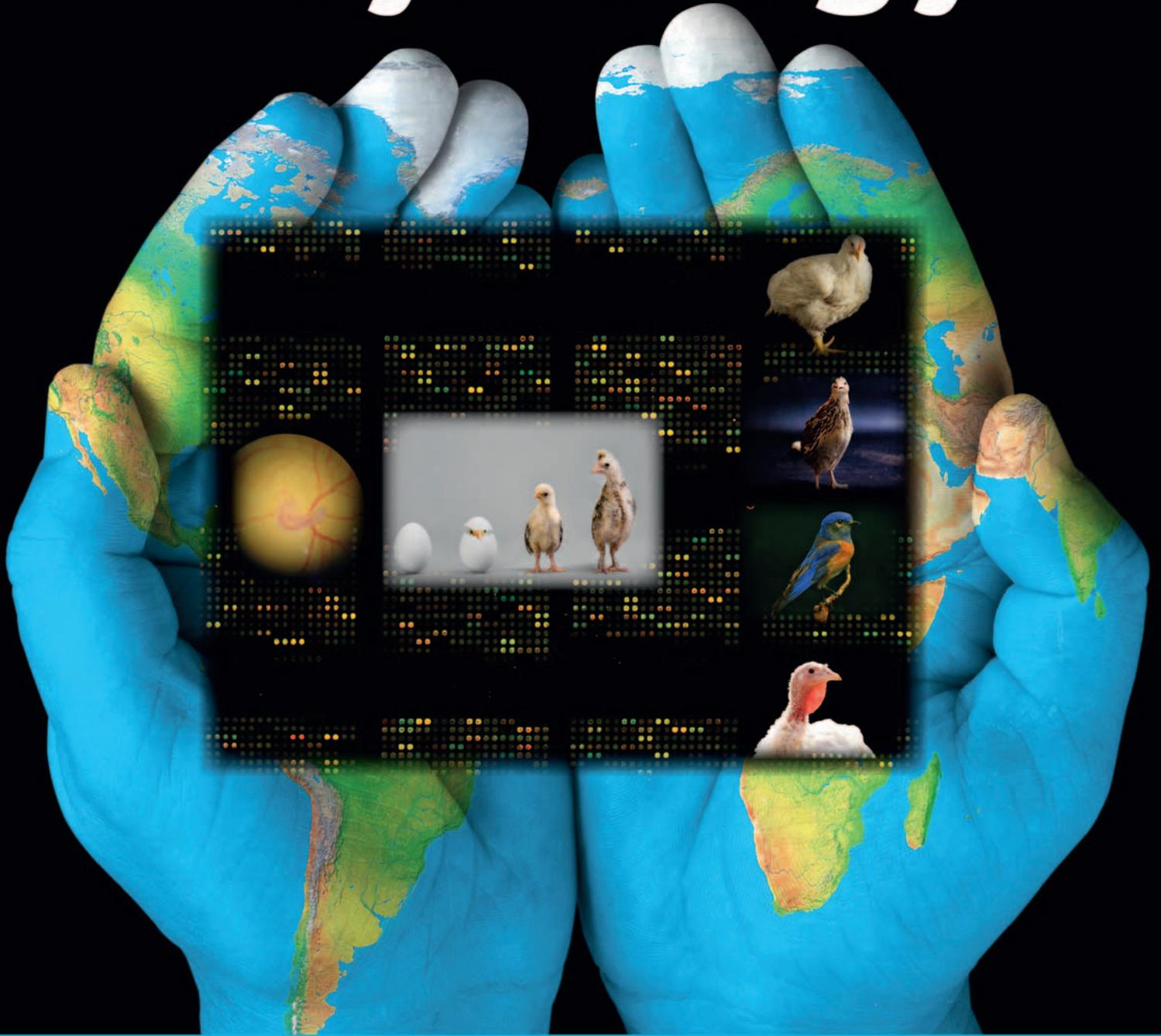


Sturkie's

Avian Physiology

Seventh Edition



Edited by
Colin G. Scanes and Sami Dridi



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Colin G. Scanes

Department of Biological Science, University of Wisconsin, Milwaukee, WI, United States;
Center of Excellence for Poultry Science, University of Arkansas, Fayetteville, AR, United States

Sami Dridi

Center of Excellence for Poultry Science, University of Arkansas, Fayetteville, AR, United States



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Physiological challenges of migration

Scott R. McWilliams¹, Marilyn Ramenofsky² and Barbara J. Pierce³

¹Department of Natural Resources Science, University of Rhode Island, Kingston, RI, United States; ²Department of Neurobiology, Physiology and Behavior, University of California, Davis, CA, United States; ³Department of Biology, Sacred Heart University, Fairfield, CT, United States

Abbreviations

ACTH Adrenocorticotrop hormone
AGRP Agouti-related peptide
AR Androgen receptor
AVT Arginine vasotocin
C-fos Fos Proto-Oncogene, an early immediate gene
CART Cocaine - and amphetamine-regulated transcript protein
CCK Cholecystokinin
CCO Cytochrome-c oxidase
CK Creatine kinase
CPT Carnitine palmitoyltransferase
CS Citrate synthase
DHT Dihydrotestosterone
DIO2 Type II iodothyronine deiodinase
DIO3 Type III iodothyronine deiodinase
ELHS Emergency life history stage
FFA Free fatty acids
FSH Follicle-stimulating hormone
GH Growth Hormone
GnIH Gonadotropin-inhibitory hormone
GnRH Gonadotropin-releasing hormone
GR Glucocorticoid receptor
GtH Gonadotropin
HOAD Hydroxyacyl CoA dehydrogenase
HPA Hypothalamic-pituitary-adrenal axis
HPG Hypothalamic-pituitary-gonad axis
ICV Intracerebroventricular
IGF-1 Insulin-like growth factor-1
IP Intraperitoneal
LH Luteinizing hormone
MDH Malate dehydrogenase
MR Mineralocorticoid receptor
MSH Melanocyte-stimulating hormone
NPY Neuropeptide Y
PFK Phosphofructokinase
PK Pyruvate kinase
POMC Proopiomelanocortin
PPAR Peroxisome proliferator-activated nuclear receptors
PSM Plant secondary metabolites
PUFA Polyunsaturated fatty acids

PRL Prolactin
T Testosterone
T3 Triiodothyronine
T4 Thyroxine
TSH Thyroid-stimulating hormone
VA opsin Vertebrate ancient opsin photopigment

47.1 Introduction

Approximately 19% of the ~10,000 species of birds in the world migrate on a regular basis (Kirby et al., 2008), and this is closer to 50% of species if only birds that breed at latitudes above 35° north and south are considered (Newton and Dale, 1996a, 1996b). The physiological feat of migration has been equated to such athletic feats in mammals as running 130 consecutive marathons (semipalmated sandpiper, *Calidris pusilla*, migrates ~5000–7500 km nonstop; Anderson et al., 2019) or completing three trips to the moon and back in a lifetime (arctic tern, *Sterna paradisaea*, migrates ~80,000 km a year over a 30 year life-span; Egevang et al., 2010). The strategies migratory birds use to complete these annual peregrinations vary among bird species with some birds completing their long-distance migration in one, nonstop flight while most fly intermittently, taking advantage of stopover sites along their routes to rest and refuel. Regardless of strategy, all avian migrants face the same physiological challenges while aloft, albeit to different extents, including: (1) burn fat at a very high rate while fasting and combatting the negative effects of lipid peroxidation, (2) maintain adequate hydration while not drinking and losing water due to elevated breathing rates, (3) obtain adequate oxygen while oxidizing fat for fuel, and especially when flying at high altitudes with low-oxygen content, (4) avoid becoming too hot (heat gained from metabolism and the environment) or too cold (heat loss to the environment), and (5) meeting these challenges under a seasonal time constraint. Additionally, birds that stop to rest

and refuel at stopover sites have the added physiological challenge of rapidly regaining energy stores with initially reduced gut size and function. Clearly, the physiological challenges associated with long-distance flight are significant and require specialized morphological and physiological adaptations and acclimatizations.

The energy costs of bird flight are substantial and have been the focus of ornithological research since the 1960's when [Greenewalt \(1960\)](#) recorded hummingbirds flying in front of a fan and examined changes in flight speed with changes in fan speeds. The ability of researchers to fly birds in a controlled environment led to significant breakthroughs not only in the field of aerodynamics but in the understanding of the physiology of flight as well. For example, classic studies of birds flying in wind-tunnels have shown that forward flapping flight is energetically more costly than running or swimming per gram body mass ([Butler, 1991](#); [Bishop and Butler, 2015](#)). Importantly, the advantage of flying on migration, instead of running and swimming, is revealed when travel distance is considered. Specifically, energy required per gram body mass to travel a given distance (i.e., the cost of transport) is considerably less for a flying migrant compared to a running or swimming migrant ([Tucker, 1970](#); [Schmidt-Nielsen, 1972](#); [Bishop and Butler, 2015](#)). With an increase in technology and the ability to track migrating birds throughout the globe, we now know the physiology of migratory flights of free-living birds to be a highly complex, synergistic process between an organism and its ever-changing environment.

In this chapter, we will review, within the context of the migration life history of birds, the neuroendocrine and physiological adaptations that allow birds to meet the challenges of long-duration flights, the preparations they implement to begin their journeys, and the in-flight adjustments they make in order to successfully complete their journeys. We will conclude with a discussion about the flexible phenotypes of birds in relation to how they physiologically respond to the challenges of migratory flight in a dynamic seasonal environment, and some of the important mysteries that remain in terms of the physiology of birds during migration.

47.2 Adaptations of birds for long-duration migratory flights

Flapping flight requires both lift to stay aloft and thrust to move forward through the air ([Tobalske, 2016](#)). Birds have evolved feathers and wings that enable them to fly because their collective shape produces lift as air flows over and around them. Combine feathers and wings with a skeletal system that is both strong yet light (hollow bones), and a muscular system that provides the power and endurance, and you have the anatomical skeletal-muscular foundation for the evolution of long-distance migration of birds.

[Bishop and Butler \(2015\)](#) provide a thorough description of the biomechanics of bird flight, and how the muscles of birds produce the power required for flight, in general, and the long-duration flapping flight used by birds in migration, in particular. Most pertinent to our review of the physiology of long-distance migration in birds is that (a) self-powered flight is the most demanding form of locomotion in terms of its energy cost per unit time—thus, fuel storage and use is critical; (b) on the other hand, flight is much more efficient than running or swimming. In short, the cost of transport for a flyer (in units of energy required for a bird of a given mass to travel a given distance) is appreciably less than that of a runner or a swimmer—thus, overcoming the fuel storage and use challenges of long-duration flapping flight allows migratory birds to travel far for their size.

47.2.1 Cardiovascular and respiratory general adaptations

The energetic costs of flapping flight have driven adaptive responses in the cardiovascular and respiratory systems of birds. In general, birds have larger hearts, lower resting heart rates, higher exercising heart rates, and higher $\dot{V}O_2$ max than nonflying mammals of similar size ([Bishop and Butler, 2015](#)). Adaptations in the vascular system of birds such as increased number of capillaries in each muscle fiber along with mitochondria that are in closer proximity to capillaries allows for efficient exchange of respiratory gasses ([Powell, 2015](#)). In addition, the structure of the avian respiratory system contributes to a bird's ability to efficiently exchange large volumes of gas as is needed during flight. Taken together the design of air sacs increases ventilation, the increased surface area in the lungs, unidirectional flow across the respiratory surface, and increased cross-current gas exchange with the blood all contribute to a bird's ability to obtain oxygen, supply oxygen to active tissue, and remove carbon dioxide from the blood at a greater rate than mammals of similar size ([Dzialowski and Crossley, 2015](#); [Scott et al., 2015](#)). In general, birds are also more tolerant of hypoxia than mammals at least in part because of differences in their sensitivity to hypocapnia (low-partial pressure of arterial blood carbon dioxide ([Scott et al., 2015](#))). Hypocapnia sensitivity of cerebral blood vessels is one of the main mechanisms in which mammals limit hyperventilation, thereby decreasing oxygen delivery to the brain, and likely limiting overall energetic output ([Ogoh and Ainslie, 2009](#); [Ainslie and Ogoh, 2010](#)). Migratory bird insensitivity to hypocapnia especially in cerebral blood vessels allows for extreme hyperventilatory rates without blood flow interference to the brain ([Faraci, 1991](#)). In turn, this hyperventilation allows for decreased arteriole partial pressure of carbon dioxide subsequently increasing arteriole partial pressure of oxygen due to the Bohr effect ([Powell, 2015](#)). Thus, birds are able to maintain

high-oxygen delivery to tissues even in low-oxygen environments such as those at high altitudes. Additional vascular adaptations that enable birds to meet the high-oxygen demands of long-duration flight while retaining essential blood solute concentrations include an overall higher hematocrit level and greater hemoglobin concentrations (Minias et al., 2013; Bishop and Butler, 2015) compared to nonmigratory birds or mammals and the maintenance of plasma levels throughout a long flight regardless of body mass changes (Carmi et al., 1993). Monthly comparison of hematocrit of White-crowned sparrows (*Zonotrichia leucophrys gambelli*) revealed that migrant subspecies were consistently greater than residents, a difference that increased 10–15% further during both seasonal stages of migration (Krause et al., 2016). Interestingly, recent experiments that directly manipulated hematocrit in short-distance migratory Yellow-rumped warblers (*Setophaga coronata*) found that birds with elevated hematocrit performed better at simulated high altitudes (in a wind tunnel) but not at lower altitudes (Yap et al., 2018); many more such manipulative experiments are needed to better understand how variation in hematocrit affects migratory flight performance.

47.2.2 Metabolism and damage control

Mitochondria generate the cellular energy required by birds (and all animals) to fuel their basal metabolism as well as that required for all activity including flapping flight (Bottje, 2015). Associated with this role as powerhouse of the cell, mitochondria are also the major site for generation of reactive species (RS)—thus an effective antioxidant protection system has evolved to reduce or avoid the negative physiological effects of RS production, the components of which are shared by all eukaryotes (Bottje, 2015; Cooper-Mullin and McWilliams, 2016; Skrip and McWilliams, 2016). Most pertinent to our review of the physiology of long-distance migration in birds is that (a) increased metabolism, like that required for long-duration flapping flight, is associated with increased RS production which may overwhelm the antioxidant system and cause oxidative imbalance or “stress” and thus damage to, for example, lipids, proteins, and DNA in cells; (b) repair of damaged structures is energetically expensive—thus, understanding how the antioxidant system of migrating birds contends with RS production is as important as understanding how the power for long-duration flight is generated.

How birds overcome 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; Munshi-South and Wilkinson, 2010; Jimenez et al., 2019), although recently a key adaptation of the master antioxidant

response of birds has been revealed (Castiglione et al., 2020). The transcription factor NF-E2-related factor 2 (NRF2) is the major cellular pathway for regulating the antioxidant response of metazoans against oxidative imbalance within cells. Under steady-state conditions, KEAP1 binds NRF2 and keeps it at low levels in the cell. Under conditions of increased metabolic rate and thus RS production, KEAP1 repression is relaxed allowing NRF2 to accumulate, bind to an antioxidant response element, and activate expression of a host of antioxidant target genes. Castiglione et al. (2020) demonstrate that a mutation in the KEAP1 coding sequence, likely caused by intra-chromosomal rearrangement, in the Neoaves ancestor has led to constitutive activation of the NRF2 master antioxidant response in living birds, and this enhanced response lowers the risk of macromolecular oxidative damage and thus a decrease in oxidative stress.

47.2.3 Immunity

The avian immune system is broadly similar between mammals and birds although most of what we know about “birds” is based on studies of domesticated chickens (reviewed in Schat et al., 2014; Kaiser and Balic, 2015). Birds and mammals have both an innate and adaptive immune response and the latter includes both cell-mediated (T-cell dependent, developed in the thymus) and humoral (B-cell dependent, developed in the Bursa of Fabricius) immune responses—note that in mammals, the B-cells are derived from bone marrow. Given the high costs of maintaining the immune system (Klasing, 2004; Hasselquest and Nilsson, 2012), birds during migration may reduce immune function to spare these costs (Hasselquest, 2007; Buehler and Piersma, 2008) or since they may encounter more pathogens they may instead upregulate immune function (Møller and Erritzøe, 1998; Buehler et al., 2010) or they could reallocate resources and so maintain immune function (Lee, 2006). The balance of evidence to date at least in terms of innate immune function suggests that it may be compromised during migration in birds (Owen and Moore, 2006; Hegemann et al., 2012; Nebel et al., 2012; Eikenaar and Hegemann, 2016) although many more such studies are needed.

47.2.4 Sensory systems and navigation

Migratory birds must be able to orient and navigate during migration, and birds have evolved several key sensory mechanisms that enable successful navigation (for example, see Mouritsen, 2015). However, this topic is beyond the scope of this chapter. Several recent reviews provide excellent entry into this realm of bird migration physiology (Berthold et al., 2003; Wiltschko and Wiltschko, 2009; Mouritsen, 2018; Muheim et al., 2018).

47.2.5 Endocrine system and the environment

Migration represents the morphological, behavioral, and physiological adaptations to seasonal environments—locations with transient resources sufficient to support breeding at one time of the year and another at a distance for survival, thus creating seasonal movements in spring and autumn. To take advantage of seasonal productivity in support of breeding and rearing young (Baker, 1938; Perrins, 1970), migratory species must maintain synchrony with the environment by relying on environmental cues in conjunction with endogenous rhythms to coordinate patterns of movement and stasis.

The endocrine system is the crucial link integrating the environmental cues with behavioral and physiological cycles that contribute to seasonal migrations. Whereas, the endocrine regulation of reproduction of Aves has been thoroughly studied, less focus and progress has been made on migration. To understand why, it is valuable to consider what migration is. It is a complicated biological process with a variety of forms extending from obligate migration that occurs on a strict time table relying on seasonally reliable resources necessary for breeding and survival to facultative forms, i.e., nomadic and irruptive movements of species that respond reactively to resources that vary unpredictably (Watts et al., 2018). Furthermore, migrations occur over multiple seasons and generations incorporating great distances, various environments, habitats, and climate. Together such variables make for a difficult system to study in its entirety. One approach that has contributed to understanding the relationship of the environment and endocrine systems is Finite State Machine Theory (Jacobs and Wingfield, 2000; Ramenofsky and Wingfield, 2007) by focusing on the unique conditions of each life history stage.

For example, the life history of a calendar migrant includes two migration stages—vernal and autumnal—that occur at separate times of the year under differing environmental conditions and regulated by unique neuroendocrine mechanisms. Each stage is composed of three sequential phases—(1) development, the initiation of molecular, biochemical, and genetic processes; (2) mature capability, where all morphological, physiological, and behavioral traits are expressed and actual migration begins; and (3) termination, the disorganization of the migratory traits and beginning of the next life history stage (Figure 47.1). Each phase is regulated by the environmental-endocrine nexus that affects its timing and progression. Current knowledge of the mechanisms regulating the two stages are not thoroughly defined but presenting migration in this format provides an integrated focus for future studies.

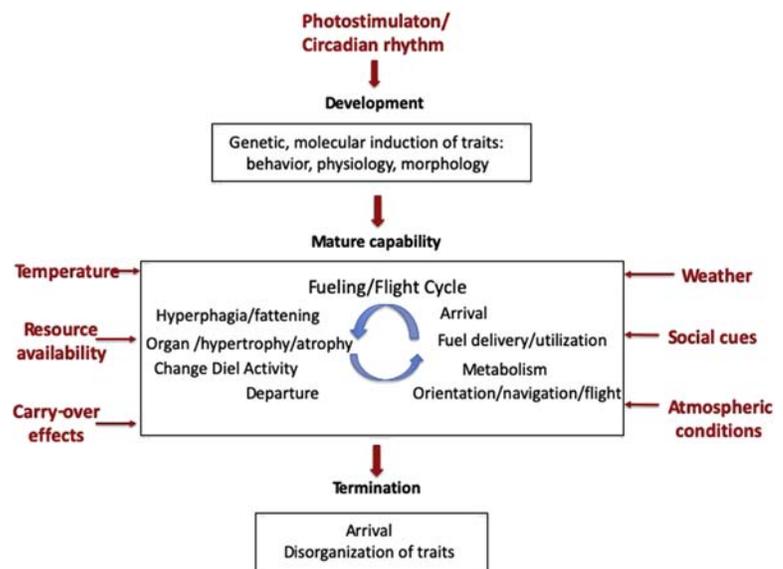
47.3 Endocrinology of migration

47.3.1 Vernal stage

47.3.1.1 Synchronization with the environment: initial predictive cue

Though not thoroughly known for all migratory species, a general consensus from many is the cue response to the vernal increase in daylength or photostimulation (Rani and Kumar, 2014; Hahn et al., 2015). The mechanism involves coincidence of the light phase of the photoperiod occurring during the peak of the circadian rhythm of photosensitivity that takes place for most species between 12 and 15 h after dawn. The reaction resides in the extraretinal photoreceptors of the basal hypothalamus in association with the putative photopigments VA opsin and Rod opsin which are

FIGURE 47.1 Three phases of the migration life history stage. Initial predictive cue of photostimulation induces the development phase and continues its effect throughout the entire stage. Local environmental and conditional cues (*red font*) affect the rate of progression through the substages of mature expression and termination.



co-expressed in the gonadotropin-releasing hormone (GnRH) and arginine vasotocin neurons (Follett et al., 1974, 1998; Meddle et al., 1997; Rastogi et al., 2013). Evidence of photostimulation was demonstrated in the First-day Release Model in which activation of the early immediate gene (*c-fos*) was detected 18 h after dawn of the first long day indicating cellular activity in the basal tuberal hypothalamus of Japanese quail (*Coturnix c. Japonica*) (Meddle et al., 1997). As a result, plasma levels of luteinizing hormone from the anterior pituitary could be detected at 22 h after dawn that in turn induced synthesis and secretion of testosterone from the gonads affecting both migration and breeding life history stages. Given that one cue, photostimulation, initiates both migration and breeding life history stages, the question becomes how are they separated to occur sequentially? Photostimulating white-crowned sparrows with low-penetration green light Wang et al. (2013) was able to separate photoperiodic responses of the migration and breeding stages. Birds developed migratory traits of mass increase, fattening, and nocturnal migratory restlessness but without gonadal recrudescence. Separation of the neuroendocrine control over initiation of migration and breeding have further support from the electrolytic lesion studies in the distinct locations of the hypothalamus in both White-throated, *Zonotrichia albicollis*, and white-crowned sparrows that demonstrated separate pathways for migratory fattening and restlessness versus gonadal development (Kuenzel and Helms, 1967; Stetson and Erickson, 1972; Yokoyama, 1976). Taken together these results suggest separate locations for photoreception and transduction for the two stages: one regulating the migratory life history and the other a more attenuated response of gonadal development and eventual breeding.

47.3.1.2 Developmental phase: hyperphagia and fattening

The initial response to photostimulation is increased food intake—hyperphagia—that leads to elevated body mass and fat stores providing fuel, lipid, and protein to support migratory flight (Ramenofsky, 1990; Lindström and Piersma, 1993). Unlike other homeostatic processes, the alterations of body mass during migration is regarded as rheostasis where the *set point* of body mass is defended but fluctuates throughout the fueling flight cycles of the stage (Mrosovsky, 1990; Jenni et al., 2000; Cornelius et al., 2013; Boswell and Dunn, 2015). The hormone action of these processes is not thoroughly understood for most migratory species but the basic principles are drawn from migratory European quail (*Coturnix coturnix*) and domesticated fowl that focus on the gene expression of opposing sets of neurons of the central melanocortin system in the arcuate nucleus of the mediobasal

hypothalamus and considered the control center for body weight (Boswell, 2005; Boswell and Dunn, 2015) (Figure 47.2). Two neuropeptides synthesized in the arcuate nucleus—neuropeptide Y (NPY) and agouti-related protein (AGRP)—act to promote feeding and mass gain. Opposing these actions are the interconnected neurons that express pro-opiomelanocortin (POMC) and cocaine-and amphetamine-regulated transcript (CART) genes. Given its basal position in the hypothalamus, the arcuate nucleus sits adjacent to the third ventricle and median eminence where the neurons are exposed to circulating levels of proteins, metabolites, and hormones that provide peripheral information. The arcuate nucleus expresses receptors for such metabolic compounds as cholecystokinin (CCK), ghrelin, corticosterone, insulin, and leptin and may serve as interpreters of metabolic state with regulatory capacity to promote or inhibit food intake via the NPY, AGRP or POMC, and CART pathways. Empirical studies using intracerebroventricular (ICV) injections into White-crowned sparrows report that while NPY stimulated food intake, the octapeptide CCK inhibited offering further support for the diverse pathways of control for feeding in a migratory bird (Richardson et al., 1992, 1993).

47.3.1.3 Thyroid hormones

Thyroid hormones play broad regulatory roles in avian physiology including metabolism, thermoregulation, breeding, molt, and migration (Groscolas and Leloup, 1986; Jenni-Eiermann et al., 2002; Zeng et al., 2013). In older literature, migratory fattening and restlessness were associated with elevated activity of the thyroid gland (Wingfield et al., 1990). Additionally, measurements of

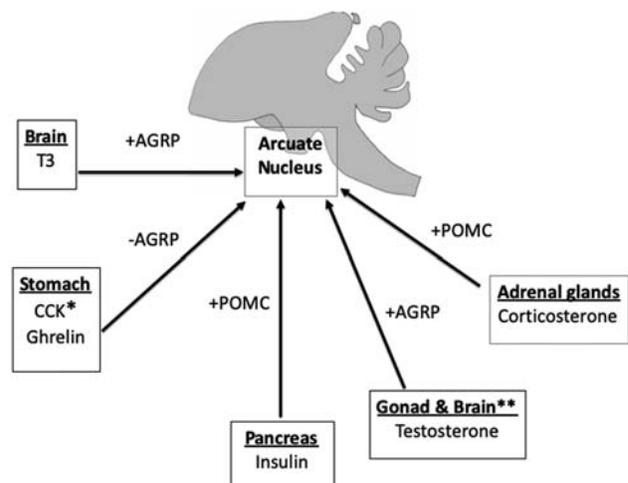


FIGURE 47.2 Suggested model for the endocrine influences on food intake via neuropeptides in the arcuate nucleus of the avian hypothalamus, * Synthesized both in gut and brain, ** possible pathway. Adapted from Boswell and Dunn (2015).

plasma levels of thyroxine (T4) and triiodothyronine (T3) were increased during the early stages of vernal migration (Chandola and Pathak, 1980; Smith, 1982; Pant and Chandola-Saklani, 1993). More recently, chemical inhibition of thyroid hormone disrupted prenuptial molt, fattening, mass gain, flight muscle hypertrophy, expression of migratory restlessness, and gonadal recrudescence while administration of T4 reversed these effects (Pérez et al., 2016, 2018). These results indicate a major role for thyroid hormones across the vernal stage.

Regarding photostimulation, thyroid hormones are considered central to molecular mechanisms regulating breeding (Rani and Kumar, 2014; Boswell and Dunn, 2017; Pérez et al., 2018). For a number of seasonally breeding birds, photoperiod is linked to release of thyroid-stimulating hormone (TSH) from the pars tuberalis of the pituitary gland. TSH stimulates expression of the biosynthetic enzyme Type II iodothyronine deiodinase to direct conversion of T4 to the biologically active T3 in the mediobasal hypothalamus that, in turn, stimulates release of GnRH from the median eminence to initiate breeding (Hahn et al., 2015; Nishiwaki-Ohkawa and Yoshimura, 2016). Evidence is accruing in Siberian hamsters and domestic chicks that the hypothalamic T3 may also exert effects on food intake and fattening through the AGRP neurons of the arcuate nucleus (Boswell and Dunn, 2017) (Figure 47.2). Whether these effects take place with photostimulation during migration are unknown but currently under investigation in a First-day Release Model with acute photostimulation of short-day white-crowned sparrows that will test directly whether long-day exposure induces expression of AGRP and increases food intake in the vernal stage.

47.3.1.4 Testosterone

Additionally, testosterone is implicated in regulating spring fattening. In a number of species, low levels of testosterone circulating during the winter stage are necessary for expression of hyperphagia and fattening in both sexes in the vernal but not the autumnal stages (Schwabl and Farner, 1989; Wingfield et al., 1990; Deviche, 1995; Ramenofsky and Nemeth, 2014), a condition challenged by others (Weise, 1967; Boswell et al., 1993). The mechanism by which testosterone could influence migratory fattening is through the androgen receptor (AR) on the arcuate nucleus stimulating the AGRP/NPY/feeding center pathways, as documented in mammals (Diano et al., 1997) (Figure 47.2). The timing of this effect is not known but could vary across migratory species.

47.3.1.5 Insulin and glucagon

The pancreas is the source of 3 proteins, insulin, glucagon, and pancreatic polypeptide; the former two are considered

major regulators of food intake in birds acting directly and/or through their effects on carbohydrate and lipid metabolism (Hazelwood, 2000). Only a few studies have investigated these in migrating birds (Goodridge, 1964; Totzke et al., 1997; Cornelius et al., 2013). What is known is that insulin and glucagon have opposite effects on plasma glucose that in turn may influence food intake. Surprisingly, intramuscular injections of either glucagon or insulin decreased feeding in captive white-crowned sparrows (Boswell et al., 1995). Plasma glucose is exceedingly high in birds even though plasma insulin falls within the normal range suggesting peripheral insensitivity to insulin (Sweazea et al., 2006). ICV administration of insulin increased feeding indicating a marked diversion from mammals and suggesting central control of food intake by insulin (Boswell et al., 1995). Besides its effect on carbohydrate metabolism, glucagon has a biphasic effect on lipid production. At elevated levels, glucagon promotes lipolysis enhancing release of free fatty acids (FFAs), a source of energy, into the circulation. At lower range, this is reversed with increased lipogenesis and fat storage (Goodridge, 1964). Testing the effects of metabolites on feeding reported a predominant sensitivity to lipid as opposed to carbohydrate, a reasonable conclusion given the major role that lipid plays during migration (Boswell et al., 1995). Taken together, it is suggestive that glucagon levels cycle throughout migration with lowest levels occurring during the migratory fattening to support lipogenesis countered by elevated levels during flight promoting lipolysis making fatty acids available for oxidation (Goodridge, 1964). More comprehensive studies on the pancreatic peptides are needed.

47.3.1.6 Glucocorticoids (Box 47.1)

Corticosterone in birds has long been associated with hyperphagia, fattening, and stress physiology in migrants, but results across numerous studies and species have not revealed consistent patterns (Landys et al., 2006; Ramenofsky, 2011; Wagner et al., 2014; Eikenaar, 2017). One of two views contributing to these divisions is the Migration Modulation Hypothesis (Holberton et al., 1996) that addresses stress physiology with the hypothesis that neotropical migrants would not show the expected stress response to capture and handling with two predictions: (1). baseline levels of corticosterone remain elevated during migration to promote hyperphagia and lipogenesis, (2). suppression of the stress response to avoid the deleterious effects of catabolism on flight muscle (Long and Holberton, 2004). The alternative view is that most migrants display a robust stress response throughout migration with plasma levels varying seasonally across the stages and in healthy birds within physiological range (Level B (Box 47.1)). Corticosterone concentration is

BOX 47.1 Aligning corticosterone, physiological state, and allostasis.

Corticosterone, the predominant adrenal steroid of birds, is associated with many aspects of the migration life history stage including behavior, metabolism, and allostasis—measure of energy requirements over time (Blas, 2015; Ramenofsky, 2011; Landys-Ciannelli et al., 2002; Romero et al., 1997). Corticosterone acts in concert with other metabolic hormones such as CCK and insulin by regulating availability of energy in the forms of circulating FFAs and glucose to maintain homeostasis (Eikenaar, 2017). To fully appreciate the multiple functions and levels of control of corticosterone, we refer to the hypothalamus-pituitary-adrenal (HPA) axis by considering its actions at three physiological states and hormone levels. Level A is considered the basic homeostasis that maintains life (Romero et al., 2009). Level B involves the activation of the HPA for fluctuations in response

to predictable, daily or seasonal demands for energy, allostatic load, across the annual life history stages. Level C, further activation of the HPA that tend to be transitory as the individual reacts to an acute and unpredictable event or stressor. The induced behavioral response is to move away or adopt an emergency life history stage (ELHS) to alleviate effects of the stress (Romero and Wingfield, 2016). To assess function of the HPA axis, two measurements of circulating corticosterone are collected: the first is the baseline measure collected within the first 3 min of capture and reflecting the current and unprovoked energetic state of the organism. The second sample is the acute or Level C collected at the peak of the response to capture and handling indicating the maximal response of the corticosterone synthesis and secretion (Figure 47.3).

regulated by the enzyme 11 β -hydroxy steroid dehydrogenase, and it acts through two cellular receptors, the high-affinity mineralocorticoid receptor (MR) and low-affinity glucocorticoid receptor (GR). Considering these multiple levels of control, corticosterone is regarded as a pleiotropic hormone with multiple effects acting in permissive roles with critical metabolic compounds that affect energy balance and allostasis including: insulin, insulin-like growth factor-1, adipose tissue lipoprotein lipase, low-density lipoprotein, FFA, NPY action (Savard et al., 1991; Remage-Healey and Romero, 2001; Landys et al., 2004a, 2006; Blas, 2015; Mishra et al., 2017), and growth hormone (GH) (Tsipoura et al., 1999). All of which contribute to the complexity and often confusion over corticosterone's action. Taking a more comprehensive view of the interactions of hormones and metabolic compounds in terms of allostasis and stress at each sub-stage may provide a more complete assessment of the role of this steroid in migration.

47.3.1.7 Leptin

The protein hormone leptin is known as a strong regulator of energy balance in mammals synthesized almost exclusively in the adipose tissue and signaling presence or deposition of fat—positive energy balance (Zhang et al., 1997). Thus it is considered a hormone with autocrine, paracrine, and endocrine functions promoting homeostasis of energy stores and has been coined an *adipostat* in mammals regulating food intake according to energy balance—fat content (Friedman-Einat et al., 2014; Friedman-Einat and Seroussi, 2019). Recent identification in birds of a leptin ortholog and characterization of leptin activity has questioned whether it functions either as a hormone or an *adipostat*. The leptin ortholog shows no expression in adipose tissue but is found in brain, adrenal

gland, and gonad. So far, the avian leptin receptor LEPR is expressed only in the pituitary. Given these diversions from mammals, it is unlikely that avian leptin is acting as a homeostatic adipostat and offers preliminary support for the Rheostasis Model during migration that would allow for greater range of body mass and fat stores (Cornelius et al., 2013; Friedman-Einat et al., 2014; Watts et al., 2018).

47.3.1.8 Ghrelin

Acting in opposition to leptin, this 28-amino-acid peptide is secreted from the stomach and other digestive organs of birds when body condition is low. Ghrelin is reported to be a GH-releasing factor in chickens and mammals that relays information to the arcuate nucleus of nutritional state. In rats, both intraperitoneal (IP) and ICV injections of ghrelin increased food intake. This effect is most apparent during fasting with ghrelin acting on the NPY/agouti-related peptide (AGRP) neurons in the arcuate nucleus (Nakazato et al., 2001). In quail, plasma ghrelin was elevated in fasted

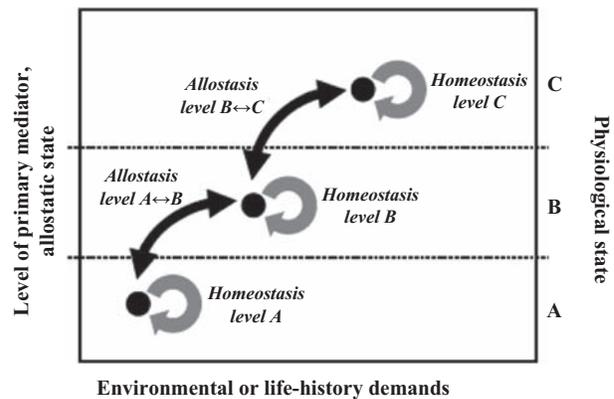


FIGURE 47.3 Description of state levels of corticosterone in relation to homeostasis, allostasis, and physiological state. With permission from Landys et al. (2006).

birds but dropped once feeding commenced. The results obtained with injections were less clear; at low concentrations, IP injections enhanced feeding but at greater dosages both IP and ICV injections decreased feeding suggesting a biphasic effect. Other studies in which ghrelin was administered reported that food intake in neonatal chicks was inhibited (Kaiya et al., 2009). Although presently controversial in domestic fowl, these results suggest that ghrelin could regulate feeding during migration, particularly when birds are lean, as they would be following flight. In a recent study, lean Garden warblers, *Sylvia borin* captured in the morning upon arrival at a stopover site on the Mediterranean Island of Ponza measured elevated plasma levels of the acylated ghrelin (Goymann et al., 2017). After refueling throughout the day in captivity, injections of the unacylated form of ghrelin decreased food intake and increased migratory restlessness at night pointing to either a biphasic effect on behavior of hormone concentration or different responses to the chemical forms of the hormone. By contrast, plasma ghrelin was not associated with nocturnal departure in fully fattened European blackbirds (*Turdus merula*) at an autumn stopover (Eikenaar et al., 2018b). These outcomes may represent species or seasonal differences calling for a more complete understanding of ghrelin's role during migration.

47.3.1.9 Prolactin

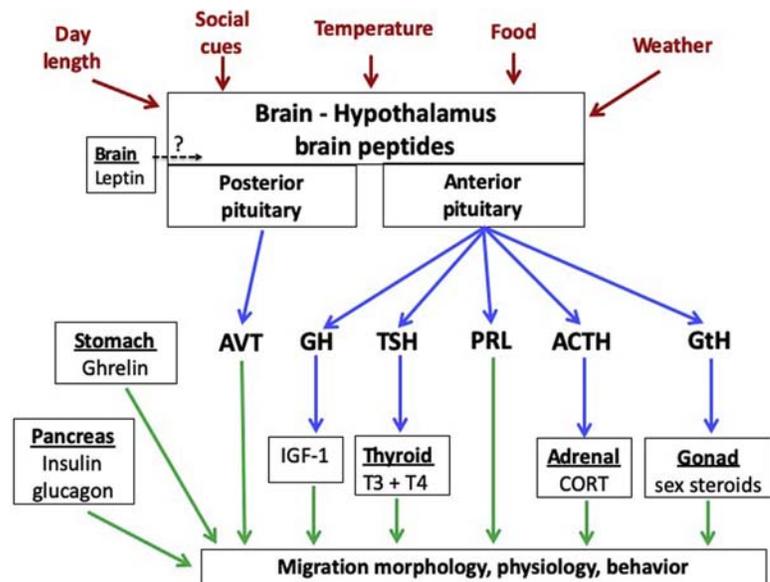
Understanding prolactin's role in migratory feeding and fattening has been problematic. Administration of this pituitary protein increases fattening in a number of migratory species (Meier and Farner, 1964; Yokoyama, 1976). Also, central effects of prolactin have been identified in

specific sites of the hypothalamus of migratory and nonmigratory birds (Yokoyama, 1976; Buntin et al., 1993). Prolactin levels, like other pituitary hormones, vary seasonally as photostimulation induces secretion of vasoactive intestinal peptide, the stimulatory hypothalamic neuropeptide that induces production and secretion of prolactin from the pituitary (Figure 47.4). This information led to the hypothesis that prolactin could be acting in conjunction with gonadal steroids and corticosterone that were also elevated with photostimulation to induce migratory fattening and restlessness. However, questions have been raised in a number of migrants as the photoinduced peak of prolactin corresponds only weakly with onset of feeding, fattening, and migratory restlessness (Hall and Gwinner, 1987; Schwabl et al., 1988; Holberton and Dufty, 2005). Timing of peak prolactin levels appears to align its function with the autumnal stages of refractoriness and postnuptial molt (Dawson et al., 2001). So, even though prolactin injections increase fattening in birds, prolactin function in relation to migratory fattening is far from resolved.

47.3.1.10 Hormones of flight muscle hypertrophy

In addition to fueling, the pectoralis flight muscles undergo hypertrophy in numerous migratory species (Fry et al., 1972; Driedzic et al., 1993; Jehl, 1997; Bauchinger et al., 2005; Banerjee and Chaturvedi, 2016) during migration that entails increased size of the muscle fibers serving to enhance contractile force and flight performance (Marsh, 1984; Gaunt et al., 1990; Evans et al., 1992; Vezina et al., 2021) (Ramenofsky et al., in prep). Though not well

FIGURE 47.4 Flow chart of the environmental cues on the neuroendocrine—endocrine system influencing migratory morphology, physiology and behavior. *Red arrows*—environmental cues influence the activity of hypothalamic brain peptides, *Blue arrows*—pituitary hormones regulated by the brain peptides affect peripheral endocrine glands. *Green arrows*—hormones of the endocrine glands regulate migratory functions. Role of leptin at present is uncertain (Friedman-Einat and Seroussi, 2019).



understood in migratory birds, anabolic steroids—testosterone and 5 α -dihydrotestosterone (DHT)—are likely candidates for regulating phenotypic changes given reports of AR gene increasing expression in flight muscles of Golden-collared manakin (*Manacus vitellinus*) during sexual displays (Fuxjager et al., 2012). Furthermore, elevations of androgen signaling via DHT, AR mRNA and the androgen dependent gene, insulin-like growth factor 1, showed increased levels of expression in White-crowned sparrows at spring departure when flight muscles were enlarging (Pradhan et al., 2018). Regulation of muscle hypertrophy could be a function of vernal photostimulation that activates androgen secretion and gonadal recrudescence (Blanchard and Erickson, 1949; Wingfield et al., 1990; Bauchinger et al., 2007). Or it is possible that testosterone secreted during the winter stage has an early priming effect on muscle as it does on fattening (Wingfield et al., 1990), something that is unknown at present. Nevertheless, the circulating levels of androgen are low as birds prepare for vernal departure suggesting intramuscular cell signaling pathways may direct muscle remodeling and thus avoiding the systemic and behavioral effects if levels of androgen were elevated at this substage (Bauchinger et al., 2007; Pradhan et al., 2018). In addition to androgen, corticosterone is implicated in flight muscle hypertrophy at vernal departure. Elevation of baseline corticosterone was associated with increased expression of the high-affinity MRs expression in White-crowned sparrows (Pradhan et al., 2019). This relationship is thought to promote the anabolic stimulation of the muscle fibers, contributing to hypertrophy. Such effects are not known for the autumnal stage.

In addition to the phenotypic changes orchestrated by the endocrine system, integral components of the muscle fibers alter during this vernal substage. Myosin heavy chain (MyHC) expression is associated with the muscle's mechanical capabilities (Reiser et al., 1996). Changes in the expression of the MyHC isoform during the development phase may represent an adaptation for upgrading the muscle mechanics for impending long-distance flight (Velten et al., 2016). Again, hormonal mechanisms regulating these molecular processes are not known but deserve further study during the autumnal stage.

47.3.1.11 Mature expression—hormones of the fueling and flight cycle

Stopover in both the vernal and autumnal stages provides the clearest example of the fueling and flight cycle as flight temporarily ceases upon arrival for rest, fueling, and then departure (Delingat et al., 2006, 2009) offering an excellent opportunity for tracking metabolic hormones. During the 4500 km journey from Africa to a stopover site along the northern Dutch coast in spring, Bar-tail godwits

(*Limosa lapponica*) cease travel for approximately one month to rest, continue prenuptial molt and refuel before continuing northward to the breeding grounds. One indication that baseline corticosterone levels align with allostatic load was noted initially by Landys-Ciannelli et al. (2002). Birds arrived in lean condition having lost on average 55.3% from their African departure body mass with elevated baseline levels of corticosterone suggesting a heightened allostatic load resulting from the “wear and tear” of a long continuous flight. Similarly, elevated baseline levels are reported in recently arrived Semipalmated sandpipers at a vernal stopover in Delaware Bay (Tsipoura et al., 1999), Gray Catbirds (*Dumetella carolinensis*) along the Gulf Coast of the United States (DeSimone et al., 2020), and Garden warblers on the Mediterranean Island of Ponza (J. Wingfield and M. Ramenofsky, in preparation). Measurements of body mass of the sandpipers throughout the period of arrival varied over a range of 10 g indicating the different stages of recovery of birds across the flock. Over this period plasma GH was negatively correlated with mass. Given the lipolytic functions of GH, the data suggest hormone action would supply fatty acids to meet the energetic demands of flight and arrival until sufficient refueling achieved positive energy balance observed in the heavier birds of the flock (Tsipoura et al., 1999). During the refueling phase of the godwits, the baseline corticosterone declined 55% from arrival. The corticosterone response levels of both the refueling and arriving birds were similar, however the peak for the arriving birds reached their maxima more rapidly suggesting a heightened sensitivity of negative feedback possibly related to allostasis and/or CNS functions required for flight (Landys-Ciannelli et al., 2002; Eikenaar et al., 2013; Romero and Wingfield, 2016). Once refueling achieved positive energy balance, godwits became aphagic while digestive organs atrophy to conserve body mass and metabolic costs for the ensuing flight (Piersma, 1998; McWilliams and Karasov, 2001). Baseline corticosterone increased around the time of departure and has been associated with the upregulation of HPA for regulating metabolic and behavioral functions for impending flight and organ remodeling (Reneerkens et al., 2002b; Eikenaar et al., 2013, 2018a; Pradhan et al., 2019). However, such upregulation was not identified in the short-hop migrant, Gray catbird (DeSimone et al., 2020) suggesting a divergence in preparation for flight depending upon species and migratory strategy. Nonetheless, studies of both captive and free-living migrants offer further support for the association of corticosterone with expression of migratory flight in the vernal and autumnal stages (Schwabl et al., 1991; Ramenofsky et al., 1999; Landys et al., 2004b; Falsone et al., 2009; Eikenaar et al., 2014; Ramenofsky and Wingfield, 2017). Taken together the results from these studies offer insight into the effects

of corticosterone and GH, providing endocrine support for the behavioral and metabolic processes during flight, at arrival, and preparation for departure during stopover.

47.3.1.12 Termination: arrival biology

Reaching the breeding grounds heralds the termination phase that includes the substage of arrival biology (Wingfield et al., 2004). This substage requires flexibility and coordination of morphology, behavior, and physiology given the quixotic environmental conditions birds may face in early spring. Observational studies note that migratory behavior changes as birds approach breeding areas and begin to search widely for optimal habitats (Hahn et al., 1995). Studies of captive birds, report changes in intensity of migratory restlessness and orientation near the conclusion of the migratory period, suggesting transition to more wandering and searching behaviors expressed even in captivity (Helms, 1963; Wiltschko et al., 1980; Ramenofsky et al., 2003). Elevated corticosterone during arrival has been proposed to support these behaviors (Ramenofsky, 2011, 2012; Romero and Wingfield, 2016) providing examples of the pleiotropic effects of corticosterone influenced by its multiple sites of control at the enzymatic, receptor, and state levels.

Field studies document that winter conditions may prevail at high altitudes and latitudes after birds arrive with storms likely forcing delay of the onset of breeding (Morton, 2002). In these cases, migrants retain elevated levels of corticosterone that promote escape to refuges until conditions on the breeding grounds improve (Reneerkens et al., 2002a; Hahn et al., 2004; Ramenofsky and Wingfield, 2007; Cornelius et al., 2013; Ramenofsky and Wingfield, 2017).

Throughout the vernal stage, hypothalamic-pituitary-gonad (HPG) axis function progresses with increasing levels of gonadotrophin (GtH), testosterone, and DHT, so males are ready to breed once females arrive and environmental conditions allow (Wingfield and Farner, 1978a; O'Reilly and Wingfield, 1995; Ramenofsky and Wingfield, 2006; Covino et al., 2015, 2017; Lymburnera et al., 2016). For females, the story differs as the final stages of oogenesis, yolk deposition, egg laying, and behaviors regulated by estrogen and progesterone are held in check under the regulation of the hypothalamic peptide gonadotropin-inhibiting hormone (GnIH) (Tsutsui et al., 2000; Bentley et al., 2009). This peptide is thought to act as a “brake” on reproduction by its central effects on sexual behavior and hypophysiotropic control of steroidogenesis and ovulation (Wingfield et al., 2016). Under extreme conditions, interactions of elevated corticosterone and GnIH may serve to extend the more mobile or nomadic phase of arrival biology until conditions improve sufficiently for GnIH levels to decline and activation of the breeding stage to proceed.

Regulation of GnIH function is not well understood, but environmental conditions appear to play a major role guiding synchronization of egg laying with the potential peak of food abundance (Perrins, 1970; Ramenofsky and Wingfield, 2017). Onset of breeding marks the termination of the vernal migratory stage.

47.3.2 Autumnal stage

47.3.2.1 Development phase

In many ways, autumnal migration appears similar to that of the vernal stage, as it can be divided into the same three phases. The traits are similar that include hyperphagia, fattening, organ remodeling, fueling flight cycles, etc. But major differences exist that provide important clues to the endocrine regulation and biological significance of each stage. For example, the recognized mechanisms that regulate activation of the vernal stage are not operating in the autumnal stage. Daylength is decreasing rather than increasing and many migrants are known to be photorefractory with a loss of responsiveness of reproductive development to long photoperiods (Dawson et al., 2001). The HPG regresses with circulating levels of GtHs and gonadal hormones decline to basal precluding further breeding attempts late in the season. For most species, both baseline and response levels of corticosterone have dropped from elevated breeding titers.

47.3.2.2 Thyroid hormones

A number of seminal studies of captive birds have identified that the rate of increase of vernal photoperiods during photostimulation exert latent effects on the timing of photorefractoriness followed by the autumnal events of post-nuptial molt and migration (Farner and Follett, 1966; Gavrilov and Dolnik, 1974; Dolnik, 1980; Moore et al., 1982, 1983). Thyroid hormones are considered central by playing organizational roles for both vernal and autumnal stages during photostimulation (Dawson et al., 2001; Pérez et al., 2016, 2018). Timing of the thyroid organizational effects is considered the basis for the separate pathways of control for the two stages (Wilson and Reinert, 1996, 1999). A further understanding is now needed for the hormonal and genomic mechanisms underlying the potential roles for thyroid hormones during autumnal migration.

47.3.2.3 Androgen

Unlike in spring, plasma levels of androgen in the autumn are basal and probably not capable of activating feeding centers in the hypothalamus. Furthermore castration during the previous winter months had no effect on autumnal fattening in white-crowned sparrows (Wingfield et al., 1990). However, both androgen and estrogen are

synthesized locally in the brain and affect autumnal behavior (Soma et al., 2002; Pradhan et al., 2010). So, it is possible that neurosteroids (steroid synthesized in the brain) could influence the arcuate nucleus via AGRP as in spring (Boswell and Dunn, 2015) to affect autumnal hyperphagia and fattening. Whether the molecular pathways associated with vernal flight muscle hypertrophy operate during the autumnal stage are unknown at present but represent intriguing possibilities.

47.3.2.4 Glucagon

One of a very few studies investigating glucagon in migratory birds during the autumnal stage in comparison with winter identified a decrease in plasma levels of glucagon and FFA in captive Red-winged blackbirds (*Agelaius phoeniceus*) while fattening for autumnal migration (Hintz, 2000). Although a surprising result, Goodridge (1964) suggested previously that seasonal patterns of circulating levels of glucagon could contribute to fluctuations in adiposity with elevated levels promoting lipolysis to mobilize energy to fuel such activities as thermogenesis during winter months and lower titers to enhance fat storage for migration. Further studies are needed to more clearly define the roles of glucagon during the autumn stage.

47.3.2.5 Mature expression—hormones of the fueling and flight cycle

Field studies focusing on the transition from breeding to autumnal departure identified that birds express individual schedules that vary according to investment and timing of breeding, molt, social interactions, age, body condition as well as local weather and wind direction (Runfeldt and Wingfield, 1985; Morton and Pereyra, 1994; Bonier et al., 2007; Sjoberg et al., 2015; Chmura et al., 2020). This asynchrony across individuals deviates markedly from the highly synchronous schedules birds express in spring driven by the initial predictive cues and strong selective pressure for birds to arrive on the breeding grounds as early as feasibly possible for reproductive advantage (Smith and Moore, 2005). Investigating the differences may help to further identify the regulatory distinctions of the two stages but very few studies have focused on seasonal comparisons at time of departure (Wingfield and Farner, 1978a).

Among the overland migrant populations of White-crowned Sparrow, body mass and fat scores reached their annual peak just prior to departure, a time when plasma levels of baseline and response corticosterone are comparable with the vernal and autumnal values but at significantly lower levels than the annual peaks reached upon arrival on the breeding grounds and during early stages of breeding (Wingfield and Farner, 1978a; 1978b; O'Reilly and Wingfield, 1995; Krause et al., 2021). By contrast, in trans-hemispheric migrant Barn swallow

(*Hirundo rustica*), the baseline levels of corticosterone prior to spring departure exceeded the values in autumn, while the response levels of autumn rose above vernal values (Raja-Aho et al., 2013). Body condition of spring birds was poor compared to autumn leading to question the role of corticosterone at the time of departure. Given the disparate results across the two species it is clear that additional studies of the physiological condition and endocrine state of birds at departure in the vernal and autumnal stages require further investigations.

47.3.2.6 Stopover: arrival

As in spring, the autumnal stopover substage provides advantageous views of the behavioral, physiological, and endocrinological states upon arrival and at departure. A pattern of elevated baseline and response corticosterone levels has been recorded in some but not all migratory species with greater titers measured in vernal than in autumnal stages (O'Reilly and Wingfield, 2003; Romero et al., 1997; Loshchagina et al., 2018; Bauer et al., 2019). When seasonal differences are detected it is suggested that allostatic load of vernal migration for these species exceeds that of autumn. Impending breeding, unpredictable and unfavorable climatic conditions and less reliable sources of food are some of the issues migrants face at higher altitudes and latitudes in spring. In species that cross extreme barriers (oceans and deserts) with routes that are comparable in both seasons, the baseline levels corticosterone may not vary to any great extent. However another mechanism for differential regulation of corticosterone is presented in Dark-eyed junco sampled during spring and autumn stopovers (Bauer et al., 2019). Neither baseline nor response corticosterone varied seasonally but negative feedback was weaker in spring than autumn suggesting a greater response to environmental perturbations. Surprisingly, these findings diverge from the increased sensitivity to capture in the spring arriving Bar-tailed godwits in comparison with refueling birds and possibly suggests a species or migratory strategy difference.

Thus, a more consistent theme arising from a variety of species captured during autumnal migration indicate only moderate elevations of baseline corticosterone, suggesting an allostatic load that falls substantially below stress-induced values Level C (Schwabl et al., 1991; Gwinner et al., 1992; Falsone et al., 2009). At such titers, corticosterone may serve to support metabolic processes supplying energy required for endurance flight in terms of protein-mediated transport of fatty acids into flight muscle and high-oxidative capacity (Lundgren and Kiessling, 1985; McFarlan et al., 2009; Price et al., 2010). Yet, a few extreme cases are reported of birds captured in flight in nearly starved condition with depleted stores of fat, atrophied flight muscle, and baseline corticosterone titers that

reach well into the realm of the acute response to stress Level C (Box 47.1). Fat stores are considered key regulators of systemic protein catabolism that can affect allostatic load, plasma corticosterone, and potentially survival (Schwabl et al., 1991; Jenni and Jenni-Eiermann, 1992; Schwilch et al., 2002; Falsone et al., 2009). Such elevated baseline levels indicate that an individual has entered the ELHS in which corticosterone metabolically promotes protein catabolism and directs a change in behavior from landing to foraging enabling recovery as long as sufficient resources can be accessed (Romero and Wingfield, 2016).

47.3.2.7 Stopover: departure

At departure from stopover sites, birds are metabolically ready for flight with elevated body mass, fat deposits, circulating triglyceride levels, and hypertrophied flight muscle (Sandberg et al., 2002; Fusani et al., 2009; Goymann et al., 2010; Covino and Holberton, 2011). Additionally, baseline levels of corticosterone correspond with orientation at take off and environmental cues conducive for flight namely favorable winds (Lohmus et al., 2003; Eikenaar and Schmaljohann, 2015; Eikenaar et al., 2017b, 2018a). In captive migrants, expression of nocturnal migratory restlessness coincides with increased baseline corticosterone (Ramenofsky and Wingfield, 2017). Taken together, departure involves the interactions of the environment, endocrine system, physiological state, and motivation to fly. The causal relationship of these variables remains to be elucidated fully.

47.3.2.8 Termination—arrival

Generally, arrival at the overwintering sites marks the end of autumnal migration with the loss of such traits as hyperphagia, fattening, flight muscle hypertrophy, and nocturnal restlessness (Romero et al., 1997; Ramenofsky, 2011). For the most part overwintering sites provide sufficient resources for survival but competition for access to roosts sites, quality food, and protection from predators can be intense given presence of resident birds as well as potential influx of breeding birds from the opposite hemisphere (Newton, 2008). Unlike the vernal stage, autumnal arrival is less synchronized, more facultative, and birds may not settle for weeks (Watts et al., 2018). To avoid competition, some cohorts arrive early or continue movement to locate in areas where food is more abundant and environmental conditions less harsh, as noted in the differential migration patterns (Ketterson and Nolan, 1976; Terrill, 1990; Newton, 2008). Given the degree of competition for resources at this stage, it is surprising that levels of androgen and corticosterone levels are basal (Wingfield and Farner, 1978a, b; Romero et al., 1997; Krause et al., 2021). However, the prospects that neurosteroids may be influencing behavior is a possibility but

unknown to date. Also, involvement of the metabolic hormones is unclear emphasizing the need for more research during the autumnal stage.

47.3.3 Conclusions to endocrine system

Comparing vernal and autumnal life history stages of migration offers insight into the adaptations of each providing a fuller appreciation of the migratory processes as a whole. In general, there are common traits that support movement in either season that include an engine (muscle) for power, fuel supplies, oriented movement, and a clock (Piersma et al., 2005; Ramenofsky and Wingfield, 2007; Dingle, 2014). Specifically, the two stages and their sub-stages diverge in terms of the environmental conditions encountered, types of available resources, reproductive states, endocrine status, age groups participating, and in many cases the migratory routes. These differences are the most revealing as they convey individual and/or population responses to the selective pressures of the environment, season, fitness, and survival supporting the premise that the two migratory stages are distinct adaptations. But before any conclusions can be fully drawn, more thorough coverage of the endocrinology of the autumnal stage is needed in addition to the studies that track plasma levels of hormones over the course of each stage. Together these points emphasize more work is needed that focuses on the molecular and genomic aspects of the endocrine system, receptor expression, and the metabolic enzymes all playing key roles in determining hormone action during both the vernal and autumnal stages as reported by (Sharma et al., 2018). Such integrative studies will provide a more complete understanding of how the environment influences migration and how individuals will cope with the challenges of climate change.

47.4 Physiological aspects of migratory preparation and long-duration flight: fueling/flight cycle

47.4.1 Introduction

Given that the vernal and autumnal migration stages occur at separate times of the year under differing environmental conditions and evidence to date suggests that the two stages are regulated by unique neuroendocrine mechanisms, we would expect some important differences in the physiology of birds during the two migration stages. In general, physiological ecologists who study migration in birds pay attention to the season in which birds are studied, but few studies have focused on how the physiology of migratory birds differs between vernal and autumnal migration. This paucity of information about the mechanistic underpinnings of physiology during the two migration stages has led us to

organize the following section around several themes (feeding and diet selection, fuel storage and fat quality, fuel use and oxidative balance) that we assume to be relatively common to both migration stages, but that may be produced by different gene-to-physiology-to-behavior mechanisms.

47.4.2 Feeding

47.4.2.1 Hyperphagia

During spring and fall migration, migratory birds increase their daily food intake (e.g., hyperphagia) in an effort to increase energy stores (fattening) to fuel their migratory flights (Odum, 1960; King and Farner, 1965). These periods of intensive feeding and fattening can last a few days to several weeks (Schaub and Jenni, 2001; Chernetsov and Mukhin, 2006; O'Neal et al., 2018), and the duration is influenced by a variety of ultimate and proximate factors such as migration strategy (e.g., long-distance, short-distance), weather, food availability, predation risk, endogenous cycles, and physiological state (Jenni and Schaub, 2003; Fusani et al., 2009; Goymann et al., 2010; Guillemette et al., 2012; Hou and Welch, 2016). For many species, the total duration of migration is composed mostly of time spent at stopovers and not in flight itself (Wikelski et al., 2003). Thus, much of the hyperphagic periods of most birds are at stopover sites. For several species of dabbling ducks, for example, the average stopover duration was 28 days and was heavily correlated with habitat quality and the availability of food (O'Neal et al., 2018). In contrast, the primary predictor of stopover duration in several species of songbirds was dependent upon the amount of fat reserves when all other factors such as weather, predation, and food availability were equal or controlled (Fusani et al., 2009; Goymann et al., 2010; Smith and McWilliams, 2014) although this generalization is based almost entirely on correlational rather than empirical experiments (Smith and McWilliams, 2014).

47.4.2.2 Balancing the energy costs of hyperphagia

Hyperphagia can inherently increase daily energy expenditure (DEE) due to the additional time required to search for and process food as well as maintain more metabolically active tissue (reviewed in Lindström, 2003). Hyperphagic birds must compensate for increased foraging costs in order to rapidly gain body stores. Thus, migratory birds exhibit behavioral and physiological adjustments during hyperphagia that help to promote fattening while keeping their DEE similar to or below nonhyperphagic periods. For example, premigratory common eiders, *Somateria mollissima*, foraged three times more than postmigration periods yet their DEE remained the same

because they reduced their heart rate during inactive times and decreased their time spent flying (Guillemette et al., 2012). Several species of migratory birds ranging in size from hummingbirds (Carpenter and Hixon, 1988) to small passerines (Wojciechowski and Pinshow, 2009) to large geese (Butler and Woakes, 2001) reduce their body temperature and so reduce energy expenditure prior to migratory flight regardless of food availability, weather conditions, or degree of fat storage.

47.4.2.3 Fasting and refeeding during migration

During migration, many birds alternate between short-term fasting while flying and intense refeeding at stop over sites. This cycle of alternating feeding and fasting influences gut morphometrics, fattening rates, and subsequently the pace of migration (Karasov and McWilliams, 2005). It is well established that the guts of migrating birds atrophy after just 1 or 2 days of fasting, and this decreased digestive capacity influences the rate at which birds can increase feeding rate and uptake of nutrients upon arrival at stopover sites (Diamond et al., 1986; Karasov and Pinshow, 2000; McWilliams and Karasov, 2005). Thus, the phenotypic flexibility in the gut of migratory birds plays a significant role in their ability to immediately refeed and fatten. Several species of migratory birds increase gut length, mass, and volume in response to increases in food intake in preparation for migratory flight (Dykstra and Karasov, 1992; McWilliams et al., 1999; McWilliams and Karasov, 2001; McWilliams and Karasov, 2005). However, digestive enzyme activity and nutrient uptake per unit of tissue did not change with an increase in food intake in several species of fasted passerines (reviewed in McWilliams and Karasov, 2005). Thus, the relevant phenotypic flexibility seems to be primarily in the size of the gut and not the chemical aspects of digestive efficiency. The digestive organ sizes of fasted birds appear to increase within one to six days upon increasing food intake (Dekinga et al., 2001; McWilliams and Karasov, 2001) and the activity of digestive enzymes, nutrient transporters, and absorption rates take 2–3 days to recover after fasting (Karasov and Hume, 1997; Karasov and Pinshow, 2000). This delay in recovery can impact the overall time it takes for a bird to become ready to migrate and thus slow the overall pace of migration.

47.4.2.4 Diet selection during migration

Many migratory bird species display seasonal shifts in diets associated with migration. For example, several passerines switch from a primarily insectivorous diet to a more frugivorous diet (Herrera, 1984; Bairlein and Gwinner, 1994; Parrish, 1997, 2000), and some arctic nesting

shorebirds switch from a diet of primarily terrestrial invertebrates to aquatic invertebrates during fall migration (Schwemmer et al., 2016). This dietary flexibility has been attributed in part to the changes in food availability linked with season (Martin and Karr, 1986; Tsipoura and Burger, 1999). For example, migratory songbirds locally congregated where fruit abundance was high (Smith and McWilliams, 2014), they consistently chose foraging sites with higher fruit availability than insect availability during migration (Martin and Karr, 1986), and migrating shorebirds chose stopover sites along the shores of the eastern United States in conjunction with horseshoe crab spawning (Tsipoura and Berger, 1999). However, food abundance does not entirely explain diet switching in birds during migration as a multitude of factors play into diet choice (see Murphy, 1994 for complete review) including the need to rapidly satisfy the elevated daily energy and nutrient demands associated with migration while eating foods that are typically nutritionally unbalanced.

Birds seem capable of discriminating between foods based on relatively small differences in key nutrients, and these nutrient-based preferences may change with nutrient demands although the evidence for this is less convincing. As an example, four species of tanagers, Blue Dacnis, *Dacnis cayana*, Flame-crested tanager, *Tachyphonus cristatus*, Green Honeycreeper, *Chlorophanes spiza*, and Short-billed tanager, *Cyanerpes nitidus*, were shown to detect differences of 1% in sugar concentration and 2% in lipid concentration in available diets (Schaefer et al., 2003). In addition, these tanagers were able to distinguish between diets that differed in protein type (casein vs. bovine serum albumin) while protein concentration remained constant (Schaefer et al., 2003). Furthermore, white-crowned sparrows preferred semisynthetic diets that differed only in certain amino acids, and their preferences for sulfur amino acids needed for feather growth increased during times of molt (Murphy and King, 1987). Yellow-rumped warblers offered several diets that varied in nutrient and energy content ate a combination of available diets that allowed them to satisfy both their energy and protein demands during nonmigratory as well as migratory periods (Marshall et al., 2016). Whether or not birds have preferences for specific amino acids during the migratory period has not yet been determined. Likewise, many species of migratory birds prefer diets containing certain types of fats (i.e., unsaturated over saturated) and certain amounts or ratios of fatty acids in their diets (Pierce and McWilliams, 2014). There is some evidence that these bird preferences for specific fats remain similar across seasons. For example, red-eyed vireos, *Vireo olivaceus*, preferred diets with more 18:1n9 than diets with more 18:0 or 16:0, and this diet preference did not change between nonmigratory and migratory periods (Pierce and McWilliams, 2005). In sum, migratory birds can discriminate between diets based on

certain nutritionally relevant components such as carbohydrates, amino acids, and fatty acids, although whether these nutrient preferences change with nutrient demands is not well documented.

Plant secondary metabolites (PSMs) may influence diet choice in migratory birds somewhat independently of the nutrient composition of foods. PSMs have been shown to increase fruit consumption in some passerines (Cipollini and Stiles, 1993; Bairlein and Simons, 1995) while decreasing consumption in others (Cipollini and Levey, 1997; Levey and Cipollini, 1998). Cedar waxwings, *Bombycilla cedrorum*, chose to eat the energy-rich fruit of *Viburnum opulus*, only when catkin proteins were simultaneously available as a protein source to help produce buffers against the acidic high-PSM fruits (Witmer, 2001). In addition, dietary PSM increased energy intake, intestinal mass, and BMR of rufous-collared sparrows, *Zonotrichia capensis*, but not the common diuca-finch, *Diuca diuca* (Barceló et al., 2016). The impact of the wide diversity of PSM on the diet choices of birds during migration and their ability to regain fuel stores remains a fruitful but largely unexplored question.

47.4.3 Fuel storage

47.4.3.1 Fats are the primary fuel

Birds fuel their high-intensity endurance exercise such as migratory flights primarily by metabolizing fat along with a small amount of protein (McWilliams et al., 2004; Guglielmo, 2010, 2018; Jenni-Eiermann, 2017). Migratory birds use primarily fat to fuel their long-duration flights because fat provides substantially more energy than an equal mass of either carbohydrate or protein (Blem, 1990) which makes it an ideal fuel for weight-economizing migratory birds (Bishop and Butler, 2015; Braun, 2015). Thus, in preparation for long-duration flights birds store appreciable energy mostly as fat (90+% of body mass increase) as well as key nutrients including protein (Jenni and Jenni-Eiermann, 1998; McWilliams et al., 2004; Bishop and Butler, 2015; Guglielmo, 2018) and antioxidants (Skrip et al., 2015a; Cooper-Mullin and McWilliams, 2016). The resulting hypertrophy of muscles and accumulation of substantial visceral, subcutaneous, and intramuscular fat stores has been long-known and well-studied (Blem, 1976, 1990; Bishop and Butler, 2015).

Given that storage of energy and key nutrients is necessary for all migratory birds, and especially those that travel long distances without the opportunity to stopover (Piersma, 1998), there is a type of “limiting factor” worth mentioning here—there are clear limits to how much storage mass can be carried for birds that also must fly. In general, the scaling of energy required to fly to that available from the muscles given their size declines as body size

increases (Pennycuik, 1975). This means that birds as heavy as ostriches cannot become airborne even if they had the largest of wings (Norberg, 1990; Marden, 1994). Such biomechanical constraints (i.e., high-wing loading expressed as grams body mass/cm² wing area) associated with flight have been invoked to explain why, for example, swans and ducks require a running takeoff to become airborne and fly (Lovvorn and Jones, 1994), the flightlessness of steamer ducks (Livezey and Humphrey, 1986), and why there are relatively few bird species that fly and eat only plants due to gut size limitations of herbivory (Dudley and Vermeij, 1992; McWilliams, 1999). However, such biomechanical constraints also apply to individuals that dramatically increase their energy and nutrient reserves or gut mass during key times of the annual cycle such as migration (Guillemette, 1994; Piersma, 1998; McWilliams, 1999), while not changing the size of their flight apparatus. For example, the accumulation of large body reserves during the prelaying period results in some female common eider unable to take off (Guillemette and Ouellet, 2005). Such thresholds for flightlessness seem best explained by biomechanical models that integrate wing morphology, muscle mass, and maximum power output required for take off (Marden, 1994). Thus, limitations associated with the power requirements of flapping flight constrain the extent of energy and nutrient storage that can be accumulated especially for larger birds.

47.4.3.2 Physiological challenges associated with fatty acids as fuels

Fats may be ideal fuels for weight-economizing migratory birds because of their high-energy density; however, the

metabolism of stored fats requires protein-mediated transport at most every step of the way from adipocyte to mitochondria (Figure 47.5) which can inhibit the very high rates of fat metabolism required for flight (McWilliams et al., 2004; Guglielmo, 2018). Birds are able to enhance their use of stored fats during migratory flights in several important ways (McWilliams et al., 2004; Price, 2010; Guglielmo, 2018). First, they may change the “quality” of their fat stores to enhance the rate of mobilization and oxidation. Fatty acid composition of stored fat changes in birds during migration primarily in response to diet and to preferential metabolism of certain fatty acids (Pierce and McWilliams, 2005; Pierce and McWilliams, 2014) and such changes in fat quality can affect flight performance during long-duration flights (Price, 2010; Guglielmo, 2018; Carter et al., 2020; McWilliams et al., 2020). Second, birds may increase the membrane proteins involved in transporting lipids into cells from the carriers in the blood plasma and the activity of cellular enzymes and so increase the oxidative capacity to use fatty acids (Guglielmo, 2010, 2018). Third, the acquisition of fat stores in birds during migration is associated with a coincident increase in antioxidant capacity to protect against oxidative damage caused by fat storage and use during long-duration flights (Skrip et al., 2015a; Cooper-Mullin and McWilliams, 2016; Skrip and McWilliams, 2016).

47.4.3.3 Fat quality is dynamic, affected mostly by diet, and changes seasonally during migration

The fatty acid composition of natural foods eaten by birds in migration can be quite variable (Pierce and McWilliams, 2014), migratory birds discriminate between foods based

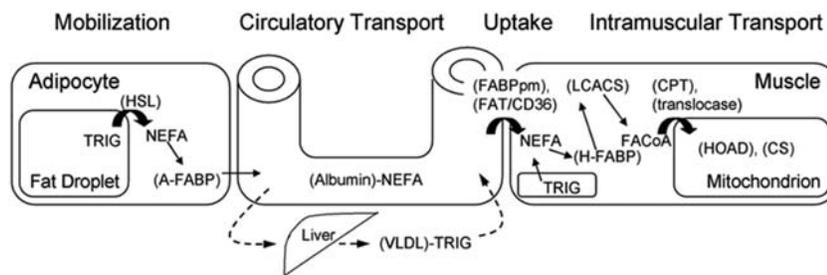


FIGURE 47.5 Lipid transport and oxidation in a bird during exercise while postabsorptive (from Price, 2010). Adipocyte triacylglycerol (TRIG) is hydrolyzed to nonesterified fatty acids (NEFAs) and glycerol through the action of hormone sensitive lipase (HSL). The extremely low-aqueous solubility of fatty acids requires the action of soluble protein carriers at every step of transport. These lipid transporters as well as key enzymes are shown in parentheses. Transport of NEFA within the adipocyte is accomplished by adipocyte fatty

acid binding protein (A-FABP). Once exported from the adipocyte, NEFA are bound by plasma albumin and carried to the muscles. In addition to using fat stores as a source of fatty acids, the liver can synthesize many fatty acids de novo or use plasma NEFA to, by esterification to glycerol, produce TRIG packaged into very low-density lipoprotein (VLDL) for release into circulation. Note that the use of plasma VLDL as a source of fatty acids for working muscles requires hydrolysis by lipoprotein lipase (LPL, not shown) at the capillary endothelium (Ramenofsky, 1990; McWilliams et al., 2004). Uptake of fatty acids from circulation into muscle is facilitated by two important fatty acid transport proteins, fatty acid translocase (FAT/CD36) and a plasma membrane fatty acid binding protein (FABPpm). Once in the muscle cells, NEFAs are bound and intracellularly transported by heart-type fatty acid binding protein (H-FABP) which also serves to increase the rate of removal of NEFA from the membrane surface. In addition to these fatty acids sourced from adipocytes and liver, TRIG can also be directly stored within muscle and be hydrolyzed to NEFA and glycerol. Intracellular NEFA are converted by long chain acyl-CoA synthetase (LCACS) to acyl Co-A (FACoA). Uptake of FACoA into the muscle mitochondrion requires several biochemical conversions carried out by two forms of carnitine palmitoyltransferase (CPT) as well as a translocase. Once in the mitochondrial matrix, FACoA enters the β -oxidation pathway and citric acid cycle where key enzymes, including 3-hydroxyacyl-CoA dehydrogenase (HOAD) and citrate synthase (CS), lead to the aerobic production of CO₂, H₂O, and ATP.

on fatty acid composition (Bairlein, 1991; Zurovchak, 1997; Boyles, 2011; Pierce and McWilliams, 2014; Rios et al., 2014), and 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, no. carbons:no. double bonds) and the essential fatty acids (e.g., 18:2n-6, 18:3n-3 along with their dominate elongation products, 20:4n-6 and 22:6n-3, respectively) with selective metabolism of certain fatty acids playing a possibly important but minor role (Blem, 1976; Pierce et al., 2005; Price and Guglielmo, 2009; Price, 2010). Note that conventional fatty acid nomenclature includes reference to the position of the double bonds relative to the methyl end of the molecule (e.g., n-6 refers to the first double bond at the sixth carbon from this end; n-6 is also referred to as omega-6 or ω -6) because the methyl end is not subject to elongation and desaturation and determines nutritional essentiality (Klasing, 1998). The implication is that migratory birds can select diets so as to achieve a certain fatty acid composition of their stored fat and muscle membranes and thereby satisfy the changing energy and nutritional demands across seasons, including that associated with endurance exercise during migration (Heitmeyer and Fredrickson, 1990; Conway et al., 1994; Bairlein, 1996; Maillet and Weber, 2006; Weber, 2009). Interestingly, behavioral preferences for certain dietary fatty acids (i.e., 18:1 and 18:2 over 18:0) were consistent across migration and nonmigration 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 (Boyles, 2011; Pierce and McWilliams, 2014). In sum, any observed seasonal changes in fatty acid composition of migratory birds are likely due primarily to diet and not to some endogenous seasonal change in diet preference for certain fatty acids or selective metabolism, although many more such studies are clearly needed.

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 on average every 10–17 days in volant birds, and at a faster rate than those in fat stores (Carter et al., 2019). Some studies have measured fatty acid composition of whole plasma [e.g., (Jensen et al., 2020)] or plasma fractions [i.e., NEFA, neutral lipids, phospholipids (Guglielmo et al., 2002c)] although we ignore such information here because seasonal changes in fatty acid composition of circulating lipids primarily reflect changes in feeding rate and diet composition rather than what is necessarily used during migratory flights when birds are fasting and must rely on stored fats (Guglielmo et al., 2002b, 2002c).

Seasonal changes in the fatty acid composition of fat stores in free-living migratory birds suggest that only a few fatty acids may be ecologically relevant and affect exercise performance (Pierce and McWilliams, 2014; Guglielmo, 2018), although given the wide variety of diets eaten by free-living birds during migration, and the relatively few such studies, such interspecific comparisons produce somewhat complicated trends (Table 47.1). In general, the 16- and 18-carbon fatty acids predominate (usually >75% of lipid stores) and the most common forms are usually the saturated 16:0 (no double bonds) and the monounsaturated 18:1n-9. During migration, 16:0 and 18:1n-9 still predominate although 16:1n-7 and two polyunsaturated fatty acids (PUFAs) considered essential for birds, 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 (Napolitano and Ackman, 1990; Egeler and Williams, 2000; Maillet and Weber, 2006; 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 ca. 20% of longer-chain 18:2n-6 and smaller amounts of 18:3n-3 PUFA (Table 47.1).

Seasonal changes in the fatty acid composition of flight muscle membrane phospholipids in free-living migratory birds confirm that only a few fatty acids may be ecologically relevant and affect exercise performance although much more information is needed (Pierce and McWilliams, 2005; Price, 2010; Guglielmo, 2018). Muscle membrane phospholipids are usually comprised of more saturated fatty acids (notably 16:0 and 18:0), less long-chain monounsaturated fatty acids (notably 18:1n-9), and more longer-chain PUFA (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., 2002c), white-throated sparrows (Klaiman et al., 2009), and semipalmated sandpipers (Maillet and Weber, 2006). Fatty acid composition of muscle membrane phospholipids changed seasonally in the two species studied to date (Table 47.1) 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., 2002c), and there was a modest increase in 18:0 during migration in both species. Klaiman et al. (2009) suggest that these differences 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

TABLE 47.1 Fatty acid composition (%) of subcutaneous fat (including neutral lipids) or whole carcass or muscle phospholipids (structural membranes) for migratory birds captured during both the nonmigration (i.e., breeding or winter) and migration (fall or spring migration) period of the annual cycle.

Species	Season	Fatty acid composition of tissue(s)							Hypothesized patterns				Tissue	Source
		14:0	16:0	16:1	18:0	18:1n-9	18:2n-6	18:3n-3	% unsaturated	18:1 18:2	16:1&18:1 18:2	n-6 ^a n-3		
Slate-colored Junco ^b (<i>Junco hyemalis</i>)	Spring migration	0.6	19.2	3.1	7.3	33.7	31.1		67.9	1.1	1.2		Whole animal	1
	Winter	0.7	14.3	3.1	6.2	27.5	41.8		72.4	0.7	0.7		Whole animal	1
White-crowned Sparrow (<i>Zonotrichia leucophrys</i>)	Spring migration	31.8	16.6	4.2	5.8	24.4	10.6	1.6	39.2	2.3	2.7	6.6	Whole animal	2
	Winter	1.5	22.3	2.8	11.6	31.1	29.3	1.0	63.2	1.1	1.2	29.3	Whole animal	2
Wood Thrush (<i>Hylocichla mustelina</i>)	Fall migration		15.2	2.4	7.6	61.6	7.6	1.3	71.6	8.1	8.4	2.6	Whole animal	3
	Breeding		24.0	4.7	13.8	34.4	12.0 ^c	3.9	55.0	2.9	3.3	2.3	Whole animal	3
Red-eyed Vireo (<i>Vireo olivaceus</i>)	Fall migration		17.5	28.0	2.5	32.8	16.1	0.2	76.9	2.0	3.8	80.5	Subcutaneous fat	4
	Breeding		29.9	2.1	6.9	39.7	14.4	4.2	56.2	2.8	2.9	3.4	Subcutaneous fat	4
White-throated Sparrow (<i>Zonotrichia albicollis</i>)	Fall & Spring migration ^d		13.5	2.1	5.9	34.0	38.0	4.1	74.1	1.0	1.1	9.3	Subcutaneous fat	5
	Winter		21.5	5.0	7.2	32.8	24.9	3.4	62.7	1.5	1.7	7.3	Subcutaneous fat	5
	Fall & Spring migration ^d		18.0		25.5	6.0	15.0 ^e	23.0 ^f	51.5	0.4	0.4	0.9	Muscle phospholipids	5
	Winter		22.1		22.0	5.9	8.1 ^e	27.9 ^f	50.0	0.7	0.7	0.5	Muscle phospholipids	5
Western Sandpiper ^g (<i>Calidris mauri</i>)	Spring migration	4.0	33.8	11.5	10.9	29.6	2.2	1.9	47.3	13.5	18.7	1.0	Subcutaneous fat	6
	Winter	6.0	36.3	8.1	17.6	18.7	2.0	2.0	34.8	9.3	13.4	0.9	Subcutaneous fat	6
Western Sandpiper ^e	Spring migration		13.8	0.6	25.7	11.9	22.3 ^h	20.3 ⁱ	59.6	6.6	6.9	1.6 ^j	Muscle phospholipids	7
	Winter		16.4	0.2	21.4	10.4	29.2 ^h	14.6 ⁱ	61.0	8.6	8.8	2.4	Muscle phospholipids	7
Canada Goose (<i>Branta canadensis</i>)	Spring migration	0.3	24.7	4.1	4.9	45.7	19.1	0.9	68.9	2.4	2.6	22.3	Subcutaneous fat	8
	Breeding	0.2	24.3	2.5	5.1	54.5	12.8	0.6	69.8	4.3	4.5	23.3	Subcutaneous fat	8
Mallard	Spring migration	1.0	17.1	2.9	6.0	51.9	19.1	2.1	74.9	2.7	2.9	9.1	Peritoneal fat	9
	Winter	1.3	21.0	3.4	7.0	44.8	18.8	3.4	68.3	2.4	2.6	5.5	Peritoneal fat	9

Only studies that measured fatty acid composition in two or more seasons (e.g., migration, nonmigration periods) are included. Fatty acid nomenclature is number of carbon atoms to number of double bonds, and the location of the first double bond from the methyl end of the fatty acid (e.g., 18:2n-6 has 18 carbons in its backbone, two double bonds, and the first double bond is at the sixth carbon from the methyl end). Fatty acids that were sometimes detected but represent <3% across all studies are excluded (i.e., 18:1n-7, 20:0, 20:3n-6, 20:5n-3, 22:5n-3) except where noted. Given the fatty acid composition of tissues, several hypotheses have been proposed to explain the pattern of change in composition during

Continued

TABLE 47.1 Fatty acid composition (%) of subcutaneous fat (including neutral lipids) or whole carcass or muscle phospholipids (structural membranes) for migratory birds captured during both the nonmigration (i.e., breeding or winter) and migration (fall or spring migration) period of the annual cycle.—cont'd

migration. Arrows denote significant changes in fatty acid composition during migration as reported by the original authors (lack of an arrow or dash indicates no significant difference between migration vs. nonmigration periods for a given species). Dashes between migration versus nonmigration rows for a given species indicate no statistical comparison was reported in the original study.

¹ Bower and Helms, 1968.

² Morton and Liebman, 1974.

³ Conway et al., 1994.

⁴ Pierce and McWilliams, 2005.

⁵ Klaiman et al., 2009.

⁶ Egeler and Williams, 2000.

⁷ Guglielmo et al. (2002a, b, c).

⁸ Thomas and George, 1975.

⁹ Heitmeyer and Fredrickson, 1990.

^a Combined n-6 fatty acids (18:2n-6, 20:4n-6) and n-3 fatty acids (18:3n-3, 20:5n-3, 22:5n-3, 22:6n-3).

^b Proportion of 18:3n-3 was not reported by season.

^c In addition, 20:4n-6, another long-chain n-6 PUFA, comprised 3.9% and 2.0% of total fatty acid composition in breeding versus fall migration periods, respectively.

^d Birds were sampled in both a fall and spring migration period, but combined here (average presented) because differences between these migration periods were relatively uncommon (exceptions for common fatty acids (>2% of total lipids): 18:0 and 18:2n-6 in muscle phospholipids, 18:3n-3 in adipose, and 18:2n-6 in intramuscular neutral lipids were different between fall versus spring migration).

^e In addition, 20:4n-6, another long-chain n-6 PUFA, comprised 8.1% and 7.5% of total fatty acid composition in winter versus migration (fall and spring) periods, respectively.

^f Proportion of 22:6n-3, another long-chain n-3 PUFA, is presented because 18:3n-3 comprised <0.5% of total fatty acid composition.

^g Males and females were separately measured during winter (December in Panama), spring migration (May in British Columbia), and fall migration (July in British Columbia), but the sexes were averaged here. Fatty acid composition of stored fat (Egeler and Williams, 2000) and pectoralis muscle phospholipids (Guglielmo et al., 2002a, b, c) during spring and fall migration were not significantly different so only fall migration is presented.

^h Proportion of 20:4n-6, another long-chain n-6 PUFA, is presented because 18:2n-6 comprised <1.9% of total fatty acid composition and unlike 20:4n-6 did not change seasonally.

ⁱ Proportion of the combined longer-chain n-3 PUFAs (i.e., 20:5 + 22:5 + 22:6) is presented because 18:3n-3 comprised <0.5% of total fatty acid composition. Significant seasonal changes were detected in only 22:5n-3 and 22:6n-3, and not 18:3n-3 or 20:5n-3.

^j The n-6/n-3 ratio for birds in fall migration was similar to that during spring migration (presented here), but was significantly lower (1.0) than during winter.

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 birds species with different migration strategies that inhabit terrestrial and/or marine ecosystems.

47.4.3.4 Physiology of protein storage and flight muscle preparation

Lean mass typically accounts for approximately one quarter of the body mass gain in passerine birds prior to migration (Klaassen and Biebach, 1994; Klaassen et al., 1997; Bauchinger and Biebach, 2001) and on average ~50% of body mass gain in several species of waders (reviewed in Lindström and Piersma, 1993). Much of the lean mass gain observed in free-living birds has been attributed to increases in the size of the gut and organs associated with flight, i.e., heart and pectoralis (flight) muscle (Marsh, 1984; Dietz et al., 1999; reviewed in Lindström and Piersma, 1993; McWilliams et al., 2004). Several hypotheses have been put forth to explain the increase in lean mass and muscle hypertrophy prior to migration including the increased power needed for flight with a larger body mass (Marsh, 1984), as a source for gluconeogenesis (Jenni and Jenni-Eiermann, 1998; Guglielmo et al., 2017) and a storage mechanism for water (Gerson and Guglielmo, 2011) (see Protein Use section below). For pectoralis (flight) muscle in particular, studies suggest the increase in size of the pectoralis muscle is the result of a concomitant increase in body size (Marsh, 1981), a result of power training before flight (Marsh and Storer, 1981), or of an endogenously regulated process that occurs independent of training or size changes (Evans et al., 1992; Bishop et al., 1998; Dietz et al., 1999).

In addition to an overall mass increase in flight muscle, the mass-specific activities of key catabolic enzymes related to the oxidation of fatty acids, overall aerobic/anaerobic capacity, burst power, and glycolytic capacity increase in flight muscle prior to migration (Marsh, 1981; Lundgren and Kiessling, 1985; Banerjee and Chaturvedi, 2016). For example, hydroxyacyl-CoA-dehydrogenase (HOAD) concentration almost doubles in the flight muscle of gray catbirds (Marsh, 1981), and CS and HOAD activity increases in reed warblers, *Acrocephalus scirpaceus*, during fattening prior to migration (Lundgren and Kiessling, 1985). Additionally, Evans et al. (1992) showed that the percentage volume of mitochondria in muscle fibers in Dunlin, *Calidris alpina*, and Sanderlings, *Calidris alba*, increased from winter to spring migration suggesting an increased aerobic capacity of the flight muscle in preparation for migration. Banerjee and Chaturvedi (2016) concluded that the pectoral muscle of premigratory, red-headed buntings, *Emberiza*

bruniceps, showed significant increases in aerobic and anaerobic capacity (CS, CCO, and MDH activity), increased fatty acid oxidation capacity [increased carnitine palmitoyl-transferase (CPT) and HOAD activity], increased glycolytic capacity (increased PFK and PK activity), and increased burst power (CK activity) compared to nonmigratory buntings (Banerjee and Chaturvedi, 2016). Thus, although the dynamics of fat stores are more extreme than that of body protein, the turnover and dynamics of body protein has important functional significance (Bauchinger and McWilliams, 2012; Bauchinger and McWilliams, 2010; Carter et al., 2019).

47.4.4 Fuel use

47.4.4.1 Patterns of change in fatty acid composition of birds during migratory stage: proposed hypotheses

Understanding how the fatty acid composition of fat stores in free-living birds changes during migration periods provides a foundation upon which to generate ecologically relevant hypotheses, informed by comparative physiology, about how fatty acid composition can affect exercise performance of migratory birds. Given that specific unsaturated fatty acids are preferentially used and more rapidly mobilized during metabolism over saturated fatty acids (Leyton et al., 1987; Raclot and Groscolas, 1995; McKenzie et al., 1998; McKenzie, 2001; Raclot, 2003; Price et al., 2008), which compensates for their relatively lower energy content and potential for ATP production (Weber, 2009; Price, 2010), one proposed hypothesis is that the proportion of unsaturated fatty acids in fat stores will increase during migration. Both studies that directly tested this hypothesis (Table 47.1) found the predicted increase in unsaturation of fat stores (Egeler and Williams, 2000; Klaiman et al., 2009), and three of the other six species studied (wood thrush, *Hylocichla mustelina*, red-eyed vireos, and mallard, *Anas platyrhynchos*) support this hypothesis. Two of the three species (slate-colored junco, *Junco hyemalis*, Canada goose, *Branta canadensis*) had a relatively similar proportion of unsaturated fatty acids in their fat stores (Table 47.1) which led Guglielmo (2018) to conclude that the most general pattern observed to date was that the proportion of unsaturated fatty acids in fat stores of migratory birds increased or stayed the same during migration (the only exception thus far is the white-crowned sparrow which had unusually high proportions of 14:0 in its fat stores during migration).

The other alternative hypotheses that have been proposed to explain the patterns in the fatty acid composition of birds during migration have focused on the essential fatty acids (18:2n-6 and 18:3n-3) and their elongation products (e.g., 20:4n-6 and 22:6n-3,

respectively). [Blem \(1980\)](#) suggested that the ratio of 18:1 to 18:2 was higher in migratory birds. Results from five of the eight species studied to date (slate-colored junco, white-crowned sparrow, wood thrush, western sandpiper, and mallard) support this alternative hypothesis ([Table 47.1](#)). [Pierce and McWilliams \(2005\)](#) noted that the ratio of long-chain monounsaturated fatty acids (16:1, 18:1) to an essential long-chain PUFA (18:2) increased during migratory periods for most of the six species studied up to that point in time. Results from six of the eight species presented in [Table 47.1](#) support this alternative hypothesis (Canada goose and white-throated sparrows were the exceptions). The potential importance of a certain ratio of n-3 and n-6 PUFAs to physiological function is long standing and is known to be strongly influenced by diet ([Hulbert et al., 2005](#)). For four of the species studied, n-3 PUFAs during both migration and nonmigration periods were <2% of all fatty acids in the whole animal (junco, white-crowned sparrow) or in separated fat stores (western sandpiper, Canada goose), and none of these four species showed the expected increase in n-6/n-3 ratio during the migration period ([Table 47.1](#)). For the other four species with more substantial n-3 fatty acids in their tissues (whole animal for wood thrush, fat stores for red-eyed vireo, white-throated sparrow, and mallard), the ratio of n-6/n-3 PUFAs consistently increased during migration compared to nonmigration periods ([Table 47.1](#)). As noted above, the changes in muscle phospholipids of birds during migration are modest compared to those observed in fat stores. The general pattern from the two studies conducted to date of reciprocal change between n-6 and n-3 PUFAs in muscle phospholipids and to a lesser extent 18:0 and 16:0 (but not fat stores; [Table 47.1](#)), provides little to no consistent support for any of the proposed hypotheses above.

Thus, the principle pattern that emerges from these few studies ([Table 47.1](#)) is that (1) there are seasonal changes in fatty acid composition of fat stores and muscle phospholipids that are associated with migration. For fat stores, the observed changes include (a) the proportion of unsaturated fatty acids either remain the same or increase during migration and (b) in particular, the relative amounts of the n-6 and n-3 PUFAs increase during migration (at least for those bird species with >2% n-3 PUFAs in their fat stores). For muscle phospholipids, reciprocal changes between primarily n-6 and n-3 PUFAs occur during migration although the direction of change differs between the two species studied to date. (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. Clearly, more studies are needed that systematically measure fatty acid composition of both fat stores (neutral lipids) and membranes

(phospholipids) in several tissues [e.g., ([McCue et al., 2009](#))] in a wide variety of migratory birds during migratory and nonmigratory seasons before these trends are confirmed and considered broadly applicable.

47.4.4.2 *The oxidative costs of burning fat as fuel*

Regulating oxidative balance is important for all air-breathing organisms such as birds because reactive pro-oxidant molecules can cause considerable cellular damage and affect health, longevity, and performance ([Halliwell and Gutteridge, 1999](#)), and 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 (RS) 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 RS production, yet they are remarkably long-lived compared to mammals ([Buttemer et al., 2010](#); [Munshi-South and Wilkinson, 2010](#); [Barja, 2014](#); [Jimenez et al., 2019](#)). Furthermore, birds use of fats 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 ([Cooper-Mullin and McWilliams, 2016](#); [Skrip and McWilliams, 2016](#)). As noted earlier, an important adaptation in Neoaves has led to the constitutive activation of the NRF2 master antioxidant response which lowers the risk of macromolecular oxidative damage in birds other than the fowl (e.g., chicken, ducks, geese ([Castiglione et al., 2020](#))). 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.

One of the challenges of studying how the antioxidant system of birds responds to the physiological challenges of migration is that the primary instigator of the oxidative challenge, increased RS production with increased metabolism, is not yet measurable in whole organisms ([Costantini, 2014](#); [Cooper-Mullin and McWilliams, 2016](#); [Skrip and McWilliams, 2016](#)). This must be inferred from measurements of key components of the antioxidant system (e.g., upregulation of antioxidant enzymes implies a response to increased RS production) and ideally simultaneous measures of RS-associated damage (e.g., upregulation

of lipid peroxidation products implies increased RS production that are insufficiently quenched by the antioxidant system). Another challenge of studying phenotypic flexibility in the antioxidant system of migratory birds is that the major site for generation of RS is the mitochondria which will vary in density and activity across tissues (Costantini, 2019) as well as with exercise and age (Cooper-Mullin and McWilliams, 2016). In addition, RS can act as both damaging molecules, as discussed above, and also as signaling molecules that can stimulate the endogenous antioxidant system (Halliwell and Gutteridge, 1999; Costantini, 2014, 2019). There are also a multitude of tests available to probe the response of the antioxidant system to ecologically relevant challenges which too often complicates comparisons across studies (Costantini, 2016, 2019; Skrip and McWilliams, 2016). Consequently, integrative studies (from mitochondria to cells to tissues to whole organism) that are also comparative (e.g., multiple tissues within the same individuals, migration state vs. nonmigration periods, multiple species that differ in migration strategy) are required to fully understand the antioxidant system of migratory birds within an ecological context. Given such integrative and comparative studies of migratory birds are largely lacking, evidence to date provides a more piecemeal view of how the antioxidant system of migratory birds changes during migration.

Does fattening and storage of oxidatively vulnerable PUFAs in preparation for migration increase RS production and an associated antioxidant response? Blackpoll warblers, *Dendroica striata*, and red-eyed vireos at a New England stopover site during fall migration (Skrip et al., 2015a), and garden warblers and barn swallows at a Mediterranean coastal stopover site during spring migration (Costantini et al., 2007), simultaneously increased their fat stores, nonenzymatic antioxidant capacity (plasma OXY), and oxidative damage (plasma d-ROMs) suggesting that fattening may incur oxidative costs and that the balance of capacity and damage may be condition-dependent. Captive-reared Northern wheatears, *Oenanthe pileata*, that were photostimulated into “migration state” in fall and that were rapidly refueling and hyperphagic increased their nonenzymatic antioxidant capacity (plasma OXY), consistent with the field studies described above, but not lipid peroxidation (red blood cell MDA) compared to control (*ad libitum*-fed) birds (Eikenaar et al., 2016). Several experimental and field studies suggest that the quality of fats consumed and stored in migratory birds affects circulating markers of oxidative damage. For example, European starlings, *Sturnus vulgaris*, fed for many months on diets with more or less n-6 PUFA had fuel stores composed of more or less n-6 PUFA, and those composed of more n-6 PUFA had consistently higher levels of plasma markers of oxidative damage (McWilliams et al., 2020). White-throated sparrows that consumed diets with more PUFA

had increased circulating oxidative damage (d-ROMs) although when given choices between diets that differed only in available antioxidants (vitamin E) these birds did not prefer antioxidant-rich diets when consuming more dietary PUFA (Alan and McWilliams, 2013). Common blackbirds captured at a stopover site in northern Germany had a higher plasma fatty acid peroxidation index, higher nonenzymatic antioxidant capacity (OXY), but similar lipid peroxidation compared to sympatric resident blackbirds (Eikenaar et al., 2017a). The lack of correspondence between plasma fatty acid composition and that of fat stores and cell membranes in the same individuals (as described earlier) may explain why oxidative damage did not change with plasma peroxidation index in this latter study. Hudsonian godwits, *Limosa haemastica*, preparing for a very long-duration migratory flight increased total antioxidant capacity and reduced oxidative damage (TBARS) but did not change metabolic enzyme activity (Gutiérrez et al., 2019). In sum, migratory birds seem to build some component of their antioxidant capacity concomitantly with fat stores and increased oxidative damage may be an inevitable consequence of increasing (or maintaining more) fat stores, especially if they are composed of mostly PUFA.

During migratory flight, do birds upregulate antioxidant capacity and thus avoid the energetically expensive repair of damaged structures? In two recent reviews, Cooper-Mullin and McWilliams, 2016 and Skrip and McWilliams, 2016 reported that free-living birds during migration, or captive birds that flew for certain periods of time, often exhibit an increase in damage to lipids and/or proteins despite an often upregulated antioxidant system composed of antioxidant enzymes, nonenzymatic sacrificial molecules, and dietary antioxidants. For example, homing pigeons, *Columba livia*, that flew further (200 km) had more oxidative damage and less serum nonenzymatic antioxidant capacity than those that flew less far (60 km) when blood was sampled w/in 15 min of returning to the roost (Costantini et al., 2008). European robins, *Erithacus rubecula*, caught during nocturnal migratory flight had elevated markers of circulating oxidative damage to proteins (protein carbonyls) compared to resting robins even though the former also had higher circulating levels of glutathione peroxidase (GPx), an enzymatic antioxidant (Jenni-Eiermann and Jenni, 1991; Jenni-Eiermann et al., 2014). In contrast, migratory common blackbirds had higher nonenzymatic antioxidant capacity (OXY) but similar lipid peroxidation compared to sympatric resident blackbirds (Eikenaar et al., 2017a). Captive zebra finches, *Taeniopygia guttata*, flown for 2 h/day for many weeks increased the coordination between the enzymatic (GPx) and nonenzymatic (OXY) components of the antioxidant system while oxidative damage remained low and similar to sedentary finches (Cooper-Mullin et al., 2019). Plasma

markers of oxidative damage did not change in European starlings over the course of daily flying for several weeks, nor before and after a single long flight, in part because of upregulation of components of their antioxidant system (Frawley et al., 2021; McWilliams et al., 2020). Thus, upregulation of the antioxidant system and, at least in one case, increased coordination of key components of the antioxidant system occurs during repeated long-duration flights, and in some but not all cases, this seems to avoid the potential increase in oxidative damage with exercise. These studies also provide an important reminder that the response of individuals to an oxidative challenge involves an interacting, multicomponent antioxidant system (Costantini, 2019).

Given that some oxidative damage may occur during a migratory flight or enforced exercise, are migratory birds able to recover from this damage in an appropriately short period of time? Migratory birds at stopover sites seem to be able to in part recover from any oxidative damage that may have occurred during migration. For example, European robins that rested during the day had lower protein damage levels (protein carbonyls) than those caught during active nocturnal flight presumably because they had time to remove or repair damaged proteins (Jenni-Eiermann and Jenni, 1991). Individual Garden Warblers sampled repeatedly at a spring stopover reduced circulating lipid peroxidation levels over time (Skrip et al., 2015a). Thus, if oxidative damage occurs, then migratory birds seem capable of repairing this damage in a relatively reasonable amount of time (i.e., days not weeks) given their usual stopover durations, although many more such studies are needed that track recovery of individuals after long-duration flights.

Does consumption of dietary antioxidants affect the upregulation of the endogenous antioxidant system associated with migratory flights? In theory, the costs of upregulating the endogenous antioxidant system could be reduced if dietary antioxidants could quench RS producing during flight (Costantini et al., 2010a; Pamplona and Costantini, 2011; Costantini, 2014). Recent experimental evidence demonstrated for the first time that an ingested fat-soluble dietary antioxidant (Vitamin E) was absorbed and transported to the mitochondria in the flight muscles of a songbird within 22.5 h, but only if the birds were regularly flying each day (Cooper-Mullin et al., 2021). Thus, actively migrating songbirds that ingest dietary antioxidants during the day at a stopover, in this case fat-soluble antioxidants, would have these available in their mitochondria to protect against RS produced during subsequent nocturnal flight(s). Several experimental studies have directly manipulated the amount and type of dietary antioxidant(s) available to migratory birds, or captive birds exposed to regular exercise, and then measured the response of the antioxidant system often in

relation to some ecologically relevant challenge (e.g., flight, high-PUFA diets). For example, European starlings fed diets supplemented or not with anthocyanins had similar plasma nonenzymatic antioxidant capacity (OXY) and oxidative damage (d-ROMs), but circulating uric acid was higher in individuals fed the low-antioxidant diet (Frawley et al., 2021). Likewise, zebra finches fed more or less anthocyanins and exercised (daily 2-h flying for months) or not had similar plasma nonenzymatic antioxidant capacity (OXY), antioxidant enzyme activity in liver (GPx, catalase, superoxide dismutase) and oxidative damage (d-ROMs); plasma uric acid was not measured in this study (Skrip et al., 2016). The suggestion from these studies is that when birds consume too little dietary antioxidants, this may not directly affect upregulation of antioxidant enzymes but may increase protein catabolism and thus circulating uric acid when flying for long durations and/or consuming high-PUFA diets. There is also evidence that consumption and physiological use of dietary antioxidants in birds may depend on their nutritional needs, energy demands, and type of dietary antioxidant (Costantini et al., 2010b; Beaulieu and Schaefer, 2013). Clearly, much more work is needed to adequately understand the role of dietary antioxidants in enabling migratory birds to maintain oxidative balance.

47.4.4.3 Carry over effects from winter to breeding

For the many birds that breed in seasonal environments, migration to more benign areas during winter has evolved along with the need to acquire energy and nutrient stores to fuel migration and, in the spring, also prepare for breeding. Life-history theory predicts that major annual cycle events such as breeding and migration are separated in time (and often space) to effectively distribute the total costs over time and to maximize the benefit-to-cost ratio given seasonal changes in resources (Lack, 1954; Dingle, 1996). However, such temporally separated events are not thereby independent in that, for example, condition of animals during one annual cycle event (e.g., in winter or on migration) can affect subsequent events (e.g., migration, reproduction). These so-called carry-over effects (Marra et al., 1998; Holmes, 2007; Harrison et al., 2011; Mitchell et al., 2011; Drake et al., 2013; Paxton and Moore, 2015) reveal links between annual cycle events that affect populations and individual fitness (Harrison et al., 2011). It has long been recognized that the extent of nutrient acquisition during spring, often prior to initiating migration, largely determines reproductive success in many waterfowl species (Ryder, 1970; Drent and Daan, 1980; Alisauskas and Ankney, 1992). As such, waterfowl provide many examples of the importance of carry-over effects (Harrison et al., 2011), the acquisition and storage of nutrient reserves at

one time or place (e.g., during the nonbreeding period) that are then used as resources at a later time and place (e.g., for breeding) (Warren et al., 2013; Sedinger and Alisauskas, 2014). Knowing the location and timing of nutrient storage during the nonbreeding period often has important conservation implications (Raveling and Heitmeyer, 1989; Abraham et al., 2005; Stafford et al., 2014; Alisauskas and Devink, 2015). Despite the importance of carry-over effects especially in migratory animals, a major gap in our understanding of these effects involves identifying the proximate causal links. All previous work has focused on how energy in the form of fat, protein, or carbohydrate stores may provide such linkages, whereas no previous studies have focused on antioxidants even though they have been proposed as an important currency that underpins life history tradeoffs (Catoni et al., 2008; Alonso-Alvarez et al., 2010) and potentially carry-over effects (Harrison et al., 2011).

Dietary antioxidants are likely an important, yet understudied, currency for carry-over effects in birds especially during spring migration for primarily three reasons. First, dietary antioxidants play important roles during the reproductive season in that breeding effort of birds promotes oxidative damage (Alonso-Alvarez et al., 2010) and domestic fowl supplemented with dietary fat-soluble antioxidants gain fitness advantages (Koutsos et al., 2003; Royle et al., 2003; McGraw et al., 2005; Williamson et al., 2006). Additionally, developing egg embryos are protected from external oxidative challenges if the females are able to deposit antioxidants in the yolk (Watson et al., 2018). Consistent with this important role of dietary antioxidants during reproduction, European starlings fed high-anthocyanin diets during spring had more elevated testosterone and more sustained breeding behaviors compared to individuals fed less antioxidants (Carbeck et al., 2018). Second, the increased metabolic rate associated with long-duration migratory flights produces pro-oxidants that must be quenched to avoid damage (Costantini, 2008; Costantini et al., 2007, 2008), and for spring migrating birds, this may reduce the antioxidant capacity available for subsequent reproduction. Importantly, dietary anthocyanins can support the metabolic function of glucocorticoids (corticosterone) and so control potential negative effects of excessive secretion of these hormones especially during long-duration flights (Casagrande et al., 2020). Third, fat-soluble antioxidants can be deposited in fat stores and so migratory birds could strategically store antioxidants prior to departure (Costantini et al., 2007), and balance their use during migratory flights so as to retain enough for investment into eggs that can subsequently enhance offspring survival and fitness (Blount et al., 2003; McGraw et al., 2005; Skrip et al., 2016). Clearly, much more study is needed to determine how female migratory birds contend with the

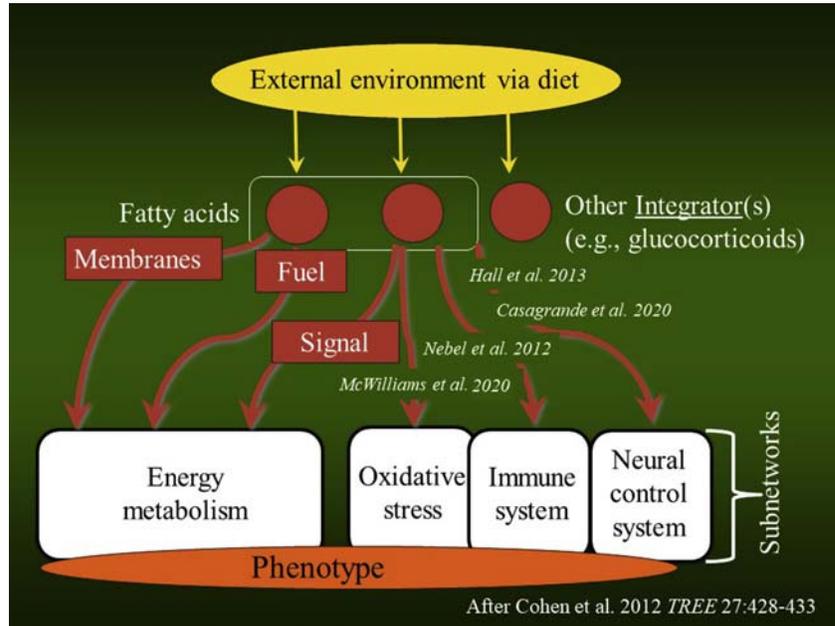
oxidative costs of migratory flights in spring while also preparing for subsequent breeding and egg laying.

47.4.4.4 *Fat quality matters*

In theory, selectively eating and hence storing certain long-chain unsaturated fatty acids may be advantageous because (1) such fatty acids may be preferentially mobilized and metabolized more quickly (fuel hypothesis); (2) such fatty acids may affect composition and key functions of lipid-rich cell membranes (membrane hypothesis); 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) (Figure 47.6). Below we briefly discuss aspects of each of these hypotheses and how they may relate to the observed effect on exercise performance of migratory birds. Other reviews should be consulted for more thorough discussion of these hypotheses and the evidence (Weber, 2009; Guglielmo, 2010; Price, 2010; Pierce and McWilliams, 2014; Guglielmo, 2018). Although we separately describe these three hypotheses for convenience, they are not mutually exclusive.

The fuel hypothesis states that enhanced exercise performance occurs because certain fatty acids are more quickly mobilized and metabolized, and this can occur in several ways (Figure 47.5): selective mobilization from adipocytes, enhanced transport to target tissues, selective uptake by and transport within muscle cells, and/or enhanced oxidation and production of ATP (McWilliams et al., 2004, Price, 2010; Guglielmo, 2018). Several studies across taxa have shown that mobilization of shorter chain SFAs and fatty acids with more double bonds (e.g., 18:2n-6) was more rapid from fat stores in rats, fish, and birds (Raclot and Groscolas, 1995; Sidell et al., 1995; Hulbert et al., 2005; Price et al., 2008; Guglielmo, 2018). Isotope tracer studies that track ingested nutrients to breath CO₂ confirm that long-chain unsaturated fatty acids are oxidized more rapidly than their saturated counterparts (e.g., 18:1 vs. 18:0) (McCue et al., 2010). Once mobilized from fat stores, fatty acids require solubilization and intracellular translocation by the family of fatty acid binding proteins (FABPs) such that an increase in the number and action of FABPs present in the cell membranes and cytosols of muscle cells increases oxidative capacity (Guglielmo et al., 1998, Guglielmo et al., 2002a; McFarlan et al., 2009; Guglielmo, 2010, 2018). Furthermore, within flight muscle cells, the rate of CPT catalysis (Figure 47.5) was relatively higher for fatty acids with more double bonds compared to their saturated forms (e.g., 18:2 and 18:3 vs. 18:0) (Price et al., 2011; Guglielmo, 2018). This evidence supports the fuel hypothesis in that certain fatty acids such as 18:2n-6

FIGURE 47.6 A simplified schematic of a physiological regulatory network that indicates how certain dietary fatty acids serve as key “integrators” that interact with multiple systems (subnetworks) and each other, thereby ensuring an appropriate match between phenotype and environmental conditions. Dietary fatty acids have been shown to influence the immune system (Nebel et al., 2012), neurogenesis (Hall et al., 2013), and neuroendocrine control of metabolism (Casagrande et al., 2020), and oxidative status (McWilliams et al., 2020). The three hypotheses (membrane, fuel, and signal), and the evidence that supports or refutes them are described in the text. After Cohen et al. (2012).



are metabolized more quickly at many steps of fatty acid oxidation although whether this is primarily responsible for enhanced exercise performance during migration periods is not yet clear (Guglielmo, 2010; Price, 2010) and discussed in the next section.

The membrane hypothesis states that the fatty acid composition of membrane phospholipids can effect key aspects of membrane structure and function (Hulbert and Else, 1999; 2000; Hulbert et al., 2005) and thus exercise performance of an organism (Valencak et al., 2003; Maillet and Weber, 2006; Maillet and Weber, 2007; Weber, 2009; Price, 2010). As described above, fatty acid composition of diet influences the phospholipid composition of muscle membranes in vertebrates, and this effect of diet on membrane composition is especially strong for dietary n-3 and n-6 compared to other fatty acids (e.g., shorter-chained saturated fatty acids (Hulbert et al., 2005; Maillet and Weber, 2006; 2007). Accordingly, the fatty acid composition of cell and subcellular membrane phospholipids converged with that of diet in migrating shorebirds that consumed marine invertebrates laden with n-3 PUFAs (Maillet and Weber, 2006, 2007). An increase in membrane PUFAs has potential functional importance for exercising animals in that (1) n-3 and/or n-6 PUFAs increase the fluidity and permeability of cell membranes (Stillwell and Wassall, 2003; Weber, 2009) and (2) n-3 and/or n-6 PUFAs are known to influence the activity of membrane-bound proteins and enzymes (e.g., UCP and -ATPases) which could affect efficiency of aerobic respiration (Hulbert and Else, 2000; Infante et al., 2001; Hulbert et al., 2005; Maillet and Weber, 2006, 2007; Gerson et al., 2008).

The signal hypothesis states that certain dietary fatty acids (most notably the n-3 and n-6 PUFAs) directly act as natural ligands for receptors that regulate the expression of genes associated with lipid metabolism (McClelland, 2004; Bordoni et al., 2006; Maillet and Weber, 2006; 2007; Weber, 2009). In particular, PUFA directly bind to and regulate the activity of peroxisome proliferator-activated nuclear receptors (PPARs) which are well known to stimulate expression of genes involved in fatty acid oxidation (Hochachka and Somero, 2002; Pawar et al., 2002; Zhang et al., 2004; Narkar et al., 2008; Weber, 2009), although the specific mechanism of action depends on the type of PPAR (Feige et al., 2006). PPAR α and β stimulate fatty acid oxidation and transport whereas PPAR γ is involved in lipid storage and adipocyte differentiation (Desvergne and Wahli, 1999; Nagahuedi et al., 2009). PPARs exhibit high affinity for n-3 PUFAs (Bordoni et al., 2006) and the upregulation of rate-limiting enzymes involved in aerobic metabolism by certain fatty acids such as 18:2n-6 (Sidell et al., 1995; Egginton, 1996; McKenzie, 2001) enables more rapid production of ATP during exercise (Guglielmo et al., 1998, 2002a; McWilliams et al., 2004). The effects of PUFAs on gene expression depend largely on the cellular concentration of PUFA, although it is not yet clear if a specific amount or ratio of dietary n-3 and n-6 fatty acids is optimal (Bordoni et al., 2006). The direct binding of certain dietary PUFAs to PPARs that then activate genes regulating lipid metabolism provides an example of “natural doping” whereby exercising animals can eat certain PUFAs, upregulate key aspects of lipid metabolism, and so enhance their exercise performance (Maillet and Weber, 2006, 2007, Weber, 2009). Such natural doping on n-3

PUFAs has been proposed for semipalmated sandpipers as they pause at key stopover sites during fall migration (Maillet and Weber, 2007). Whether this is a most interesting but unusual case in migratory birds deserves further investigations. In addition, these same essential PUFAs are used to build eicosanoids (e.g., prostaglandins, thromboxanes, leukotrienes, and lipoxins) that act locally on the cells that produce them or are nearby, and in this sense they are classified as hormones with signaling properties. At present, the importance of eicosanoids in birds during migration has not been directly studied and only proposed as an explanation (Klaiman et al., 2009; Carter et al., 2020), although their involvement in regulating a wide variety of physiological systems (e.g., immunity, development and growth, thermoregulation, and oviposition) suggests some attention may be worthwhile.

47.4.4.5 Testing the fuel, membrane, and signal hypotheses

Empirical evidence somewhat supports all of 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 (Leyton et al., 1987; Geiser and Learmonth, 1994; Raclot and Groscolas, 1995; McKenzie et al., 1998; Wagner et al., 2004; Pierce et al., 2005; Price et al., 2008; Price and Guglielmo, 2009; Petersson et al., 2010). Our own recent work and that of colleagues has confirmed that songbirds with stored fat composed of more n-6 PUFA have improved exercise performance during short-term intense exercise (Pierce et al., 2005; Price and Guglielmo, 2009; Price, 2010). Price and Guglielmo (2009) used a cleverly designed sequence of feeding and fasting protocols to produce white-throated sparrows with fat stores and muscle membranes composed of different fatty acids. Consequently, they were able to demonstrate that the enhanced exercise performance of sparrows was associated with the fatty acid composition of fat stores rather than muscle membranes. The implied mechanism for the enhanced performance, in this case higher peak metabolic rates, included both faster mobilization rates of n-6 fatty acids from adipose as well as selective uptake of fatty acids into muscle cells and intramyocyte transport (Price and Guglielmo, 2009; Price, 2010). As correctly pointed out by Price (2010), a crucial untested assumption of this proposed mechanism for producing higher peak metabolic rates is that rate of fatty acid supply, and not some other factor such as oxygen supply or oxidative capacity, is the physiological limitation responsible for these whole-animal changes in exercise performance. In vivo studies that examine *selective* uptake and intracellular transport rates of certain fatty acids in muscle

cells during exercise would be quite informative, especially if combined with diet and feeding regime manipulations that allow the effect of fatty acid composition of fat stores to be isolated from that of the other mechanisms.

Birds during migration, however, may be optimizing energy efficiency rather than maximizing metabolic rate and so may not need to maximize rate of fatty acid supply, as is often assumed. Energy efficiency in this case refers to flying further for a given amount of fuel energy or flying as far but expending less fuel energy. A possible mechanism for such enhanced efficiency that is consistent with the fuel hypothesis includes, for example, the documented higher transport rates of unsaturated fatty acids reducing the energy needed for transport of fatty acids (Price, 2010). Evidence in support of this enhanced flight efficiency idea comes from a study of European starlings from a migratory population in southern Germany that were fed for many months specially formulated diets that differed only in the amount of n-6 and n-3 fatty acids—the fatty acid composition of their fat stores was likewise different as expected. During the fall migration period, and after several weeks of flight-training in a wind tunnel, starlings composed of more n-6 (and n-3) PUFA used substantially less energy (ca. 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). This experimentally demonstrated that migratory birds can enhance fuel economy when composed of more n-6 PUFAs, a result consistent with the fuel hypothesis although it does not by itself definitively refute the other proposed hypotheses. As discussed further below, this 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 having 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 certain types of PUFA and metabolic rate (Wu et al., 2001, 2004; Turner et al., 2003).

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 was 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 refuted the membrane hypothesis. For example, as discussed above, 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) 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 that differed in the MUFA, n-3, and n-6 composition of flight muscle membranes. They found effects of membrane composition on activity of several flight muscle oxidative enzymes in warblers but not on multiple whole-animal performance measures including BMR, peak metabolic rate, and energy expenditure and duration of wind tunnel 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 that were consistent over the 4-month experiment (Carter et al., 2020). Carter et al. (2020) found effects of membrane composition on activity of several flight muscle oxidative enzymes (Carter et al., 2021) but also on multiple whole-animal performance measures including BMR, peak metabolic rate, and rate of energy expenditure during >2-h wind tunnel flights. Specifically, birds with higher concentrations of 18:2n-6 in membranes and fat stores had higher BMR and peak metabolic rates, although this pattern was evident early in the fall and not later in the fall 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 suborganismal measures are affected by 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.

The natural doping hypothesis proposes that birds (in this case shorebirds) during migration enhance their exercise performance by selecting high n-3 diets (marine prey such as *Corophium volutator* in the case of semipalmated sandpipers) and thereby (a) incorporate these PUFAs into membrane phospholipids and affect membrane function (membrane hypothesis), and (b) (signal hypothesis) binding of n-3 PUFAs to PPARs that then activate the expression and activity of key genes and enzymes that instigate the metabolic pathways involved in enhancing the oxidative metabolism of fatty acids (Maillet and Weber, 2006, 2007, Weber, 2009). Some support for the mechanisms proposed by the signal hypothesis comes from recent studies of Gray catbirds sampled throughout their annual cycle. During premigratory fattening periods, catbirds had increased mRNA expression of certain PPARs and key target genes (Corder et al., 2016; DeMoranville et al., 2019), and these PPAR isoforms from catbirds were activated by certain fatty acids (i.e., 18:1, 20:5n-3) tested on mammal cell lines (Hamilton et al., 2018). Whether dietary n-3 fatty acids (and n-6 PUFA) act as important natural ligands and so determine these seasonal changes in PPAR expression in migratory catbirds remains unknown (Corder et al., 2016; DeMoranville et al., 2019). In one of the most comprehensive and relevant tissue-to-whole animal experimental studies of migratory birds to date, yellow-rumped warblers fed more n-3 PUFAs and that had membranes composed of more n-3 PUFA decreased PPAR- β mRNA abundance, activity of muscle oxidative enzymes, and overall oxidative capacity, and this was not associated with any whole-animal performance effects, in direct opposition to the natural doping, signal hypothesis (Dick and Guglielmo, 2019). The potential to enhance whole-animal performance as proposed by the signal hypothesis may also pertain to the essential n-6 PUFAs. As noted earlier, Carter et al. (2020) concluded that the results from their study of European starlings that were fed and composed of more n-6 PUFAs, and then flown for long durations in a wind tunnel, were most consistent with the signal hypothesis. These same starlings composed of more 18:2n-6 increased the expression of PPAR α in the liver and LPL in the pectoralis; however, this occurred only in starlings that flew daily for 2 weeks in the wind tunnel and not untrained birds fed the same diet, and no such effect of diet was observed on the expression of other PPAR transcription factors, PGC-1 coactivators, and key metabolic genes (i.e., CD36, MCAD, CS, PLIN2, and avUCP) in the pectoralis muscle and the liver (DeMoranville et al., 2020). The dependency of the signaling effect of n-6 PUFA on flight training suggests something more complex than a simple direct diet influence.

The three proposed hypotheses (fuel, membrane, and signal) are not mutually exclusive, and each has garnered some support. Given that the use of fats as fuel requires storage, protein transport at many steps of the ways, up- and downregulation of metabolic enzymes (Figure 47.5), and that dietary fatty acids affect the composition of stored fat as well as membranes and can act as signaling molecules, we should not be surprised that this multifaceted fat metabolism system can be affected by diet and exercise in multiple ways. We know from both experimental and correlative studies that the fatty acid composition of diet largely determines that of fat stores and muscle membranes and that there is seasonal variation in the composition of the fat stores and membranes. Thus, the study of how dietary fatty acids affect fat metabolism at large as well as exercise performance in birds during migration presents a very tractable and ecologically relevant opportunity to test these various hypotheses. Especially intriguing and potentially informative are recent transcriptomic analyses (Dick, 2017) that revealed upregulation of key fatty acid metabolism pathways in captive yellow-rumped warblers in fall (vs. winter) while 45 other metabolic pathways were downregulated including those related to muscle growth, inflammation and immune function, and hormone signaling. The extreme challenges of migration may require such metabolic tradeoffs (Guglielmo, 2018), as has also been suggested in terms of an energy savings-oxidative cost tradeoff for birds during migration (McWilliams et al., 2020).

47.4.4.6 Fatty acid transport really matters

Metabolizing fatty acids at very high rates is quite difficult compared to the alternative, more soluble, carbohydrate and protein fuels used predominately by mammals during exercise (Guglielmo, 2010, 2018). As discussed in the next section, fatty acid oxidation in the flight muscles of migratory birds is enhanced by increasing the activity of key mitochondrial enzymes (e.g., HOAD and CPT) although the primary metabolic limitation seems more related to fatty acid transport through the circulation and its uptake by muscle cells (Guglielmo, 2010, 2018). The hypothesized mechanisms for effective and adequately rapid transport of fatty acids from fat stores into muscle cells in migratory birds has been extensively discussed elsewhere (McWilliams et al., 2004; Guglielmo, 2018) and above. In brief, migratory birds in general and birds during active migration, in particular, rely somewhat on augmented circulatory pathways to enhance fatty acid utilization, but the more important determinants of fatty acid flux seems to occur at the muscle cell level—specifically, protein-mediated transport of fatty acids across the muscle cell membrane [e.g., fatty acid translocase (FAT/CD36), plasma membrane fatty acid binding protein (FABPpm)] and

within cells [e.g., heart-type fatty acid binding protein (H-FABP)] seems most likely to limit the overall rate of fatty acid metabolism in migratory birds (Figure 47.5). See Bishop and Butler (2015) for a more thorough treatment of this topic.

47.4.4.7 Protein use during flight and water balance

It is well established that birds catabolize lean mass as a protein source during flight with significant reductions in pectoralis muscle, leg muscle, digestive organs, and liver masses among other organs (Åkesson et al., 1992; Bauchinger and Biebach, 1998, 2001; Battley et al., 2000). Unlike lipids and carbohydrates, birds have no specific storage form for proteins (except very small endogenous amino acid pools). Proteins are stored in functional tissue such as flight muscle, digestive organs including the liver, and even skin (Marsh, 1984; Bauchinger and Biebach, 1998; Battley et al., 2000). Thus, the use of protein during flight causes a concomitant loss of structure and/or function. In red knots, *Calidris tenuirostris*, all organs (flight muscle, leg muscle, intestines, liver, kidney, stomach, heart, spleen, and skin) except brain and lungs decreased in mass during their long-duration flight from Australia to China (Battley et al., 2000). This lean mass loss in organs coincided with a 40% decrease in mass-specific BMR after migration suggesting a significant functional consequence in the organs contributing to BMR (Battley et al., 2000).

Several hypotheses explain why birds utilize protein during long-duration flights including the need for proteins as an adaptive reduction in muscle mass to conserve energy (Pennycuik, 1998), as intermediaries in the citric acid (Kreb's) cycle (Jenni and Jenni-Eiermann, 1998; Jenni-Eiermann, 2017), in tissue maintenance and repair (Lindström and Piersma, 1993; Guglielmo et al., 2001), and as a water source (Gerson and Guglielmo, 2011; Jenni-Eiermann, 2017; Groom et al., 2019). It is well understood that exercising mammals use proteins as a fuel source for gluconeogenesis and as intermediaries in the citric acid cycle (Aragón, 1981; Dohm, 1986). Jenni and Jenni-Eiermann (1998) concluded that the use of protein for the maintenance of citric acid cycle intermediaries is important in permitting the high rates of fatty acid oxidation required to meet the increased metabolic demands of long-duration flight in migratory birds. Guglielmo et al. (2001) found elevated plasma creatine kinase (CK) in migrating western sandpipers, and bar-tailed godwits as compared to nonmigrants in the same year suggesting that birds undergo a moderate amount of flight-induced muscle damage during migration and therefore must repair this damage before continuing their migration. However, the extent to which this damage impacts the recovery time at stopover sites and ultimately the pace of migration is still unclear.

Models of water use during flight suggest that water may be an important factor in limiting flight duration (Carmi et al., 1992; Klaassen, 1996). Protein catabolism provides 5.9 times more water per kilojoule than lipid catabolism (Jenni and Jenni-Eiermann, 1998) and thus can provide an invaluable source of water for fasting, flying birds (Gerson and Guglielmo, 2011; Jenni-Eiermann, 2017; Groom et al., 2019). The rate of protein catabolism during flight has been shown to be directly related to ambient relative humidity. Gerson and Guglielmo (2011) found that Swainson's thrushes *Catharus ustulatus* flown in a wind-tunnel at moderately low-ambient humidity had greater lean mass loss, increased metabolic water production, and higher uric acid levels (indicative of protein catabolism) than birds flown in moderately high humidity. Additionally, Groom et al. (2019) found that lean mass loss in birds exposed to low and high-ambient humidity was independent of metabolic rate in Swainson's thrushes with flown birds having similar protein catabolism as birds at rest. Birds have been shown to be effective at controlling blood plasma volumes regardless of thermal dehydration or dehydration incurred during flight (Carmi et al., 1993). Gerson and Guglielmo (2011) suggest that birds may utilize the protein-for-water strategy in an effort to maintain osmotic homeostasis since the plasma osmolarity of the thrushes was unaffected by ambient humidity during flight.

Although several species of birds have been shown to be sensitive to dehydration in ambient temperatures below 20°C in wind-tunnel studies (Torre-Bueno, 1978; Giladi and Pinshow, 1999; Engel et al., 2006), studies of trans-Saharan migrants suggest that energy savings may supersede any limitations set by water loss as migrants fly at higher ambient temperatures and lower humidity than expected given our current understanding from wind tunnel studies (Schmaljohann et al., 2008, 2009). Notably, access to drinking water may be a factor in a bird's decision to depart a stopover site and continue migration. For example, Garden warblers at a spring migration stopover site in the Mediterranean Sea that were captured with large fat stores and then given no access to water, were more likely to depart that night (i.e., had the greatest zugunruhe activity) compared to warblers with similar fat loads and access to water as well as those with less fat loads regardless of access to water (Skrip et al., 2015b). The degree to which freely available water influences departure of birds from a stopover site deserves further study, especially given the impact of climate change on worldwide water distribution.

The amount of protein used during long flights and the sources of these proteins appears to also be influenced in part by the level of fat storage, at least in passerines. Garden warblers, pied flycatchers *Ficedula hypoleuca*, Willow warblers *Phylloscopus trochilus*, and Barn swallows consumed protein primarily from flight muscle when fat stores comprised greater than 20% of total dry body mass.

However, when fat stores reached critically low levels (i.e., 5–10% of total dry body mass), protein catabolism greatly increased and the protein mass of all organs decreased with significant reductions in the digestive organs as well as flight muscle masses (Schwilch et al., 2002). This pattern of protein use suggests an adaptive response in birds to the interaction of fuel use, energy requirements, and flight capability. When fat stores are adequate, reduction in flight muscle coincides with reductions in overall body mass (thus conserving energy) without compromising flight capability. However, when fat stores are nearing depletion, protein requirements increase and so birds rely more heavily on protein stores in nonuse organs such as the digestive tract as well as flight muscle. Although this is an adaptive response to meeting the energetic needs of the bird during flight, it appears to be at the detriment of flight capability.

47.4.4.8 Rebuilding protein stores after flight

The loss of proteins from structural and functional tissue during flight naturally requires that birds replenish what has been lost prior to their next flight. Birds arriving at a stopover site replenish protein reserves first before storing fat (Atkinson et al., 2007). For example, mass gain in red knots at Delaware Bay, USA, comprised ~15% fat when birds were below 133 g and ~84% fat above 133 g suggesting that birds have a critical body mass level where they must first rebuild protein stores before they are able to begin refattening (Atkinson et al., 2007). Since much of the protein used during flight is taken from digestive organs, fasted birds must rebuild their guts before returning to maximum digestive capacity and food intake (McWilliams and Karasov, 2001; Gannes, 2002; Pierce and McWilliams, 2004; Muñoz-García et al., 2012). Passerine birds require 1–3 days for their digestive system to fully recover from fasting (Karasov and Pinshow, 2000; McWilliams and Karasov, 2001; Gannes, 2002) and this recovery may be diet-dependent (Pierce and McWilliams, 2004; Muñoz-García et al., 2012). For example, fasted and food restricted white-throated sparrows fed a fruit diet (low protein) were unable to increase food intake rates to pre-fasted levels and thus regain body stores in three days of refeeding whereas sparrows fed a grain diet (high protein) were able to fully recover food intakes to prefast levels and regain energy stores in 24 h (Pierce and McWilliams, 2004). Muñoz-García et al. (2012) fed blackcaps, *Sylvia atricapilla*, diets containing 3% (low) and 20% (high) protein with labeled leucine to determine the extent to which these birds relied on dietary (exogenous) or endogenous sources of protein to rebuild their guts. Blackcaps fed a low-protein diet incorporated less exogenous protein into their tissue than blackcaps fed the high-protein diet. Interestingly, blackcaps incorporated more

exogenous protein into their gut than their pectoral muscle but were unable to rebuild their intestines at a similar rate as the blackcaps fed a high-protein diet (Muñoz-García et al., 2012). However, the rate of rebuilding of protein stores (i.e., gut tissue) in migrating blackcaps was influenced by the availability of drinking water when the water content of food was low (Mizrahy et al., 2011). Blackcaps with limited access to drinking water and fed food with low-water content had no increase in lean mass nor fat mass during a simulated stopover period whereas birds provided with unlimited access to drinking water and/or food with high-water content were able to gain lean and fat mass (Mizrahy et al., 2011). This finding, along with that of Skrip et al. (2015) discussed above, suggests that freely available water at stopover sites may play a much larger role than previously thought in enabling birds to rebuild energy and protein stores and complete migration. A full understanding of the interaction between the protein-for-water strategy and the availability of drinking water at stopover sites deserves further investigation.

47.4.5 Temperature regulation during flight

Much of what is known about the body temperature fluctuations of birds during flight has been from wind tunnel studies of captive birds in short duration flights (Aulie, 1971; Torre-Bueno, 1976; Hudson and Bernstein, 1981). For example, pigeons increase their core body temperature (hyperthermia) during short-duration wind tunnel flights at ambient temperatures between 25 and 29°C (Aulie, 1971), and this hyperthermia seems to limit the length of flight bouts in pigeons and European starlings (Aulie, 1971; Torre-Bueno, 1976). More recently, studies on wild birds using implanted data loggers have found that hyperthermia may play a much greater role in limiting the duration of migratory flights than previously assumed (Guillemette et al., 2016, 2017); however, this may only be relevant for the larger aquatic species with continuous, fast-flapping flight (Guillemette et al., 2017). Common eiders allow their body temperatures to rise on average 1°C by the end of a typical flight and spend a significant portion (36%) of their daily time budget behaviorally cooling their body temperatures from previous flight bouts (Guillemette et al., 2017). Thus, eiders are heat dumping in between migratory flights. Less is known about temperature regulation to avoid hyperthermia during migratory flight in passerines as there are no studies to our knowledge that have used data loggers to track migratory temperature fluctuations in songbirds. Given the few studies to date on free-living birds, it would be beneficial to investigate the role of hyperthermia in regulating the duration of flight in migratory birds, especially in light of climate change.

47.4.6 Flight at high altitude

Birds are preadapted to low-oxygen conditions since the design of their respiratory and circulatory systems makes their oxygen uptake highly efficient, although several aspects of their physiology enable regular flying at high altitude during migration (see Bishop and Butler, 2015 for a thorough treatment of this topic). For example, birds such as bar-headed geese, *Anser indicus*, that fly regularly at high altitudes produce more hemoglobin, more red blood cells, and more myoglobin (the hemoglobin equivalent in muscle cells) as they prepare for migration which enhances their blood's capacity to bind and transport oxygen (Scott and Milsom, 2006). In addition, relatively larger lungs, and more and deeper penetrating blood capillaries in their heart and flight muscles compared to other geese further facilitates oxygen transport. Bar-headed geese also have a special form of an enzyme (nicknamed COX) involved in energy production within their muscle cells (Scott et al., 2011).

47.5 Beyond systems

Migration is one of the most complicated life history stages given the diverse habitats traversed, distances covered, multiple routes, and daily fluctuations of climatic conditions to which birds are exposed in vernal and autumnal stages. To be successful, this life history stage requires flexibility of morphology, physiology, and behavior in tight coordination with environmental information that initially regulates preparation for the stage and subsequently influences the timing, duration, and amplitude or intensity of the response throughout the fueling and flight cycle and eventually termination. The endocrine system plays major roles integrating environmental information with the molecular and cellular physiology as presented here. But, questions remain including: (1) how does seasonal variation of resources and routes affect fueling and flight, (2) does the endocrine status of vernal and autumnal migrants affect their responses to the conditions of specific habitats *en route*, and (3) are the apparent seasonal differences in the endocrine pathways exerting similar effects on fueling or are there multiple ways in which such regulatory systems have evolved?

A fundamental aspect of the life history of migratory birds is the ability to flexibly modify their physiology to satisfy the changing demands associated with migration. Such physiological flexibility is possible only because the network structure of molecules and regulatory relationships that maintain and adjust homeostasis (i.e., the Physiological Regulatory Network, PRN *structure*) can remain the same while the concentrations and relative strengths of the

relationships (i.e., the PRN *state*) can change depending on conditions (e.g., age, seasons, and migration; Cohen et al., 2012). In this chapter, we have outlined key components of the PRN *structure* (e.g., Figure 47.6) and how the PRN *state* is adjusted within individuals during migration. However, our review also makes clear that there remain major gaps in our understanding of both (a) the network of specific molecules and regulatory relationships that maintain and adjust homeostasis (i.e., PRN *structure*) and especially (b) how the concentrations of key molecules and the relative strengths of certain regulatory relationships change with the context and the conditions of vernal and autumnal migration (i.e., PRN *states*). For example, the biochemical mechanisms involved in using fats as fuel, or those responsible for maintaining redox homeostasis and limiting oxidative damage, are usually considered distinct physiological systems (i.e., separate PRN *structures*) that dynamically respond to changing conditions. However, we have emphasized here that there are physiological linkages between fat metabolism and oxidative status that require a more systems-level, integrative approach to fully understand how migratory birds respond to their changing environment(s), and the conditions of vernal and autumnal migration. Furthermore, phenotypic flexibility of physiological traits requires that the capacity of a physiological system is matched to the prevailing demand but can be modulated in response to changes in demand as to provide some limited excess capacity (“enough but not too much”) (Diamond, 1991; Hammond and Diamond, 1997; McWilliams and Karasov, 2014). The level of so-called “spare capacity” and the full extent of phenotypic flexibility and its required time course provide important insights into constraints on whole-animal performance, diet diversity, and ecological niche (Piersma and Gils, 2011; McWilliams and Karasov, 2014). Given this systems-level perspective, the following related questions remain outstanding: (1) for a given physiological system (e.g., fat metabolism, oxidative status, and immune function), what is the PRN *structure* for migratory birds and how does PRN *state* change within individuals during migration, (2) what are the key physiological linkages between these systems that influence the limits to animal performance, and (3) what is the time course for such phenotypic flexibility of key physiological traits given that birds during migration are often time-limited?

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