

## REVIEW

# A unifying, eco-physiological framework for animal dormancy

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## Abstract

1. Various animals across the tree of life express some form of programmed dormancy (e.g. hibernation, diapause) to maximize fitness in highly seasonal environments. The integrated phenotype of animals undergoing programmed dormancy is strikingly similar among diverse groups; however, research on programmed dormancy has historically been phylogenetically siloed. A broad comparative approach could clarify new angles for answering fundamental questions about programmed dormancy evolution.
2. To advance this approach, we present a cross-taxonomic framework describing dimensions that distinguish animal dormancies and provide a set of core traits that animals regulate as they progress through the eco-physiological phases of deep, programmed dormancy.
3. We use this universal framework to explore the ultimate drivers and evolutionary consequences of dormancy across the tree of life. Deep, programmed dormancy appears to be a predictable and repeated adaptation to highly seasonal environments that draws on a conserved suite of ancestral traits. We highlight evidence for molecular convergence in signalling pathways coordinating environmental sensing and energy metabolism in the insect and mammal lineages, separated by 700 million years of evolution and representing independent colonizations of highly seasonal environments.
4. Lastly, we discuss the utility of this new framework and highlight opportunities and challenges for researchers to continue advancing our understanding of dormancy through a broad, comparative lens.

## KEYWORDS

diapause, hibernation, hypometabolism, metabolic suppression, seasonality, torpor, winter

## 1 | INTRODUCTION

Across the tree of life, the term 'dormancy' is used to describe physiological adjustments that enhance survival in temporarily hostile environments (Cáceres, 1997; Geiser, 1998; Hand, 1991; Košťál, 2006). Dormancies have been documented in all animal phyla except Echinodermata (Hand, 1991), and are described using a wide variety of taxon-specific names and definitions (Table 1). Within and among these groups, dormancies span an extremely broad range of physiological states, from the nearly inert, 'latent life' state called cryptobiosis exemplified by Tardigrades (Jönsson et al., 2019) to more subtle

state of hypometabolism exhibited by some active high latitude ungulates (in winter; Arnold, 2020) and polar bears (in summer; Nelson et al., 1983; Whiteman et al., 2015).

Animals undergoing different types of dormancies resemble one another in how behaviour, energy metabolism and environmental sensing are regulated, and these processes are often underpinned by deeply conserved regulatory pathways (Hand et al., 2016). Despite these striking similarities, dormancy research is strongly phylogenetically siloed, with little crosstalk among fields in the primary literature (Box 1). The phylogenetic siloing of these closely related research fields inhibits our ability to answer evolutionary,

**TABLE 1** Glossary of terminology used to refer to animal dormancies across and among taxa

Term	Taxa	Definition	Citation
Aestivation	Vertebrates and invertebrates	'a state of aerobic hypometabolism that is probably best described as a survival strategy for dealing with arid conditions, but is also typically associated with lack of food availability and frequently with high environmental temperatures'	Storey (2002)
	Birds and Mammals	'torpor in summer/at high ambient temperatures'	Geiser (2010)
Brumation	Ectotherms	'The winter dormancy that is observed in ectothermic species, [in which] animals are dependent on the temperature of their surroundings and are forced to stay torpid until temperatures rise'	Wilkinson et al. (2017)
	Reptiles	'winter dormancy in ectothermic vertebrates that demonstrate physiological changes which are independent of body temperature'	Mayhew (1965)
	Amphibians	'The pre-winter reduced activity and reduced metabolic rates of poikilotherms'	Borzée et al. (2019)
Daily heterothermy or torpor	Birds and Mammals	A maximum torpor bout duration of less than 24 hr with consistent association with the circadian rhythm of body temperature; a minimum metabolic rate during torpor of $>0.1 \text{ ml O}_2 \text{ g}^{-1} \text{ hr}^{-1}$ and a minimum body temperature above $10^\circ\text{C}$	Ruf and Geiser (2015)
	Birds and Mammals	Torpor 'lasting for several hours during the rest phase'	Geiser (2013)
Diapause	Animals	'a programmed arrest of development ... that may or may not be associated with some degree of metabolic depression'	Hand et al. (2016)
	Invertebrates	'[a dormancy] maintained by an internal physiological responses rather than an external environmental factor'	Cáceres (1997)
	Insects	'A more profound, endogenously and centrally mediated interruption that routes the developmental programme away from the direct morphogenesis into an alternative diapause programmed of succession of physiological events; the state of diapause usually precedes the advent of adverse conditions and the end of diapause need not coincide with the end of adversity'	Košťál, (2006)
	Insects	'an environmentally preprogrammed period of arrested development, characterized by metabolic depression that can occur during any stage of insect development'	Hahn and Denlinger (2011)
Dormancy	Animals	'Dormancy describes a state of reduced (but not complete lack of) metabolism, i.e., hypometabolism'	Withers and Cooper (2010)
	Insects	'A generic term covering any state of suppressed development (developmental arrest) which is adaptive (that is ecologically or evolutionarily meaningful and not just artificially induced), and usually accompanied with metabolic suppression'	Košťál (2006)
	Invertebrates	'An all-encompassing term that includes any form of resting stage, regardless of cues required for induction or termination'	Cáceres (1997)
Hibernation	Animals	'A general term applied to all animals that seek a local refuge (a hibernaculum) in which to overwinter'	Ultsch (1989)
	Insects	A type of diapause entered 'in polar and temperate regions'	Košťál et al. (2017)
	Reptiles	'the general reduction in activity ... following cold-acclimation or cold-acclimatization ... equivalent to brumation'	Gatten (1978)
	Birds and Mammals	A maximum torpor duration of more than 24h, with strong suppression or even complete arrest of the circadian clock; a minimum metabolic rate in torpor of $<0.1 \text{ ml O}_2 \text{ g}^{-1} \text{ hr}^{-1}$ and a minimum body temperature below $10^\circ\text{C}$	Ruf and Geiser (2015)
	Birds and Mammals	'Multiday torpor predominantly throughout winter'	Geiser (2013)
	Mammals	A 'strategy for winter survival [in which] animals sink into a deep torpor where metabolic rate is $<5\%$ of normal, body temperature falls to $0\text{--}5^\circ\text{C}$ , and physiological function are strongly suppressed'	Storey (2003)
Quiescence	Invertebrates	'[a dormancy] Induced and maintained by adverse environmental conditions; includes hibernation, aestivation, anhydrobiosis, and cryptobiosis'	Cáceres (1997)
	Insects	'direct inhibition of development by conditions below or above developmental thresholds ... [quiescence is] an immediate response (without central regulation) to a decline of any limiting environmental factor(s) below physiological thresholds with immediate resumption of the processes if the factor(s) rise above them'	Košťál (2006)

### BOX 1 A phylogenetic siloing of fields studying programmed dormancy

We searched ISI Web of Science on 11 April 2019 for studies from 1900 to 2019 that incorporated ideas from more than one taxonomic (animal) group as a central part of their work (see Appendix 1 in Supporting Information for methods of our literature search). Of 13,223 primary literature studies on diapause, hibernation or brumation, only five studies (Appendix 1, Table S2) set their study in the context of more than one type of animal dormancy according to our criteria. These five studies were focused on either insects or killifish, and our search did not reveal any primary literature on mammalian hibernation that included reference to either brumation or diapause. By using insights from other taxa, these studies illustrate that many shared gene expression and metabolic pathways regulate programmed dormancy across taxa, but the precise wiring of those pathways often differs (Duerr & Podrabsky, 2010; Kučerová et al., 2016; Wang et al., 2018; Xu et al., 2012). It is striking that cross-taxon synthesis in the primary literature has only begun to appear in the past decade. This almost complete siloing of research fields is restricting progress in many areas of research. The siloing of fields is less apparent in the secondary literature (e.g. reviews and syntheses), where researchers have repeatedly emphasized striking similarities in dormancy across animal taxa (Baumgartner & Tarrant, 2017; Hahn & Denlinger, 2011; Hand et al., 2016; Lyons et al., 2013; Malan, 2014; Melvin & Andrews, 2009; Ruf & Geiser, 2015; Schiesari & O'Connor, 2013; Secor & Carey, 2016; Staples, 2016; Storey & Storey, 2004, 2013; Ultsch, 1989). However, this has yet to be fully taken-up by the primary research literature.

ecological, and mechanistic questions about dormancy. For example, ecological and mechanistic similarities among taxa may offer fundamental insight into how natural selection shapes dormancy evolution. Phylogenetic siloing also means parallel research questions and discoveries are more likely to go unrecognized in adjacent fields. Researchers are likely missing opportunities to cross-pollinate hypotheses and research approaches. Unifying these fields has the potential to advance research on both mechanisms and evolution of dormancy.

Because these research fields have been phylogenetically siloed almost since their inception, the concepts and terminology used in each field are also taxon-specific and difficult to apply broadly. Dormancy is often conceptually divided into two discrete 'types' (Andrewartha, 1952; Cáceres, 1997; Hand, 1991; Košťál, 2006; Levesque et al., 2016), but the defining features that delineate the dichotomy are taxon-specific and have been the subject of considerable controversy. In the insect literature, dormancy is generally

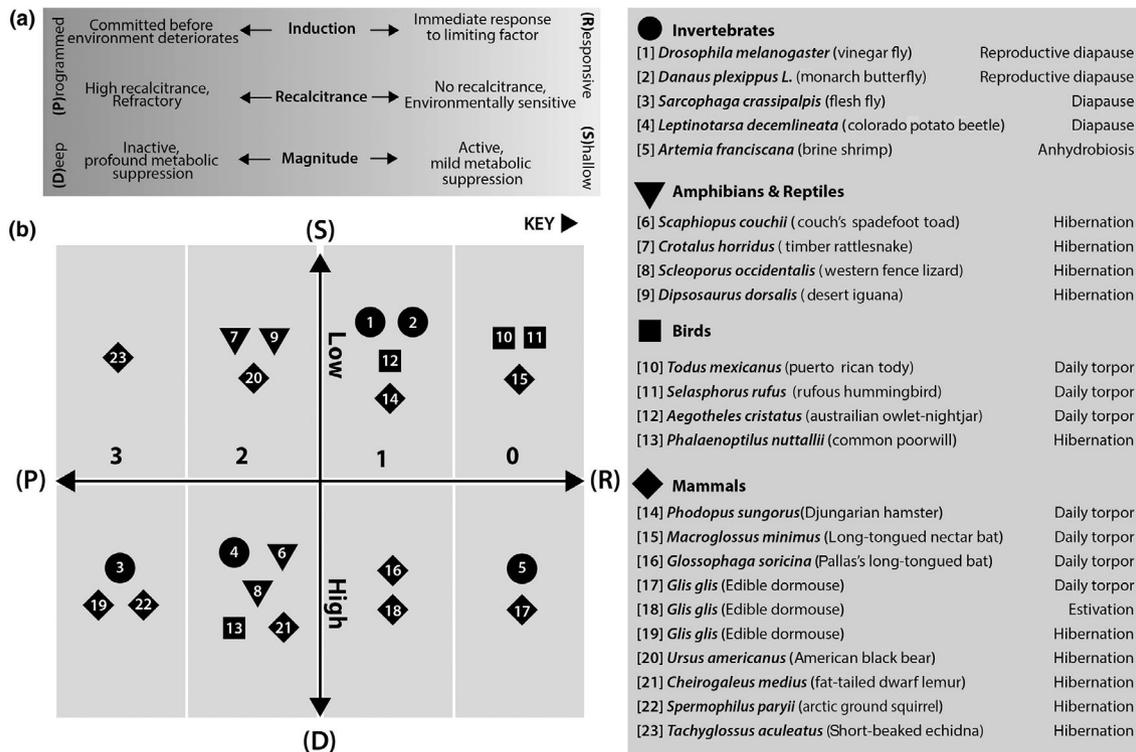
classified as quiescence or diapause, which can be differentiated principally by the role environmental cues play in controlling onset and completion of dormancy (Table 1). In the mammalian and bird literature, the dichotomy is set between daily torpor and hibernation, which are generally differentiated by the duration and magnitude of metabolic suppression (Table 1; Ruf & Geiser, 2015). Some aspects of these definitions do not translate well across taxa, and the dichotomy-driven view of dormancies has proved too rigid to adequately describe the diverse dormancies that exist within a single taxonomic group. In the insect literature, the wide range of variation in the control of the initiation and termination of dormancy lead to debates about whether specific dormancies qualify as 'diapause', particularly given that many insects with a dormancy characterized as diapause transition to a state known as post-diapause quiescence relatively early in winter (Hodek, 2002), and may have considerable variation in the degree of suppression in processes such as locomotion, growth, and even development (Košťál et al., 2000; Tatar & Yin, 2001). In the mammalian literature, metabolic flexibility in protoendothermic species (e.g. tenrecs or tropical and sub-tropical bats) that use a mix of daily torpor- and hibernation-like strategies across the heterothermic period have been difficult to integrate with the broader daily torpor-hibernation dichotomy (Nowack et al., 2020; Treat et al., 2018; van Breukelen & Martin, 2015). We need a flexible concept of dormancy that transcends phylogenetic divisions and captures ecologically relevant axes of dormancy to facilitate phylogenetically broad comparative dormancy research.

With this goal in mind, we propose a universal framework comprised of three components—axes, core traits and phases of dormancy—that can be used to classify, compare and contrast dormancies across animal taxa. We illustrate how this framework can be used to explore commonalities in the evolutionary/ecological drivers and consequences of dormancy. Finally, we highlight opportunities for cross-pollination and areas of the proposed framework that will benefit from quantitative expansion. We focus on insects and mammals because the vast majority of research has focused on these taxa and they reflect our research expertise, but we highlight examples from other taxa throughout to illustrate that the framework is generalizable beyond these groups, and we have developed the terminology in consultation with researchers from a wide range of animal dormancy fields. Nonetheless, we acknowledge that others may find that our focus on the big picture commonalities results in oversimplifications and generalizations in some instances.

## 2 | INTEGRATING ANIMAL DORMANCY RESEARCH IN A UNIVERSAL FRAMEWORK

### 2.1 | Major axes of dormancy

We suggest that there are three axes that can differentiate dormancy types across animal taxa (Figure 1a). The first two axes, **Induction** and **Recalcitrance**, together capture the degree to which the dormancy is endogenously programmed and centrally mediated (i.e.



**FIGURE 1** The major axes distinguishing animal dormancies. (a) The three axes of dormancy, which differentiate deep, programmed dormancies from shallow, responsive dormancies (see text for further description of axes). (b) Using the framework to classify dormancies of invertebrates, amphibians and reptiles, birds and mammals. We compiled information from the literature on the degree of programming and metabolic suppression (as a measure of magnitude) of representative dormancies for some well-studied dormancy models (Table S4). Some species or individuals may display multiple types of dormancy in different life stages or in response to different environmental challenges, and these dormancies can be compared within the framework as well. *Glis glis* [17, 18, 19] is included here as a well-described example. We collapsed induction and recalcitrance into one axis describing the degree of programming (P = programmed, R = responsive), with grades of 0 (responsive induction, low recalcitrance); 1 (programmed induction, low recalcitrance); 2 (programmed induction and moderate recalcitrance), or 3 (programmed induction, high recalcitrance). We characterized dormancy magnitude (D = Deep, S = shallow) as a dichotomous variable (high/low) based on the degree of metabolic suppression (per cent of basal or standard metabolic rate in a dormant animal compared to a similarly staged non-dormant animal), where high corresponds to >90% for endotherms and >70% for poikilotherms. Note that feeding rate was used in *Drosophila melanogaster* as no metabolic rate data were available. Species key is on the right

driven by central nervous system and endogenous time-keeping mechanisms), versus a direct response to an adverse environment. The third axis, **Magnitude**, describes the dormancy-specific degree of plasticity in a range of traits, including metabolic rate (described fully in Section 2.2).

The **Induction** axis describes the process by which animals are committed to entering the dormancy program, as opposed to continuing the active season lifecycle (Košťál, 2006). Induction of dormancy is classified as responsive when dormancy is initiated immediately and in direct response to a factor (often environmental, such as temperature, water or nutrients) crossing a physiological threshold. For example, food restriction induces spontaneous torpor in deer mice *Peromyscus maniculatus* regardless of season (Tannenbaum & Pivorun, 1984, 1988). Induction is programmed when the animal is committed to entering dormancy prior to the onset of environmental deterioration, often allowing for an extended preparation period during which the animal remodels its physiology and other traits (see Phases of Dormancy). Induction can be programmed in two distinct ways: (a) Obligate dormancies occur at a set life stage (in the case of

annual life cycles such as insects) or set time of year determined by the endogenous circannual clock, regardless of environmental conditions (Andrewartha, 1952; Danks, 1987; Harlow & Menkens Jr., 1986; Košťál, 2006; Nelson et al., 2010; Pengelley & Asmundson, 1969); (b) Facultative dormancy occurs only if animals receive the appropriate environmental cues (also known as token stimuli, often photoperiod and temperature; Harlow & Menkens Jr., 1986; Ryan et al., 2018; Tauber & Tauber, 1981; Vornanen et al., 2009) to induce dormancy; if those cues are not detected then the animal will proceed with the active season life cycle. The sensitive period for detecting cues used for facultative induction may occur well in advance of dormancy initiation, or even in the parental generation in insects with more than one generation per year (Denlinger, 1972).

The **Recalcitrance** axis describes the strength of the endogenous lock preventing an animal from breaking dormancy prematurely. An animal with a high degree of recalcitrance will remain in dormancy for weeks, if not months, once the dormancy program is initiated, even if environmental conditions become permissive. High recalcitrance of dormancy ensures that dormancy is not prematurely terminated

during a mild spell and may extend beyond the duration of adverse conditions. Experimentally, recalcitrance can be measured as either the time taken or proportion of individuals that resume active season physiology and behaviour after entering dormancy when transferred to or held under permissive conditions (French, 1982; Košťál, 2006; Pengelley & Fisher, 1963; Tauber & Tauber, 1976; Wooding & Hardisky, 1992). Dormancy recalcitrance differs systematically among species and populations (Masaki, 2002), and it also declines as dormancy progresses. As a useful starting point for species- or population-level comparisons, recalcitrance should be measured early in dormancy, ideally immediately after initiation (see Phases). The molecular and physiological mechanisms underlying variation in dormancy recalcitrance (and thus timing of spring emergence) are an active area of research in both mammalian and insect dormancy literature (e.g. Hut et al., 2014; Powell et al., 2020).

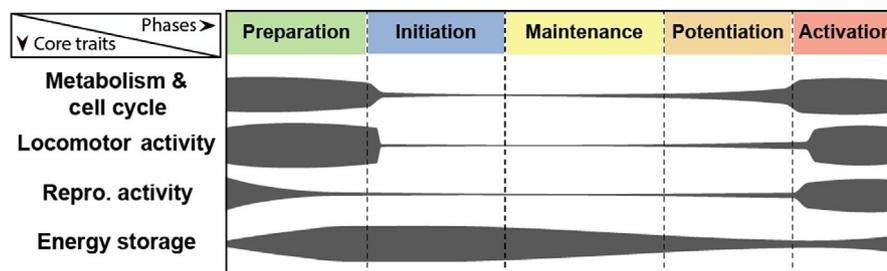
The third axis, **Magnitude**, describes the degree of dormancy-specific plasticity in the core physiological and behavioural traits, relative to a non-dormant animal at a similar life stage. The degree of metabolic suppression is a common metric of dormancy magnitude that is already widely used across taxa (Guppy & Withers, 1999; Ruf & Geiser, 2015). Additional traits such as activity and energy storage allow for a multivariate characterization of magnitude (see Section 2.2).

We chose some well-studied examples of dormancies to illustrate how this framework can provide a semi-quantitative characterization of major dormancies that transcend phylogenetic divisions (Figure 1b). Using this cross-taxonomic framework illustrates that there is a cluster of animals that express deep, programmed dormancies, including representatives from insects, birds, mammals and amphibians. More broadly, we find examples of eutherian dormancies that fall across the full length of each proposed axes, whereas poikilotherms (invertebrates, reptiles and amphibians) are only found in six of these categories, and birds only occupy three. Although endothermy apparently allows for diverse dormancy strategies in eutherians, birds are more constrained. In invertebrates, the degree of programming appears to be more closely linked to the magnitude of the dormancy. Within a dormancy sub-type (e.g. diapause, hibernation) there is a range of variation in both programming and magnitude, and all sub-types cover more than one quadrant. For example, insect diapause includes dormancies ranging from the shallow and relatively responsive reproductive dormancy of *Drosophila melanogaster* [1], to the

deep and highly programmed dormancy of *Sarcophaga crassipalpis* [3]. Aestivation generally refers to a responsive dormancy that occurs in response to food or water shortages (Storey & Storey, 2012), but there are reported instances of aestivation that fall within the quadrant of deep, programmed dormancy (see [21, 24]; Bieber & Ruf, 2009; Dausmann et al., 2004; Hoelzl et al., 2015; McNab, 2002). Tropical and sub-tropical dormancies are often characterized by greater flexibility (Dausmann et al., 2004; Faherty et al., 2018; Fietz & Dausmann, 2007; Geiser, 2020; Lovegrove et al., 2014), and thus are classified as more responsive in terms of induction and recalcitrance. Finally, even within a species or individual, dormancies in different life stages, or in response to different environmental challenges, may fall into different quadrants (e.g., see [17, 18, 19]). Additional work is required to develop these into truly quantitative indices, but our capacity to do so depends on cross-talk among fields to facilitate the collection of comparable data across taxa.

## 2.2 | Core traits and phases of dormancy

In contrast to historic views of dormancy as a state of suspended animation, we know now that the dormant period is a dynamic stage made up of distinct, sequential phases (Carey et al., 2003; Denlinger, 2002; Hand et al., 2016; Hirche, 1996; Košťál, 2006). Animals gradually modify their behaviour, morphology and physiology in predictable, ordered ways as they proceed through dormancy. The second component of our framework is a working model of how the core traits that form the integrated dormancy phenotype are organized and regulated throughout the phases of dormancy (Figure 2). The broad working model we propose here is intended to apply across the animal phylogeny and is thus based on patterns for which there is evidence across taxa. In general, our discussion reflects evidence for the pattern across taxa, but in some instances, there is excellent evidence for the pattern in one taxon but it has only been examined a handful of times in other taxa. Thus, our working model is a hypothesis that should motivate quantitative assessments of its generality (see Section 4 and Box 2). With this in mind, citations throughout this section are intended to be used as starting points for researchers interested in comparative physiology and ecology of dormancy, and thus they may not be exhaustive or comprehensive.



**FIGURE 2** Phases and Core Traits of dormancy. During dormancy, animals proceed through distinct phases (columns, described in detail in the text) during which core phenotypic traits (rows) are up-and down-regulated (corresponding to width of grey bands). Adjacent phases may temporally overlap, not all phases occur in all species and trait regulation will vary across species

Here we outline our working model using dormancy literature from a wide range of animal taxa. The first component of this working model is the set of core traits. Core traits refer to quantifiable traits that can provide a multivariate and comparative characterization of how the physiology, morphology and behaviour of an animal undergoing dormancy changes, from active season to active season, thus making up the integrated dormancy phenotype. The most fundamental core traits are a decrease in the cell cycle (in at least some tissues) and metabolic rate during dormancy (compared to a similarly staged non-dormant animal). A decrease in either locomotor activity or reproductive function is also frequently diagnostic in animals that are dormant in otherwise active life stages. Finally, energy storage becomes essential as dormancies increase in their degree of programming (particularly the degree of recalcitrance, which usually underlies dormancies of longer duration).

The second part of our working model organizes the regulation of these core traits into distinct phases that facilitate intra- and inter-specific comparisons using biological time rather than calendar time. This is critical because, using only calendar time, dormancy phenology varies geographically according to season length, complicating comparisons of biochemical and physiological data. To overcome this challenge, insect physiologists divided deep, programmed dormancy into a set of eco-physiological phases, which describe sequential modifications to physiology and behaviour that insects undergo during transitions into and out of dormancy (Danks, 1987; Košťál, 2006). Experimental transcriptomic studies support the biological relevance of these phases (Dowle et al., 2020; Košťál et al., 2017). With this utility in mind, our phases of dormancy build on those defined by Košťál (2006) and expand their utility to all animals.

In line with Košťál, the full set of phases are defined using deep, programmed dormancies, in part because these dormancies are the most organized and predictable. All dormancies share the **Initiation** and **Activation** phases, which describe the traditional 'beginning' and 'end' of dormancy proper, but dormancies that are more responsive (lacking induction and/or with low recalcitrance) will lack some phases that are critical for deep, programmed dormancy (e.g. **Preparation**). Finally, although these phases and traits are focused on winter dormancies, which are well-studied, we expect tropical and sub-tropical dormancies that fall within the deep, programmed dormancy quadrant to be fundamentally similar.

### 2.2.1 | Preparation: Animals begin to accumulate energy stores while suppressing or halting reproduction

A key characteristic of programmed dormancy is that it is initiated in advance of the onset of adverse conditions. The first phase of the dormancy program is thus preparation, during which animals remodel their morphology and physiology in anticipation of dormancy proper. During the preparation phase, animals remain active with high metabolic rates and begin to store energy that will fuel metabolism during later phases. Most animals will accumulate internal

lipid stores, doubling or even tripling adiposity levels (Baumgartner & Tarrant, 2017; Carey et al., 2003; Dark, 2005; Derickson, 1976; Fitzpatrick, 1976; Hahn & Denlinger, 2007; Seymour, 1973). For some small mammals (e.g. chipmunks), energy may be stored externally in food caches rather than in adipose tissue. Insects, some amphibians and fish accumulate storage proteins and carbohydrates (e.g. glycogen; Costanzo et al., 2013; Denlinger, 2002; Hahn & Denlinger, 2011; Hyvärinen et al., 1985; Vornanen et al., 2009). These glycogen stores provide crucial fuel for anaerobic metabolism in species that undergo deep, programmed dormancy in anoxic environments (i.e. crucian carp; Vornanen et al., 2009). There are hints from a range of taxa that internal lipid stores are increased through some combination of hormonally controlled hyperphagia, increased digestive efficiency and decreased energy demands (Bean et al., 1983; Dark, 2005; Florant & Healy, 2012; Schwartz et al., 2015). In addition to a general hyperphagia, preference for specific nutrients may change during preparation (Staples, 2016). For example, many mammals increase their preference for unsaturated lipids (Frank, 1994; Munro & Thomas, 2004; Staples, 2016). Some combination of dietary shifts, endogenous remodelling of nutrients and selective trafficking alters the composition of fatty acids stored internally and in the make-up of cell membranes (Arnold et al., 2011; Carey et al., 2003; Košťál, 2010; Ruf & Arnold, 2008; Seebacher, 2005).

In many animals, the suppression or halting of reproductive activity is a key part of dormancy preparation. Inhibition of reproductive physiology is often permissive for dormancy expression (i.e. reproductive hormones suppress dormancy expression; see Table 2 and **Activation**). There are exceptions to this general rule particularly in bats, echidnas and bears, where species maintain or even specifically express reproductive behaviours and activity during programmed dormancy (McAllan & Geiser, 2014). For example, several bat species are able to maintain spermatogenesis and accessory organs during dormancy (Gustafson, 1979; McAllan & Geiser, 2014; Willis, 2017), and male echidnas and bats participate in copulation during arousals from dormancy (Morrow & Nicol, 2009; Thomas et al., 1979). Female bats and echidnas may maintain pregnancy during programmed dormancy, however, gestational development is usually suspended until dormancy is complete (McAllan & Geiser, 2014; Morrow & Nicol, 2009; Nicol & Morrow, 2012; Orr & Zuk, 2013; Oxberry, 1979; Racey, 1973; Wimsatt, 1969) but see (Willis et al., 2006). In contrast, bears gestate and lactate during programmed dormancy. In the case of bears, this energetically intensive feat is associated with altered blood biochemistry and more shallow metabolic depression relative to non-reproductive individuals (Tøien et al., 2011; Wright et al., 1999).

### 2.2.2 | Initiation: Animals cease feeding and activity and seek a sheltered microclimate before increasing the magnitude of metabolic suppression

During initiation, animals seek microhabitats (often sheltered, but Common Poorwills and some tree-roosting bats are notable exceptions to this rule; see Turbill, 2008; Turbill & Geiser, 2008; Woods & Brigham, 2004; Woods et al., 2019) and dramatically depress or cease

**TABLE 2** Conserved neuroendocrine signalling molecules involved in programmed dormancies

Conserved signalling molecules or systems	Core traits	Role	Relevant citations
Insulin signalling (mammals)/ insulin-like signalling (insects)	Metabolism, Energy storage	Signalling decreases with active metabolic suppression and increases when dormancy ends	Florant and Healy (2012), Hoehn (2004), Ragland and Keep (2017), Sim and Denlinger (2013) and Tessier et al. (2015)
Retinoic acid receptor & Thyroid hormone (RXR/TH; vertebrates) Ultraspiracle and Juvenile hormone (USP/JH; invertebrates)	Metabolism, Energy storage	Bioavailability is gradually suppressed as animals prepare for dormancy and then increases when dormancy ends	Dardente et al. (2014) Denlinger (2002), Denlinger et al. (2011), Epperson and Martin (2002), Hut et al. (2014), Liu et al. (2017), Vermunt et al. (1999), Wheeler and Nijhout (2003) and Zhang and Denlinger (2012)
Neuropeptide Y (NPY; vertebrates) Neuropeptide F (NPF; invertebrates)	Energy storage	Transition from high to low expression suppresses feeding behaviour as animals prepare to enter dormancy	Boswell et al. (1993), Huybrechts et al. (2004) and Levin et al. (2013)
Ghrelin (vertebrates)	Energy Storage	Strong down-regulation associated with suppression of feeding behaviour as animals prepare to enter dormancy	Florant and Healy (2012) and Healy et al. (2010)
Leptin (mammals) Unpaired 2 (Upd2; insects)	Energy Storage, Metabolism	Permissive peak associated with fattening as animals prepare to enter dormancy followed by decrease associated with metabolic suppression	Florant and Healy (2012), Freeman (2004) and Kubrak et al. (2014)
Steroid hormones (Testosterone [vertebrates], Ecdysteroids [invertebrates])	Repro. activity, Metabolism?	Bioavailability may begin to increase as animals become sensitive to cues they use to end dormancy; bioavailability tends to rapidly increase when dormancy ends	Andò et al. (1992), Darrow et al. (1988), Denlinger (2002), Lee et al. (1990), Ragland et al. (2011) and Richter et al. (2016)

locomotor activity (Carey et al., 2001; Hahn & Denlinger, 2007). Energy storage has reached maximum levels by this time.

Many species cease all feeding at the onset of initiation (including one fish; Penttinen & Holopainen, 1992), and animals often dramatically decrease their digestive system volume (Cramp et al., 2009; Hahn & Denlinger, 2011; Hume et al., 2002; Martin et al., 2008; Naya et al., 2009). The gut microbiome of many animals is also modified as animals begin fasting during initiation (Bailey et al., 2010; Carey et al., 2013; Gosling et al., 1982; Liu et al., 2016; Secor & Carey, 2016; Sommer et al., 2016). For animals that consume food intermittently during dormancy, such as food-caching rodents, some bats, bears and some insect larvae (Avery, 1985; Boyles et al., 2006; Goddeeris et al., 2001; Humphries et al., 2003; Kirby et al., 2019; Krofel et al., 2016; López et al., 1995; Pigeon et al., 2016; Turbill, 2008), digestive system volume may still be reduced, but maintaining a more active gut throughout winter is likely to increase overall maintenance costs (Humphries et al., 2003).

During initiation, metabolic rate is suppressed to a fraction of active season metabolic rates, through some combination of active inhibition of metabolic pathways and passive suppression due to low temperatures (Baumgartner & Tarrant, 2017; Hahn & Denlinger, 2007; Humphries et al., 2003; Staples, 2016). In most cases, the mechanisms underlying metabolic suppression are still an open question and active field of research (Hand et al., 2011; Mathers & Staples, 2019). The cell cycle is arrested leading to a cessation of growth and development (Carey et al., 2003; Dowle et al., 2020; Hand et al., 2016).

For terrestrial ectotherms, including insects, reptiles and amphibians, body temperatures may fall below the freezing point of body tissues during

dormancy in high latitude or altitude environments; thus, developing freeze tolerance or resistance is a critical process that occurs during initiation (Costanzo et al., 2013; Storey & Storey, 2013; Toxopeus & Sinclair, 2018). Endothermic hibernators defend a minimum body temperature using internal heat production when environmental temperatures fall below a critical threshold, and thus their body temperature rarely approaches freezing; however, some endotherms (e.g. arctic ground squirrels) allow their body temperature to drop as low as  $-2^{\circ}\text{C}$  and thus must also employ some mechanisms (supercooling) to prevent freezing (Barnes, 1989). Stress signalling cascades may be progressively activated during the initiation phase, leading to increased levels of some protective molecules (e.g. molecular chaperones, cryoprotectants and antioxidants; Carey et al., 1999; Joanisse & Storey, 1996; King & MacRae, 2015; Lee, 2010; Moreira et al., 2016; Storey, 2010; Wijenayake et al., 2018). Although some underlying commonalities in regulation of stress hardiness may be useful to characterize dormancy, we did not feel the evidence was of sufficiently high agreement and quality to include this in the core traits at this time.

### 2.2.3 | Maintenance: Metabolic suppression reaches a maximum and may be interspersed with periodic arousals. Energy stores are gradually depleted

During the maintenance phase of programmed dormancy, animals exhibit deep and prolonged suppression of metabolic rate, and sustained low body temperature (provided the environment is below active season body temperature). The blood of animals including

molluscs, reptiles, amphibians, and mammals becomes hypercapnic and these animals undergo respiratory acidosis (Malan, 2014). Hypercapnia may be a useful marker of dormancy progression but has not yet been investigated in a sufficiently wide range of animals to justify inclusion as a core trait.

Metabolic suppression may be punctuated by periodic arousal cycles during which metabolic rate increases and endotherms regain euthermic body temperatures (Staples, 2016). Although these arousal cycles are best known in rodent hibernators, they also occur in at least two insect species, one fish species, one lizard species and one bird species (Campbell et al., 2008; Crozier, 1979; Rismiller & McKelvey, 2000; Sláma & Denlinger, 1992; Woods et al., 2019; Figure 3). In both insects and mammals studied to-date, the period of these metabolic cycles increases to a maximum during the maintenance phase (Geiser et al., 1990; Sláma & Denlinger, 1992; Zervanos et al., 2010).

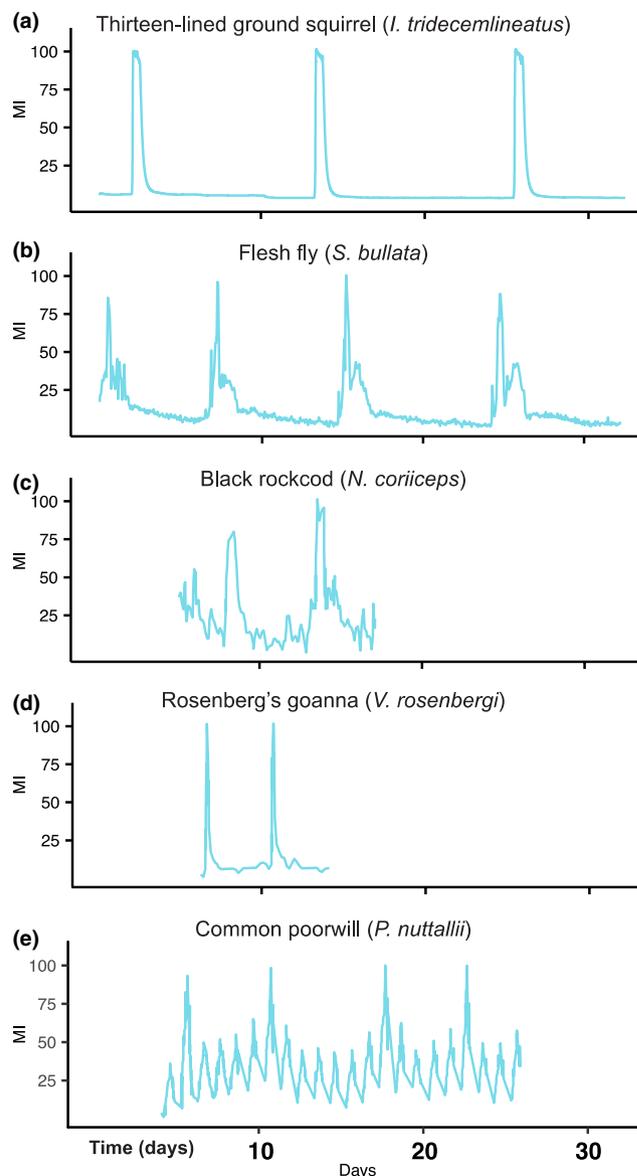
Nutrient stores are usually gradually depleted during the maintenance phase (but see Lehmann et al., 2016), and fuel preferences may shift correspondingly. Lipids are the primary fuel that animals catabolize during dormancy provided oxygen is not limiting, but proteins and carbohydrates may become more important later in dormancy, during anoxia or hypoxic periods, or under especially low environmental temperatures (Adedokun & Denlinger, 1985; Andrews, 2019; Boutilier et al., 1997; Buck & Barnes, 2000; Vornanen, 2011; Vornanen & Paajanen, 2006).

**2.2.4 | Potentiation: The magnitude and recalcitrance of dormancy is gradually reduced, and animals are sensitized to the environmental cues that trigger the return to growing season physiology. Animals become competent to resume growing season activities when the environment becomes permissive**

The endogenous lock put in place during initiation must be released so that animals can respond to cues that signal the return of favourable environmental conditions. Until those cues are detected, animals remain dormant, but the dormancy is now exogenously controlled. The potentiation phase includes the period over which the endogenous lock on development and activity is gradually released, until active season behaviour resumes. The mechanisms by which the endogenous lock is released is an active research area in both insect and mammal fields (Dowle et al., 2020; Hut et al., 2014; Meyers et al., 2016).

In the insect literature, this phase is currently referred to as 'termination' followed by 'post-diapause quiescence' (Košťál, 2006). In the mammalian literature, this phase has been referred to as the 'emergence period' (French, 1982), and 'termination' refers to the end of the final torpor bout or emergence from the hibernacula. We suggest '**potentiation**' as a term that could be adopted across fields and captures the gradual sensitization of the organism to cues that will trigger the resumption of activity, development, growth and (in many cases) reproduction.

The covert nature of potentiation makes this phase very difficult to detect unless manipulative experiments can be performed. In insects,



**FIGURE 3** Distinctive, multi-day cycles in metabolic activity (transformed to unitless measure Metabolic Intensity (MI) for easier visual comparison, where 100 is equal to the maximum metabolic activity measured in that study) are a feature of the maintenance phase in many small mammals (a, MI represents core body temperature, unpublished data, Matthew T. Andrews), a few insect species (b, MI represents metabolic rate, unpublished data, Daniel A. Hahn and Chao Chen), at least one fish (c, MI represents heart rate, figure adapted from Campbell et al., 2008), one lizard species (d, MI represents core body temperature, figure adapted from Rismiller & McKelvey, 2000) and one bird species (e, MI represents inferred body temperature, figure adapted from Woods et al., 2019)

this phase is diagnosed by a rapid increase in metabolic rate, or rapid development, upon return to permissive conditions (Hodek, 1996; Košťál, 2006). In mammals, torpor bout duration shortens, or mammals may experience pre-emergent euthermic intervals but retain the ability to express torpor (Geiser et al., 1990; Sláma & Denlinger, 1992; Tøien et al., 2011; Williams et al., 2014; Zervanos et al., 2010).

Potentiation may comprise a large portion of the dormant period in some species. Instances where bat species and some bears apparently

become intermittently active during dormancy to feed and/or drink are consistent with an extended potentiation phase (Avery, 1985; Ben-Hamo et al., 2013; Boyles et al., 2006; Brigham, 1987; Dunbar et al., 2007; Kirby et al., 2019; Krofel et al., 2016; Lausen & Barclay, 2006; Pigeon et al., 2016; Whitaker & Rissler, 1992, 1993). Activity in bat species is often associated with more permissive environmental conditions (e.g. warmer temperatures) and may be related to an individual's dehydration status or body condition (Ben-Hamo et al., 2013; Boyles et al., 2006; Brigham, 1987; Lausen & Barclay, 2006).

The gradual decrease in dormancy recalcitrance that occurs during potentiation culminates in the animal being responsive to environmental cues that will trigger the resumption of development and activity. Thus, potentiation plays a critical role in synchronizing spring phenology of populations. The ability to respond to environmental cues is associated with increased synthesis and release of regulatory factors including many neuroendocrine hormones (Table 2) and with restored competency of target tissues (Fujiwara et al., 1995; Košťál, 2006; Košťál et al., 2017; Yamada & Mizoguchi, 2017). In some cases, the reproductive system may begin or resume development and activity, however, full competency of the reproductive axis usually requires that animals enter the activation phase (Barnes et al., 1986; McAllan & Geiser, 2014; Morrow & Nicol, 2009; Nicol & Morrow, 2012; Oxberry, 1979; Racey, 1973; Richter et al., 2016; Williams, Buck, et al., 2017; Wimsatt, 1969). Potentiation phase ends when activity and development resume, following the onset of favourable environmental conditions.

In some species or sub-groups within species (e.g. male Arctic ground squirrels), dormancy ends spontaneously without the need for external stimuli (Körtner & Geiser, 2000; Košťál, 2006; Williams, Buck, et al., 2017). In these cases, the potentiation phase does not occur.

### 2.2.5 | Activation: Animals resume growing season activities, rebuild tissues catabolized during dormancy, and repair accumulated damage. Activation is completed when the growing season life stage is fully realized, and physiological processes have reached full intensity

Once the appropriate cues or internal stimulus have been received, growing season processes must be restarted in a set order. In juvenile animals, growth and development must resume prior to reproductive maturation. Animals already in the adult life stage may initiate or resume reproductive activities (e.g. gestation) immediately upon entering activation.

Our fine scale understanding of the order of events during activation is limited. In insects, transcriptomic work suggests that metabolism and cellular growth/proliferation are up-regulated together before morphogenesis, growth and development; however, some of the regulatory differences leading to activation must begin in an earlier phase (i.e. during potentiation; Dowle et al., 2020; Meyers et al., 2016;

Ragland et al., 2011). Similarly, we know that the same neuroendocrine systems are involved in both the inhibition and activation of reproduction in mammals as part of the dormancy program, but the connections between these systems differ between preparation/initiation and potentiation/activation (Dardente et al., 2014; Follett, 2015; Hut et al., 2014).

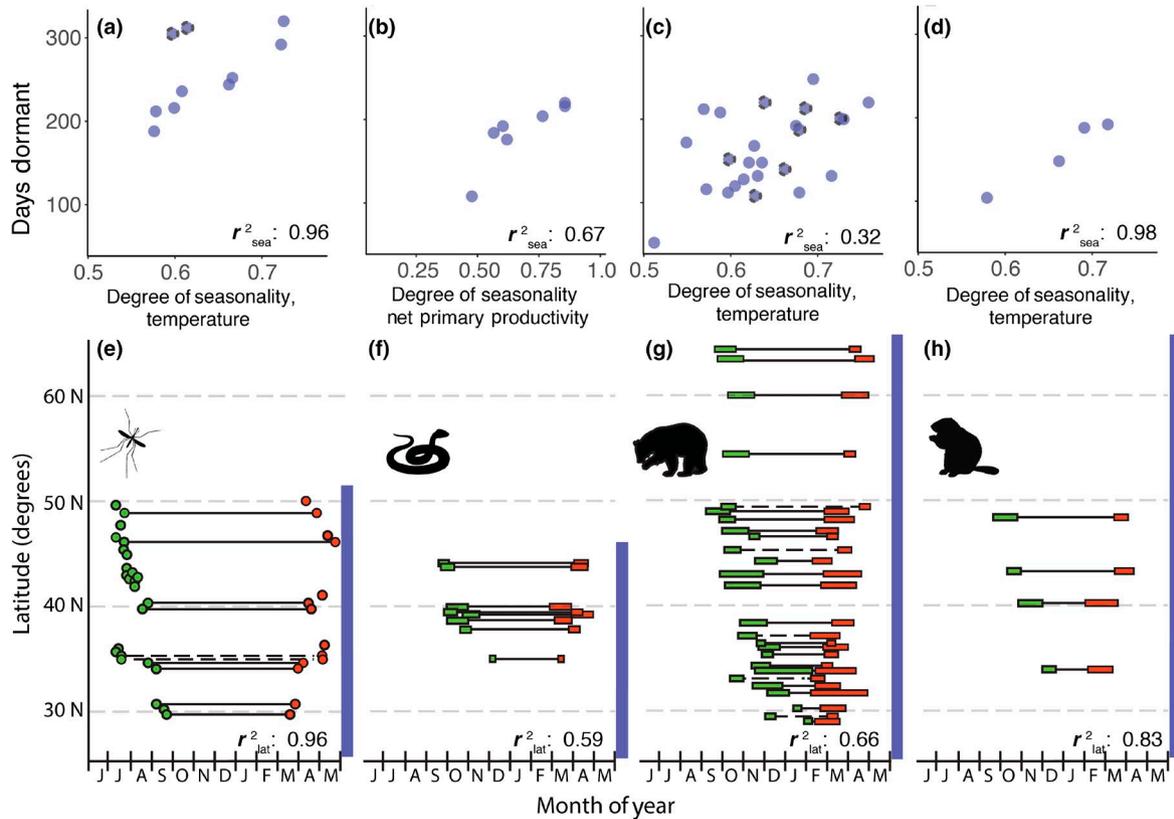
Feeding resumes soon after the onset of activity but may ramp up slowly (Schwartz et al., 2013). The slow onset of feeding may result in part from regrowth and remodelling of the gut (micro-villi, etc.) and the microbiome, with spring microbiotas reflecting a repopulation of an active season microbiota profile once feeding resumes (Carey et al., 2013).

The last two phases, during which animals end dormancy and return to growing season physiology, are the least understood parts of the dormancy program in all taxa.

## 3 | EVOLUTION AND ECOLOGY OF DORMANCY ACROSS ANIMALS

### 3.1 | Seasonality as a end major selective pressure underlying deep, programmed dormancy

Considering animal dormancies across the entire animal phylogeny allows us to broadly explore the association between seasonality and the major axes of dormancy. Deep, programmed dormancies such as mammalian hibernation and insect diapause are an important component of the annual cycle in seasonal environments (Carey et al., 2003; Hand et al., 2016). Seasonality can be quantified based on the predictability and magnitude of fluctuations in temperature, precipitation and primary productivity (Kreitzman & Foster, 2010; Lisovski et al., 2017; Williams, Ragland, et al., 2017). Seasonality increases with latitude, is greater in terrestrial and freshwater compared to marine habitats, and is greater in northern continental compared to southern oceanic climates (Lisovski et al., 2017; Sunday et al., 2011). Correspondingly, deep, programmed dormancy (diapause or hibernation compared to quiescence or daily torpor) is more common at high latitudes in North American mammals (Ruf & Geiser, 2015), in continental compared to oceanic climates in invertebrates (Convey, 1996; Sinclair et al., 2003), and in terrestrial and freshwater compared to marine taxa (Cáceres, 1997). The duration of dormancy increases with degree of seasonality within and among taxa (Figure 4), reflecting the longer winters at high latitudes. Exceptions to latitudinal patterns in dormancy duration occur at high altitude sites, which ecologically resemble higher latitude populations (Figure 4, dashed lines). In insects, latitudinal clines in diapause duration have been linked to genetic variation in both induction (Bradshaw & Holzapfel, 2001; Lehmann, Lyytinen, et al., 2015), and recalcitrance (Masaki, 2002; Posledovich et al., 2015). The contribution of recalcitrance to dormancy duration in other taxa has not been well documented, due to the complexity of laboratory manipulations required to isolate the factors setting dormancy duration. Dormancy magnitude, as measured by metabolic suppression, is also greater in diapausing insects from higher



**FIGURE 4** The duration of programmed dormancy across taxa is positively correlated with greater environmental seasonality. (a–d) We compiled data on dormancy duration for four North American species (a, *Wyeomyia smithii* [Pitcher plant mosquito]; b, *Elaphe obsoleta* [Ratsnake]; c, *Ursus americanus* [American black bear]; d, *Marmota monax* [Woodchuck]) and calculated dormancy duration as number of days between the earliest initiation day and latest activation day reported. Degree of seasonality temperature and primary productivity were determined using latitude and longitude from each population matched to seasonality index values from Lisovski et al., 2017 for  $1 \times 1$  degree squares across North America (see Table S5;  $R^2$  values from linear models including elevation as a continuous predictor are indicated in the lower right hand corner in each panel). Each blue circle corresponds to a different population; circles with dashed, black outline indicate populations resident above 500 m elevation. Results from linear models and additional details are provided in Table S6. (e–h) Because seasonality indices are highly correlated with latitude in North America (Temperature:  $R^2 = 0.62$ ,  $p < 4.9e-8$ ; Net primary productivity:  $R^2 = 0.41$ ,  $p < 0.002$ ; Precipitation:  $R^2 = 0.35$ ,  $p < 0.041$ ), similar patterns are evident when data are plotted by latitude (e–h,  $R^2$  for models substituting latitude for degree of seasonality indicated in lower right of each panel). Vertical, blue bars to the right of each panel indicate species latitudinal range above  $25^\circ\text{N}$ . (e) Green-filled circles show critical photoperiod (CP) for diapause induction across *W. smithii* populations collected at different latitudes in North America, whereas orange-filled circles show CP for diapause termination. CPs were determined experimentally in controlled laboratory environments. Black lines connect induction and termination CPs from the same populations. CPs for both periods were not determined for all populations. Dashed lines are populations from altitudes  $>500$  m. (f–h) Green and orange-filled bars show range or mean  $\pm 1$  SD, depending on data provided from each study, of dormancy initiation and activation respectively. Dashed lines show populations from altitudes  $>500$  m

latitudes (Lehmann, Piironen, et al., 2015). In endotherms, the magnitude of dormancy, has not been widely assessed across populations under controlled conditions apart from the small study by Fenn et al. (2009), which is largely inconclusive because of its small sample size and confounding effects of age and sex. Diapause induction, recalcitrance and magnitude have a distinct genetic basis in insects, suggesting that they can evolve independently to match dormancy characteristics to ecological conditions (Dambroski & Feder, 2007; Masaki, 2002). An important next step is to systematically evaluate the ways that induction, recalcitrance and magnitude in multiple core traits coevolve in diverse taxa and testing whether coevolution of these traits is associated with particular aspects of seasonal environments (see Box 2).

### 3.2 | Origins of deep, programmed dormancy

Deep, programmed dormancy occurs broadly across the tree of life, spanning invertebrate and vertebrate lineages that split around 700 MYA (Figure 5). Extant invertebrates and vertebrates evolved from ancestors that lived in a cold and weakly seasonal ocean and the emergent groups (arthropods, molluscs and vertebrates) independently colonized more seasonal terrestrial and freshwater habitats multiple times (Lozano-Fernandez et al., 2016). The molecular machinery used to regulate the core traits involved in deep, programmed dormancy originated prior to this split. Photoperiodic sensing and daily timing is ubiquitous (Bradshaw & Holzapfel, 2007; Hut & Beersma, 2011; Kreitzman & Foster, 2010; Nelson et al., 2010), and the bases for this system

## BOX 2 Key questions raised by an eco-physiological framework for animal dormancy

### Ecological drivers of dormancy evolution

- Do particular aspects of seasonal environments (water and food availability, temperature, etc.) covary with the magnitude of core traits across taxa, or are the interactions between seasonal constraints and core traits taxon-specific?
- Are there predictable patterns in the relative duration of phases of the dormancy program that underlie ecologically associated phenological variation?

### The physiological & molecular origins of dormancy programs

- In the diving response, some organs and regulatory processes play a critical role in facilitating longer dives, whereas others are less important (Hochachka, 2000; Hochachka & Somero, 2002). Which core traits and regulatory processes are crucial to extending dormancy duration and resistance to biochemical stressors during this period? Are these critical traits taxa-specific?
- What is the molecular basis of recalcitrance? Do clock genes play a similar role in this process across taxa?
- To what extent are molecular pathways implicated in deep, programmed dormancies involved in regulating core traits in similar ways in more responsive dormancies?
- What are the limits to maintaining suppressed metabolism for long periods? Does the existence of metabolic cycles outside of mammals indicate a shared constraint? Are the regulatory mechanisms shared or distinct?

### Dormancy and life-history evolution

- Are there predictable and repeated 'adaptive walks' across dormancy axes that animals take in evolving deeper and more programmed dormancies (e.g. increases in magnitude precede increases in recalcitrance)?
- Is there a greater diversity of dormancies that exist and fall along all major axes of the dormancy program (i.e. can we 'fill out' more of the quadrants in Figure 1)? What factors constrain or facilitate the evolution of shallow, programmed dormancies across taxa?

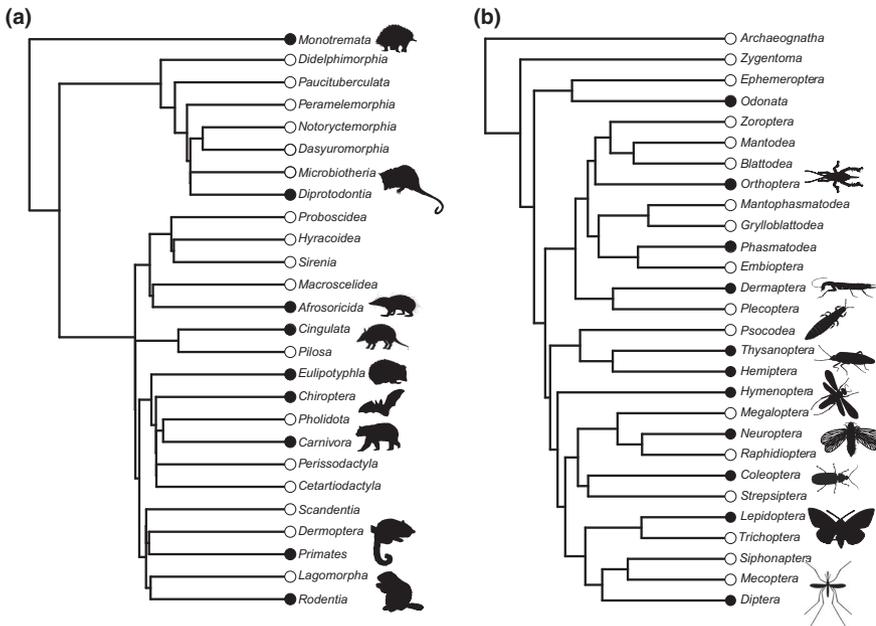
evolved early in the tree of life (cyanobacteria; Brunner et al., 2008; Dvornyk et al., 2003; Hut & Beersma, 2011; Simons, 2009). The molecular mechanisms that coordinate metabolic arrest are also ancestral, having evolved in response to hypoxia in ancient oceans (Hochachka et al., 1993; Seebacher, 2018). However, the organization of these ancestral, component parts into a stereotypical dormancy program appears to have been repeatedly derived. Within birds and mammals, heterothermy is ancestral, but hibernation and daily torpor are seen as derived phenomena that build on this ancestral capacity (van Breukelen

& Martin, 2002; Carey et al., 2003; Lovegrove, 2017; Malan, 2014; Ruf & Geiser, 2015). In insects, diapause displays rapid evolution, limited phylogenetic conservation of the diapausing life stage and apparent evolutionary convergence of gene regulation through diapause, suggesting that diapause has evolved convergently many times in many clades (Danks, 1987; Ragland & Keep, 2017; Tauber et al., 1985). The repeated co-opting and coordination of ancestral physiological systems to support derived functionality (i.e. programmed dormancy) is thus analogous to the mammalian diving response, where the ancestral constituent traits are brought together in highly stereotypical ways to achieve extreme intensities and duration of a complex compound of traits (Hochachka, 2000; Hochachka & Somero, 2002). Identifying those traits that are critical for extending dormancies will be important to further defining core traits (see Box 2).

Supporting this view of repeated exaptation of ancestral building blocks, there are many examples of shared molecular mechanisms coordinating programmed dormancy, particularly in pathways that integrate environmental signals and control energy metabolism (Table 2). For example, the homologous receptors Retinoic acid receptor (*Rxr*; vertebrates) and Ultraspiracle (*Usp*; invertebrates) both appear to regulate availability of thyroid hormones (vertebrates) and juvenile hormone/ecdysteroids (invertebrates). These systems influence reproductive and metabolic amplitude across programmed dormancy, and there is evidence that they control cyclic metabolic activity during the maintenance phase (Denlinger et al., 1984; Magnus & Henderson, 1988; Schwartz et al., 2013). Insulin and insulin-like signalling pathways in mammals and insects are also regulated in similar patterns during programmed dormancy, perhaps because they converge on secondary signalling pathways that modulate cell cycle activity and metabolism (Barbieri et al., 2003; Sim & Denlinger, 2013).

## 3.3 | Evolutionary and life-history consequences

Animals expressing dormancy also share broader aspects of their life history. Dormancy leads to a slowing of biological time and enhanced maintenance of cellular homeostasis, including increased resistance to some types of stress (Carey et al., 2003; Hoekstra et al., 2020; Schmidt et al., 2005). Dormancy decreases mortality rates and slows senescence, leading to life span extension in both insects and mammals (Tatar et al., 2001; Tatar & Yin, 2001; Turbill et al., 2011, 2013; Turbill & Prior, 2016). Some of these life span extension effects likely arise from the thermodynamic effects of low temperatures on the rate of living (Flouris & Piantoni, 2014; Stark et al., 2018), but evidence from a range of taxa suggests that actuarial senescence is delayed due to a shut-down of neuroendocrine signalling, independent of temperature (Tatar et al., 2001; Tatar & Yin, 2001). Along with life span extension, dormancy is associated with delayed development and maturity, later age at first reproduction and reduced investment into reproduction (Schmidt et al., 2005; Tatar et al., 2001; Turbill et al., 2011). Higher diapause propensity is genetically correlated with longer life span, higher resistance to some types of stress and extended development times in *Drosophila melanogaster* (Schmidt et al., 2005), suggesting that dormancy invokes a shift towards a slower life-history



**FIGURE 5** Distribution of programmed dormancy across the mammalian (a) and insect (b) phylogenies. Orders containing species that express programmed dormancy are indicated by filled circles (Heldmaier et al., 2004). Most highlighted orders represent deep, programmed dormancy but a few represent shallow, programmed dormancy (e.g. Monotremata and Carnivora). See Table S6 for references. Mammal phylogeny from (Fritz et al., 2009) and insect phylogeny from (Wiens et al., 2015). Silhouettes and licenses are from phylopic.org

strategy, perhaps driven by a reallocation of resources towards somatic maintenance and away from reproduction. Our comparative framework raises questions about whether dormancy evolution and shifts in life history across taxa occur via similar processes (see Box 2). At the molecular level, this life-history shift may be facilitated by alterations to insulin signaling, a highly pleiotropic pathway which regulates growth, energy metabolism and life span, and is involved in dormancy regulation in a wide range of taxa (see Table 2; McGaugh et al., 2015; Sim & Denlinger, 2008; Sparkman et al., 2012; Williams et al., 2006; Wolkow et al., 2000).

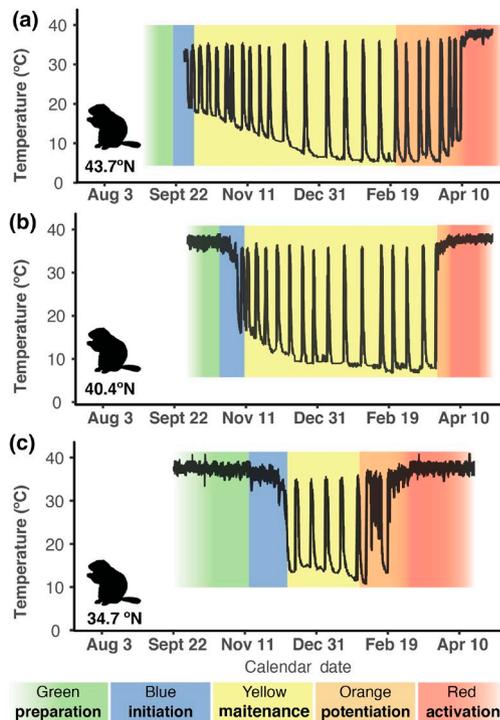
#### 4 | OPPORTUNITIES AND OUTLOOK

Our framework uses three main components (axes, phases and core traits) to categorize and quantifying ecologically relevant variation in dormancies across animal taxa. The axes (induction, recalcitrance and magnitude) provide an experimentally tractable means of categorizing dormancy that can be compared among species across the animal phylogeny, and they capture the ecologically relevant aspects of dormancy more richly than traditional dichotomies such as diapause/quiescence or hibernation/daily torpor. Induction and recalcitrance are ecologically important because they together determine the length of dormancy, and their underlying physiological and molecular mechanisms are the material that evolution acts on to fine-tune dormancy duration to environmental conditions. The magnitude of dormancy is ecologically important because it determines strategies of energy acquisition (e.g. requirements for energy storage during preparation, locomotor performance during dormancy setting ability to forage) and allocation (e.g. maintenance costs during dormancy, setting rates of energy depletion). Using these three axes allows us to clearly separate the shallow reproductive diapause of *Drosophila melanogaster* from the deep programmed diapause of *Sarcophaga bullata*, and to differentiate between an annual aestivation seen in *Cheirogaleus medius* and the more responsive aestivation displayed by *Glis glis*.

The phases allow us to compare experimental data according to biological rather than calendar time, and, by using diagnostic traits that occur across taxa, open up opportunities for comparative research. Applying these phases to a mammalian hibernator suggests that the relative length of phases differs along a latitudinal gradient (Figure 6), suggesting that increased duration of dormancy does not simply reflect extension of a single phase (e.g. maintenance). While we do not expect researchers to abandon field-specific terminology, signposting phases in which experimental data are collected using this framework will facilitate an integration of fields in the primary literature, addressing the extreme siloing that we documented in our literature search.

The core traits are useful because they can provide a multi-faceted quantitation of the degree of intra- and interspecific variation in dormancy magnitude and regulation. For this benefit to be realized, we need a standardized way of measuring the degree of plasticity in each trait. We suggest that, for comparative purposes, researchers report the maximum change in core traits relative to specified active season values (e.g. reproductive or non-reproductive). Defining degree of suppression is already common in the case of metabolic rate, allowing us to compare the degree of metabolic suppression of poikilotherms and mammals (e.g. Guppy & Withers, 1999; Ruf & Geiser, 2015), and extending this approach can be used to quantify the degree of energy accumulation and depletion and the degree of reduction in locomotor and reproductive activity. Conceptualizing these core traits as components of the dormancy program that can be tweaked independently suggests core molecular and metabolic pathways that may be altered in animals expressing similar dormancy types.

A unification of fields of dormancy research offers broad opportunities for cross-pollination of research questions and hypotheses. For example, in the insect literature, clines in clock gene allele frequency underlie evolved differences in diapause induction and initiation timing, and these alleles are under selection due to climate change (Bradshaw & Holzapfel, 2001;



**FIGURE 6** Qualitatively delineated phases in the dormancy program may not vary proportionally in duration with dormancy period across latitudes or by species. (a–c) Body temperature traces from hibernating Woodchucks (*Marmota monax*, data from S. Zervanos). Body temperature traces from each population were qualitatively divided into phases of dormancy (Green, Preparation; Blue, Initiation; Yellow, Maintenance; Orange, Potentiation; Red, Activation). Duration of each phase can vary among individuals and populations, and it will vary inter-annually within populations

Pruisscher et al., 2018). Similar clines in timing also exist in other taxa (Figures 4 and 6), but we do not know the extent to which they share a common mechanism (see Box 2; Fenn et al., 2009; Grabek et al., 2019; Lane et al., 2011, 2019; Zervanos et al., 2010). The mammalian literature has shown that diet during preparation may influence the magnitude and duration of maintenance phase. Does diet meaningfully influence programmed dormancy in insects and other animals that have a greater ability to modify lipids endogenously? Other interesting avenues include the role of sex steroids in phenology (e.g. protandry) outside of ground squirrels (Richter et al., 2016; Williams, Buck, et al., 2017), the prevalence of hypercapnia and respiratory acidosis in insects (Malan, 2014) and common mechanisms by which dormancy recalcitrance is reduced during maintenance and potentiation phases (Dowle et al., 2020; Hut et al., 2014; Košťál, 2006; Meyers et al., 2016; Powell et al., 2020; Wadsworth et al., 2013).

Inevitably, creating a broad and generalizable framework requires glossing over some exceptions and system-specific details. Some of the physiological and ecological processes that are discussed here as analogous across species will not appear so as we learn more, researchers working on animals outside the insect and mammal systems that we have focused on will no doubt have insights that will require

the framework to adapt and expand. Broad application of the framework will require substantial conceptual and experimental work from researchers across fields. However, we hope that the framework outlined here will provide a starting point for that work to take place. We strongly believe that a broad and phylogenetically inclusive dormancy framework will facilitate a better understanding of both the mechanisms and origins of dormancy, stimulating forward momentum and novel directions for the broader field of dormancy research.

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#### AUTHORS' CONTRIBUTIONS

All authors contributed equally to developing the ideas and writing the manuscript.

#### DATA AVAILABILITY STATEMENT

There are no data to archive for this manuscript.

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## SUPPORTING INFORMATION

Additional supporting information may be found online in the Supporting Information section.

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