesis in the sense that key metabolic enzymes and other sub-organismal measures are affected by the fatty acid composition of membranes; however, these studies have not consistently found the predicted effects on whole-animal exercise performance, given differences in membrane composition alone.

Thus, the picture that emerges is that the observed seasonal changes in fatty acid composition matter for migrating songbirds in that they affect the energy savings–oxidative cost trade-off during endurance flights. Given that these seasonal changes in fatty acid composition are primarily determined by diet, and songbirds (and perhaps other migrants) can discriminate between diets based on their fatty acid composition, an important next step involves better understanding the micronutrient composition of natural foods and how this influences diet selection (and thus fat composition) of animals during migration.

Oxidative costs of high-intensity exercise and the responses of the antioxidant system

The seasonal shifts in fatty acid composition may enhance flight efficiency and metabolic performance, but may also carry potential physiological costs (e.g. increased vulnerability to oxidative damage). Regulating oxidative balance is important for all air-breathing organisms because reactive pro-oxidant molecules can cause considerable cellular damage, and affect health, longevity and performance (Halliwell and Gutteridge, 1999); PUFAs are especially susceptible to lipid peroxidation (Hulbert et al., 2007; Montgomery et al., 2012). This has led to a rich literature relating variation in membrane fatty acid composition to size-related variation in metabolic rate in mammals and birds (Hulbert and Else, 1999, 2000), and in turn to variation in reactive species production, life span and aging (Harman, 1956; Speakman, 2005; Speakman and Selman, 2011; Speakman and Garratt, 2013; Herborn et al., 2016). In this context, birds have often been portrayed as exceptional vertebrates in that they display relatively high metabolic rates, with the associated increased reactive species production, yet they are remarkably long-lived compared to mammals (Barja, 2014; Munshi-South and Wilkinson, 2010; Jimenez et al., 2019; Buttemer et al., 2010). Furthermore, the use of fats by birds as their primary fuel during high-intensity endurance exercise, such as migratory flights (Jenni and Jenni-Eiermann, 1998; Guglielmo, 2010), has potential acute oxidative costs because fats – and especially PUFAs – are highly susceptible to oxidative damage (Skrip and McWilliams, 2016; Cooper-Mullin and McWilliams, 2016). For more information about how birds overcome potential redox imbalance, see Box 3.

Several recent reviews (McWilliams et al., 2022, 2021) have described the dynamic response of the antioxidant system of birds during migration periods and during a given long-duration flight. Four key themes emerge, although more such studies are needed to verify these patterns (Fig. 2). First, migratory birds and bats seem to build some component of their antioxidant capacity (Fig. 2A) concomitantly with fat stores (Skrip et al., 2015; Costantini et al., 2007, 2018; Gutiérrez, 2019; Dick and Guglielmo, 2019), but not always (Eikenaar et al., 2020), and increased oxidative damage may be an inevitable consequence of increasing (or maintaining more) fat stores (Costantini et al., 2007; Skrip et al., 2015; Eikenaar et al., 2020), especially if they are mostly composed of PUFA (McWilliams et al., 2020; Alan and McWilliams, 2013).

Second, upregulation of the antioxidant system (Fig. 2) in experimental or natural long-duration flights seems to avoid the potential increase in oxidative damage with exercise (Bairlein et al., 2015; McWilliams et al., 2020; Frawley et al., 2021; DeMoranville et al., 2020; Costantini et al., 2013), but not in all cases (Costantini et al., 2008). Enzymatic antioxidants [including glutathione peroxidase (GPx) and superoxide dismutase (SOD) (Fig. 2B) and catalase (CAT)] may serve as a first line of defense for birds faced with an oxidative challenge. For example, European robins (*Erithacus rubecula*) caught during nocturnal migratory flight had higher GPx activity compared to birds on stopover (Jenni-Eiermann et al., 2014), and yellow-rumped warblers flown in a wind tunnel had higher SOD after flight than individuals at rest (Dick and Guglielmo, 2019). European starlings fed a diet not supplemented with anthocyanin, which is a dietary antioxidant, had decreased GPx activity immediately after flight, whereas GPx activity did not change after flight for starlings fed a diet supplemented with anthocyanins (Frawley et al., 2021). Furthermore, zebra finches (*Taeniopygia castanotis*) flown for short bursts had similar serum GPx, CAT and SOD activity after flight compared to unflown control birds (Costantini et al., 2013). Zebra finches flown for 2 h had elevated GPx activity immediately after flight, and this acute increase in GPx activity was consistently observed even after ≈2 weeks and 6 weeks of daily flight, indicating that birds were able to rapidly downregulate GPx activity when the oxidative challenge had passed (Cooper-Mullin et al., 2019). Interestingly, daily flight by zebra finches over 1.5 months increased coordination between the enzymatic (GPx) and non-enzymatic components of the antioxidant system (Cooper-Mullin et al., 2019).

Box 3. How birds overcome potential redox imbalance

How birds overcame the potential constraints of redox imbalance (so-called ‘oxidative stress’) associated with their relatively high baseline and active metabolic rates has been the subject of much conjecture (Buttemer et al., 2010; Jimenez et al., 2019; Munshi-South and Wilkinson, 2010); however, recently a key adaptation of the master antioxidant response of birds (see Glossary) has been revealed (Castiglione et al., 2020). The transcription factor NF-E2-related factor 2 (NRF2) is part of the major cellular pathway for regulating the antioxidant response of metazoans against oxidative imbalance within cells, and Kelch-like ECH-associated protein (KEAP1) serves as a biosensor for reactive oxygen species (see Glossary) that negatively regulates NRF2 activity. Under steady-state conditions, KEAP1 binds NRF2 and keeps it at low levels in the cell. Under conditions of increased metabolic rate – and thus increased reactive oxygen species production – KEAP1 repression is relaxed, allowing NRF2 to accumulate, bind to an antioxidant response element (ARE) and activate expression of a host of antioxidant target genes. Castiglione et al. (2020) have demonstrated that a mutation in the KEAP1-coding sequence, likely caused by intrachromosomal rearrangement, in the Neoaves ancestor led to constitutive activation of the NRF2 master antioxidant response in living birds and this enhanced response upregulates antioxidant gene expression and thus lowers the risk of macromolecular oxidative damage in avian cells and tissues. A different ancient mutation, a stop codon in KEAP1, has been recently discovered in Equids (including horses) that both enables increased mitochondrial respiration while decreasing oxidative stress in tissues (Castiglione et al., 2025). For migratory birds, this constitutive activation of the antioxidant response may require birds to maintain a more robust and costly endogenous antioxidant system, although consumption of dietary antioxidants could reduce or alleviate these costs.

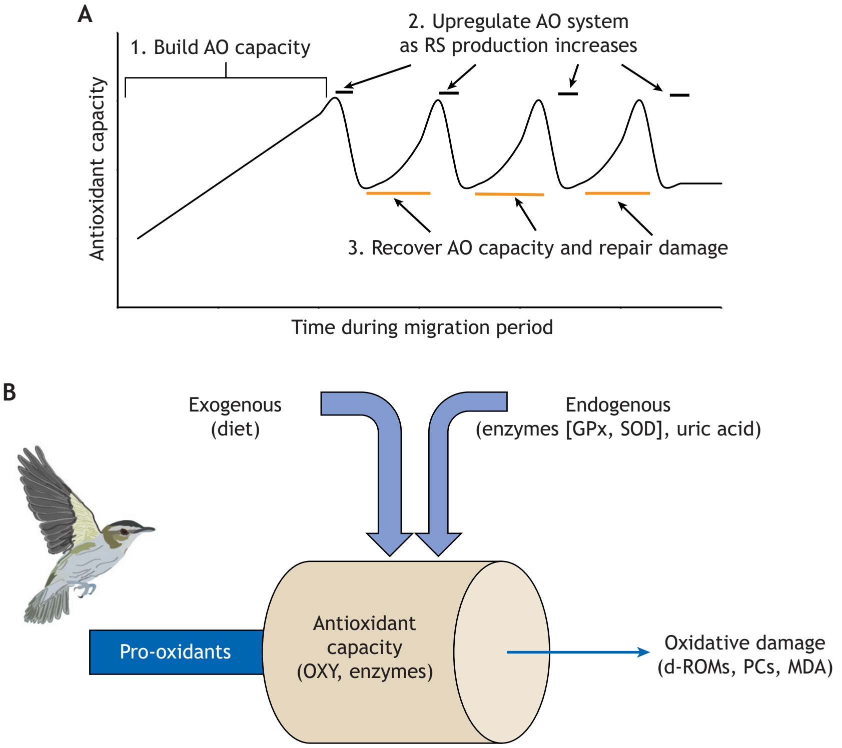


Fig. 2. Dynamic response of the antioxidant system in birds during successive long-duration flights over the migration period. (A) Birds build antioxidant (AO) capacity in preparation for a given flight and then, during flight, upregulate their AO system to combat the reactive species (RS) production that increases during fat-fueled high-intensity exercise. After each flight, birds recover their AO capacity and repair any oxidative damage that accumulated during the flight. (B) The antioxidant capacity of all animals is needed to combat pro-oxidants or reactive oxygen species produced during metabolism to avoid oxidative damage. Animals can increase antioxidant capacity by consuming dietary antioxidants (exogenous) and by increasing their own (endogenous) antioxidant enzymes [e.g. glutathione peroxidase (GPx) and superoxide dismutase (SOD)] or sacrificial molecules (e.g. uric acid in birds). The overall antioxidant capacity of the organism can be assessed by measuring the activity of these antioxidant enzymes, as well as the non-enzymatic component with the OXY absorbent test plus uric acid. Oxidative damage can be assessed in blood as protein carbonyls (PCs) or malondialdehyde (MDA), or using the d-ROMs test, which is often preferred because it includes products of the lipid oxidation cascade, as well as protein and nucleic acid oxidation (Cooper-Mullin and McWilliams, 2016; Skrip and McWilliams, 2016).

Likewise, non-enzymatic endogenous antioxidants, including sacrificial molecules such as glutathione (GSH) and uric acid (Fig. 2B), consistently increase after flight, suggesting they may be functionally important. European starlings flown in wind tunnels had elevated serum uric acid immediately after up to 6 h of flight (Carter et al., 2020; McWilliams et al., 2020; Frawley et al., 2021). White-crowned sparrows (*Zonotrichia leucophrys*) that were flown at high speeds in a hop/hover wheel (Tsahar et al., 2006) and pigeons (*Columba livia*) flown for 4 h (Gannes et al., 2001) also had increased uric acid concentrations after flight. Serum uric acid was also higher in garden warblers (*Sylvia borin*), pied flycatchers (*Ficedula hypoleuca*) and European robins on active migration compared to birds at rest or refueling on stopover (Jenni-Eiermann and Jenni, 1991). Given that it is a byproduct of protein catabolism during exercise, uric acid may serve as a particularly important antioxidant for flying birds. In contrast, other components of non-enzymatic antioxidant capacity [as measured with the OXY-adsorbent (OXY) test] usually decrease after flight (Costantini, 2008) – especially after more extensive flights (DeMoranville et al., 2020) – and the extent of this acute change in OXY after flight depends on the acute response of enzymatic antioxidants such as GPx when regular daily flying is prolonged (Cooper-Mullin et al., 2019).

Third, if oxidative damage occurs during long-duration exercise then migratory birds seem capable of repairing this damage (Fig. 2A) in a relatively reasonable amount of time (i.e. days not weeks) given their usual stopover durations. The first evidence of potential acute recovery on stopover came from actively migrating European robins caught flying at night through a Swiss mountain pass in autumn (Jenni-Eiermann et al., 2014). Birds captured at night out of flight had higher oxidative damage to proteins (circulating protein carbonyls) than birds captured while resting during the day (Jenni-Eiermann et al., 2014). However, the timeframe over which recovery occurred was unknown, because damage was not tracked over time within individuals. The first study to track oxidative damage in relation to time after a long-distance flight found that circulating oxidative damage to lipids (d-ROMs) decreased among recaptured garden warblers the longer they were at a Mediterranean stopover site in spring [between 1 and 192 h (8 days)]; opportunistic intra-individual sampling (n=2) confirmed that damage decreased within birds over a matter of days (Skrip et al., 2015). More recently, Eikenaar et al. (2020) longitudinally tracked changes in damage within individuals and confirmed that migrating songbirds can recover from oxidative damage on stopover. Northern wheatears (*Oenanthe oenanthe*) caught out of spring migration in Germany and held in captivity for 3 days decreased their oxidative damage to polyunsaturated fats (MDA) and appeared to stabilize that damage at a consistent level, suggesting that there may be a threshold of low damage or an ‘oxidative set-point’ (Eikenaar et al., 2020) that birds seek to reach before taking their next long-distance flight. Taken together, these three studies provide the first evidence that songbirds are capable of recovering from oxidative damage after flight. How they do so, however, remains an unanswered question. Do birds repair damaged molecules or replace them, or do both? Do resources available at a given stopover site or the physiological condition of an individual bird influence how birds address oxidative damage? The minimum time within which birds begin to recover after a flight is also uncertain. Migrating songbirds held in handling bags for short periods before blood sampling (30 min, Costantini et al., 2007; 20–192 min, Skrip et al., 2015) exhibited no change in oxidative measures. However, gray catbirds (*Dumetella carolinensis*) caught during autumn migration and kept overnight had increased uric acid and decreased levels of residual total antioxidant capacity within at least a 12 h period (Cohen et al., 2008).

Birds at stopover sites also seem capable of recovering their antioxidant capacity while there (Fig. 2A). An experimental study with flight-trained European starlings demonstrated recovery of antioxidant capacity after long-distance flight (DeMoranville et al., 2025), and free-living garden warblers on the island of Ponza, Italy, after a spring crossing of the Sahara Desert and Mediterranean Sea reduced markers of lipid damage with time on stopover (Skrip et al., 2015). There is evidence that restoration of antioxidant capacity in metabolically active tissues is mediated by the transcription of antioxidant enzyme proteins. For example, during recovery, these same flight-trained starlings had greater mRNA levels of antioxidant enzymes in the liver (CAT, SOD2 and GPX1) and pectoralis (SOD2) compared to unflown starlings, while lipid damage levels were similar (DeMoranville et al., 2021).

Fourth, when birds consume too few dietary antioxidants, this may not directly affect upregulation of antioxidant enzymes but may increase protein catabolism and, thus, circulating uric acid (Fig. 2B) when flying for long durations and/or consuming high-PUFA diets. For example, consumption of dietary antioxidants by flight-trained European starlings affected the response of enzymatic antioxidants as well as non-enzymatic antioxidants (DeMoranville et al., 2021; Frawley et al., 2021), and had a multitude of related effects: antioxidant consumption reduces corticosterone production in flight-trained birds, and, thus, potentially protects against the costs of high glucocorticoids (Casagrande et al., 2020) and enhances the breeding condition of males (Carbeck et al., 2018). There is also evidence that consumption and physiological use of dietary antioxidants in birds may depend on their nutritional needs, energy demands and the type of dietary antioxidant (Beaulieu and Schaefer, 2013; Costantini et al., 2010). For example, Cooper-Mullin et al. (2021) used stable isotope-labelled vitamin E to reveal that consumed dietary antioxidants are absorbed and reach the muscle mitochondria of zebra finches but only when they are regularly exercised (2 h of regular daily flying).

Recent experiments with actively migrating birds in autumn in New England, USA have revealed the benefits of consuming dietary antioxidants, and how antioxidant capacity and fat stores interactively influence the time passerines spend on stopover (Cooper-Mullin and McWilliams, 2022). For example, gavage-feeding dietary anthocyanins to hermit thrushes (*Catharus guttatus*) on an *ad libitum* diet boosted their ability to build non-enzymatic antioxidant capacity (OXY; Cooper-Mullin and McWilliams, 2022). Furthermore, birds on an *ad libitum* diet increased OXY compared to birds on a diet designed to maintain their weight at capture (Cooper-Mullin and McWilliams, 2022). Studies in mammals have identified anthocyanins as enhancers of the NRF2 antioxidant pathway that activates the expression of antioxidant genes (Shih et al., 2007; Aboonabi and Singh, 2015; Aboonabi et al., 2020; Tian et al., 2018). Dietary antioxidants may also help songbirds increase enzymatic antioxidant capacity by stimulating the same pathway. For example, European starlings supplemented with anthocyanins had higher mRNA levels of antioxidant enzymes associated with combating reactive species production in the mitochondria (SOD2) and lipid peroxidation in the peroxisomes (CAT) of the flight muscles compared to unsupplemented birds (DeMoranville et al., 2021). Intraindividual variation in the ability to utilize antioxidants in response to various energetically demanding scenarios must exist for phenotypic flexibility of the antioxidant system to persist (Piersma and van Gils, 2011); we found evidence of such individual-level, condition-dependent modulation of OXY and uric acid during long-duration flight (DeMoranville et al., 2025). Specifically, a subset of birds that expended energy in the upper 50% range (>0.51 kJ min^{-1}) seemed to either deplete OXY or increase levels of uric acid – a potent antioxidant – whereas the remaining birds did not change these circulating measures (OXY and uric acid). How exogenous and endogenous antioxidants interact in birds on stopover (Fig. 2B) while recovering or refueling still needs more investigation.

Conclusion

The main metabolic ‘gears’ that mobilize carbohydrates and/or fats to fuel short-duration high-intensity to long-duration low-intensity locomotion are broadly conserved across taxa, and the evolution of fat-fueled, high-intensity endurance (the ‘fourth gear’) is a comparatively rare innovation, in part because of important physiological constraints. Oxidizing fat at high rates requires a tightly integrated suite of physiological adaptations, including dense muscle mitochondria, enhanced fatty acid transport, efficient lipid mobilization and delivery, specialized muscle architecture, ample oxygen supply, and a sufficient antioxidant system. A central framework emerging from our synthesis is the pervasive role of phenotypic flexibility, which manifests in seasonal, reversible and dramatic changes in phenotype, which enables volant migrant animals to meet the extreme performance demands of their journey. For example, seasonal changes in fat quantity and quality occur that include remodeling of fatty acid composition, which alters the efficiency, speed and cost of fat oxidation during flight. Migratory birds counter the oxidative costs through seasonal upregulation of antioxidant defenses, strategic dietary intake of antioxidant-rich foods and dynamic regulation of oxidative enzymes.

Migratory flying animals are natural models of extreme endurance, capable of sustaining aerobic power outputs that rival or exceed those of elite human athletes, while simultaneously managing oxidative stress, thermal loads and dehydration without external fuel intake. The biochemical, physiological and structural adaptations that allow such feats from selective lipid biochemistry to rapid organ remodeling offer comparative models for sports science, space medicine and military performance. For example, lessons from volant migrants could inspire new strategies for sustaining human endurance in low-resource environments, enhancing thermoregulation under heat stress, preventing muscle and organ damage during prolonged exertion, and interventions for oxidative damage in contexts ranging from aging to critical care.

The next frontier is integrating these mechanistic insights into the broader spectrum of environmental challenges that shape migration. Climate change is a central driver, but it interacts with other pressures such as habitat loss, degradation and fragmentation, shifts in food web structure, light and noise pollution, and the spread of novel pathogens to create a more complex and unpredictable migratory landscape. Thermal stress from rising temperatures will compound dehydration risks while aloft and at stopover sites, while increasingly erratic wind, precipitation and storm patterns will make the duration and energetic cost of flights less predictable. Habitat loss and altered phenology can reduce both the quantity and quality of fueling opportunities, with knock-on effects for lipid composition, antioxidant defenses and performance capacity. Understanding how migratory animals navigate this shifting set of challenges will require coupling controlled mechanistic experiments with long-term landscape-scale monitoring across gradients of environmental stress.

Acknowledgements
Literally a small army of scientists have been involved in the empirical research that we describe in this Review. For our own empirical studies, we are thankful to the many members of the McWilliams and Bauchinger labs (University of Rhode Island and Jagellonian University, respectively), and to Barbara J. Pierce (Sacred Heart University), our primary collaborator, who provided stimulating discussions on key topics. Major logistical support was provided by the animal care staff, technical staff and scientists at the Max Planck Institute for Ornithology, Seewiesen, Germany, and at the Advanced Facility for Avian Research (AFAR), University of Western Ontario, Canada. For the work carried out in Germany, special thanks to Carola Schmidt-Wellenburg, Sophia Engel, Ninon Ballerstaedt, Lillie Langlois, Michelle Boyles, Olivia Fatica, Katherin Carbeck, Susan Forrest, Pietro D'Amelio, Kristen

DeMoranville, Wolfgang Goymann, Lisa Trost, Amadeusz Bryla, Mackiej Dzialo, Edyta Sadowska, Stefania Casagrande and Ulf Bauchinger, who helped with the windtunnel experiments; B. Helm, B. Kempenaers, H. Gwinner, B. Biebach and M. Starck for regular stimulating discussions; and H. Biebach for having the foresight and fortitude to create the windtunnel at MPIO, Seewiesen. For the work carried out in Canada, special thanks to Andrew Gould, Mikaela Rebuli, Eddie Price, Alex Gerson, Wales Carter, Liam Corcoran, Clara Cooper-Mullin and the entire staff at AFAR for providing necessary infrastructure, animal care assistance and logistical help throughout the experiment. Special thanks to Chris Guglielmo for having the foresight and fortitude to create the windtunnel at AFAR and for the opportunity to use it.

Competing interests

The authors declare no competing or financial interests.

Funding

The authors' research was supported by grants from the National Science Foundation to S.R.M. and B. J. Pierce (IBN-9983920 and IOS-1354187), from the U.S. Department of Agriculture to S.R.M. (RIAES-538748), by an OPUS grant from the Narodowe Centrum Nauki to U. Bauchinger (UMO-2015/19/B/NZ8/01394) and by the University of Rhode Island, College of the Environment and Life Sciences.

Special Issue

This article is part of the special issue 'The Integrative Biology of Exercise', guest edited by Erika Eliason, Christopher Guglielmo, Natalie Holt and Monica Daley. See related articles at https://journals.biologists.com/jeb/issue/229/7.

References

Abbott, S. K., Else, P. L., Atkins, T. A. and Hulbert, A. J. (2012). Fatty acid composition of membrane bilayers: importance of diet polyunsaturated fat balance. *Biochim. Biophys. Acta* **1818**, 1309-1317. doi:10.1016/j.bbamem.2012.01.011

Aboonabi, A. and Singh, I. (2015). Chemopreventive role of anthocyanins in atherosclerosis via activation of Nrf2–ARE as an indicator and modulator of redox. *Biomed. Pharmacother.* **72**, 30-36. doi:10.1016/j.biopha.2015.03.008

Aboonabi, A., Singh, I. and Rose' Meyer, R. (2020). Cytoprotective effects of berry anthocyanins against induced oxidative stress and inflammation in primary human diabetic aortic endothelial cells. *Chem-Biol. Interact.* **317**, 108940. doi:10.1016/j.cbi.2020.108940

Alan, R. R. and Mcwilliams, S. R. (2013). Oxidative stress, circulating antioxidants, and dietary preferences in songbirds. *Comp. Biochem. Physiol.* **164B**, 185-193. doi:10.1016/j.cbpb.2012.12.005

Alexander, D. E. (2015). *On the Wing: Insects, Pterosaurs, Birds, Bats and the Evolution of Animal Flight*. New York, NY: Oxford University Press.

Anaparasan, L., Hobson, K. A. and McNeil, J. N. (2023). Effect of rearing conditions on fatty acid allocation during flight in nectivorous lepidopteran Mythimna unipuncta. *Front. Ecol. Evol.* **11**, 1055534. doi:10.3389/fevo.2023.1055534

Anderson, A. M., Duijns, S., Smith, P. A., Friis, C. and Nol, E. (2019). Migration distance and body condition influence shorebird migration strategies and stopover decisions during southbound migration. *Front. Ecol. Evol.* **7**, 251. doi:10.3389/fevo.2019.00251

Andersson, A., Sjodin, A., Hedman, A., Olsson, R. and Vessby, B. (2000). Fatty acid profile of skeletal muscle phospholipids in trained and untrained young men. *Am. J. Physiol. Endocrinol. Metab.* **279**, 744-751. doi:10.1152/ajpendo.2000.279.4.E744

Arnold, W., Giroud, S., Valencak, T. and Ruf, T. (2014). Ecophysiology of omega fatty acids: a lid for every jar. *Physiology* **30**, 232-240. doi:10.1152/physiol.00047.2014

Arrese, E. L. and Soulages, J. L. (2010). Insect fat body: energy, metabolism, and regulation. *Annu. Rev. Entomol.* **55**, 207-225. doi:10.1146/annurev-ento-112408-085356

Ayre, K. J. and Hulbert, A. J. (1997). Dietary fatty acid profile affects endurance in rats. *Lipids* **32**, 1265-1270. doi:10.1007/s11745-006-0162-5

Bairlein, F. (1991). Nutritional adaptations to fat deposition in the long-distance migratory Garden Warbler (Sylvia borin). Proceedings of the 20th International Ornithological Congress, volume 20, pp. 2149-2158. Christchurch, New Zealand.

Bairlein, F. (1996). Fruit-eating in birds and its nutritional consequences. *Comp. Biochem. Physiol.* **113A**, 215-224. doi:10.1016/0300-9629(95)02091-8

Bairlein, F. and Gwinner, E. (1994). Nutritional mechanisms and temporal control of migratory energy accumulation in birds. *Annu. Rev. Nutr.* **14**, 187-215. doi:10.1146/annurev.nu.14.070194.001155

Bairlein, F., Fritz, J., Scope, A., Schwendenwein, I., Stanclova, G., Van Dijk, G., Meijer, H. A. J., Verhulst, S. and Dittami, J. (2015). Energy expenditure and metabolic changes of free-flying migrating northern bald ibis. *PLoS ONE* **10**, e0134433. doi:10.1371/journal.pone.0134433

Barja, G. (2014). The mitochondrial free radical theory of aging. *Prog. Mol. Biol. Transl. Sci.* **127**, 1-27. doi:10.1016/B978-0-12-394625-6.00001-5

Bauchinger, U. and McWilliams, S. R. (2010). Extent of phenotypic flexibility during long-distance flight is determined by tissue-specific turnover rates: a new hypothesis. *J. Avian Biol.* **41**, 603-608. doi:10.1111/j.1600-048X.2010.05137.x

Beaulieu, M. and Schaefer, H. M. (2013). Rethinking the role of dietary antioxidants through the lens of self-medication. *Anim. Behav.* **86**, 17-24. doi:10.1016/j.anbehav.2013.05.022

Beenakkers, A. M. T. (1969). Carbohydrate and fat as a fuel for insect flight. A comparative study. *J. Insect Physiol.* **15**, 353-361. doi:10.1016/0022-1910(69)90281-9

Beenakkers, A. M. T., Van Der Horst, D. J. and Van Marrewijk, W. J. A. (1984). Insect flight muscle metabolism. *Insect Biochem.* **14**, 243-260. doi:10.1016/0020-1790(84)90057-X

Bennett, A. F. (1991). The evolution of activity capacity. *J. Exp. Biol.* **160**, 1-23. doi:10.1242/jeb.160.1.1

Biebach, H. (1990). Strategies of trans-Sahara migrants. In *Bird Migration: Physiology and Ecophysiology* (ed. E. Gwinner). Berlin: Springer-Verlag.

Bishop, C. M. and Guglielmo, C. G. (2022). Flight. In *Sturkie's Avian Physiology* (ed. C. G. Scanes and S. Dridi), 7th edn, pp. 391-435. London, UK: Academic Press. doi:10.1016/B978-012747605-6/50016-X

Blem, C. R. (1976). Patterns of lipid storage and utilization in birds. *Am. Zool.* **16**, 671-684. doi:10.1093/icb/16.4.671

Boyles, M. (2011). Seasonal diet preferences for fatty acids differ between species of migratory passerine, are affected by antioxidant level, and relate to the fatty acid composition of wild fruits. *Masters in Environmental Science*, University of Rhode Island, Kingston, RI, USA.

Brooks, G. A. and Mercier, J. (1994). Balance of carbohydrate and lipid utilization during exercise: the "crossover" concept. *J. Appl. Physiol.* **76**, 2253-2261. doi:10.1152/jappl.1994.76.6.2253

Brown, J. J. and Chippendale, G. M. (1974). Migration of the monarch butterfly, Danaus plexippus: Energy sources. *J. Insect Physiol.* **20**, 1117-1130. doi:10.1016/0022-1910(74)90218-2

Buttemer, W. A., Abele, D. and Costantinit, D. (2010). From bivalves to birds: oxidative stress and longevity. *Funct. Ecol.* **24**, 971-983. doi:10.1111/j.1365-2435.2010.01740.x

Canavoso, L. E., Stariolo, R. and Rubiolo, E. R. (2003). Flight metabolism in Panstrongylus megistus (Hemiptera: Reduviidae): the role of carbohydrates and lipids. *Mem. Inst. Oswaldo Cruz* **98**, 909-914. doi:10.1590/S0074-02762003000700009

Carbeck, K. M., Demoranville, K. J., D'amelio, P. B., Goymann, W., Trost, L., Pierce, B., Bryla, A., Dzialo, M., Bauchinger, U. and McWilliams, S. R. (2018). Environmental cues and dietary antioxidants affect breeding behavior and testosterone of male European starlings (*Sturnus vulgaris*). *Horm. Behav.* **103**, 36-44. doi:10.1016/j.yhbeh.2018.05.020

Carter, W. A., Cooper-Mullin, C. and McWilliams, S. R. (2018). Turnover of muscle lipids and response to exercise differ between neutral and polar fractions in a model songbird, the zebra finch. *J. Exp. Biol.* **221**, jeb168823. doi:10.1242/jeb.168823

Carter, W. A., Whiteman, J. P., Cooper-Mullin, C., Newsome, S. D. and McWilliams, S. R. (2019). Dynamics of individual fatty acids in muscle fat stores and membranes of a songbird and its functional and ecological importance. *Physiol. Biochem. Zool.* **92**, 239-251. doi:10.1086/702667

Carter, W. A., Demoranville, K. J., Pierce, B. J. and McWilliams, S. R. (2020). The effects of dietary linoleic acid and hydrophilic antioxidants on basal, peak, and sustained metabolism in flight-trained European starlings. *Ecol. Evol.* **10**, 1552-1566. doi:10.1002/ece3.6010

Carter, W. A., Demoranville, K. J., Pierce, B. J. and McWilliams, S. R. (2021). Dietary linoleic acid, antioxidants, and flight training influence the activity of oxidative enzymes in European Starlings (*Sturnus vulgaris*). *J. Comp. Physiol. B Biochem. Syst. Environ. Physiol.* **191**, 357-370. doi:10.1007/s00360-021-01345-1

Casagrande, S., Demoranville, K. J., Trost, L., Pierce, B. J., Bryla, A., Dzialo, M., Sadowska, E. T., Bauchinger, U. and McWilliams, S. R. (2020). Dietary antioxidants attenuate the endocrine stress response during long-duration flight of a migratory bird. *Proc. R. Soc. B* **287**, 20200744. doi:10.1098/rspb.2020.0744

Castiglione, G. M., Xu, Z., Zhou, L. and Duh, E. (2020). Adaptation of the master antioxidant response connects metabolism, lifespan and feather development pathways in birds. *Nat. Commun.* **11**, 2476. doi:10.1038/s41467-020-16129-4

Castiglione, G. M., Chen, X., Xu, Z., Dbouk, N. H., Bose, A. A., Carmona-Berrio, D., Chi, E. E., Zhou, L., Boronina, T. N., Cole, R. N. et al. (2025). Running a genetic stop sign accelerates oxygen metabolism and energy production in horses. *Science* **387**, eadr8589. doi:10.1126/science.adr8589

Chown, S. L. and Nicolson, S. W. (2004). *Insect Physiological Ecology: Mechanisms and Patterns*. Oxford, UK: Oxford University Press.

Clerc, J. C. (2015). An investigation of tree bat migration ecology using fatty acid signatures. *MSc thesis in Biology*, Humboldt State University, Arcata, CA, USA

Cohen, A., Hau, M. and Wikelski, M. (2008). Stress, metabolism, and antioxidants in two wild passerine bird species. *Physiol. Biochem. Zool.* **81**, 463-472. doi:10.1086/589548

Conway, C. J., Eddleman, W. R. and Simpson, K. L. (1994). Seasonal changes in fatty acid composition of the wood thrush. *Condor* **96**, 791-794. doi:10.2307/1369482

Cooper-Mullin, C. and McWilliams, S. R. (2016). The role of the antioxidant system during intense endurance exercise: lessons from migrating birds. *J. Exp. Biol.* **219**, 3684-3695. doi:10.1242/jeb.123992

Cooper-Mullin, C., Carter, W. A. and McWilliams, S. R. (2019). Acute effects of intense exercise on the antioxidant system in birds: does exercise training help? *J. Exp. Biol.* **222**, jeb210443. doi:10.1242/jeb.210443

Cooper-Mullin, C. and McWilliams, S. R. (2022). Fat stores and antioxidant capacity affect stopover decisions in three of four species of migratory passerines with different migration strategies: an experimental approach. *Front. Ecol. Evol.* 10:762146. doi:10.3389/fevo.2022.762146

Cooper-Mullin, C., Carter, W. A., Amato, R. S., Podlesak, D. and McWilliams, S. R. (2021). Dietary antioxidants reach the mitochondria in the flight muscles of birds but only if they exercise. *PLoS ONE* **16**, e0253264. doi:10.1371/journal.pone.0253264

Costantini, D. (2008). Oxidative stress in ecology and evolution: lessons from avian studies. *Ecol. Lett.* **11**, 1238-1251. doi:10.1111/j.1461-0248.2008.01246.x

Costantini, D., Cardinale, M. and Carere, C. (2007). Oxidative damage and anti-oxidant capacity in two migratory bird species at a stop-over site. *Comp. Biochem. Physiol.* **144C**, 363-371. doi:10.1016/j.cbpc.2006.11.005

Costantini, D., Dell'ariccia, G. and Lipp, H.-P. (2008). Long flights and age affect oxidative status of homing pigeons (*Columba livia*). *J. Exp. Biol.* **211**, 377-381. doi:10.1242/jeb.012856

Costantini, D., Rowe, M., Butler, M. W. and McGraw, K. J. (2010). From molecules to living systems: historical and contemporary issues in oxidative stress and antioxidant ecology. *Funct. Ecol.* **24**, 950-959. doi:10.1111/j.1365-2435.2010.01746.x

Costantini, D., Monaghan, P. and Metcalfe, N. B. (2013). Loss of integration is associated with reduced resistance to oxidative stress. *J. Exp. Biol.* **216**, 2213-2220.

Costantini, D., Lindecke, O., Pētersons, G. and Voigt, C. C. (2018). Migratory flight imposes oxidative stress in bats. *Curr. Zool.* **65**, 147-153. doi:10.1093/cz/zoy039

Coulson, S. Z., Guglielmo, C. G. and Staples, J. F. (2024). Migration increases mitochondrial oxidative capacity without increasing reactive oxygen species emission in a songbird. *J. Exp. Biol.* **227**, jeb246849. doi:10.1242/jeb.246849

Demoranville, K. J., Carter, W. A., Pierce, B. J. and McWilliams, S. R. (2020). Flight training in a migratory bird drives metabolic gene expression in the flight muscle but not liver, and dietary fat quality influences select genes. *Am. J. Physiol. Regul. Integr. Comp. Physiol.* **319**, R637-R652. doi:10.1152/ajpregu.00163.2020

Demoranville, K. J., Carter, W. A., Pierce, B. J. and McWilliams, S. R. (2021). Flight and dietary antioxidants influence antioxidant expression and activity in a migratory bird. *Integr. Org. Biol.* **4**, obab035. doi:10.1093/iob/obab035

Demoranville, K. J., Carter, W., Cooper-Mullin, C., Corcoran, L., Pierce, B. J. and McWilliams, S. R. (2025). Flying stimulates the antioxidant system and protects against oxidative damage in a migratory songbird, yet diet quality has little effect. *J. Avian Biol.* **2025**, e03379. doi:10.1002/jav.03379

Dick, M. F. and Guglielmo, C. G. (2019). Dietary polyunsaturated fatty acids influence flight muscle oxidative capacity but not endurance flight performance in a migratory songbird. *Am. J. Physiol. Regul. Integr. Comp. Physiol.* **316**, R362-R375. doi:10.1152/ajpregu.00206.2018

Dingle, H. (2014). *Migration: the Biology of Life on the Move*. New York: Oxford University Press.

Dixit, A. S., Chetri, R. and Singh, N. S. (2022). Utilization of biomolecules as fuel energy and their physiological mechanism during migration in birds – a review. *J. Environ. Biol.* **43**, 1-10. doi:10.22438/jeb/43/1/MRN-1901

Egeler, O. and Williams, T. D. (2000). Seasonal, age, and sex-related variation in fatty-acid composition of depot fat in relation to migration in western sandpipers. *Auk* **117**, 110-119. doi:10.1093/auk/117.1.110

Egevang, C., Stenhouse, I. J., Phillips, R. A., Petersen, A., Fox, J. W. and Silk, J. R. (2010). Tracking of Arctic terns *Sterna paradisaea* reveals longest animal migration. *Proc. Natl. Acad. Sci. USA* **107**, 2078-2081. doi:10.1073/pnas.0909493107

Eikenaar, C., Hegemann, A., Packmor, F., Kleudgen, I. and Isaksson, C. (2020). Not just fuel: energy stores are correlated with immune function and oxidative damage in a long-distance migrant. *Curr. Zool.* **66**, 21-28. doi:10.1093/cz/zoz009

Fernández-Elías, V. E., Ortega, J. F., Nelson, R. K. and Mora-Rodriguez, R. (2015). Relationship between muscle water and glycogen recovery after prolonged exercise in the heat in humans. *Eur. J. Appl. Physiol.* **115**, 1919-1926. doi:10.1007/s00421-015-3175-z

Frawley, A. E., Demoranvilee, K. J., Carbeck, K. M., Trost, L., Bryla, A., Dzialo, M., Sadowska, E. T., Bauchinger, U., Pierce, B. and McWilliams, S. R. (2021). Season, anthocyanin supplementation, and flight training have mixed effects on the antioxidant system of migratory European Starlings. *Ornithology* **138**, 1-16. doi:10.1093/ornithology/ukab023

Gannes, L. Z., Hatch, K. A. and Pinshow, B. (2001). How does time since feeding affect the fuels pigeons use during flight. *Physiol. Biochem. Zool.* **74**, 1-10. doi:10.1086/319315

Geiser, F. and Learmonth, R. P. (1994). Dietary fats, selected body temperature and tissue fatty acid composition of agamid lizards (*Amphibolurus nuchalis*). *J. Comp. Physiol.* **164B**, 55-61. doi:10.1007/BF00714571

Gerson, A. R. and Guglielmo, C. G. (2011). Flight at low ambient humidity increases protein catabolism in migratory birds. *Science* **333**, 1434-1436. doi:10.1126/science.1210449

Gleeson, T. T. (1991). Patterns of metabolic recovery from exercise in amphibians and reptiles. *J. Exp. Biol.* **160**, 187-207. doi:10.1242/jeb.160.1.187

Gordon, M., Blickhan, R., Dabiri, J. and Videler, J. (2017). *Animal Locomotion: Physical Principles and Adaptations*. CRC press.

Guglielmo, C. (2010). Move that fatty acid: fuel selection and transport in migratory birds and bats. *Integr. Comp. Biol.* **50**, 336-345. doi:10.1093/icb/icq097

Guglielmo, C. (2018). Obese super athletes: fat-fueled migration in birds and bats. *J. Exp. Biol.* **221**, jeb165753. doi:10.1242/jeb.165753

Guglielmo, C. G., Williams, T. D., Zwingelstein, G., Brichon, G. and Weber, J.-M. (2002). Plasma and muscle phospholipids are involved in the metabolic response to long-distance migration in a shorebird. *J. Comp. Physiol.* **172B**, 409-417.

Gutiérrez, J. S. (2019). Oxidative status and metabolic profile in a long-lived bird preparing for extreme endurance migration. *Sci. Rep.* **9**, 17616. doi:10.1038/s41598-019-54057-6

Halliwell, B. and Gutteridge, J. M. (1999). *Free Radicals in Biology and Medicine*. Oxford: Clarendon Press.

Harman, D. (1956). Aging: a theory based on free radical and radiation chemistry. *J. Gerontol.* **11**, 298-300. doi:10.1093/geronj/11.3.298

Heitmeyer, M. E. and Fredrickson, L. H. (1990). Fatty acid composition of wintering female mallards in relation to nutrient use. *J. Wildl. Manag.* **54**, 54-61. doi:10.2307/3808900

Herborn, K. A., Daunt, F., Heidinger, B. J., Granroth-Wildling, H. M. V., Burthe, S. J., Newell, M. A. and Monaghan, P. (2016). Age, oxidative stress exposure and fitness in a long-lived seabird. *Funct. Ecol.* **30**, 913-921. doi:10.1111/1365-2435.12578

Hoppeler, H. and Weibel, E. R. (1998). Limits for oxygen and substrate transport in mammals. *J. Exp. Biol.* **201**, 1051-1064. doi:10.1242/jeb.201.8.1051

Hulbert, A. J. and Else, P. L. (1999). Membranes as possible pacemakers of metabolism. *J. Theor. Biol.* **199**, 257-274. doi:10.1006/jtbi.1999.0955

Hulbert, A. J. and Else, P. L. (2000). Mechanisms underlying the cost of living in animals. *Annu. Rev. Physiol.* **62**, 207-235. doi:10.1146/annurev.physiol.62.1.207

Hulbert, A. J., Pamplona, R., Buffenstein, R. and Buttemer, W. A. (2007). Life and death: metabolic rate, membrane composition, and life span of animals. *Physiol. Rev.* **87**, 1175-1213. doi:10.1152/physrev.00047.2006

Hunter, P. (2007). The nature of flight. The molecules and mechanics of flight in animals. *EMBO Rep.* **8**, 811-813. doi:10.1038/sj.embor.7401050

Husak, J. F., Keith, A. R. and Wittry, B. N. (2015). Making Olympic lizards: the effects of specialised exercise training on performance. *J. Exp. Biol.* **218**, 899-906. doi:10.1242/jeb.114975

Infante, J. P., Kirwan, R. C. and Brenna, J. T. (2001). High levels of docosahexaenoic acid (22:6n-3)-containing phospholipids in high-frequency contraction muscles of hummingbirds and rattlesnakes. *Comp. Biochem. Physiol.* **130B**, 291-298. doi:10.1016/S1096-4959(01)00443-2

Jenni, L. and Jenni-Eiermann, S. (1998). Fuel supply and metabolic constraints in migrating birds. *J. Avian Biol.* **29**, 521-528. doi:10.2307/3677171

Jenni-Eiermann, S. and Jenni, L. (1991). Metabolic responses to flight and fasting in night migrating passerines. *J. Comp. Physiol.* **161**, 465-474.

Jenni-Eiermann, S., Jenni, L., Smith, S. and Costantini, D. (2014). Oxidative stress in endurance flight: an unconsidered factor in bird migration. *PLoS ONE* **9**, e97650. doi:10.1371/journal.pone.0097650

Jimenez, A. G., O'Connor, E. S. and Elliott, K. H. (2019). Muscle myonuclear domain, but not oxidative stress, decreases with age in a long-lived seabird with high activity costs. *J. Exp. Biol.* **222**, jeb211185. doi:10.1242/jeb.211185

Joyner, M. (2008). Endurance exercise performance: The physiology of champions. *J. Physiol.* **586**, 35-44. doi:10.1113/jphysiol.2007.143834

Karasov, W. H., Kohl, K. D. and Caviedes-Vidal, E. (2025). The dynamic gut: the vertebrate gastrointestinal tract and associated microbiome exhibit physiological flexibility and adaptations to diet. *J. Exp. Biol.* **228**, 250395. doi:10.1242/jeb.250395

Kirby, J. S., Stattersfield, A. J., Butchart, S. H. M., Evans, M. I., Grimmett, R. F. A., Jones, V. R., O'Sullivan, J., Tucker, G. M. and Newton, I. (2008). Key conservation issues for migratory land- and waterbird species on the world's major flyways. *Bird Conserv. Int.* **18**, S49-S73. doi:10.1017/S0959270908000439

Klaiman, J. M., Price, E. R. and Guglielmo, C. G. (2009). Fatty acid composition of pectoralis muscle membrane, intramuscular fat stores and adipose tissue of migrant and wintering white-throated sparrows (*Zonotrichia albicollis*). *J. Exp. Biol.* **212**, 3865-3872. doi:10.1242/jeb.034967

Klasing, K. C. (1998). *Comparative Avian Nutrition*. New York: CAB International.

Kooyman, G. L., Castellini, M. A. and Davis, R. W. (1981). Physiology of diving in marine mammals. *Annu. Rev. Physiol.* **43**, 343-356. doi:10.1146/annurev.ph.43.030181.002015

Krüger, F., Clare, E. L., Symondson, W. O. C., Keišs, O. and Pētersons, G. (2014). Diet of the insectivorous bat Pipistrellus nathusii during autumn migration and summer residence. *Mol. Ecol.* **23**, 3672-3683. doi:10.1111/mec.12547

Levin, E., McCue, M. D. and Davidowitz, G. (2017). More than just sugar: allocation of nectar amino acids and fatty acids in a Lepidopteran. *Proc. R. Soc. B* **284**, 20162126. doi:10.1098/rspb.2016.2126

Leyton, J., Drury, P. J. and Crawford, M. A. (1987). Differential oxidation of saturated and unsaturated fatty acids in vivo in the rat. *Br. J. Nutr.* **57**, 383-393. doi:10.1079/BJN19870046

Li, X., Zhou, Y. and Wu, K. (2023). Biological characteristics and energy metabolism of migrating insects. *Metabolites* **13**, 439. doi:10.3390/metabo13030439

Maggini, I., Noakes, M. J., Hawkes, L. A. and Hegemann, A. (2022). Editorial: Ecophysiological adaptations associated with animal migration. *Front. Ecol. Evol.* **10**, 1022173. doi:10.3389/fevo.2022.1022173

Maillet, M. and Weber, J.-M. (2006). Performance-enhancing role of dietary fatty acids in a long-distance migrant shorebird: the semipalmated sandpiper. *J. Exp. Biol.* **209**, 2686-2695. doi:10.1242/jeb.02299

Maillet, M. and Weber, J.-M. (2007). Relationship between n-3 PUFA content and energy metabolism in the flight muscles of a migrating shorebird: evidence for natural doping. *J. Exp. Biol.* **210**, 413-420. doi:10.1242/jeb.02660

Maina, J. N. (2000). What it takes to fly: the structural and functional respiratory refinements in birds and bats. *J. Exp. Biol.* **203**, 3045-3064. doi:10.1242/jeb.203.20.3045

McClelland, G. B. and Lyons, S. A. (2025). Follow the fat. Regulation of metabolic substrates in trout. *Am. J. Physiol. Regul. Integr. Comp. Physiol.* **328**, R559-R561. doi:10.1152/ajpregu.00060.2025

McClelland, G. B., Lyons, S. A. and Robertson, C. E. (2017). Fuel use in mammals: conserved patterns and evolved strategies for aerobic locomotion and thermogenesis. *Integr. Comp. Biol.* **57**, 231-239. doi:10.1093/icb/icx075

McGuire, L. P. and Guglielmo, C. G. (2009). What can birds tell us about the migration physiology of bats? *J. Mammal.* **90**, 1290-1297. doi:10.1644/09-MAMM-S-084R.1

McGuire, L. P., Fenton, M. B. and Guglielmo, C. G. (2013). Phenotypic flexibility in migrating bats: seasonal variation in body composition, organ sizes and fatty acid profiles. *J. Exp. Biol.* **216**, 800-808. doi:10.1242/jeb.072868

McGuire, L. P., Jonasson, K. A. and Guglielmo, C. G. (2015). Bats on a budget: torpor-assisted migration saves time and energy. *PLOS ONE* **9**, e115724. doi:10.1371/journal.pone.0115724

McKechnie, A. E. (2022). Regulation of body temperature: patterns and processes. In *Sturkie's Avian Physiology*, 7th edn (ed. C. Scanes and S. Dridi), pp. 1231-1264. London, UK: Academic Press. doi:10.1016/B978-0-12-819770-7.00025-6

McKenzie, D. J., Higgs, D. A., Dosanjh, B. S., Deacon, G. and Randall, D. J. (1998). Dietary fatty acid composition influences swimming performance in Atlantic salmon (*Salmo salar*) in seawater. *Fish Physiol. Biochem.* **19**, 111-122. doi:10.1023/A:1007779619087

McWilliams, S. R. and Karasov, W. H. (2001). Phenotypic flexibility in digestive system structure and function in migratory birds and its ecological significance. *Comp. Biochem. Physiol. A* **128**, 579-593. doi:10.1016/S1095-6433(00)00336-6

McWilliams, S. R. and Karasov, W. H. (2005). Migration takes guts: digestive physiology of migratory birds and its ecological significance. In *Birds of Two Worlds* (ed. P. Marra and R. Greenberg), pp. 67-78. Washington, D.C: Smithsonian Institution Press.

McWilliams, S. R. and Karasov, W. H. (2014). Spare capacity and phenotypic flexibility in the digestive system of a migratory bird: defining the limits of animal design. *Proc. R. Soc. B* **281**, 20150308. doi:10.1098/rspb.2014.0308

McWilliams, S. and Pierce, B. J. (2006). Diet, body composition, and exercise performance: why birds during migration should be careful about what they eat. *Physiologist* **49**, C1-C57.

McWilliams, S., Kearney, S. and Karasov, W. (2002). Diet preferences of warblers for specific fatty acids in relation to nutritional requirements and digestive capabilities. *J. Avian Biol.* **33**, 167-174. doi:10.1034/j.1600-048X.2002.330207.x

McWilliams, S., Guglielmo, C., Pierce, B. and Klaassen, M. (2004). Flying, fasting, and feeding in birds during migration: a nutritional and physiological ecology perspective. *J. Avian Biol.* **35**, 377-393. doi:10.1111/j.0908-8857.2004.03378.x

McWilliams, S. R., Pierce, B., Wittenzellner, A., Langlois, L., Engel, S., Speakman, J. R., Fatica, O., Demoranville, K., Goymann, W., Trost, L. et al. (2020). The energy savings-oxidative cost tradeoff for migratory birds during endurance flight. *eLife* **9**, e60626. doi:10.7554/eLife.60626

McWilliams, S., Carter, W., Cooper-Mullin, C., Demoranville, K., Frawley, A., Pierce, B. and Skrip, M. (2021). How birds during migration maintain (Oxidative) balance. *Front. Ecol. Evol.* **9**, obab035. doi:10.3389/fevo.2021.742642

McWilliams, S. R., M. Ramenofsky, and Pierce, B. J. (2022). Physiological challenges of migration. In *Sturkie's Avian Physiology* (ed. C.G. Scanes and S. D), 7th edn, pp. 1311-1352. Academic Press.

Mesquita, P. H. C., Rhodes, E. M., Yap, K. N., Mueller, B. J., Hill, G. E., Hood, W. R. and Kavazis, A. N. (2024). Mitochondrial remodelling supports migration in white-crowned sparrows (Zonotrichia leucophrys). *Proc. Biol. Sci.* **291**, 20242409.

Minter, M., Pearson, A., Lim, K. S., Wilson, K., Chapman, J. W. and Jones, C. M. (2018). The tethered flight technique as a tool for studying life-history strategies associated with migration in insects. *Ecol. Entomol.* **43**, 397-411. doi:10.1111/een.12521

Montgomery, M. K., Hulbert, A. J. and Buttemer, W. A. (2012). Metabolic rate and membrane fatty acid composition in birds: a comparison between long-living parrots and short-living fowl. *J. Comp. Physiol.* **182B**, 127-137. doi:10.1007/s00360-011-0603-1

Moyes, C. D., Suarez, R. K., Hochachka, P. W. and Ballantyne, J. S. (1990). A comparison of fuel preferences of mitochondria from vertebrates and invertebrates. *Can. J. Zool.* **68**, 1337-1349. doi:10.1139/z90-201

Munshi-South, J. and Wilkinson, G. S. (2010). Bats and birds: exceptional longevity despite high metabolic rates. *Ageing Res. Rev.* **9**, 12-19. doi:10.1016/j.arr.2009.07.006

Nagahuedi, S., Popesku, J. T., Trudeau, V. L. and Weber, J.-M. (2009). Mimicking the natural doping of migrant sandpipers in sedentary quails: effects of dietary n-3 fatty acids on muscle membranes and PPAR expression. *J. Exp. Biol.* **212**, 1106-1114. doi:10.1242/jeb.027888

Napolitano, G. E. and Ackman, R. G. (1990). Anatomical distribution of lipids and their fatty acids in the semipalmated sandpiper *Calidris pusilla* L. from Shepody Bay, New Brunswick, Canada. *J. Exp. Mar. Biol. Ecol.* **114**, 113-124. doi:10.1016/0022-0981(90)90023-6

Newton, I. (2008). *The Migration Ecology of Birds*. New York: Academic Press, Inc.

O'brien, D. M. (1999). Fuel use in flight and its dependence on nectar feeding in the hawkmoth Amphion floridensis. *J. Exp. Biol.* **202**, 441-451. doi:10.1242/jeb.202.4.441

Pernow, B. (1971). Muscle Metabolism During Exercise. Proceedings of a Karolinska Institutet Symposium Held in Stockholm, Sweden, September 6–9, 1970 (ed. B. Pernow and B. Saltin), Plenum Press.

Petersson, A., Pickova, J. and Brannas, E. (2010). Swimming performance at different temperatures and fatty acid composition of Arctic charr (*Salvelinus alpinus*) fed palm and rapeseed oils. *Aquaculture* **300**, 176-181. doi:10.1016/j.aquaculture.2010.01.017

Pi, A., Villivalam, S. D. and Kang, S. (2023). The molecular mechanisms of fuel utilization during exercise. *Biology (Basel)* **12**, 1450.

Pierce, B. and McWilliams, S. R. (2014). The fat of the matter: how dietary fatty acids can affect exercise performance. *Integr. Comp. Biol.* **54**, 903-912. doi:10.1093/icb/icu098

Pierce, B. J., McWilliams, S. R., Place, A. R. and Huguenin, M. A. (2004). Diet preferences for specific fatty acids and their effect on composition of fat reserves in migratory red-eyed vireos (*Vireo olivaceous*). *Comp. Biochem. Physiol.* **138A**, 503-514. doi:10.1016/j.cbpb.2004.06.014

Pierce, B. J., McWilliams, S. R., O'connor, T., Place, A. R. and Guglielmo, C. (2005). Effect of dietary fatty acid composition on depot fat and exercise performance in a migrating songbird, the red-eyed vireo. *J. Exp. Biol.* **208**, 1277-1285. doi:10.1242/jeb.01493

Piersma, T. and van Gils, J. A. (2011). *The Flexible Phenotype: a Body-Centred Integration of Ecology, Physiology, and Behaviour*. New York: Oxford University Press.

Pigliucci, M. (1996). How organisms respond to environmental changes: from phenotypes to molecules (and vice versa). *Trends Ecol. Evol.* **11**, 168-173. doi:10.1016/0169-5347(96)10008-2

Price, E. R. (2010). Dietary lipid composition and avian migratory flight performance: development of a theoretical framework for avian fat storage. *Comp. Biochem. Physiol.* **157A**, 297-309. doi:10.1016/j.cbpa.2010.05.019

Price, E. R. and Guglielmo, C. G. (2009). The effect of muscle phospholipid fatty acid composition on exercise performance: a direct test in the migratory white-throated sparrow. *Am. J. Physiol.* **297R**, R775-R782. doi:10.1152/ajpregu.00150.2009

Price, E. R., Krokfors, A. and Guglielmo, C. G. (2008). Selective mobilization of fatty acids from adipose tissue in migratory birds. *J. Exp. Biol.* **211**, 29-34. doi:10.1242/jeb.009340

Price, E. R., Bauchinger, U., Zajac, D. M., Cerasale, D. J., McFarlan, J. T., Gerson, A. R., McWilliams, S. R. and Guglielmo, C. G. (2011). Migration- and exercise-induced changes to flight muscle size in migratory birds and association with IGF1 and myostatin mRNA expression. *J. Exp. Biol.* **214**, 2823-2831. doi:10.1242/jeb.057620

Quinn, J. T., Hamilton, D. J. and Herbert, C. E. (2017). Fatty acid composition and concentration of alternative food of Semipalmated Sandpipers (*Calidris pusilla*) in the upper Bay of Fundy, Canada. *Can. J. Zool.* **95**, 565-573. doi:10.1139/cjz-2016-0246

Raclot, T. and Groscolas, R. (1995). Selective mobilization of adipose tissue fatty acids during energy depletion in the rat. *J. Lipid Res.* **36**, 2164-2173. doi:10.1016/S0022-2275(20)39200-2

Rios, J. M., Barcelo, G. F., Narvaez, C., Maldonado, K. and Sabat, P. (2014). Feeding and digestive responses to fatty acid intake in two South American passerines with different food habits. *J. Comp. Physiol. B* **184**, 729-739. doi:10.1007/s00360-014-0832-1

Rogers, E. J., Sommers, A. S. and McGuire, L. P. (2019). Seasonal dynamics of lipid metabolism and energy storage in the brazilian free-tailed bat. *Physiol. Biochem. Zool.* **92**, 386-395. doi:10.1086/704107

Ruf, T., Valencak, T., Tataruch, F. and Arnold, W. (2006). Running speed in mammals increases with muscle n-6 polyunsaturated fatty acid content. *PLoS ONE* **1**, e65. doi:10.1371/journal.pone.0000065

Schlichting, C. D. and Pigliucci, M. (1998). *Phenotypic Evolution: a Reaction Norm Perspective*. Sunderland, MA: Sinauer Associates.

Shih, P.-H., Yeh, C.-T. and Yen, G.-C. (2007). Anthocyanins induce the activation of phase II enzymes through the antioxidant response element pathway against oxidative stress-induced apoptosis. *J. Agric. Food Chem.* **55**, 9427-9435. doi:10.1021/jf071933i

Skrip, M. and McWilliams, S. R. (2016). Oxidative balance in birds: an atoms-to-organisms-to-ecology primer for ornithologists. *J. Field Ornithol.* **87**, 1-20. doi:10.1111/jofo.12135

Skrip, M., Bauchinger, U., Goymann, W., Fusani, L., Cardinale, M., Alan, R. and McWilliams, S. R. (2015). Migrating songbirds on stopover prepare for, and recover from, oxidative challenges posed by long-distance flight. *Ecol. Evol.* **5**, 3198-3209. doi:10.1002/ece3.1601

Speakman, J. R. (2005). Body size, energy metabolism and lifespan. *J. Exp. Biol.* **208**, 1717-1730. doi:10.1242/jeb.01556

Speakman, J. R. and Garratt, M. (2013). Oxidative stress as a cost of reproduction: beyond the simplistic trade-off model. *BioEssays* **36**, 93-106. doi:10.1002/bies.201300108

Speakman, J. R. and Selman, C. (2011). The free-radical damage theory: accumulating evidence against a simple link of oxidative stress to ageing and lifespan. *BioEssays* **33**, 255-259. doi:10.1002/bies.201000132

Stager, M., Velotta, J. P., Cheviron, Z. A. and Senner, N. R. (2024). Assessing the evidence for treating developmental plasticity and phenotypic flexibility as different phenomena. *Funct. Ecol.* **2024**, 1-13. doi:10.1111/1365-2435.14590

Thomas, V. G. and George, J. C. (1975). Plasma and depot fat fatty acids in Canada Geese in relation to diet, migration, and reproduction. *Physiol. Zool.* **48**, 157-167. doi:10.1086/physzool.48.2.30155649

Tian, X., Xin, H., Paengkoum, P., Paengkoum, S., Ban, C. and Sorasak, T. (2018). Effects of anthocyanin-rich purple corn (Zea mays L.) stover silage on nutrient utilization, rumen fermentation, plasma antioxidant capacity, and mammary gland gene expression in dairy goats1. *J. Anim. Sci.* **97**, 1384-1397. doi:10.1093/jas/sky477

Tsahar, E., Arad, Z., Izhaki, I. and Guglielmo, C. G. (2006). The relationship between uric acid and its oxidative product allantoin: a potential indicator for the evaluation of oxidative stress in birds. *J. Comp. Physiol. B* **176**, 653-661. doi:10.1007/s00360-006-0088-5

Turner, N., Else, P. L. and Hulbert, A. J. (2003). Docosahexaenoic acid (DHA) content of membranes determines molecular activity of the sodium pump: implications for disease states and metabolism. *Naturwissenschaften* **90**, 521-523. doi:10.1007/s00114-003-0470-z

Voigt, C. C., Sörgel, K. and Dechmann, D. K. N. (2010). Refueling while flying: foraging bats combust food rapidly and directly to power flight. *Ecology* **91**, 2908-2917. doi:10.1890/09-2232.1

Voigt, C. C., Rosner, E., Guglielmo, C. G. and Currie, S. E. (2019). Fatty acid profiles of the European migratory common noctule bat (*Nyctalus noctula*). *Sci. Nat.* **106**, 33. doi:10.1007/s00114-019-1627-8

Wagner, G. N., Balfry, S. K., Higgs, D. A., Lall, S. P. and Farrell, A. P. (2004). Dietary fatty acid composition affects the repeat swimming performance of Atlantic salmon in seawater. *Comp. Biochem. Physiol.* **137A**, 567-576. doi:10.1016/j.cbpb.2003.11.005

Weber, J.-M. (1988). Design of exogenous fuel supply systems: adaptive strategies for endurance locomotion. *Can. J. Zool.* **66**, 1116-1121. doi:10.1139/z88-163

Weber, J.-M. (2009). The physiology of long-distance migration: extending the limits of endurance metabolism. *J. Exp. Biol.* **212**, 593-597. doi:10.1242/jeb.015024

Weber, J.-M. (2011). Metabolic fuels: regulating fluxes to select mix. *J. Exp. Biol.* **214**, 286-294. doi:10.1242/jeb.047050

Weber, J.-M. and Haman, F. (2004). Oxidative fuel selection: adjusting mix and flux to stay alive. *Int. Congr. Ser.* **1275**, 22-31. doi:10.1016/j.ics.2004.09.043

Wojciechowski, M. S. and Pinshow, B. (2009). Heterothermy in small, migrating passerine birds during stopover: use of hypothermia at rest accelerates fuel accumulation. *J. Exp. Biol.* **212**, 3068-3075. doi:10.1242/jeb.033001

Wu, B. J., Else, P. L., Storlien, L. H. and Hulbert, A. J. (2001). Molecular activity of Na+/K+-ATPase from different sources is related to the packing of membrane lipids. *J. Exp. Biol.* **204**, 4271-4280. doi:10.1242/jeb.204.24.4271

Wu, B. J., Hulbert, A. J., Storlien, L. H. and Else, P. L. (2004). Membrane lipids and sodium pumps of cattle and crocodiles: an experimental test of the membrane pacemaker theory of metabolism. *Am. J. Physiol.* **287**, R633-R641. doi:10.1152/ajpcell.00486.2003

Zurovchak, J. G. (1997). Nutritional role of high-lipid fruits in the diet of migrant thrushes. *Ph.D. Dissertation*, Rutgers University, NJ, USA.