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5 Title: Neural programming of seasonal biology in birds and mammals: a modular perspective.

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8 Authors: Tyler J Stevenson*, Timothy A Liddle, Calum Stewart, Christopher J Marshall,

9 Gaurav Majumdar.

10

11

12 Affiliation: Institute of Biodiversity, Animal Health and Comparative Medicine, University

13 of Glasgow, Glasgow G61 1QH, United Kingdom.

14

15 * Corresponding author:

16 Tyler Stevenson

17 235 Jarrett Building

18 Garscube Campus

19 Inst. Biodiversity, Animal Health and Comparative Medicine

20 University of Glasgow

21 Glasgow, G61 1QH

22 e. tyler.stevenson@glasgow.ac.uk

23

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30 Abstract (250)

31 Most animals in the temperate zone exhibit robust seasonal rhythms in physiology and
32 behavior. The integration of predictive and supplementary environmental cues (e.g.,
33 nutrients) involves a series of discrete, and interconnected brain regions that span
34 hypothalamic, thalamic, mesencephalic, and limbic regions. These adaptive changes in
35 neuroendocrine structures and cellular plasticity have likely evolved to support species-
36 specific seasonal life-history transitions. Despite significant advances in our understanding of
37 ecological responses to different environmental cues, there remains a paucity in literature on
38 how these diverse cues impact the underlying neural and cellular substrates. To date, the
39 predominant scientific approach has focussed on neuroendocrine responses to annual changes
40 in daylength, referred to as photoperiod, due to the robust physiological changes to light
41 manipulations in laboratory settings. Here, we highlight the relatively few animal models that
42 have been effectively used to investigate how predictive day lengths, and supplementary cues
43 are integrated across hypothalamic nuclei, and discuss the key findings of how seasonal
44 rhythms in physiology are governed by adaptive neuroendocrine changes. We discuss how
45 specific brain regions integrate environmental cues to form a multiple modal system that have
46 evolved in to optimize timing of seasonal physiology. Overall, the review aims to highlight
47 the existence of a modular network for the control of seasonal rhythms and indicates that
48 natural selection can operate independently on different neuroanatomical and cellular
49 substrates to support an organism's fitness.

50

51 **Introduction**

52 Most long-lived (i.e., >1yr) animals that inhabit temperate zones evolved neural mechanisms
53 to time seasonal transitions in life-history traits (Wingfield et al., 1992, Ball, 1993, Stevenson
54 et al., 2017). In some cases, there are simple stimulus-response events in which
55 environmental cues, such as precipitation or social context, induce a seasonally adaptive
56 specialized change in physiological stability (Hahn and MacDougall-Shackleton, 2008).
57 There are also endogenous annual programs that anticipate the future and function to prepare
58 an individual for predictable environmental change (Lincoln, 2019). These endogenous
59 programmed changes in seasonal physiology are termed circannual rhythms, as the
60 physiological oscillations will continue in the absence of any change in the environment
61 (Helm and Stevenson, 2015). In this review, we will first discuss the current understanding of
62 circannual rhythmicity in the central nervous system. Then, we will cover how different
63 environmental cues are integrated across hypothalamic, limbic, and cortical brain regions,
64 functioning to fine-tune the timing of seasonal physiology. An exhaustive overview of the
65 neural response across all birds and mammals is beyond the scope of this review but instead,
66 the paper will focus on a few select animal models. A comparative approach that draws from
67 mouse and rat literature will be employed to propose a multi-modal neural system for the
68 control of seasonal rhythms with examples focusing on sex-dependent and -independent
69 control of reproductive physiology.

70

71 **Programming seasonal physiology**

72 Some of the best examples of endogenous seasonal rhythmicity in life history traits are
73 observed in temperate birds (Wingfield et al., 2008). Studies in African stonechats
74 (*Saxicola torquatus*) held in constant photoperiod and temperature conditions maintain
75 oscillations in gonadal size and molt for up to 7.5 years (Gwinner and Dittami, 1990). The

76 period length of the oscillation averaged 9.1 ± 1.9 months for the duration of the study
77 resulting in nine complete cycles. Female stonechats exhibit an initial short period (i.e., 9-10
78 months) for the first three years and then subsequently lengthened annual rhythmicity to
79 nearly 12 months thereafter. Endogenous circannual rhythms in migration and reproduction
80 have been identified across a wide range of bird species and include Siberian stonechats
81 (*Saxicola maurus*) (Helm et al., 2009), Pied flycatchers (*Ficedula hypoleuca*) (Helm et al.,
82 2019), and Spotted munia (*Lonchura punctulata*) (Budki et al., 2012). The Golden-mantled
83 ground squirrel (*Citellus lateralis*) is one of the most studied animal model and is particularly
84 appropriate for the study of mammalian circannual programs. Under constant laboratory
85 conditions of 12L:12D photoperiod and approximately 2°C temperature, ground squirrels
86 displayed annual cycles of hibernation and active phases consistent with wild conspecifics
87 (Pengelley and Fisher, 1957). The precise neurobiological basis of circannual timing remains
88 elusive, although the pars tuberalis of the anterior pituitary gland (Lincoln and Hazlerigg,
89 2010) and tanycytes (Lewis and Ebling, 2017) along the third ventricle of the hypothalamus
90 have been proposed as potential substrates.

91 The annual change in daylength is a predictive environmental cue that is used by many
92 birds (Dawson et al., 2001) and mammals (Goldman, 2001) to entrain endogenous programs
93 in seasonal rhythms. The neurobiology of photoperiodism, or the neural coding of day length,
94 is the best understood exogenous cue due to the robust changes in physiology (Farner and
95 Follett, 1966; Hazlerigg and Wagner, 2006). Other environmental stimuli, such as social
96 cues, temperature, and nutrient availability have been shown to influence sex-dependent
97 seasonal reproduction to local environmental conditions (Ball and Ketterson, 2008, Tolla and
98 Stevenson, 2020). Over the past couple decades, the use of immediate early gene expression
99 in midbrain, hypothalamic, limbic, and cortical brain regions have shown a network of
100 cellular activity that reflects the neural coding of social behavior in birds, mammals, and even

101 fish (Newman, 1999; Goodson, 2005). The patterns of immediate early gene activation and
102 distribution of neuropeptides (e.g., vasotocin/vasopressin) provides insights on how seasonal
103 social behaviour including aggression, affiliation, copulatory and parental behaviour are
104 regulated (Goodson, 2005). Social behaviour has also been shown to effect gene expression
105 related to seasonal reproduction in starlings (Perfito et al., 2015). Annual changes in
106 temperature have long been known to impact timing of reproduction in birds (Visser, 2008)
107 and emergence of hibernation in mammals (Inouye et al., 2000). External and visceral
108 temperatures are detected and communicated to discrete neurons in the anterior
109 hypothalamus/preoptic area (AH-POA) that integrate both warm- and cold-temperatures (Tan
110 and McKnight, 2018). How these cells integrate local and transitive temperatures (e.g.,
111 vernal, autumnal) is not fully understood. This paper will discuss the neural integration of
112 predictive and supplementary environmental cues and present a modular network for the
113 timing of seasonal physiology.

114

115 **Mammalian and Avian Animal Models for Mechanisms of Seasonal Rhythms**

116 There was an exponential increase in the number of yearly publications on seasonality in
117 mammals and birds from the 1970s to early 2000s (Fig.1A). The ecological perspective
118 applied to seasonal rhythms in Great tit (*Parus major*) and Blue tit (*Cyanistes caeruleus*)
119 (Visser et al., 2010) populations, along with Golden-mantled ground squirrel (Mrosovsky,
120 1975) and Red deer (*Cervus elaphus*) (Guinness et al., 1971), have been invaluable for
121 interpreting how environmental cues are integrated at morphological and physiological
122 levels. For many reasons, our understanding of the neural mechanisms that control seasonal
123 rhythms have relied on relatively few animal models that adapted well to laboratory
124 conditions. Animal models used for most laboratory-controlled experiments include
125 biomedical mice, rats, sheep, hamsters, and chickens (Fig.1B). Studies of seasonal rhythms in

126 sheep have largely focused on veterinary medicine (Scheerlinck et al., 2008) and basic
127 science (Lehman et al., 2002). The large hypothalamic and pituitary tissue obtained from
128 sheep presents as a valuable system to uncover the role of reproductive neuropeptides
129 (Weems et al., 2015) and photoperiodic (Lincoln et al., 2003) control of seasonal rhythms.
130 White-footed mice (*Peromyscus leucopus*) has been used as a model organism for the study
131 of mammalian seasonality for decades and is currently the second most common model
132 documented within publications referencing seasonality (Fig.1B). In wild and laboratory
133 conditions, white-footed mice exhibit reliable, and predictable physiological responses to
134 changing light conditions. They also exhibit a short-term form of hibernation referred to as
135 torpor, in response to decreasing day lengths (Lynch et al, 1978). A significant advantage of
136 using white-footed mice has been the availability of a quality genome since 2002 (Waterston
137 and Pachter, 2002), that has facilitated gene-behavior relationship analyses. Siberian hamster
138 (*Phodopus Sungorus*) with its recently available genome sequence (Bao et al., 2019) has also
139 been a useful model due to the small size, robust physiological rhythms in response to
140 photoperiodic changes facilitating large scale studies. In Siberian hamsters, short
141 photoperiods drive significant decreases in body mass, which lead to a large drop in energy
142 requirements for thermoregulation to survive winter conditions (Heldmaier and Steinlechner,
143 1981). They lose body mass through a period of food restriction which recovers to a
144 seasonally appropriate mass after food availability which reflects programmed circannual
145 processes (Ebling and Barrett, 2008). Siberian hamsters are also seasonal breeders, having
146 offspring in summer when resources are abundant. To facilitate this, short days drive
147 significant gonadal regression and subsequent recrudescence in both males and females
148 (Gorman and Zucker, 1995).

149 In birds, Japanese quail (*Coturnix japonica*) is widely regarded as a model species for
150 the study of avian seasonal reproduction in a laboratory setting (Huss et al, 2008). Benefits of

151 selecting quail are high rate of maturation (approximately 6 weeks) and fast growth rate
152 (Boon et al, 2000). Furthermore, the Japanese quail shows an extremely robust photoperiodic
153 response including testes mass, with some reports suggesting an approximately 200-250-fold
154 increase following the onset of reproductive investment (Sachs, 1967; Yasuo et al, 2006).
155 Perhaps most crucially for the investigation of seasonal rhythms, the Japanese quail has a
156 rapid and robust neuroendocrine response to variable photoperiods (Yasuo et al, 2006).
157 Another avian model, red-headed buntings (*Emberiza bruniceps*), exhibit robust shifts in
158 locomotor behaviour that accurately mimics a major life history transition: migration. Short,
159 winter-like photoperiods maintain a non-migratory state and the switch to long summer-like
160 photoperiods induces pre-migratory fattening followed by nocturnal migratory behavior (i.e.
161 zugunruhe) (Kumar et al. 2010; Stevenson and Kumar, 2017). An important adaptation for
162 seasonal migration is weight gain and fat storage, which is visible in the sub-cutaneous fat
163 stores. This weight gain is induced by hyperphagia (Bairlein, 1985) and/or a diet-selection
164 shift in response to changes in the environmental photoperiod (Bairlein, 1998). The bunting
165 model provides a unique system where seasonal rhythms of the metabolic regulation at
166 behavioral, physiological, neuroanatomical, or molecular level can be studied.

167

168 **Modular basis for the neuroendocrine control of seasonal physiology**

169 The neural integration of environmental and endogenous programs is limited to a few discrete
170 regions (Ball, 1993). Some brain regions have functional connections with seasonal programs
171 in physiology, such as the AH-POA control of body temperature (Satinoff E et al., 1976) and
172 sex-specific reproductive behavior (Nance et al., 1977) (Fig.2). Although the control of
173 feeding behavior is primarily driven by the arcuate nucleus in the hypothalamus, other neural
174 substrates such as the ventromedial nucleus, lateral hypothalamus and mesencephalic regions
175 contribute to long-term changes in body mass and metabolism (Elmqvist et al., 1999) (Fig.2).

176 Here, we will cover the neural structures and cellular components that underlie how
177 hypothalamic and extra-hypothalamic regions form modular networks for the control of
178 seasonal rhythms. Using commonalities across mammalian and birds models described
179 above, the perspective that evolutionary pressures can shape independent variation in the
180 neural modular control of seasonal physiology and establish the range of different
181 morphological and phenotypic variation will be presented.

182

183 **Modular control of seasonal physiology in birds**

184 *Anterior hypothalamus-preoptic area, mediobasal-hypothalamus, and the photoperiodic*
185 *response*

186 Research on seasonal biology in birds has focused mostly on the photoperiod based neural
187 control of reproduction. Of this, Gonadotropin releasing hormone (GnRH) which is a highly
188 conserved neuropeptide required for sexual reproduction in all amniotes (Fernald and White,
189 1999) has been a focus for a bulk of studies. GnRH neurons are localized to the AH-POA and
190 control seasonal rhythms in bird and mammalian reproduction (Stevenson et al., 2012a). Both
191 environmental and endogenous programs in the control of seasonal rhythms must act either at
192 the level of the neuronal GnRH cell, release of GnRH into the pituitary gland, or the receptor
193 of GnRH cells on gonadotropes in the anterior pituitary gland. Annual changes in
194 photoperiodic control of GnRH synthesis have evolved to facilitate different degrees of
195 adaptive flexibility in seasonal timing (MacDougall-Shackleton et al., 2009). Photoperiod
196 also regulates the release of GnRH from the median eminence into the anterior pituitary gland
197 by a local circuit that involves pars tuberalis thyrotropin-stimulating hormone- β signalling to
198 3rd ventricle ependymal cells (Nakao et al., 2008) to control tanycytes retraction (Yamamura
199 et al., 2004) that functions to block or permit neuropeptide communication. The current
200 proposition is that annual changes in photoperiod provides dual neuroendocrine control over

201 seasonal rhythms in reproduction, by acting at the level of GnRH synthesis in the AH-POA
202 and GnRH release into the median eminence (Dawson et al., 2001; Stevenson et al., 2012b).
203 Integration of photoperiodic cues by the GnRH system is dependent on light detection by
204 photoreceptor(s) localized in the hypothalamus. Across avian taxa, multiple light responsive
205 opsin photoreceptors are known to be present in hypothalamus like rhodopsin, melanopsin,
206 neuropsin, VA opsin etc with recent evidence suggesting vertebrate ancient opsin (VA opsin)
207 and neuropsin (Opn5) to be the leading candidates for deep brain photoreception (Pérez et al.,
208 2019). VA opsin neurons co-localize with GnRH neurons and may directly regulate
209 expression levels (Pérez et al., 2022).

210

211 *Distributed neural network integrates social cues*

212 Social cues modulate GnRH synthesis and release in birds. In European starlings (*Sturnus*
213 *vulgaris*), males that are housed with a female had significantly more GnRH-expressing
214 neurons compared to singly housed birds and suggest that visual, auditory, or tactile stimuli
215 from a female enhanced neuroendocrine regulation of reproduction (Stevenson and Ball,
216 2009). Social cues also impact GnRH release by affecting the ependymal layer expression
217 Deiodinase type-2 (*Dio2*) enzyme. The presence of a potential male mate significantly
218 increased *Dio2* expression in female starlings which was positively associated with increased
219 follicle volume, a direct consequence of elevated gonadotropin secretion (Perfito et al., 2015).
220 The discovery of Gonadotropin-inhibitory hormone (GnIH) opened an entirely new avenue of
221 research into how supplementary cues impact reproduction (Tsutsui et al., 2021). GnIH is
222 primarily localized to the paraventricular nucleus in the hypothalamus and directly inhibits
223 GnRH release (Bentley et al., 2003). *GnIH* expression reflects the social environment as
224 paired starlings have reduced levels in the hypothalamus and resulted in the facilitation of
225 gonadotropin release (Calisi et al., 2011). Integration of social cues by AH-POA GnRH, and

226 PVN GnIH expressing cells must include visual, auditory, and tactile cues that are distributed
227 across neural networks. A ‘social behavior network’ consisting of highly interconnected
228 limbic and cortical brain regions in mammals (Newman, 1999) and has been adapted to birds
229 (Goodson, 2005). This social behavior network contains multiple neuropeptides such as
230 vasotocin and oxytocin that guide seasonal changes in affiliation, aggression, and sociality
231 (e.g., gregarious) (Goodson et al., 2005). These findings illustrate the multiple hypothalamic
232 and extra-hypothalamic neural structures and specific cellular populations converge on GnRH
233 to regulate seasonal timing in reproduction.

234

235 *Dorsomedial- and mediobasal-hypothalamus and the control of energy stability*

236 While behavioural, physiological, and molecular studies have been done on several species of
237 migratory birds and animals as such, few studies have been done on the neurobiological or
238 anatomical correlates of metabolism associated with migration. Recent research in red headed
239 bunting suggested that the dorsomedial hypothalamus (DMH) and median eminence (ME)
240 may serve as crucial neurobiological substrates for the metabolic needs associated with
241 migration (Majumdar et al., 2021). Clever comparisons of neurogenesis and expression of
242 neuropeptide Y (NPY) between a non-migratory seasonal bird which shows no weight gain in
243 response to changing daylengths and migratory buntings provided for the first evidence that
244 MBH in birds also serves as neurogenic niche as demonstrated in mammals (Lee et al., 2010).
245 One hypothesis is that this neurogenic niche is involved in diet related weight gain (Lee et al.,
246 2012). Presence of strong correlations of body mass gain with hypothalamic neurogenesis in
247 response to high calorie diet and photoperiod otherwise absent in the non-migratory birds

248 hints that hypothalamic neurogenesis may be a regulator of weight gain and metabolism
249 across species (Majumdar et al., 2021).

250 Buntings undergo two migrations, spring migration towards breeding grounds and
251 autumn migration towards overwintering grounds. Transcriptome profiling of hypothalamic
252 and liver tissues of spring migrants revealed an interesting upregulation of calcium binding
253 gene, ATP2A suggesting that increased calcium uptake is involved in energy stability
254 (Sharma et al., 2018). ATP2A gene is responsible for the increased transport of fat from the
255 liver and thus can aid in minimizing the risk of developing of metabolic syndrome like fatty
256 liver disease. A similar upregulation of genes associated with myelin sheath and focal
257 adhesion were found in MBH (Sharma et al., 2018). The spring and autumn migration shows
258 contrasting physiological characteristics with a seasonal metabolic plasticity, particularly in
259 the accumulation, mobilization, and utilization of fat. Consistent with previous results,
260 seasonal life history events such as migration depend on pyruvate decarboxylase along with
261 malate dehydrogenase gene was found indicating a requirement of acetyl-CoA to support
262 migratory behavior (Majumdar et al., 2021). Not surprisingly mRNA levels of fatty-acid
263 synthase were also found along with differences in adipose triglyceride lipase and lipoprotein
264 lipase suggest that triglycerides and/or free fatty acids are the main metabolic substrates for
265 spring migration (Sharma and Kumar, 2019, Majumdar et al., 2021). A contrast of expression
266 between spring and autumn migration was also found in fatty acid binding protein and fatty
267 acid translocases demonstrating a differential fat fuel supply (Sharma and Kumar 2019).

268 Seasonal transitions in life-history traits are often energetically demanding (Murphy
269 and Ebling, 2011). Recent studies in Black- and Red-headed buntings has shown a significant
270 shift of the MBH transcriptomic landscape (Trivedi et al., 2014, Majumdar et al., 2015,
271 Sharma et al., 2019, Majumdar et al., 2021). While comparing the seasonal non-migratory
272 with the migratory states in migratory black-headed buntings where bunting display a

273 significant weight gain, fatty-acid synthase was expressed at higher levels in the
274 hypothalamus during premigratory and migratory stages. Trivedi and colleagues (2014) argue
275 an increased lipogenic activity during photostimulated premigratory and migratory states is
276 required to ensure sufficient energy stores are available. In comparison, genes involved in
277 glucose metabolism were less effected by seasonal migratory life history transitions. In Red
278 headed buntings which were exposed to one single long photoperiod of different lengths, only
279 succinate dehydrogenase and malate dehydrogenase showed a daylength-dependent change in
280 MBH expression (Majumdar et al., 2015). This may mean that although molecular regulation
281 of metabolism parallels the physiology, light may also influence metabolism directly by
282 acting on hypothalamic substrates.

283

284 **Modular basis of the neural control of seasonal rhythms in mammals**

285 *Distributed network for photoperiodic control of seasonal physiology*

286 Nocturnal duration of melatonin is the primary mechanism in which day lengths are encoded
287 in the mammalian brain (Goldman, 2001). Melatonin binds to melatonin receptor 1c subtype
288 to drive seasonal programs in physiology (Prendergast, 2010). The action of melatonin is
289 widely distributed in the mammalian brain with most species having expression in the
290 suprachiasmatic nuclei, median eminence/pars tuberalis, dorsomedial nucleus of the
291 hypothalamus, and multiple thalamic and mesencephalic regions (Weaver et al., 1989).
292 Similar to birds, thyrotropin-stimulating hormone- β expression is a cellular correlate of
293 daylength and guides seasonally appropriate morphological changes in tanycytes along the 3rd
294 ventricle (Hanon et al., 2008). In long-day breeding rodents, the short-day induced tanycytes
295 deiodinase type-3 expression is the earliest identified molecular change, and the long-term
296 exposure to constant winter-like daylengths results in inhibition in levels (Stevenson and
297 Prendergast, 2013). The photoperiodic regulation of tanycytes extension and retraction is

298 likely a conserved mechanism in amniotes to control GnRH release. Unlike birds, GnRH
299 synthesis remains relatively constant across seasonal states in rodents (Bernard et al., 1999).
300 Instead, multiple neurotransmitters including dopamine, serotonin, glutamate, gamma-
301 aminobutyric acid, and neuropeptides (e.g., kisspeptin, RF-amide related peptide-3) function
302 to regulate GnRH activity (Malpoux et al., 1999). Since the discovery of kisspeptin (Seminara
303 et al., 2003), several laboratories such as Gregory Demas (Greives et al., 2006) and Valerie
304 Simonneaux (Saenz de Miera et al., 2014) groups have shown that expression in the
305 anteroventral periventricular nucleus is positively related to reproductive state, and that
306 injections elevate gonadotropin release. These data indicate that a conserved AH-POA and
307 median eminence pathway for the neuroendocrine control of GnRH activity and release is
308 function similarly in birds and mammals. The divergence and diversification of birds over
309 150 million years ago (Brusatte et al., 2015) likely resulted in the loss of kisspeptin signalling
310 and modulatory inputs from anteroventral periventricular hypothalamic cellular populations.
311 How and where other neuromodulatory inputs such as dopamine, integrate melatonin
312 signalling of day length is poorly understood.

313

314 *Arcuate nucleus controls programmed changes in energy stability*

315 Arcuate, ventromedial, and lateral hypothalamic nuclei are well established brain regions for
316 the control of feeding and energy stability (Elmquist et al., 1999). The neuropeptide,
317 proopiomelanocortin (POMC) is an evolutionary conserved pleiotropic gene that exhibits
318 large scale seasonal changes in expression (Helfer and Stevenson, 2020). Across mammalian
319 species, increased body mass, one parameter of energy balance, is positively associated with
320 arcuate *Pomc* expression in hamsters (Bao et al., 2019), rats (Ross et al., 2015) and sheep
321 (Archer et al., 2004). Recent work has identified that VGF nerve growth factor (VGF) is
322 expressed in tanycytes and infusions of one derivative, TLQP-21 reduced body weight and

323 food intake (Lewis et al., 2017; Lisci et al., 2019). Both *Pomc* and *VGF* are expressed at high
324 levels in long photoperiod Siberian hamsters compared to short photoperiod housed animals
325 (Bao et al., 2019; Barrett et al., 2005). Indeed, a complex relationship between neural and
326 peripheral systems functions to maintain programmed seasonal changes in energy balance
327 and photoperiodic switches in these two neuropeptides likely integrate both circulating
328 hormonal signals of satiety and hunger, with the anticipation of future summer, or winter
329 conditions (Stevenson and Helfer, 2019).

330 Undoubtedly, neural modules that govern the integration of environmental cues
331 interact to coordinate seasonal physiological responses. The integration of supplementary
332 environmental cues by the master molecular of reproduction, GnRH, is one good example
333 (Fig.3). First order neurons in the circuits driving hunger and feeding behaviour are well
334 positioned to relay energy status to the GnRH neural network, suppressing fertility when food
335 sources are scarce, and the organism falls into negative energy status. These neurons express
336 the neuropeptides agouti-related peptide (AgRP) and neuropeptide Y (NPY) (Hahn et al.,
337 1998), and rodent studies have shown that virtually all AgRP neurons are GABAergic
338 (Horvath et al., 1997; Marshall et al., 2017). Direct AgRP neuron signalling on GnRH
339 neurons are well established. Evidence from light and electron microscopy provide extensive
340 morphologic evidence of synapses between AgRP neuron terminals and the proximal regions
341 of GnRH neurons, including in humans (Campbell et al., 2001). Electron microscopy further
342 reveals these synapses are symmetric in nature (Tsuruo et al., 1990; Turi et al., 2003). The
343 observed effects of NPY neuron signalling on GnRH neurons suggest a predominantly
344 inhibitory role. Applying NPY receptor agonists to GnRH neurons show that they are largely
345 inhibited by activation of the NPY Y1 receptor (Roa and Herbison, 2012), while a small
346 subset of neurons was excited by agonists for the Y4 receptor. Additionally, there is evidence
347 in GnRH neurons from nasal explants that suggests Y1 receptor activation inhibits GnRH

348 neurons by activating G protein-coupled inwardly rectifying potassium channels (Klenke et
349 al., 2010). For example, 70% of GnRH neurons are excited by *Pomc* derived alpha-
350 melanocortin stimulating hormone (MSH) acting on melanocortin-3 (MC3R) and -4 receptor
351 (MC4R) and induce, an excitatory affect (Roa and Herbison, 2012). Immunohistochemical
352 studies demonstrate terminals that are immunoreactive for adrenocorticotrophic hormone
353 (ACTH) (Leranth et al. 1988) and beta-endorphin (Chen et al. 1989), both cleavage products
354 of *Pomc*, synapse with GnRH neuron cell bodies. There are fewer functional studies but
355 MC3R and MC4R knockout leads to a decrease in litter size (Begrache et al. 2011) and fewer
356 ovarian corpora lutea suggesting less frequent ovulation in females (Sandrock et al. 2009),
357 indicating a direct negative effect on fecundity. Altogether, these data suggest that *Pomc* may
358 play a supplemental but not necessary role in stimulating GnRH neurons, but more research
359 is necessary to define their exact role.

360 Another way in which GnRH neuron activity can be assayed is by measuring changes
361 in circulating luteinizing hormone (LH) release, as LH pulses are invariably preceded and
362 driven by pulsatile GnRH release (Clarke and Cummins, 1982; Levine et al., 1982; Moenter
363 et al., 1992). Of the substrates expressed by AgRP neurons, the most evidence for modulation
364 of LH release comes from examining the effect of NPY. NPY administration in rodents often
365 stimulates LH secretion (Bauer-Dantoin et al., 1991). This perhaps stems from NPY acting
366 directly upon gonadotrophs, as NPY signalling and Y1 receptor activation potentiates LH
367 release in response to GnRH signalling (Hill et al., 2004). It should also be noted that AgRP
368 neurons may suppress GnRH neurons indirectly by inhibiting excitatory afferents (Padilla et
369 al., 2017), thus possessing multiply levels at which AgRP neurons can modulate GnRH
370 neuron activity and LH release.

371

372 **Future directions**

373 This review has predominantly focused on the role of neural modules involved in
374 reproduction and energy balance, and how the function of a few neuropeptides governs
375 seasonal physiology, respectively. The conjecture proposed was discrete neural substrates
376 control key physiological processes and that each module (e.g., AH-POA, Arcuate) has
377 autonomous functionality. The independent neuropeptidergic activity is a mechanism for
378 evolutionary pressures to act to shape how an organism times physiological, and behavioral
379 traits to environmental cues. Most research has used non-traditional animal models that have
380 lacked genomic information, and the ability to shape gene-environment studies. The past
381 decade has observed an explosion in the ability to sequence nucleic acids with whole
382 genomes, epigenomes, transcriptomes, and proteomes sequenced rapidly and at ever
383 increasing affordability. These high-throughput analyses are essential to uncover the entire
384 complement of genomic plasticity, and neuroanatomical specificity of seasonal control of
385 physiology. Research is currently stymied due to two relatively complex issues: genome
386 modifications and mathematical modelling. Current approaches to manipulate genome
387 function rely on short-hairpin RNA that are packaged into viral vectors. Although this
388 strategy is useful for short-term disruption in transcript levels, it is limited in the ability to
389 assess long-term inhibition of target genes. The development of cluster regularly interspaced
390 short palindromic repeats (CRISPR) and related associated protein-9 (Cas9) has ushered in a
391 new era in which select targets can be over-expressed, and mutated, to facilitate analyses of
392 genome function, and neuroanatomical specificity required for seasonal studies. Some
393 progress has already been achieved in non-traditional animal models such as Japanese quail
394 (Lee et al, 2019). Lastly, the large sequencing databases available, and soon, will reveal a
395 new challenge for seasonal biologists, the abundance of potential genes/transcripts/proteins
396 across different neural substrates, and understanding how the timing of each level is
397 coordinated across neural networks. Here, mathematical modelling using artificial

398 intelligence will be essential to handle the mass amounts of data in a logical, and meaningful
399 way. Early work using an information theory approach with contingency-constancy
400 modelling to both ecological (Wingfield et al., 1992) and neuroendocrine (Stevenson and
401 Ball, 2011) levels of analyses provide a strong foundation to build complex models that can
402 incorporate the wide range of brain regions and cellular processes that control seasonal
403 physiology.

404

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408

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702

703 Figure legends**704 Figure 1 – PUBMED database for publications on seasonality in amniotes.**

705 Analyses of search terms for ‘seasonal’ and ‘mammal’ or ‘bird’ indicates an
706 exponential increase in the number of publications over the past 50 years (A). Break
707 down of the number of publications for a select group of highly seasonal animals
708 including sheep, mouse, rat, chicken, hamster, squirrel, and quail (B).

709

710 Figure 2 – Modular basis for the neural integration of environmental cues.

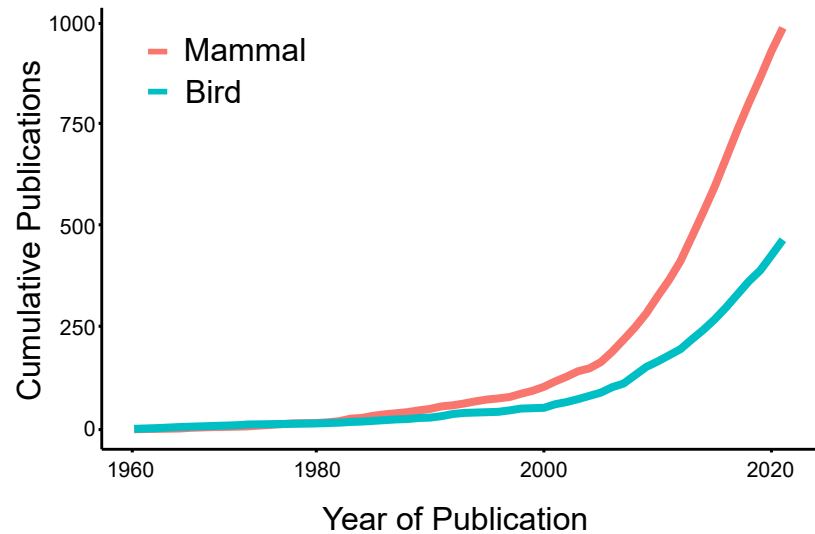
711 In both mammal and avian species, the pars tuberalis and median eminence integrate
712 daylength cues and code photoperiodism. Environmental cues such as temperature,
713 nutrient availability and social cues have some overlapping, but many distinct neural
714 regions that guide seasonal timing of reproduction, body temperature, energy
715 stability and sociality.

716

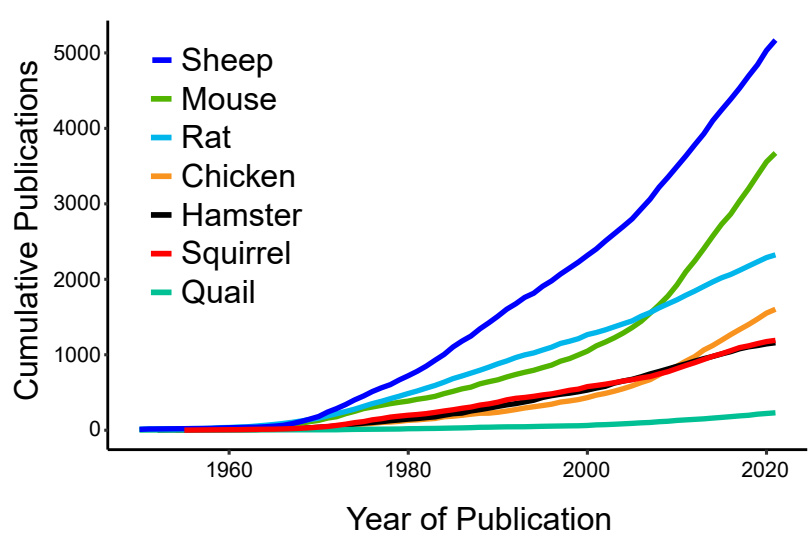
**717 Figure 3 – Convergence of neural and cellular substrates on GnRH for seasonal
718 rhythms in reproduction.**

719 Gonadotropin-releasing hormone (GnRH) is an evolutionary conserved neuropeptide
720 that controls reproduction in all vertebrates. GnRH neurons receive inputs from
721 many neural substrates involved in the integration of social, temperature, nutrient
722 and photic cues. Abbreviations: Agouti-related peptide (AgRP), Androgen receptor
723 (AR), Arginine vasopressin (AVP), Arginine vasocotin (AVT), Deiodinase type-3
724 (Dio3), Estrogen receptor (ER), Gamma aminobutyric acid (GABA), Gonadotropin-
725 releasing hormone-2 (GnRH-2), Kisspeptin-1 (Kiss1), Neuropeptide Y (NPY),
726 Oxytocin receptor (OXT-R), Proopiomelanocortin (Pomc), Progesterone receptor
727 (PR), Thyrotropin-stimulating hormone- β (Tsh β), Vasotocin 1a receptor (V1aR).

A)



B)



Predictive cue

Photoperiod

Pars tuberalis
Median eminence

Supplementary cues

Temperature

Anterior hypothalamus
Preoptic area
Dorsomedial hypothalamus

Nutrients

Arcuate nucleus
Ventromedial hypothalamus
Lateral hypothalamus
Nucleus of the solitary tract

Social cues

Amygdala
Preoptic area
Anterior hypothalamus
Ventromedial hypothalamus
Periaqueductal grey
Lateral septum

