How to get the most bang for your buck: the evolution and physiology of nutrition-dependent resource allocation strategies

Enoch Ng'oma[1], Anna M. Perinchery[1], and Elizabeth G. King[1]

[1]Division of Biological Sciences, University of Missouri, Columbia, MO 65211

Abstract

All organisms utilize resources to grow, survive, and reproduce. The supply of these resources varies widely across landscapes and time, imposing ultimate constraints on the maximal trait values for allocation-related traits. Consequently, an impressive diversity of phenotypically plastic strategies evolves in response to changes in resource availability. In this review, we address three key questions fundamental to our understanding of the evolution of allocation strategies and their underlying mechanisms. First, we ask: how diverse are flexible resource allocation strategies among different organisms? We find there are many, varied, examples of flexible strategies that depend on nutrition. However, this diversity is often ignored in some of the best-known cases of resource allocation shifts, such as the commonly observed pattern of lifespan extension under nutrient limitation. A greater appreciation of the wide variety of flexible allocation strategies leads directly to our second major question: what conditions select for different plastic allocation strategies? Here, we highlight the need for additional models that explicitly consider the evolution of phenotypically plastic allocation strategies and empirical tests of the predictions of those models in natural populations. Finally, we consider the question: what are the underlying mechanisms determining resource allocation strategies? Although evolutionary biologists assume differential allocation of resources is a major factor limiting trait evolution, few proximate

mechanisms are known that specifically support the model. We argue that an integrated framework can reconcile evolutionary models with proximate mechanisms that appear at first glance to be in conflict with these models. Overall, we encourage future studies to 1) mimic ecological conditions in which those patterns evolve, and 2) take advantage of the 'omic' opportunities to produce multi-level data and analytical models that effectively integrate across physiological and evolutionary theory.
Keywords: resource availability, resource allocation, phenotypic plasticity, evolutionary theory, proximate mechanisms, ecological context

1. The central importance of the interplay between resource acquisition and allocation

The amount of resources available to organisms, whether the source is sunlight, plant matter, or prey animals, is inherently variable over the landscape and across time. This variability presents a fundamental challenge to all organisms, from the smallest microorganisms to the largest plants and animals, all who must coordinate the acquisition of resources from the environment with allocation of those resources among the many competing functions and structures that contribute to the organisms' fitness. When faced with variation in available resources, individuals could respond in one of two ways: (1) maintaining the same relative proportion allocated to each trait or (2) exhibiting phenotypic plasticity in resource allocation by altering the relative amount of resources allocated to one trait versus others. When the optimal allocation strategy changes with resource availability, selection will favour the evolution of a phenotypically plastic allocation strategy.

The inescapable link between the amount of resources available to an organism and subsequent allocation of those resources means it is critical to consider how allocation strategies change across a range of resource availabilities. There are many examples of flexible strategies that depend on availability. For example, an adaptive shift in resource allocation is thought to underlie the commonly observed pattern of lifespan extension under dietary restriction (reviewed in [1–5]. Likewise, sexually selected traits often show strong condition dependence (i.e. dependence on acquisition), also thought to result from an adaptive shift in allocation (reviewed in [6,7]. Even the current obesity epidemic in modern human populations is often hypothesized to result from a mismatch between a selective environment favouring increased storage under high resources and the modern environment of constant high resource availability [8] (see [9] for a recent review). To understand this wide diversity in allocation strategies in the natural world, we must understand how different ecological conditions select for different strategies and what mechanistic changes underlie these strategies.

Understanding how and why this coordination of resource allocation with availability evolves has implications for nearly all areas of biology. Energetic costs to biological structures and functions (i.e. allocation trade-offs) are assumed to be universal and a major factor limiting trait evolution [10,11]. Typically, less attention is focused on the role of variation in the acquisition of resources, though it is no less important in determining trait values, and can obscure the detection of functional trade-offs. In a seminal paper, van Noordwijk and de Jong introduced the Y model—a mathematical model linking resource acquisition and resource allocation [12], which has been a central concept in the field of life history evolution. In the Y model, two traits

draw from a single resource pool, with trait values determined by the proportion of resources allocated to each (Figure 1 [12]). One of the key strengths of this model is its simplicity and generality; it can be applied to diverse questions such as why and how organisms age, what limits crop yields in different environments, why some species produce hundreds of offspring while others produce very few, and what constrains the evolution of fitness. While the Y model provides a conceptual starting point to understand the evolution of acquisition and allocation, in the Y model the underlying mechanisms governing these processes are treated as a black box. Likewise, our empirical knowledge of the genetic and physiological mechanisms underlying these processes is still limited, due in large part to their vast complexity [13,14]. The allocation of resources is thought to influence nearly all the major structures and functions of an organism, is affected by an array of interacting physiological pathways, is variable across the lifetime of the organism, and interacts with many different environmental factors. To achieve a complete understanding of how resource allocation trade-offs govern these processes, we must explicitly consider its interaction with resource acquisition and integrate across genomics, physiology, and evolution.

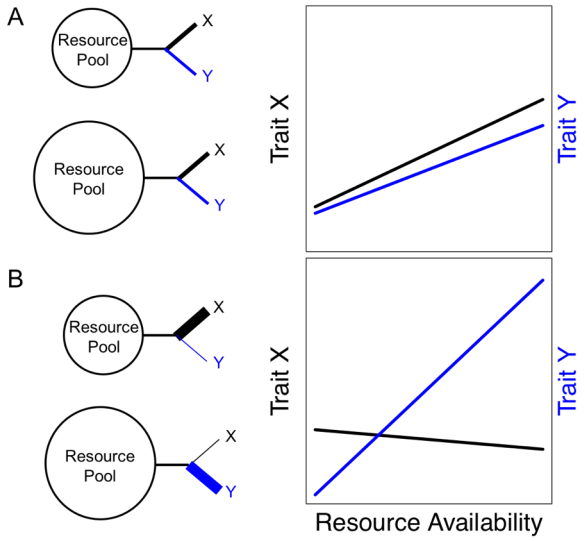

Figure 1: Expectations for trait values for two traits involved in a resource allocation trade-off when A) there is no phenotypic plasticity in allocation in response to resource availability, and B) there is phenotypic plasticity in allocation with increasing proportions allocated to trait Y as resource availability increases.

As we advance our ability to collect “omic” data at multiple levels (genomics, transcriptomics, proteomics, metabolomics, etc.) and in multiple environments, achieving this integration is becoming increasingly feasible. A major challenge now is making sense of multi-level, multi-environment data, and pulling out emergent themes that will help us better understand the complex processes underling trade-offs and linking these with evolutionary models. We argue that resource allocation is a natural focal point in this effort. This relatively straightforward concept has the potential to integrate knowledge across fields and address key questions facing the intersection between evolutionary and molecular biology.

In this review, our goals are to: 1) detail the diversity of resource allocation strategies in response to environmental fluctuations in resource availability, 2) review the evolutionary explanations for these strategies and highlight where new models are needed, and 3) assess the prospects and strategies for understanding the genetic and physiological mechanisms underlying resource allocation strategies.

2. The diversity of phenotypically plastic resource allocation strategies in the natural world

In the wild, organisms vary widely between species and populations in how they respond to variation in resource acquisition, with a diverse array of examples of phenotypically plastic resource allocation strategies (Table 1). Variation in resource acquisition can result from variation in resource availability in the environment, and/or from differences among individuals in their ability to acquire resources. By far the

largest challenge in describing broad patterns of phenotypic plasticity in allocation strategies is to directly quantify resource acquisition and the amount of those resources allocated to different traits. In only a very few cases have resource acquisition and allocation been successfully estimated in terms of energy units (e.g. [15–18]). In the majority of studies, these patterns must instead be inferred indirectly from phenotypic patterns.

The problem of estimating acquisition can be avoided in part when acquisition can be experimentally manipulated via resource restriction. When resource levels are restricted, the expectation for resource-based trait values is that they will also decrease. When trait values increase instead or remain constant, it suggests increased allocation to that trait (Figure 1). A well-examined example of this type of pattern is the commonly observed increase in lifespan (hypothesized to be due to increased allocation to somatic maintenance) under food restriction coupled with reduced reproduction (reviewed in [1–5]). The majority of the work on the response of lifespan to food restriction has been focused on model organisms. While there are several examples in non-model species that show a similar response (Table 1), not all species live longer on food restriction [19], including some species of water striders [20], house flies [21], squirrel monkeys [22], and rotifers [23,24]. Additionally, several species show a marked *increase* in reproductive allocation under low resource conditions (flatworms [25], guppies [26], rotifers [24]), demonstrating reproductive allocation does not always decrease under food restriction. Another trade-off that is particularly well characterized in terms of differential resource allocation is the trade-off between flight capability and reproduction in several wing dimorphic insect species (reviewed in [27–30]). In these species, there

exist discrete flight capable (macropterous) and flightless (micropterous or apterous) morphs. Wing morphology displays phenotypic plasticity in response to several environmental variables including rearing density, a likely correlate with acquisition, with different species displaying very different responses. In aphids and planthoppers, induction of flight capable morphs increases in response to crowding and low nutrition [31,32], while in crickets, group rearing and other stressors increase induction of flightless morphs [33,34]. Both of these examples, the lifespan-reproduction trade-off and the flight capability-reproduction trade-off, demonstrate the wide variation in allocation patterns across different species.

Most experimental manipulations of acquisition simply consider a single “low” and single “high” resource environment, and often the diet used is artificial and quite different from the organism's natural diet. Recently, the community has begun to take a “nutritional geometry” perspective, considering wider ranges of nutritional conditions, both in terms of caloric content and individual diet components (i.e. protein, carbohydrate, and lipid content), as well as a wider range of the timing of resource level changes across an organism's lifetime [35–37]. These efforts provide a much more complete picture of how an organism responds to diet, but also increase complexity, which can make interpreting the results in an evolutionary context a challenge when patterns are highly dynamic. To best place diet manipulations in an evolutionary context, we need ecological studies that characterize typical diet sources, and the degree of natural variation in resource availability experienced by populations in the wild. For many populations, this goal will be a challenge.

Overall, a broad view of trait variation reveals many varied examples of phenotypic plasticity in resource allocation in response to variation in acquisition (Table 1). Often, patterns vary substantially among closely related species (e.g. [20,22,23,25]), among populations of the same species (e.g. [20,26]), or between different inbred strains [38]. These examples argue against any hard and fast, universal resource allocation strategies in response to variation in acquisition and lead to the key questions of why and how environmental variation in resource availability leads to the evolution of different resource allocation strategies.

3. How and why do phenotypically plastic resource allocation strategies evolve?

There is a long and rich history of theoretical evolutionary models addressing both optimal resource allocation patterns in different environmental conditions (i.e. life history evolution models; e.g. [39–43]; see [10,44] for extensive reviews), and the evolution of phenotypic plasticity [45–51]. However, there are few models that specifically focus on the evolution of phenotypically plastic resource allocation in response to variation in resource availability. While this category might seem to be a special case, there is reason to expect general models of phenotypic plasticity might not be fully applicable to variation in resource availability. Resource availability places an ultimate constraint on the maximal trait values for allocation-related traits, and in that way, it is fundamentally different from other types of environmental conditions. The dependency creates the somewhat paradoxical situation in which no plasticity in allocation will lead to plasticity in trait values, as they will necessarily decrease with resource availability (Figure 1).

Thus, it is critical for theoretical models to explicitly consider variability in resource availability when predicting how plastic allocation strategies will evolve.

One emergent property of models that do explicitly consider the interplay between acquisition and allocation is that environmental predictability (i.e. whether current resource availability is correlated with future availability) is a major determinant of the evolution of phenotypically plastic resource allocation patterns [52–54]. In a model considering allocation to flight capability versus reproduction, [52] showed completely opposite patterns of plasticity in allocation are expected to evolve in environments with predictable versus unpredictable patterns of resource availability. Fischer and co-workers [53,54] showed that, in response to short term resource availability fluctuations, populations should evolve to allocate toward somatic maintenance under low food conditions. However, this response is more complicated. If conditions are low enough to be indicative of low survival probability, allocation to survival is not favoured. Rather, a terminal investment strategy, investing heavily in reproduction at the expense of survival, is favoured.

One area where models of the evolution of condition-dependent (i.e. acquisition-dependent) resource allocation strategies is well developed is in the field of sexual signalling. In many cases, male advertisements to females are dependent on the condition of the male, producing so-called 'honest' signals (e.g. [55,56]; for reviews see [57–59]. This condition dependence can be continuous (e.g. call duration in male gray tree frogs [55]) or a discrete polymorphism such as in (sexually dimorphic mandible growth in stag beetles [60]). There are several models considering how the benefits and costs of increased allocation toward a sexual signal change depending on an

individual's condition [58,59,61], with models predicting low condition individuals that allocate more toward sexual signals experience lower benefits and/or higher costs depending on the assumptions of the model (see [59]). These models are a subset of models considering allocation strategies in poor condition as a 'best of a bad lot' strategy [44]. In essence, it does not pay to invest heavily in a sexual signal if one simply does not have enough resources to produce a high-quality signal that will attract many mates.

The majority of evolutionary models focus solely on why, not how, allocation patterns evolve, ignoring the underlying mechanisms. Often, this is a sensible strategy, given that when mechanisms don't act as ultimate constraints, evolutionary endpoint will remain the same, irrespective of the specifics of the mechanistic underpinning. Nevertheless, evolutionary models that incorporate explicit mechanisms, can be highly informative in explaining the mechanisms underlying evolutionary patterns. For example, [62] integrated physiological parameters such as oxidative damage associated with faster growth and resource allocation to damage repair in a model predicting when compensatory growth (increased allocation to growth following a period of food restriction) should evolve. Only by explicitly incorporating the physiological mechanisms of damage and repair, were they able to simulate patterns of compensatory growth that matched observations. Compensatory growth never arose using a simple optimality framework, demonstrating that explicitly incorporating physiology can fundamentally change the predictions of life history models in some cases. We encourage the development of evolutionary models that integrate proximate mechanisms as a way to

expand our understanding of the evolution of resource allocation strategies in multiple systems.

4. Genetic and physiological mechanisms underlying phenotypic plasticity in resource allocation

It is clear organisms have evolved the ability to shift the allocation of resources in response to their nutritional state in many different ways, but *how* do they accomplish this change? What physiological changes accompany a shift in allocation strategy and what genes are involved? Not surprisingly, the greatest progress in the effort to uncover the mechanisms governing the coordination between acquisition and allocation comes from model organisms (e.g. yeast, worms, flies, and mice) that have been the focus of studies for decades. However, the relatively recent "omic" technologies available, and the decreasing cost of these technologies, make it increasingly feasible to gather data at multiple levels of the genotype to phenotype map in multiple environments for nearly any organism, opening up the possibility of moving beyond unnatural manipulations in model organisms and toward more ecologically relevant contexts.

a. Evolutionary endocrinology suggests key role of hormones in resource allocation

At first glance, resource acquisition and allocation might seem hopelessly complex, casting doubt on the prospect of uncovering the proximate mechanisms involved in the relatively subtle variation, at least when compared to mutants, in natural populations. However, an emergent theme from several systems, including many of the above detailed examples in model organisms, is the key role of hormone pathways as major determinants of resource allocation. These discoveries have spurred the

expansion of the field of “evolutionary endocrinology” [63–65]. For instance, we have learned a great deal about the mechanisms governing allocation of resources in response to environmental changes from genetic screens and mutational analysis in model organisms (e.g. [65–67]). Here, we review some examples in model and non-model systems, focusing on resource allocation plasticity in the response of reproduction-lifespan trade-off to hormonal signalling. The relevant hormone pathways include insulin, ecdysone, juvenile hormone and testosterone.

i. Lessons from studies of large effect mutations

Studies that have yielded the most insights have tended to focus on mutations of large effect. For example, Upd2 (unpaired 2) is a cytokine-like protein located upstream in the insulin pathway that is a functional homolog of human leptin [68] and causes a nutrient dependent effect on growth. It mediates production of Dilps (Drosophila insulin-like peptides) in *Drosophila* in the fed state, and subsequent secretion of insulin in response to dietary fat. Rajan and Perrimon [68] knocked down Upd2 function and found fat body-specific reduction in growth and metabolism. In small mammals and humans, leptin together with AMPK (AMP-activated protein kinase) control appetite thus regulating nutrient intake [69]. Other studies have found that leptin also mediates energetic trade-offs with the immune system [70]. These studies demonstrate a direct connection between nutrient availability and allocation.

Another set of studies sequentially perturbed insulin/insulin-like signalling pathway (IIS) and ecdysone signalling in ovarian somatic cells of *D. melanogaster* to explore three nutrition-sensitive developmental processes that contribute to variation in ovary size and ovariole number. Larvae exposed to poor diet (containing 1% sucrose)

showed slowed rate of development compared to larvae on rich media (20% sucrose). These studies concluded that ecdysone signalling regulated the rate of increase in ovary volume in general while IIS conferred the same effect before larvae attained critical weight [71,72]. Green and Extavour [73] further showed that IIS activity underlies phenotypic plasticity and variation in ovariole number across *Drosophila* species. This nutrient-dependent development of the ovary illustrates the role of hormonal signalling in plastic allocation of nutrients.

Perhaps one of the most significant contributions emerging from mutation studies is that IIS/target of rapamycin (TOR) signalling pathways are critical in the regulation of lifespan in many species. In several model organisms (including fly, mice and worm), reduced IIS which is typically assayed via mutational analysis, phenocopies nutrient deprivation, resulting in longer-lived individuals (e.g. [74–76]). In poor nutritional conditions or via disruption of the energy balance, many organisms shift limited resources from growth and reproduction to maintenance and survival functions, leading to significant delay in the onset of age-related conditions including cancer [77,78]. In addition, a suppressed IIS or removal of germ-line produce life extending effects by activating the forkhead transcription factor (FOXO) which is conserved across *C. elegans* (*daf*-16), *D. melanogaster* (dFOXO) and mammals (FOXO3a) [79–82]. In mammals, amino acid stimulation negatively regulates mTORC1 via a polypeptide encoded by long non-coding RNA [83].

At the whole-body level, AMPK regulates metabolic energy balance by affecting feeding behaviour and circadian rhythms [69]. While the active IIS promotes anabolic processes and storage, AMPK plays a catabolic role in active tissues utilizing glucose.

When availability of nutrients is low, the elevated AMP to ATP ratio activates AMPK, with subsequent gain in health span and longevity in *D. melanogaster* [69,84]. AMPK is a conserved modulator of lifespan in flies and mammals linking energy sensing to longevity, and is emerging as a major mechanism accounting for variation in longevity [69,84,85].

ii. Lessons from studies with more ecological context

Hormone pathways have also been implicated in nutrient allocation shifts in non-model systems. Studies in flies and beetles have suggested the IIS as a major pathway involved in resource distribution. An exonic indel polymorphism in the Insulin-like Receptor (*InR*) gene was identified as a functional direct candidate target of natural selection wild *D. melanogaster* [86,87]. In rhinoceros beetles, horn size is highly sensitive to nutrition and to perturbations in the IIS than are other body structures [88]. The precise details about how nutrients are mobilized toward competing traits have perhaps been best characterized in the wing dimorphic sand cricket, *Gryllus firmus*. Juvenile hormone (JH) levels determine the morph, and trigger a whole host of processes leading to differential allocation of actual resource components toward flight capability versus reproduction. Flight capable morphs preferentially metabolize amino acids and convert a larger proportion of fatty acids to triglycerides while flightless morphs preferentially metabolize fatty acids and convert a larger proportion of amino acids to ovarian protein [89]. Adult crickets on low food diets allocate proportionally fewer resources toward flight capability [17,18], however, whether this diet-dependent shift is also mediated through JH has not yet been established. Juvenile hormone

signalling is also involved in nutrition-based sex-specific mandible development via *doublesex* gene in the staghorn beetle [60,90].

These studies support the hypothesis that the evolution of allocation patterns ultimately results from the evolution of key endocrine pathways [63–65], potentially providing a simple theme in complex web of traits at various levels. Thus, while there is no denying acquisition and allocation of resources are highly complex processes, it is clear that hormone pathways serve as major mediators in many cases.

iii. Understanding the underlying genetics of natural variation

Most of the above-described studies that identify key genes (except a few e.g. [86,87]) rely on evidence from large effect mutations or major perturbations and they have been very successful at identifying genes involved in the regulation of metabolism and resource allocation and of the effects of large alterations to individual genes. Our knowledge of the genetic basis of *natural* variation in metabolism and resource allocation is severely lacking in comparison, a predicament that is shared by the majority of complex traits [91–93]. The large effect genetic mutants identified via classical genetic techniques are typically not segregating in natural populations, which is not surprising given the central role of the pathways involved [94]. Additionally, despite the fact that several large effect mutations have been found to influence lifespan in *D. melanogaster* [3,95], mapping studies and evolution experiments using natural populations have not independently identified these same genes as important contributors to natural genetic variation (e.g. [3,96–98]), with few exceptions [86,87]. There are several possible explanations for this large disconnect regarding genes in these hormone pathways: 1) they do not contribute to natural genetic variation, 2) their

effects are subtle and thus difficult to detect, 3) their effects stem from *trans* regulatory changes affecting gene expression [99]. Large effect mutant studies may represent the extreme tail of effect size distribution in nature [14], or, in the case of increase in longevity, different mechanisms altogether may induce altered nutrient signaling pathways in captive populations due to absence of stressors [92,93,100].

Identifying the specific genetic variants underlying resource allocation phenotypes is a major challenge shared by all complex traits. In general, complexity is expected to increase as we move from higher level phenotypes such as lifespan and reproduction down to genotype and it often becomes more difficult to identify causation along the way. The challenge is increased when also considering how trait values are influenced by the environment (e.g. nutrition). The overall challenge and strategies associated with identifying the genetic variants associated with phenotypes has been reviewed elsewhere [14]. One of the strongest messages to emerge from modern quantitative genetics is that the genotype to phenotype map is more complex than some anticipated or hoped for (reviewed in [101]. Within this complexity, our goals should be to find the main roads and general patterns.

One potential strategy to aid in this effort is the development of large stable mapping panels as community resources in several model systems. These populations encompass greater amounts of genetic variation and increased mapping resolution relative to two-parent mapping populations [102] and have the advantage of being able to measure multiple phenotypes in multiple environments for the same set of lines. Multiparental populations (MPPs) thus hold promise to produce new hypotheses and analytical methods, as well as improved experimental designs. Since the 1990s, several

synthetic animal and plant panels have been generated (listed in [103] for genetic mapping of quantitative traits, and new ones have emerged (e.g. [104,105]). These have been used to understand mechanisms of diverse biological processes from complex diseases in humans and mice (e.g. [106,107], toxicity resistance in flies (e.g. [108,109]) to crop improvement (e.g. [88]), and methods development (e.g. [103,110,111]). These resources improve the prospects of both targeted studies and systems genetic approaches to leverage what is known about hormone pathways to reveal mechanistic bases of plastic resource allocation in natural organisms.

b. Integrating genetic and physiological mechanisms into evolutionary perspectives of resource allocation

As with the above evolutionary models, traditionally, questions surrounding proximate mechanisms have been considered separately from evolutionary questions, with a more recent movement toward integration across sub-disciplines. In particular, a major question surrounding hypothesized resource-based trade-offs is the degree to which the proximate mechanism underlying trade-offs stems from functional resource competition, or whether some other mechanism (e.g. hormone signaling), produces the relationship between traits. Here, we argue that these proximate mechanisms are not in conflict with the conceptual framework of the Y model.

i. Challenge of a resource-based Y model

In recent years, the Y model of resource allocation, as a framework to explain proximate mechanisms underlying life history trade-offs has been criticized by some as inadequate, leading some to seek revision of life history theory (see views and exchanges in [112–116]). The challenge to a resource-centred model is based on new

empirical data showing that 1) abrogation of reproduction does not always extend lifespan, 2) some mutations that extend lifespan do not affect, or in fact, increase fecundity, and 3) male and female organisms of several species respond differently to interventions that increase lifespan. The most notable of these are studies in *C. elegans* [117,118] and *D. melanogaster* [119,120] in which gonad ablation failed to increase lifespan, while ablation of the germline only, doubled lifespan. Evidence suggests this effect is mediated largely by the insulin/IGF-1 system, which is thought to integrate molecular signals from the germ line and those from the somatic gonad to determine lifespan, rather than direct redistribution of resources. This hormonal signalling alternative has spurred a vigorous debate (see [114,115] whose reconciliation, in our view, depends on the eventual and successful integration of proximate mechanisms of trade-offs into evolutionary theory.

ii. Is the new data really in conflict with the Y model?

We have reviewed above, case studies that directly or indirectly offer support for a resource model of life history evolution. Of particular note are studies demonstrating preferential amino acid metabolism and allocation of fatty acids to either flight or reproduction in winged vs wingless cricket morphs [89,121–125]. These works represent compelling evidence for differential resource allocation associated with the flight capability-reproduction trade-off. In addition, a study that manipulated resource availability confirmed the predictions of the Y mode for this trade-off. Studies that fail to find the trade-off or find a positive relationship do not logically invalidate those that observe a negative correlation. Further, the bulk of known mechanisms have been described in non-natural laboratory mutant organisms with limited or zero selection

pressures as experienced in the wild [92,93,100]. Although, the evidence for the connection between signalling and resource allocation is unclear, this absence of evidence should not be treated as evidence of absence.

iii. Opportunities for integration of fields

Conceptual dichotomies where available empirical data do not sufficiently fit standing theoretical principles are not new to biology. These apparent conflicts have fuelled progress of the broad field and successfully led to the integration of once thought disparate fields – Mendelian, molecular, and quantitative genetics in the last century (see [126]). Instead of asking whether survival costs are best explained either by literal resource competition or by resource-free hormonal signalling, it may be useful to explore how the two may be related parts that integrate into the observed trade-off. This strategy can redirect research into looking for potential connections between nutrients and signals and factors that affect that connection. There is strong evidence that hormonal signalling is involved in nutrient sensing mechanisms implicated in aging [127], and that these mechanisms are at the base of appetite regulation and redistribution of nutrients [69]. It is thus possible to see how hormonal signalling may regulate optimal allocation and account for the evolution of diverse resource allocation strategies. Therefore, new data showing that signals regulate lifespan do not, presently, preclude the evolutionary significance of resource constraints, particularly in natural settings. It is completely fitting with evolutionary theory to expect organisms to use specific cues to indicate environmental conditions such as food availability. Thus, when results find that a single amino acid level can change how organisms allocate resources [89], an

evolutionary interpretation is that that amino acid is what is cueing the organism about the environment, not that actual resource levels are not important to the response.

We do not know yet whether one or more proximate explanations govern a given trade-off. A possible scenario to emerge may negate the notion of a single proximate mechanistic explanation since there may be unique proximate explanations in different species and/or environmental settings. For example, [128] investigated a related trade-off between larval survival and adult size, in wild-living *D. melanogaster* and found that larval age predicted survival in temperate regions, while larval weight predicted survival in tropical regions, concluding that thermal evolution of resource allocation involved the ability to access glycogen reserves. Similarly, Wayne et al, [129] found that ovariole number increased in response to maternal starvation and suggested evolutionary association between maternal environment and the reproductive system of female offspring. Further, [130] documented intra-sex differences in lifespan response to resource availability in redback spider and found that DR extended lifespan in mated, but imposed cost in unmated females. These examples likely suggest multiple mechanistic possibilities defining a given phenotypic trade-off in different species or within species in different environments. Whether the trade-off is affected by diet, temperature, or behaviour, molecular signalling could lead to changes in how resources are allocated. It will benefit both fields if future studies take advantage of the 'omic' technologies to step up cross-field approaches in the search for mechanisms governing these traits in nature.

5. Future Directions

In this review, we have attempted to argue that a resource-based Y model is uniquely favoured to facilitate integration of evolutionary life history theory with proximate mechanisms underlying the near-ubiquitous trade-offs in life history traits. In doing so we have brought to the fore two key areas where significant progress is attainable, especially with the aid of 'omic' approaches: 1) increasing the ecological context in which studies are performed, and 2) increasing the level of integration between fields.

A major gap in our understanding of life history trade-offs in general, and the relationship between survival and reproduction in particular, is a general paucity of studies focusing on the underlying mechanisms in natural species, and lack of concordance between results of mutational studies in model species and those from studies of natural variation in the few cases where these have been undertaken. Here, we have attempted to show the wide variety of plastic resource allocation strategies in response to environmental fluctuations in availability that exist among natural populations and species. Understandably, many of the patterns so far uncovered have been demonstrated using laboratory studies with explicit diet manipulations (at most, three diet variations). We support this approach but, in addition, advocate for a broader, more realistic consideration of experimental diets. In this direction, studies taking 'nutritional geometry' approaches discussed earlier have the potential to provide a broader understanding of how organisms respond to changes in diet. In addition to considerations of mere nutritional content, experimental diets should attempt to mimic the natural diet of the organism as closely as possible, and the natural range of

availability in the field in order to ensure that results most reflect evolutionarily relevant patterns that occur in nature.

Secondly, we have highlighted gaps in theoretical evolutionary models that address both optimal resource allocation patterns, and the evolution of phenotypic plasticity. To our knowledge, very few models specifically focus on evolution of phenotypically plastic resource allocation in response to variation in resource availability. We encourage the development of evolutionary models that integrate proximate mechanisms as a way to expand our understanding of the evolution of resource allocation strategies in multiple systems. In addition, testing the predictions of models predicting the evolution of different resource allocation strategies should be a major priority. Natural systems where patterns of availability differ among populations and species, can also inform these questions. Alternatively, experimental evolution approaches, where resource availability can be altered in a controlled way, and different types of variability across time can be induced, are potentially a powerful way to test these models. An experimental evolution approach could also allow for tracking change across the genotype to phenotype map in an integrative way, tracking changes in proximate mechanisms as evolution occurs.

Overall, viewing phenotypes within a framework of resource acquisition and allocation allows for a natural integration of physiology, genetics, and evolution. Studies that measure phenotypes at multiple levels (genomic, physiological, organismal levels) and in multiple resource environments provide a potentially productive path forward.

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Competing interests

We have no competing interests.

Author's contributions

EGK and EN conceived the idea and wrote the manuscript; AMP and EN compiled Table 1, EN, AMP and EGK provided editorial comments. All authors gave final approval for publication.

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Table 1: Examples of resource allocation strategies in some life history traits across the animal kingdom.

Trade-off	**Taxa**	**Increased allocation with low resource availability**	**Selected examples**
Flight capability/reproduction	*Prokelisia marginata*	flight	[31]
	Gryllus rubens	flightlessness	[33]
	Gryllus firmus	flightlessness	[34]
Flight/survival/ body mass/reproduction	*Speyeria mormonica*	reproduction	[131]
Flight/storage	*Trichoptera* spp.	short lived species: storage; long lived species: no change	[132]
Growth/development time/body size	*Scathophaga stercoraria*	growth	[133]
Growth/reproduction	*Daphnia magna*	growth	[134]
Growth/reproduction/stor	*Paroedura*	growth	[135]

age	*picta*		
Growth/reproduction/ sprint speed	*Anolis sagrei*	survival	[136]
Reproduction/ dispersal	*Gryllus firmus*	adults to dispersal; juveniles to reproduction	[17,18]
	Aphidoidea	dispersal	[32]
Reproduction/storage	*Drosophila melanogaster*	storage	[137]
Soma/reproduction	*Poecilia reticulata*	reproduction	[26]
Somatic growth/ survival	*Macaca mulatta, Saimiri* sp.	*M. mulatta to survival; Saimiri* sp *no effect*	[22]
Survival/ reproduction	*Theraphosidae*	survival	[138]
	Synchaeta pectinata	reproduction	[24]
	Odocoileus	survival	[139]

virginianus		
Callosobruchus maculatus	survival	[140]
Asobara tabid	survival	[141]
Anastrepha ludens	survival	[142]
Notiophilius buguttatu	survival	[143]
D. melanogaster	survival	[1,5,144–146]
Larus michahellis	survival	[147]
Homo sapiens	survival	[67,148]
Rhabditophora	reproduction	[25]
10 rotifer species	most to survival	[23]
Drosophila melanogaster	survival	[36]

	Eupelmus vuilletti	reproduction according to nutrient	[16]
	Ceratitis capitata	females: reproduction males: survival	[149]
Male survival/reproduction	*Saccopteryx bilineata*	survival	[150]
Survival/reproduction/ dispersal	*Gerris* spp	reproduction	[20]