



Comparative endocrinology of aging and longevity regulation

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Hormones regulate growth, development, metabolism, and other complex processes in multicellular animals. For many years it has been suggested that hormones may also influence the rate of the aging process. Aging is a multifactorial process that causes biological systems to break down and cease to function in adult organisms as time passes, eventually leading to death. The exact underlying causes of the aging process remain a topic for debate, and clues that may shed light on these causes are eagerly sought after. In the last two decades, gene mutations that result in delayed aging and extended longevity have been discovered, and many of the affected genes have been components of endocrine signaling pathways. In this review we summarize the current knowledge on the roles of endocrine signaling in the regulation of aging and longevity in various animals. We begin by discussing the notion that conserved systems, including endocrine signaling pathways, “regulate” the aging process. Findings from the major model organisms: worms, flies, and rodents, are then outlined. Unique lessons from studies of non-traditional models: bees, salmon, and naked mole rats, are also discussed. Finally, we summarize the endocrinology of aging in humans, including changes in hormone levels with age, and the involvement of hormones in aging-related diseases. The most well studied and widely conserved endocrine pathway that affects aging is the insulin/insulin-like growth factor system. Mutations in genes of this pathway increase the lifespan of worms, flies, and mice. Population genetic evidence also suggests this pathway’s involvement in human aging. Other hormones including steroids have been linked to aging only in a subset of the models studied. Because of the value of comparative studies, it is suggested that the aging field could benefit from adoption of additional model organisms.

Keywords: aging, longevity, lifespan, senescence, hormone, signaling, endocrine, insulin-like growth factor

INTRODUCTION

Aging is the process of progressive decline in the biological functions of cells and organs that causes most organisms to suffer from exponentially increasing mortality rates over time. The exact underlying causes of aging at the cellular level remain obscure. The most popular theory has been the free-radical theory of aging put forward by Harman (1956). This theory suggests that reactive oxygen species produced by mitochondria as a result of normal metabolism cause irreversible damage to DNA and protein that accumulates over a lifetime, and eventually causes the breakdown of homeostasis. There is a large amount of correlative evidence supporting this theory. However, direct evidence for the free-radical theory of aging is still scarce. To date, there have been a number of *in vivo* studies using transgenic/knockout mice with alterations in a wide variety of genes that affect the levels of free-radicals or oxidative stress. So far, most of these genetic manipulations have failed to show an effect on lifespan (reviewed in Perez et al., 2009). Thus the search for the underlying mechanisms of aging continues.

In recent years, forward genetics studies have discovered gene mutations that result in delayed aging and extended longevity, and many of the affected genes are components of endocrine signaling pathways. In retrospect, this should not have been surprising in

view of the fact that the extension of lifespan is a massively complex phenotype that likely requires varying pleiotropic actions in different tissue and cell types, and would have to be synchronized at the organismic level. The endocrine system is known to regulate metabolism, growth, and homeostasis throughout the body, and by comparison, it is logical that the various mechanisms that oppose the underlying aging process would also be under the control of hormonal signaling systems.

This review will focus on our current understanding of the roles that hormonal signaling plays in the regulation of longevity in animals. We concentrate on so-called “cell-non-autonomous” mechanisms of aging, in which aging-related changes at the cellular level are caused by signals released from other cells rather than by an intrinsic factor within the cell itself. It should be noted that the relevant literature on the comparative endocrinology of aging is vast. We have attempted to focus on major endocrine signaling pathways that have been demonstrated to regulate longevity in order to paint a broad picture of the current state of the field. Throughout this article we refer to the concept of aging and longevity being “regulated.” This is not intended to signify a presumption that aging is “programmed,” but rather that the rate of aging can be promoted and inhibited by various factors including endocrine signaling.

CONSERVED ROLES OF ENDOCRINE SIGNALING IN LONGEVITY REGULATION

The role of the endocrine system in human aging was first proposed in the late 1800s by Charles-Édouard Brown-Séquard who has been called one of the fathers of endocrinology for his role in the demonstration that the adrenal glands produce hormones that are essential for life (Tattersall, 1994). Unfortunately, his attempts to extend his own life by subcutaneously injecting animal seminal fluid and testicular extracts were misguided, but they launched a fad in the early twentieth century of similar attempts to extend life (Haber, 2004). It is now known that in worms (Hsin and Kenyon, 1999), flies (Flatt et al., 2008), fish (Robertson, 1961), rats (Drori and Folman, 1976), and possibly humans (Hamilton and

Mestler, 1969), removal of the gonads (or germline in *C. elegans*) actually extends lifespan. These findings may indicate a conserved role of gonadal hormones in longevity regulation, but a hormone involved in mediating this effect has so far been identified only in *C. elegans* (Yamawaki et al., 2010).

Direct evidence for the involvement of hormonal signaling in longevity came after the identification of the first single gene mutations in *C. elegans* that extended lifespan (Friedman and Johnson, 1988; Kenyon et al., 1993; Kimura et al., 1997). These were components of a widely conserved endocrine signaling pathway that is orthologous to the Insulin and Insulin-like growth factor Signaling pathways in mammals, and is therefore referred to as the “IIS pathway,” (see **Figure 1A**). Mutations in genes encoding components

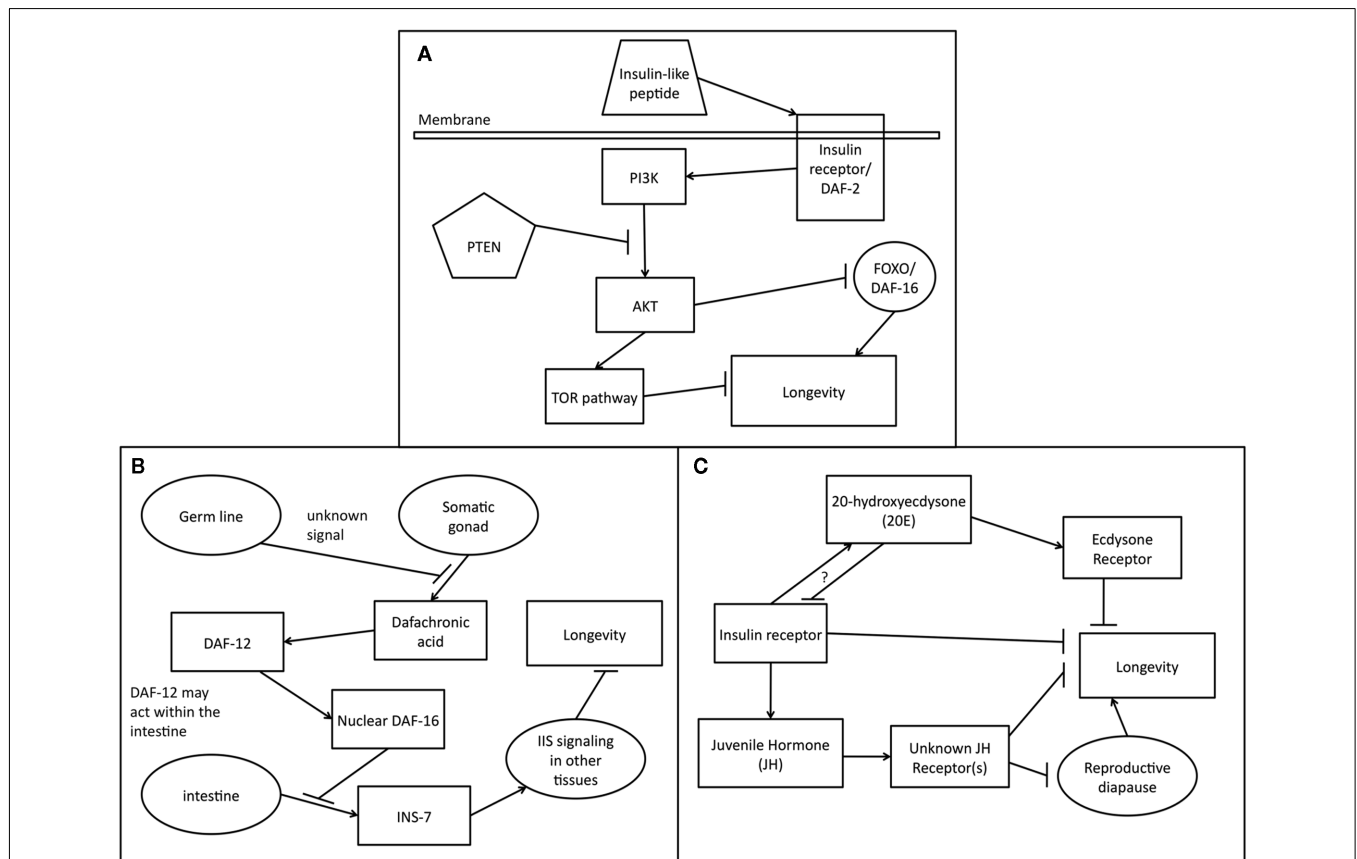


FIGURE 1 | Endocrine signaling pathways affecting longevity.

(A) Role of the conserved IIS signaling pathway in longevity regulation.

Insulin-like peptides bind to an insulin/IGF receptor on the plasma membrane. Ligand binding causes dimerization of the receptor, activating the intracellular tyrosine kinase domain. Phosphorylation by the receptor kinase domain activates the PI3 Kinase (PI3K). The signaling activity of PI3K, antagonized by the PTEN phosphatase, activates the Akt kinase. Akt phosphorylates FOXO/DAF-16 which is then sequestered in the cytosol. In the absence of IIS signaling, FOXO translocates to the nucleus and activates transcription of longevity promoting genes. AKT signaling also opposes longevity by activating the TOR pathway, which inhibits autophagy, a pro-longevity process. **(B)** Endocrine signaling in the *C. elegans* germline longevity pathway. The germ line stem cells send an unknown signal that allows other tissues to detect that they are present. When the germ line stem cells are ablated, the somatic gonad

releases the steroid dafachronic acid that binds to the nuclear hormone receptor DAF-12. It is unclear exactly where DAF-12 acts to receive this signal but the intestine is a possible location. As a result of signaling via DAF-12, DAF-16/FOXO activity increases in the nuclei of intestinal cells. This in turn leads to signaling from the intestine to the other tissues that informs them about status of the DAF-16/FOXO in the intestine. IIS signaling in the intestine can down regulate the expression of INS-7 and this may be one mechanism by which intestinal DAF-16/FOXO controls other tissues. **(C)** Regulation of longevity by 20-hydroxyecdysone (20E) and juvenile hormone (JH) in insects. JH suppresses reproductive diapause which promotes longevity. JH may also negatively affect longevity in other ways. The receptor(s) to which JH binds is unknown. 20E activates the ecdysone receptor which may reduce longevity. IIS engages in cross talk with both JH and 20E and also reduces longevity via other signaling pathways.

of this pathway in *Drosophila* were later found that also extended lifespan (Clancy et al., 2001; Tatar et al., 2001b). In mice, mutations that reduce the levels of insulin-like growth factor 1 (IGF-1) were shown to extend lifespan (Flurkey et al., 2001; Coschigano et al., 2003). Hypomorphic mutations in IIS pathway component genes in humans also have been associated with extended longevity (Suh et al., 2008; Tazearslan et al., 2011). The conserved role of the IIS pathway in longevity regulation is a central theme in the comparative endocrinology of aging.

The conservation of molecular mechanisms that regulate longevity is suggested also by the effects of caloric restriction on lifespan in different animal species. It was observed in 1935 that rats fed fewer total calories while receiving sufficient vitamins and other nutrients to prevent malnutrition exhibited an extended lifespan (Mccay et al., 1935). Since then, this life-extending intervention has been tested and demonstrated to be effective in the major model systems *C. elegans* (Klass, 1977), *Drosophila* (Chapman and Partridge, 1996; Mair et al., 2003), and mice (Cheney et al., 1980), as well as in a diverse range of other species including spiders, rotifer, guppies, and many others (Comfort, 1963; Fanestil and Barrows, 1965; Austad, 1989). Caloric restriction seems to not only extend the duration of life but also the, “health span,” or the period during which an animal remains free of aging-related diseases. This is demonstrated by the fact that caloric restriction delays a large number of aging-related diseases and conditions in rodents, monkeys, and humans, including cancer, cardiovascular disease (CVD), diabetes, sarcopenia, and immunosenescence, among others (Cheney et al., 1980; Weindruch and Walford, 1982; Weindruch et al., 1986; Black et al., 2003; Fontana et al., 2004; Messaoudi et al., 2006; Colman et al., 2008, 2009). Many different variations in the protocols of caloric restriction exist, and the methods used for different species differ. The exact effects and extent of longevity enhancement often vary depending on the strain and the different protocols used, and these effects have been reviewed extensively elsewhere. It is not surprising that the effects of caloric restriction would be complex given the complexity of the underlying aging process and its dependence on many different genes. Given this complexity, the nearly universal ability of caloric restriction to extend lifespan would seem to support the notion that it is regulated by conserved genetic mechanisms. The exact processes that mediate the effects of caloric restriction are still unclear.

A possible conserved role of endocrine signaling in longevity regulation is suggested by the fact that caloric restriction causes alterations in hormonal signaling levels in various species. In rodents, caloric restriction reduces insulin levels (Masoro et al., 1992) and IGF-1 levels (Breese et al., 1991; D’Costa et al., 1993), increases corticosterone levels (Sabatino et al., 1991), and decreases serum thyroid hormone levels (Herlihy et al., 1990). The effects on thyroid hormone, which regulates metabolic rate, would seem to suggest that a reduction in metabolic rate could be involved in extending lifespan, but energy expenditure in calorically restricted rats was found to be higher than expected based on body composition (Selman et al., 2005). Rats that stood in cool water for 4 h a day, 5 days a week throughout life consumed 44% more food than controls, but their longevity was not different despite their increased energy expenditure (Holloszy and Smith, 1986).

Drosophila also did not show reduced metabolic rate under caloric restriction (Hulbert et al., 2004). Metabolic rate was found to be uncorrelated with lifespan in an analysis of data from hundreds of species (De Magalhaes et al., 2007). Rather, age at sexual maturity was found to be positively correlated with lifespan, suggesting that factors that regulate growth and maturation may be connected with longevity regulation (Prothero, 1993; De Magalhaes et al., 2007).

In humans caloric restriction can also reduce serum IGF-1 levels, insulin levels, and the levels of sex steroids, in addition to other hormonal changes (see the section below on the endocrinology of human aging). Salutary effects of caloric restriction have been reported in humans, but any possible effects on lifespan have yet to be determined (reviewed in Fontana and Klein, 2007). In *Drosophila*, ablation of the cells in the nervous system that secrete insulin-like peptides (ILPs), called the median neurosecretory cells (mNSCs), resulted in the loss of most of the increased longevity caused by caloric restriction, indicating that the function of these cells is required for the extension of lifespan observed (Broughton et al., 2010). Mutation in the *Drosophila* insulin receptor substrate 1 (IRS-1) gene, *chico*, results in lower IIS signaling and increases lifespan, and subsection of these mutant flies to caloric restriction produced different effects depending on the amount of dietary restriction. The effects were consistent with the idea that the *chico* mutants were already subject to some of the same effects caused by dietary restriction, as mild dietary restriction could extend their lifespans but more severe restriction caused them to die sooner than controls (Clancy et al., 2002). This suggests overlap between the mechanisms of lifespan extension in caloric restriction and reduction in IIS signaling. In *C. elegans* however, caloric restriction by both reduction of food availability and mutations that reduce efficiency of the eating process, are independent of the IIS signaling pathway (Lakowski and Hekimi, 1998; Houthoofd et al., 2003). One way this was demonstrated was by showing that already long-lived mutants with reduced IIS signaling could be made to live even longer by caloric restriction. Long-lived Ames dwarf mice also live even longer when subjected to caloric restriction (Bartke et al., 2001), but, long-lived growth hormone receptor knockout mice do not (Bonkowski et al., 2009).

ADVANCES IN THE ENDOCRINOLOGY OF AGING IN MODEL SYSTEMS

In this section we discuss the major findings that relate to the endocrinology of aging in each of the major model organisms: *C. elegans*, *Drosophila*, and rodents. Both widely conserved and species-specific mechanisms have been discovered in each of these models, and by comparing the results from multiple organisms one can formulate better hypotheses regarding human aging (see **Table 1**).

C. ELEGANS

The first mutation found to extend lifespan in *C. elegans* was in the *age-1* gene (Klass, 1983; Friedman and Johnson, 1988). This gene was shown to encode a homolog of PI3 kinase, which is a downstream component of the intracellular pathway that transduces signals from the IIS pathway (see **Figure 1A**). A later analysis found that second generation homozygous null *age-1* mutant worms

Table 1 | Characteristics of aging model organisms.

Organism	Lifespan	Advantages	Disadvantages	Endocrine pathways linked to longevity
<i>C. elegans</i>	~2 weeks	Short lifespan, easy to work with, genetically tractable	Lacks distinct endocrine tissues and various other tissue types, very distant from humans	IIS, steroids
<i>Drosophila</i>	~3 months	Short lifespan, easy to work with, genetically tractable, has a wide range of tissue types, has adult stem cells	Distant from humans	IIS, ecdysone, JH
Honey bee	Varies depending on caste	Social structure affects lifespan allowing study of plasticity of aging	Distant from humans	Vitellogenin, JH, possibly IIS
Long-lived bivalves	Centuries	Exceptionally slow aging rate	Distant from humans	None so far
Zebrafish	~4–5 years	Vertebrate, genetically tractable, small size, cheap to maintain	Longer lifespan than mice	None so far
Killifish	~3 months	Vertebrate, exceptionally short lifespan, small size, cheap to maintain	New model	None so far
Salmon	Several years	Vertebrate, special case of programmed aging	Large size, relatively long lifespan	Corticosteroids, sex steroids, possibly IGF
Mouse	~2–3 years	Mammal, relatively short-lived, many genetic tools available	Expensive to work with	GH, IGF, Insulin, klotho, angiotensin II, possibly thyroxine, possibly sex steroids
Naked mole rat	~20–30 years	Mammal, very slow aging rate for size	New model	None so far
Non-human primates	Years to decades	Very similar to humans	Difficult and expensive to work with	None so far
Humans	~80 years	Research is highly relevant for improving health	Limited ability to do experiments	IGF

lived almost 10 times longer than wild type worms (Ayyadevara et al., 2008). Subsequently, mutations in various other components of this pathway were shown to be involved (Kenyon et al., 1993). Many of these mutants that exhibited long adult lifespans were so-called dauer formation mutants; that is, mutants with an altered tendency to enter the dauer larval state.

The *C. elegans* dauer larva is an alternative larval stage that can survive for months without feeding and is very resistant to stress (Cassada and Russell, 1975). Formation of dauer larvae is promoted by low nutrient availability in the environment, and also by high levels of a dauer pheromone produced by all individuals (Golden and Riddle, 1984). This stage allows the worms to survive until more food becomes available. Various dauer formation (*daf*) mutations have been found that either prevent dauer formation or cause constitutive dauer formation (Riddle et al., 1981). The observation has been that mutations that increase dauer formation tend to increase adult lifespan as well. The gene *daf-2* is the *C. elegans* insulin receptor homolog and the major down stream effector of the pathway is *daf-16*, which is a FOXO family transcription factor that is required for the lifespan extension effects produced by mutation of *daf-2* and other pathway components (Kenyon et al., 1993; Kimura et al., 1997). Signaling through the IIS pathway leads to sequestration of DAF-16/FOXO in the cytosol, thereby suppressing its anti-aging activity (Figure 1A).

daf-2 mutant worms live two to three times longer than wild type worms. It is noteworthy that mosaic analysis showed that *daf-2* mutation only in certain cells was capable of extending lifespan for the whole organism, indicating a cell-non-autonomous

effect which may be mediated by endocrine signaling (Apfeld and Kenyon, 1998). Some but not all mutations in *daf-2* cause reduced fecundity in addition to varying levels of lifespan extension, indicating lifespan can be decoupled from reduced reproductive costs (Gems et al., 1998). Furthermore it was shown that RNAi knockdown of *daf-2* during development reduced fecundity but did not extend lifespan, whereas knockdown only during adulthood extended lifespan without affecting fecundity (Dillin et al., 2002). This indicates that the effects of IIS mutants on lifespan in the adult stage are actually dependent on the levels of IIS during adulthood, rather than “left over” longevity factors of some kind from the larval stage during which the dauer formation decision is made.

C. elegans has about 40 ILP genes in its genome (www.wormbase.org). It is thought that these ILPs functioned by binding to the receptor tyrosine kinase DAF-2 (Olinski et al., 2006). Some of these molecules function as DAF-2 receptor agonists while others were proposed to act as antagonists (Pierce et al., 2001; Li et al., 2003; Murphy et al., 2007). However, the functions of most of the ILPs remain unknown, and it is not clear whether all of them interact with DAF-2. Vertebrates have a subgroup of insulin-like molecules called the relaxin/insulin-like family that function by binding to G protein-coupled receptors (Hsu et al., 2002; Hoffmann and Opazo, 2011).

Other signaling pathways have been implicated in regulating aging in worms including transforming growth factor TGF β signaling which seems to act partly through modulation of IIS signaling (Shaw et al., 2007; Narasimhan et al., 2011). Serotonin

signaling was also shown to promote aging via an effect on the IIS pathway (Murakami and Murakami, 2007).

Of particular interest is the observation that signaling in certain specific tissues is required for longevity enhancement in a number of cases. Disabling sensory input to certain neurons can extend or reduce lifespan for the whole organism (Apfeld and Kenyon, 1999; Alcedo and Kenyon, 2004; Bishop and Guarente, 2007). *daf-16* expression is normally required for lifespan extension in *daf-2* mutants. Expression of *daf-16* only in the intestine is sufficient to rescue the lifespan extension in long-lived *daf-2* mutants that lack DAF-16/FOXO in other tissues (Libina et al., 2003). DAF-16 down-regulates expression of one of the ILPs, INS-7. INS-7 is a DAF-2 agonist, and when DAF-16 activity is increased in the intestine, it leads to increased DAF-16/FOXO activity throughout the body by reducing levels of INS-7 secreted by the intestine (Murphy et al., 2007). In long-lived *daf-2* mutants, replacement of *daf-2* only in neurons was found to reduce the lifespan to wild type levels (Wolkow et al., 2000). However the role of neuron-specific IIS was found to be minor in a later study (Libina et al., 2003). A mutation which alters mitochondrial function can extend lifespan even when present only in certain cells, indicating cell-non-autonomous functions even for a mutation affecting a fundamental metabolic process (Durieux et al., 2011).

Steroid hormones have also been shown to contribute to longevity regulation in *C. elegans* (Jia et al., 2002; Broue et al., 2007; Gerisch et al., 2007). Mutations of an enzyme involved in steroid hormone synthesis called DAF-9 extend lifespan, and this extension also requires a nuclear hormone receptor called DAF-12, but does not require DAF-16/FOXO (Jia et al., 2002). Long-lived *daf-9* mutants are returned to normal lifespan by treatment with bile acid-like steroids called dafachronic acids (Gerisch et al., 2007), which are endogenous ligands of DAF-12 (Motola et al., 2006). These findings suggest that DAF-9 generates dafachronic acid, which promotes aging by interacting with DAF-12. In contrast, treatment with another steroid, called pregnenolone, which can be found in vertebrates, extended lifespan in worms, and this extension also required DAF-12 (Broue et al., 2007). Thus, steroid signaling via DAF-12 is capable of both promoting and opposing aging, and in fact, different mutations in *daf-12* itself can either shorten or extend lifespan (Fisher and Lithgow, 2006). It is also noteworthy that null mutations of *daf-12* further extend the already long lifespans of strong *daf-2* (insulin receptor) mutants, but they block the lifespan extension caused by weak *daf-2* mutations (Gems et al., 1998).

When the *C. elegans* germline cells are ablated, lifespan is increased, and *daf-9* and *daf-12* are required for this effect, along with *daf-16* (Hsin and Kenyon, 1999; Gerisch et al., 2001; Arantes-Oliveira et al., 2002). Removal of the entire gonad does not extend lifespan, and it was shown that the somatic gonad tissue, which expresses *daf-9* (Gerisch et al., 2001), was required for the lifespan extension due to removal of the germline (Yamawaki et al., 2008). However, in already long-lived DAF-2 deficient worms, removal of the entire gonad extended lifespan even further, allowing them to live six times longer than wild type and remain healthy and active throughout most of this time (Arantes-Oliveira et al., 2003). This indicates that strong reduction in IIS signaling eliminates the need for the signal normally provided by the somatic gonad. The

hormone responsible for this anti-aging signal has been identified as the steroid dafachronic acid, which binds to DAF-12 (Gerisch et al., 2007; Yamawaki et al., 2010). Germline removal causes DAF-16/FOXO to accumulate in the nuclei of intestinal cells and this mediates the increase in lifespan (Lin et al., 2001; Libina et al., 2003). It is speculated that dafachronic acid released by the somatic gonad activates DAF-12 in the intestinal cells, which in turn enhances DAF-16 nuclear localization and promotes longevity by down-regulating intestinal secretion of INS-7, leading to lower IIS levels throughout the body (**Figure 1B**), but this has not yet been confirmed. The factors that determine whether DAF-12 promotes or opposes aging remain unknown. A gene called *kri-1* and a transcription elongation factor called TCER-1 are required for DAF-16 nuclear localization and transcriptional activity to be promoted by germline removal but not by IIS reduction (Berman and Kenyon, 2006; Ghazi et al., 2009). There is presumably another endocrine pathway that signals the presence or absence of the germ line to the rest of the body but this pathway has not yet been identified. Many other open questions exist regarding the roles of endocrine signaling in regulating longevity in response to germ line removal (reviewed in Kenyon, 2010).

DROSOPHILA

The fruit fly *Drosophila* has several advantages as a model for studying endocrinology of aging. Flies have several distinct endocrine glands and a wider range of tissue types in general than *C. elegans*. Also, unlike *C. elegans* which lack dividing somatic stem cells in the adult stage, *Drosophila* have now been shown to possess adult somatic stem cells in at least five different tissues (Margolis and Spradling, 1995; Micchelli and Perrimon, 2006; Ohlstein and Spradling, 2006; Singh et al., 2007, 2011; Voog et al., 2008).

IIS signaling regulates longevity in *Drosophila*. The *Drosophila* genome contains seven insulin-like peptide (dILP) genes and one insulin receptor (INR), and signaling through the INR by each of the dILPs promotes growth in flies (Brogiolo et al., 2001). The dILPs are expressed in different spatiotemporal patterns during development (Brogiolo et al., 2001). Three of the dILPs are produced and secreted by a collection of neurons called mNSCs and this secretion can be regulated by the availability of nutrients in larvae (Ikeya et al., 2002). Genetic ablation of the mNSCs slows growth and larval development, and increases lifespan (Rulifson et al., 2002; Broughton et al., 2005). Loss of the mNSCs also interferes with the lifespan extension resulting from caloric restriction by yeast dilution (Broughton et al., 2010). A null mutation of the gene encoding dILP2 extended lifespan but null mutations in the other dILP genes did not (Gronke et al., 2010). It is noteworthy that the developmental expression patterns of progenitors of the two tissues indicates homology between the mNSCs in flies and the insulin secreting pancreatic beta cells in vertebrates (Wang et al., 2007b).

Some hypomorphic mutations in the gene encoding the single INR were shown to extend female *Drosophila* lifespan by up to 85% while causing dwarfism and preventing maturation of the gonads (Tatar et al., 2001b). Mutations of many genes encoding components of the INR signaling pathway, such as the PI3K and AKT homologs, cause normal or reduced lifespan or are lethal, which is not surprising due to the important roles of this pathway

in normal growth and development (Clancy et al., 2001). However, heterozygous and homozygous mutations in the IRS gene homolog, *chico*, extend fly lifespan (Clancy et al., 2001; Tu et al., 2002a). They can also further extend lifespan in long-lived female flies that also carry a mutation which prevents oogenesis, indicating that reduction of fertility is not the mechanism by which the longevity of *chico* mutants is extended (Clancy et al., 2001). Also, *chico* heterozygotes have normal size and normal fertility and are nevertheless longer-lived than wild type although not as long-lived as the homozygotes (Clancy et al., 2001).

As in *C. elegans*, several studies have demonstrated in *Drosophila* that tissue-specific modifications can extend the lifespan of the whole organism, indicating cell-non-autonomous effects that may be mediated by endocrine signaling. The transcription factor dFOXO is the *Drosophila* homolog of *C. elegans* DAF-16 and functions downstream in the IIS pathway (see **Figure 1A**). Overexpression of dFOXO in the head fat body (the equivalent of adipose tissue in mammals) during adulthood modulated expression of one of the ILPs and extended lifespan (Giannakou et al., 2004; Hwangbo et al., 2004). Overexpression of dFOXO in the head fat body only during the early adult period was found to be sufficient for increasing lifespan and did not adversely affect fecundity (Giannakou et al., 2007). Autophagy, or macroscopic cellular self-digestion, has been proposed as a cell-autonomous longevity mechanism. Increasing levels of autophagy only in the fly nervous system by overexpression of an autophagy protein increases fly lifespan by 50%, indicating likely cell-non-autonomous effects on other tissues (Simonsen et al., 2008). Olfactory neuron signaling has also been shown to regulate lifespan in *Drosophila* (Libert et al., 2007).

Because caloric restriction and many lifespan-extending IIS mutations often result in reduced fecundity in various model systems, it has often been suggested that there is a trade-off between investment of energy in reproduction or in somatic maintenance (i.e., repairing mutations and damage etc.). In *Drosophila*, dietary restriction extends lifespan and reduces fecundity (Chapman and Partridge, 1996; Mair et al., 2003). However, it is frequently possible to decouple positive longevity effects from negative fecundity effects. When additional quantities of the amino acid methionine were provided to flies during dietary restriction, the fecundity was restored to the level of wild type flies without reducing the extension in lifespan caused by the reduced calorie intake (Grandison et al., 2009). In *Drosophila*, there is a cost of mating for females in that their lifespan is reduced by mating (Chapman and Partridge, 1996). If this were caused by transfer of resources from somatic maintenance to reproduction, then it would be expected that sterile females would have reduced costs of mating, but in fact it was found that their costs were increased (Ueyama and Fuyama, 2003). The cost of mating has been found to be mediated by a signaling molecule in male seminal fluid called sex peptide (Wigby and Chapman, 2005). Ablation of germ cells in flies has been found to extend lifespan (Flatt et al., 2008). Whether this effect is mediated by endocrine signaling as in *C. elegans* is currently unknown.

The phyla to which *Drosophila* and *C. elegans* belong, Arthropoda and Nematoda respectively, are both members of the superphylum ecdysozoa (Mallatt and Winchell, 2002; Dunn et al.,

2008). The most significant common feature that members of these phyla share is that during early development they periodically shed their cuticle or exoskeleton and produce a new larger one to accommodate continued growth. This process is termed ecdysis, and it gives the super phylum its name. Ecdysis is stimulated by a steroid hormone called 20-hydroxyecdysone (20E), which is the active form of a prohormone called ecdysone (Thummel, 1996; Nakagawa and Henrich, 2009). A group of hormones called juvenile hormones (JH) that are sesquiterpenoid lipids also participate in the regulation of growth and development along with 20E, and the presence or absence of JH is what determines whether a larva will undergo ecdysis or metamorphosis in response to 20E (reviewed in Dubrovsky, 2005).

Both 20E and JH regulate a wide variety of processes in insects, and they have been implicated in the regulation of adult longevity (**Figure 1C**). JH is secreted by a gland called the corpus allatum (Altaratz et al., 1991). *Drosophila* and some other insects can undergo so-called reproductive diapause during their adult stage, which in many ways resembles the dauer in *C. elegans* (Tatar et al., 2001a). In this condition, oogenesis and mating cease, stress resistance increases, metabolism decreases, and longevity is increased (Tatar et al., 2001a). Reductions in JH signaling control entry into diapause (Tatar, 2004). Treatment with a JH analog blocks diapause in *Drosophila* (Tatar et al., 2001a). When the corpus allatum is removed in other insects, their lifespan can be increased (Tatar and Yin, 2001). Removal of the corpus allatum in monarch butterflies that undergo reproductive diapause doubled longevity whereas injection with JH halved it (Herman and Tatar, 2001). Long-lived *inr* mutants have reduced JH signaling, and treatment with JH reduces their lifespan back to wild type levels (Tatar et al., 2001b; Tu et al., 2005). When fly larvae were treated with a JH analog their lifespan was reduced but early life fertility was increased (Flatt and Kawecki, 2007). Flies selected for 19 generations for survival in somewhat toxic levels of JH analog overcame some of the lifespan reduction; these flies were longer-lived than wild type in the absence of JH (Flatt and Kawecki, 2007). The exact roles that JH plays in regulating aging are still being studied but the indications are that it promotes aging in insects.

Long-lived female *inr* mutants also have reduced 20E levels, which may be related to the fact that their ovaries are undeveloped, and the ovaries are the major site of 20E synthesis (Tu et al., 2002b). The 20E and IIS signaling pathways engage in cross talk during growth and development (Colombani et al., 2005; Walkiewicz and Stern, 2009). Flies heterozygous for mutations in the ecdysone receptor have increased longevity with no negative effects on reproduction (Simon et al., 2003). A mutant involved in 20E biosynthesis also has increased longevity (Simon et al., 2003). A more recent study involving adult-specific inactivation of the ecdysone receptor by RNAi or dominant negatives found that there was a mild lifespan extension in males, but in females lifespan was decreased (Tricoire et al., 2009). This harmful effect was prevented in a sterile mutant (Tricoire et al., 2009). There are many interesting similarities between 20E signaling in flies and dafachronic acid signaling in worms that suggest that these are homologous pathways (reviewed in Galikova et al., 2011).

MICE AND RATS

In vertebrates, the IIS signaling pathway has diverged into two distinct pathways, those of insulin and IGFs. Mammals have three IIS ligands, insulin, IGF-1, and IGF-2, and an insulin receptor and IGF-1 receptor (IGF-1R; reviewed in Taguchi and White, 2008). Insulin regulates metabolism, and IGF regulates development, growth, cell survival, proliferation, and other effects. IGF-1 is secreted by the liver in response to growth hormone from the anterior pituitary gland; signaling by IGF-1 is responsible for the growth-promoting effects of growth hormone (Liu and Leroith, 1999). IGF-1 is also secreted by peripheral tissues and this pool of IGF-1 can compensate for the loss of liver-derived IGF-1, which normally accounts for most of the IGF-1 in the serum (Yakar et al., 1999). IGF-1R signaling is essential for postnatal survival in mice, making it difficult to study using knockouts (Liu et al., 1993).

The observation that caloric restriction in rats increased lifespan was followed by work showing that pituitary hormone secretion was inhibited during this state (McCay et al., 1935; Mulinos and Pomerantz, 1940). It was later demonstrated that removal of the pituitary gland retarded some effects of aging (Everitt and Cavanagh, 1965; Olsen and Everitt, 1965). The Snell and Ames dwarf mice that have mutations in transcription factors (Pit-1 and Prop-1) that prevent the normal development of the anterior pituitary were discovered many decades ago (Snell, 1929; Schaible and Gowen, 1961). More recently, these mutant mice were studied and found to be long-lived (Brown-Borg et al., 1996; Flurkey et al., 2001). These dwarf mice lack the hormones GH, prolactin (PRL), and thyroid-stimulating hormone (TSH). Increasing PRL levels in these mice back to essentially normal levels by transplanting pituitary glands into them (which secrete only PRL constitutively) did not decrease their long lifespans, suggesting PRL is not involved (Flurkey et al., 2001). Treatment of Snell dwarf mice with the thyroid hormone thyroxine throughout their adulthood reduced their lifespan somewhat (Vergara et al., 2004). Hypothyroid mice have slightly increased longevity, suggesting that some but not all of the lifespan extension in dwarf mice may be due to reduced thyroid hormone levels (Ooka et al., 1983).

Interestingly, when dwarf mice were treated with GH and thyroxine for 11 weeks, they were able to grow significantly more than they normally would. Males became fertile, but they still had increased longevity, suggesting that retarded growth and reduced fertility are not the causes of increased longevity (Vergara et al., 2004). When the pituitary gland is removed in adults, lifespan is still extended, just as caloric restriction begun in adults also extends lifespan despite the fact that the animals are already fully grown (Weindruch and Walford, 1982; Powers et al., 2006). Mice expressing an antagonist of GH have reduced growth but do not live longer, further indicating that these effects can be uncoupled (Coschigano et al., 2003).

Knockout of the growth hormone receptor gene, or the growth hormone releasing hormone receptor gene, results in significantly increased longevity and reduced cancer rates (Zhou et al., 1997; Coschigano et al., 2000; Flurkey et al., 2001; Ikeno et al., 2009). Both of these mutants have extremely low levels of IGF but the former also has high levels of GH, whereas the latter has none. These results indicated that IGF itself was probably involved in regulating longevity. Heterozygous IGF-1R mutant females were shown to

have increased lifespan, although the control group had elevated mortality in this study (Holzenberger et al., 2003). It has been reported that another group was unable to reproduce this increase in lifespan (unpublished data cited in Ladiges et al., 2009). Mice that overexpress IGF or GH have reduced lifespans (Steger et al., 1993; Zaina et al., 2003). However, overexpression of IGF specifically in the hearts of mice actually increased their median lifespan, although maximum lifespan was not significantly changed, and thus the aging rate itself may not have been affected (Li and Ren, 2007). IGF can also be a protective signal for heart cells (Ren et al., 1999).

When the insulin receptor was knocked out specifically in adipose tissue, these mice had increased health parameters and lived 18% longer (Bluher et al., 2003; Katic et al., 2007). Fat itself may have negative effects on longevity as evidenced by the fact that surgical removal of fat can increase lifespan in rodents (Muzumdar et al., 2008). However, mice subjected to caloric restriction that had amounts of adipose tissue similar to those of the mice whose fat was surgically removed lived even longer (Muzumdar et al., 2008). A study in which the IRS-1, a downstream signaling component of the insulin and IGF pathways, was knocked out showed increased lifespan in mice (Selman et al., 2008). When IRS-2 was knocked out specifically in the brain of mice, they also lived longer (Taguchi et al., 2007).

In vertebrates IGF is bound and transported by a conserved family of high affinity IGF binding proteins (IGFBPs) numbered 1–6, and virtually all IGF found in the blood is bound by IGFBPs. The IGFBPs have equal or higher affinity for IGF than the IGF-1R, so they can be inhibitory but can also act to potentiate IGF signaling in some cases (Duan and Xu, 2005). Some of the IGFBPs, notably IGFBP-4, a principally inhibitory binding protein, can be cleaved by a protease called “pregnancy-associated plasma protein A” (PAPP-A; Lawrence et al., 1999). Deletion of the PAPP-A gene increases mouse lifespan by around 40% and delays some effects of aging (Conover and Bale, 2007; Vallejo et al., 2009). PAPP-A may promote aging by releasing IGF from inhibitory IGFBPs (cleaved IGFBPs lose affinity for IGF), thereby increasing pro-aging IGF signaling levels (Conover, 2010).

Mutation of a gene called *klotho* was shown to reduce lifespan greatly, and the mutants exhibited signs of apparent accelerated aging (Kuro-O et al., 1997). Subsequently, the extracellular domain of *klotho* was found in the bodily fluids and shown to act as a hormone (Imura et al., 2004). Overexpression of *klotho* can increase the longevity of mice, suggesting more strongly that it may be involved in normal aging; it may function by suppressing insulin or IGF signaling (Kurosu et al., 2005). It has also been shown to affect other signaling pathways that may be relevant for aging (Liu et al., 2007; Wang and Sun, 2009).

Other forms of hormonal signaling have not been studied nearly as well in mice as the GH–IGF axis. Gonadal signaling has been implicated in longevity regulation. In rats, castration can increase lifespan (Drori and Folman, 1976). When the ovaries of young female mice were transplanted into older female mice whose ovaries had been removed before puberty, the lifespan of the recipients was increased by 40% relative to controls that received sham surgeries (Cargill et al., 2003). Removal of the ovaries of old mice and replacing them directly with young ovaries also extended

lifespan of the recipients (Mason et al., 2009). Estrogen levels fall in female mammals after cessation of reproductive cycling, and this change is associated with an increased risk of CVD (Jacobsen et al., 1999). Female mice that received transplanted young ovaries after having undergone cessation of reproductive cycling were protected from the normal increase in cardiovascular risk (Mason et al., 2011). These results suggest a cell-non-autonomous effect on longevity mediated by endocrine signaling from the ovary, possibly involving estrogen, but this has yet to be determined.

In mice and most other vertebrates, the thymus, the major site of T-lymphocyte production, undergoes striking involution starting at puberty, causing it to be replaced with adipose tissue. Involution continues progressively throughout life until the organ is only a small fraction of its size at puberty, and this is thought to account for some of the reductions in immune system function that occur with age (reviewed in Taub and Longo, 2005). When old rats were castrated, the thymus regenerated, and immune functions were rejuvenated, but treatment of castrated rats with testosterone reversed these effects (Greenstein et al., 1986; Utsuyama and Hirokawa, 1989). The same effects have been found in mice and humans as well (Sutherland et al., 2005). Glucocorticoids have long been implicated in promoting thymic involution (Wyllie, 1980). It has recently been shown that testosterone signaling induces thymocytes to produce glucocorticoids, and mice that lack the glucocorticoid receptor in the thymus are completely protected from thymic involution (Chen et al., 2010). Incidentally, long-lived PAPP-A mutant mice are also protected from thymic involution (Vallejo et al., 2009).

Cell-non-autonomous effects in aging were demonstrated decades ago when it was shown that bone marrow cells from old mice were competent to repopulate bone marrow in young transplant recipients, but bone marrow cells from young individuals were not able to aid old recipients (Harrison, 1975a,b). Marrow cells can be transplanted serially and last through the lives of several generations of mice, suggesting that an intrinsic limit on cell divisions did not limit lifespan (Siminovitch et al., 1964). Adult tissue stem cells often exhibit defects in replicative capacity, or are lost altogether with age (Kuhn et al., 1996; Maslov et al., 2004; Nishimura et al., 2005; Waterstrat and Van Zant, 2009; Zhou et al., 2010). Recent studies have shown that aged muscle stem cells in old individuals could be rejuvenated by exposure to blood from young animals, suggesting that hormones in the blood regulate the aging-related changes in muscle stem cells (Conboy et al., 2005; Brack et al., 2007). FoxO3, a *daf-16* homolog inhibited by the IGF pathway was shown to oppose the aging of neural stem cells (Renault et al., 2009).

LESSONS FROM OTHER ANIMAL SPECIES

In this section we discuss results of studies on the aging of three non-traditional model organisms that provide unique insights into the endocrine regulation of longevity. Some of the aging mechanisms in these organisms may not be directly relevant to humans, but understanding the diversity of regulatory mechanisms which evolution has produced is useful when considering the kinds of differences that may exist between model systems and humans (see **Table 1**).

SOCIAL INSECTS

Social insects like bees, ants, and termites provide interesting models for aging research because workers are typically much shorter-lived than queens giving examples of massively different lifespan being produced by the same genome. Queens in many species can live 100 times longer than their workers (Keller and Genoud, 1997). This additional longevity does not appear to be a result of increased oxidative stress resistance (Corona et al., 2005; Schneider et al., 2011). The difference in longevity between highly reproductively active queens and sterile female workers is also of interest because it suggests that investment in reproduction does not necessarily preclude “somatic maintenance” from taking place. In various mammal and bird species, it has also been found that reproductive investment is unconnected with lifespan (Ricklefs and Cadena, 2007). There have also been a number of examples from other model systems that show that fecundity and longevity can be decoupled (Gems et al., 1998; Ueyama and Fuyama, 2003; Vergara et al., 2004; Liu et al., 2005; Copeland et al., 2009; Grandison et al., 2009).

Honey bee workers begin adult life performing tasks in the hive and then transition to foraging for resources outside. Foragers have higher external mortality rates (due to predation and other hazards) but they also have more rapid declines in cognitive ability and stress resistance, and they experience exponential aging-related increases in mortality (Behrends et al., 2007; Remolina et al., 2007; Rueppell et al., 2007a,b). The lifespan of a worker is 4–8 weeks; the main determinant of lifespan is the age at which they transition to foraging (Amdam et al., 2004). This transition is promoted by JH signaling, and JH levels increase as the transition draws nearer (Jaycox et al., 1974; Fluri et al., 1982). During the winter months in temperate climates, workers become so-called “winter bees” that survive 6 months to a year; in this state their JH levels are very low (Fluri et al., 1982).

Workers are sterile and do not produce eggs but they nevertheless synthesize an evolutionarily conserved egg yolk protein called vitellogenin (Rutz and Luscher, 1974). Nurse bees use the vitellogenin to generate a secretion called royal jelly that is used to feed larvae, the queen, and other bees (Amdam et al., 2003). Young hive bees express vitellogenin at extremely high levels but expression declines with age (Fluri et al., 1982). Knockdown of vitellogenin by RNAi increases JH levels and speeds up the transition to foraging, thus reducing lifespan (Guidugli et al., 2005). Increased JH signaling also downregulated vitellogenin (Pinto et al., 2000). It has been suggested that the antagonism between these two key signals is important for regulating the transition to foraging, and thus longevity (Amdam and Omholt, 2003).

Honey bees have two ILP genes and two INR genes (Ament et al., 2008). Queens have lower IIS signaling levels than workers, and nurse bees have lower levels than foragers (Corona et al., 2007; Ament et al., 2008). This is consistent with the idea that reduced IIS extends lifespan in other organisms, but IIS also usually correlates with nutrition levels and it seems to work oppositely in honey bees (Ament et al., 2008). This unique regulatory mechanism may have evolved to maintain survival of bees with high levels of stored nutrients in order prevent loss of those resources by the colony as a whole (Munch and Amdam, 2010).

SALMON

The Pacific Salmon of the genus *Oncorhynchus* are semelparous and usually die immediately after spawning. In the period leading up to sexual maturation and spawning they undergo a series of degenerative changes that resemble the effects of aging in other vertebrates. Most organs including kidney, liver, spleen, heart, and digestive tract degenerate; arteriosclerotic lesions develop in the arteries; the thymus involutes and immune functions are lost; neurodegeneration occurs, and amyloid aggregates are deposited in the brain (Robertson and Wexler, 1960; Robertson et al., 1961; Maldonado et al., 2000, 2002). Unlike most species, this senescence process in salmon is generally accepted as being evolutionarily “programmed” due to its high degree of stereotypy (Austad, 2004a).

It is believed that elevated levels of corticosteroid hormones are responsible for many of the degenerative changes in salmon (Mcquillan et al., 2003). The interrenal gland, the teleost fish homolog of the adrenal gland, undergoes hyperplasia, and corticosteroid levels become elevated fivefold or more during maturation and spawning (Hane and Robertson, 1959; Robertson and Wexler, 1960). Implantation of pellets infused with cortisol in young fish caused the same degenerative changes to occur prematurely (Robertson et al., 1963). Some Chinook salmon can mature without ever migrating out to sea, and most of these can survive a round of spawning and return to repeat the process. It was shown that the iteroparous salmon that do not die after spawning did not exhibit the same elevations in corticosteroids as semelparous members of the same species (Barry et al., 2001). When the gonad was removed from salmon before maturation, interrenal hyperplasia was prevented and lifespan was extended (Robertson, 1961). Gonadectomy prevented hypersecretion of corticosteroids, and this was rescued in gonadectomized fish by injections of androgens (Fagerlund and Donaldson, 1969). Sex steroids can directly regulate corticosteroid secretion in salmon (Mcquillan et al., 2003). Based on these results, it is believed that gonadal sex steroids regulate programmed death in salmon. It is interesting that androgen and corticosteroid signaling also seem to regulate post-mating programmed death of males in some species of dasyurid marsupials (McDonald et al., 1986; McCallan, 2006).

The GH-IGF axis promotes growth and is nutritionally regulated in fish including salmon (Duan, 1998; Beckman et al., 2004), but there have so far been no studies directly linking IGF signaling to aging in salmon. However, it is interesting to note that IGF promotes synthesis of sex steroids in salmon gonads (Maestro et al., 1997) and stimulates release of gonadotropins luteinizing hormone (LH) and follicle stimulating hormone (FSH; Furukuma et al., 2008). In salmon, in the year before spawning, a period of rapid body growth and gonadal development takes place during which plasma IGF positively correlates with body size and Estradiol levels (Campbell et al., 2006). Increased plasma IGF levels were found in salmon with more advanced gonadal development, suggesting that IGF may be involved in linking the timing of body growth and sexual maturation in preparation for spawning (Onuma et al., 2010). The evidence is consistent with the idea that IGF signaling promotes sexual maturation and sex steroid synthesis, which in turn promotes aging-like programmed

post-spawning death by inducing hypersecretion of glucocorticoids. The major lesson from these studies in salmon is that, at least in this species, endocrine signaling systems may actively promote a programmed aging process. While most other species including humans almost certainly do not undergo this sort of stereotyped programmed aging process, there may still be parallels. For instance, sex steroid-induced glucocorticoid secretion is involved in age-related thymic involution even in mammals (Chen et al., 2010).

NAKED MOLE RAT

The naked mole rat, *Heterocephalus glaber*, is a mammal that is approximately the same size as a mouse but lives about 10 times longer; the oldest reported naked mole rat lived 28.3 years (Buffenstein and Jarvis, 2002). Naked mole rats live in burrows and eat giant tubers that they find underground. They have a reduced threat from predators and seem to have evolved increased lifespan as a result (Buffenstein, 2005). It was thought that their extended lifespan might be due to higher resistance to oxidative stress, but it was shown that young naked mole rats actually have higher levels of oxidative damage than young mice (Andziak et al., 2006). Interestingly, naked mole rats are also extremely resistant to cancer, and tumors have never been observed in them (Seluanov et al., 2009). In naked mole rat colonies, one female and between 1 and 3 males breed, but mating is repressed in all other colony members. There is no difference in lifespan between breeders and non-breeders, and breeding continues until death (Buffenstein and Jarvis, 2002). However, in related species of mole rats, breeders have been shown to live considerably longer than non-breeders (Dammann and Burda, 2006; Dammann et al., 2011).

Information on endocrinology in naked mole rats is still limited (Edrey et al., 2011). Naked mole rats are somewhat insulin resistant and glucose intolerant (Kramer and Buffenstein, 2004). Increased insulin sensitivity has been proposed as a major mechanism of life extension. Naked mole rats have also been found to have very low thyroid hormone levels relative to other rodents (Buffenstein et al., 2001). They also show a low metabolic rate compared with mice. Since they live underground, they do not receive sunlight and are unable to synthesize vitamin D, but they are nevertheless able to regulate calcium levels (Buffenstein et al., 1994). In mice, the anti-aging hormone *klotho* inhibits vitamin D induced apoptosis, and *klotho* knockout mice have severe vitamin D toxicity (Kuro-O et al., 1997; Medici et al., 2008). Comparative studies of naked mole rats should provide insights into the endocrinology of aging in the future.

HUMANS AND OTHER PRIMATES

A number of endocrine signaling changes occur during normal aging in humans. In females one of the most significant changes is menopause, after which estrogen levels are greatly reduced (Lindsay et al., 1996). Menopause occurs at an average age of 51, and the timing of menopause (early or late) was found to be predictive of lifespan (Snowdon et al., 1989; Jacobsen et al., 1999). Hormone replacement therapy can reduce mortality rates in post-menopausal women younger than 60 (Salpeter et al., 2009). Most mammals exhibit a similar cessation of ovulation with aging, but interestingly, menstrual cycles continue basically up until death in

our closest relative the chimpanzee (Lacrouse et al., 2008). Male testosterone levels decrease with age after puberty, and this has been termed “andropause” (Tenover, 1994; Feldman et al., 2002). Testosterone replacement therapy may have a number of beneficial effects in elderly men (reviewed in Bain, 2010). In males, the FSH and LH levels increase with advancing age (Morley et al., 1997; Feldman et al., 2002). In females, mean FSH and LH levels increase before menopause and then increase even further following menopause (Chakravarti et al., 1976; Lee et al., 1988; Lenton et al., 1988). Thyroid hormones decline in both sexes (Hesch et al., 1977; Mariotti et al., 1995). Basal levels of glucocorticoids generally do not change (Jensen and Blichert-Toft, 1971) but cortisol may increase somewhat (Van Cauter et al., 1996). Basal levels of aldosterone decrease (Flood et al., 1967). Basal levels of glucagon are unchanged in the elderly but the liver’s sensitivity to it may change (Simonson and DeFronzo, 1983). Growth hormone secretion (Rudman et al., 1981; Ho et al., 1987), and total serum IGF-1 levels go up during puberty and then fall with increasing age (Johanson and Blizzard, 1981; Poehlman and Copeland, 1990; Brabant et al., 2003; Veldhuis et al., 2005). About 99% of serum IGF is bound to IGF-BPs, and levels of free IGF-1 decrease with age but free IGF-2 remains stable with age (Frystyk et al., 1994; Juul et al., 1997). By a different method, serum free IGF-1 was also found to increase (Janssen et al., 1998).

A number of studies have found that certain inflammatory cytokines, such as interleukin-6 (IL-6) and tumor necrosis factor alpha (TNF α), are elevated in healthy elderly people (Wei et al., 1992; Ershler et al., 1993; Hager et al., 1994; Ferrucci et al., 2005), but some studies have found conflicting results (Peterson et al., 1994; Beharka et al., 2001). Elevated levels of TNF α have been implicated in promoting the apoptosis of myocytes that leads to aging-related sarcopenia (Carbo et al., 2002; Visser et al., 2002; Pistilli et al., 2006; Schaap et al., 2009). One source of higher levels of inflammatory mediators may be adipose tissue, which increases in quantity and redistributes to different locations in older humans and mice (Morin et al., 1997; Wu et al., 2007; Kuk et al., 2009; Koster et al., 2010). Adipose tissue also secretes a number of other endocrine signaling molecules (reviewed in Galic et al., 2010), and some of these may be involved in controlling the sensitivity of tissues to the action of insulin (Xu et al., 2003; Menzaghi et al., 2007; Serrano et al., 2009; Lim et al., 2010). The prevalence of insulin resistance increases with age in humans, monkeys, and rodents (Narimiya et al., 1984; Frazee et al., 1987; Lane et al., 1995; Gomez-Perez et al., 2011). Insulin resistance eventually develops into type two diabetes (Groop, 1999), which also increases in prevalence with age (Cowie et al., 2006).

One of the biggest endocrine changes found in human aging is the 5- to 10-fold decrease in levels of dehydroepiandrosterone (DHEA), a steroid secreted by the adrenal glands (Orentreich et al., 1992; Ravaglia et al., 1996). Higher levels of this hormone have been linked with better health outcomes and one study has found a correlation between higher levels of DHEA and increased longevity in males (Enomoto et al., 2008). Treatment of elderly people with DHEA resulted in beneficial effects including improvement of insulin sensitivity and reduction of inflammatory cytokines (Weiss et al., 2011).

Understanding human aging is the ultimate goal of most aging research, but theories are difficult to test directly in humans. For instance, it is still unclear whether caloric restriction affects lifespan in humans, but there is evidence that even short term caloric restriction provides many of the health benefits seen in other animals, and protection from aging-related diseases such as atherosclerosis (Fontana et al., 2004; Fontana and Klein, 2007). Studies of caloric restriction in rhesus monkeys have shown reduced cancer rates, delayed immune system senescence, other beneficial health effects, and extended longevity (Mattison et al., 2003; Mes-saoudi et al., 2006; Colman et al., 2009). Hormonal changes in humans subjected to caloric restriction include an increase in cortisol (Fichter et al., 1986), and reductions of thyroid hormones (Roth et al., 2002; Fontana et al., 2006), leptin (Bergendahl et al., 2000; Chan et al., 2003), insulin (Fontana et al., 2004; Weiss et al., 2006), and testosterone in men (Cangemi et al., 2010). It is noteworthy that GH, IGF, and DHEA levels did not change with caloric restriction in humans (Smith, 1996; Walford et al., 2002; Heilbronn et al., 2006). However when protein intake is restricted in humans, IGF levels were decreased (Fontana et al., 2008).

There is conflicting evidence regarding IGF signaling and aging in humans. Recently a number of studies have found association between polymorphisms in genes encoding IGF pathway components and longevity. These include the IGF-1 receptor and downstream signaling components such as PI3K, AKT, and FOXO3a (Bonafe et al., 2003; Kuningas et al., 2007; Suh et al., 2008; Willcox et al., 2008; Anselmi et al., 2009; Li et al., 2009; Pawlikowska et al., 2009). A variant of the human klotho gene may also be associated with human longevity (Arking et al., 2002). In women, combinations of polymorphisms in IIS pathway genes that were expected to decrease signaling were associated with increased longevity (Van Heemst et al., 2005). In addition polymorphisms in the IGF-1R that were associated with longevity have been shown to be hypomorphic (Suh et al., 2008; Tazearslan et al., 2011). These results agree with the findings in animal models that IIS signaling and its downstream signaling pathway promote aging. Humans with mutations in the growth hormone receptor who have reduced IGF-1 levels can survive to old age (Laron, 2005). However, humans with hypopituitarism and deficiencies in growth hormone who are not treated with growth hormone have reduced lifespan (Besson et al., 2003). Patients with acromegaly (excessive growth hormone and IGF-1 levels) also have reduced lifespan, especially when untreated (Bates et al., 1993).

A large number of studies over the last decade have looked for associations between serum IGF-1 levels in humans and risk of dying from all-causes over a subsequent follow-up period. Some of these have found no association between serum IGF-1 levels and risk of all-cause mortality (Laughlin et al., 2004; Saydah et al., 2007; Kaplan et al., 2008; Hu et al., 2009; Yeap et al., 2011). However, some studies did find that lower levels of serum IGF-1 (Cappola et al., 2003; Roubenoff et al., 2003; Friedrich et al., 2009), or serum IGF bioactivity (Brugts et al., 2008), were associated with greater all-cause mortality risk. At least one study also found that higher IGF-1 levels were associated with greater all-cause mortality risk (Andreassen et al., 2009), and two studies found greater risk for subjects with both low and high levels (Van Bunderen et al., 2010; Friedrich et al., 2011). Based on these results, it is still unclear

whether infusions of IGF would be beneficial or detrimental in older people.

ATHEROSCLEROSIS AND CARDIOVASCULAR DISEASE

Cardiovascular disease, which includes heart attack, stroke, and heart failure is by far the most common aging-related cause of death in elderly humans (Xu et al., 2010). Incidences of CVD increase exponentially with age (Driver et al., 2008). The underlying cause of most CVD is atherosclerosis, a disease of the arteries in which complex lipid-containing inflammatory lesions called atheromatous plaques form beneath the endothelial cell lining. Treatments (drugs and diets) that reduce plasma low density lipoprotein (LDL) levels protect against atherosclerosis in humans (Gould et al., 1998) even in people who already have extremely low LDL levels (Leeper et al., 2007). Atherosclerosis does not occur in rodents unless they are fed an “atherogenic” high fat, high cholesterol diet (Armstrong and Heistad, 1990), and animals normally have much lower LDL levels than the average for humans (Mills and Taylaur, 1971). Mice are particularly resistant to atherosclerosis, but apolipoprotein E (ApoE) and LDL receptor (LDLR) knockout mice, which have massively elevated LDL levels, do develop atherosclerosis early in life (Plump et al., 1992; Zhang et al., 1992; Ishibashi et al., 1994). Humans who are deficient in the LDL receptor, which removes LDL from the blood, are also extremely prone to atherosclerosis at an early age (Mabuchi et al., 1986). LDL particles are actively transported through the endothelial cell layer to the subendothelial matrix (Vasile et al., 1983; Ishibashi et al., 1994) where they bind to negatively charged proteoglycan molecules, and accumulate (Skalen et al., 2002; Tabas et al., 2007; Nakashima et al., 2008). The aggregated LDL particles eventually provoke a complex inflammatory response involving recruitment of immune cells, leading to further plaque development (reviewed in Galkina and Ley, 2009).

The arteries change with age and become more susceptible to atherosclerosis (reviewed in Lakatta et al., 2009). The changes include a thickening and stiffening of the extracellular matrix-rich inner layer of the artery wall (the intima) and an increase in the number of vascular smooth muscle cells in this zone (Virmani et al., 1991; Orlandi et al., 1993; Nagai et al., 1998; Li et al., 1999; Wang et al., 2003, 2007a). Atherosclerosis preferentially occurs at sites of thickened intima (Orlandi et al., 2000; Nakashima et al., 2007). In mice, rabbits, and monkeys, when young and old animals were fed atherogenic diets, the older animals developed more advanced and more severe atherosclerosis than the younger ones in the same time period (Clarkson et al., 1969; Spagnoli et al., 1991; Orlandi et al., 2000; Collins et al., 2009). The progression of atherosclerosis in humans is accelerated in the premature aging diseases, Werner syndrome and Hutchinson–Gilford Progeria, despite a lack of elevated LDL or other risk factors (Cohen et al., 1987; Gordon et al., 2005; Hennekam, 2006; Cao et al., 2007; Olive et al., 2010) and in a mouse model of premature aging (Fenton et al., 2004).

Insulin-like growth factor 1 signaling seems to be involved in regulating the rate of the underlying aging process, and this may promote the arterial remodeling that increases susceptibility to atherosclerosis. In recent years, some association studies have found that higher levels of IGF-1 are associated with increased risk of CVD (Fischer et al., 2004; Kawachi et al., 2005; Schneider

et al., 2008; Andreassen et al., 2009). However, some studies have shown the opposite result, that lower levels of IGF-1 predict higher risk of CVD (Juul et al., 2002; Vasan et al., 2003; Laughlin et al., 2004; Johnsen et al., 2005; Friedrich et al., 2009). Some studies also found no association between IGF-1 levels and CVD (Saydah et al., 2007; Yeap et al., 2011); one found that both high and low levels showed increased risk of CVD (Van Bunderen et al., 2010). Humans with a genetic polymorphism in the promoter of the IGF-1 gene that resulted in an average of 18% less IGF-1 in their serum were found to be at higher risk for heart attack (Vaessen et al., 2001). Hypopituitarism and acromegaly, which cause a deficiency or excess, respectively, in activity of the GH–IGF-1 axis, both cause increased risk of CVD (Rosen and Bengtsson, 1990; Clayton, 2003).

The role of IGF in atherosclerosis has been extensively studied. ApoE knockout mice that were engineered to have a genetic polymorphism that results in 20% less circulating IGF-1 had an increased atherosclerotic plaque burden compared with control ApoE knockout mice (Shai et al., 2011). Infusion of recombinant IGF-1 into the blood of ApoE knockout mice resulted in decreased plaque burden (Sukhanov et al., 2007). However, overexpression of IGF-1 in VSMCs in ApoE knockout mice did not reduce the plaque burden but the plaques showed signs of increased stability (Shai et al., 2010). Overexpression of IGF-1 in smooth muscle tissue does cause VSMC proliferation and hyperplasia (Wang et al., 1997). PAPP-A, which increases IGF bioavailability by cleaving inhibitory IGFBPs, is enriched in atherosclerotic plaques, and in the blood in people with coronary artery disease and unstable atherosclerotic plaques (Bayes-Genis et al., 2001a; Beaudoux et al., 2003; Lund et al., 2003; Heider et al., 2010). Knockout of PAPP-A in mice extends lifespan, as mentioned previously, and also delays aging-related pathology, including reduced degenerative cardiovascular changes (Conover et al., 2010a). Knockout of PAPP-A in ApoE knockout mice reduced the size of their atherosclerotic lesions (Harrington et al., 2007), and overexpression of PAPP-A in ApoE knockout mice increased lesion size (Conover et al., 2010b). Overexpression of a protease-resistant form of IGFBP-4, a major PAPP-A target (Parker et al., 1995; Bayes-Genis et al., 2001b), inhibits smooth muscle cell growth in mice (Zhang et al., 2002). Infusion of the protease-resistant form of IGFBP-4 into hypercholesterolemic pigs reduced the size of their atherosclerotic lesions, and this effect was prevented by simultaneous infusion of IGF-1 (Nichols et al., 2007). ApoE knockout mice that also lack IGF-2 have reduced atherosclerotic lesion size compared with control ApoE knockout mice, suggesting that IGF-2 promotes atherosclerosis (Zaina et al., 2002). Constitutive IGF-1R tyrosine kinase activity was found in VSMCs from old rats but not young rats (Li et al., 2008). It has been suggested that IGF-1 in the blood protects against plaque rupture by inhibiting VSMC apoptosis (Conti et al., 2011). Based on the evidence discussed above, it seems likely that IGF signaling, especially by IGF-2, also plays a role in promoting atherosclerosis, perhaps at the level of paracrine signaling within the arterial intima. IGF also protects the heart by inhibiting cardiomyocyte apoptosis (Lee et al., 1999), which normally causes an aging-related decline in heart function even in the absence of disease (Olivetti et al., 1997).

There is evidence to suggest that signaling by the hormone angiotensin II plays a role in promoting aging-related changes in the arteries. Angiotensin II is the final and most active product of the renin–angiotensin system whose primary role is to regulate blood pressure (Mehta and Griendling, 2007). Angiotensin II induces vasoconstriction by binding to and activating angiotensin type 1 receptors (AT1) on vascular smooth muscle cells. Angiotensin signaling might play a role in aging. Knockout of the major isoform of AT1 in mice (AT1a) increases lifespan (Benigni et al., 2009). Long-term treatment of rats with inhibitors that reduce angiotensin signaling protected against aging-related changes in the cardiovascular system and also extended their lifespans (Basso et al., 2007). Double knockout mice lacking both AT1a and ApoE had significantly smaller atherosclerotic lesions at 60 weeks of age than mice lacking only ApoE, indicating that AT1 signaling promotes atherosclerosis progression (Eto et al., 2008). The arterial walls of aged mice and non-human primates contain higher levels of angiotensin-converting enzyme (ACE), angiotensin II, and other components of the angiotensin signaling pathway (Wang et al., 2003, 2007a). Treatment of young rats with angiotensin II causes changes in their artery walls that reproduce changes that normally occur with aging (Wang et al., 2005). Angiotensin II increases expression of the IGF-1R in VSMCs, and this may be involved in the mechanism by which angiotensin II promotes VSMC proliferation (Du et al., 1999).

CANCER

The second most common cause of death in the elderly is cancer (Xu et al., 2010). Rates of cancer incidence increase with age but actually fall after the ninth decade (Driver et al., 2008). Cancer seems to be linked to the rate of the underlying aging process, in that processes like speciation and selective breeding that can alter lifespan also affect the rate of cancer incidence (Miller, 1991). Caloric restriction reduces cancer rates in mice and non-human primates (Weindruch and Walford, 1982; Weindruch et al., 1986; Colman et al., 2009). *C. elegans* mutants with extended longevity, including IIS mutants, have reduced growth of germ line tumors (Pinkston et al., 2006; Pinkston-Gosse and Kenyon, 2007). Dwarf mice, GH receptor knockout mice, and PAPP-A knockout mice have reduced and/or delayed cancer occurrence (Ikeno et al., 2003, 2009; Conover et al., 2010a). Humans with a variety of mutations that confer congenital IGF-1 deficiency are protected from cancer (Shevah and Laron, 2007). A number of association studies have found that higher serum IGF levels correlate with higher risk for specific cancers (Chan et al., 1998; Hankinson et al., 1998; Ma et al., 1999; Yu et al., 1999; Probst-Hensch et al., 2001; Renehan et al., 2004; Gunter et al., 2009), and general cancer mortality in elderly men (Major et al., 2010). IGFs promote growth, proliferation, and protection against apoptosis, and are directly involved in promoting tumorigenesis (reviewed in Pollak, 2008). High levels of insulin may also increase the risk of cancer in humans (Pisani, 2008). Reductions in IIS signaling seem to protect against cancer but a major question is whether this is caused by a delay in the aging process or simply an inhibition of tumor growth due to the reduced availability of an important growth factor. The fact that GH-deficient mice are resistant to chemical carcinogenesis suggests

that a reduction in the GH–IGF-1 axis may actually increase resistance to DNA mutation (Ramsey et al., 2002). FOXO transcription factors, which are inhibited by IIS signaling, have been shown to act as tumor suppressors (Paik et al., 2007), and FoxO3a has been shown to activate DNA repair (Tran et al., 2002). After a tumor has already formed, many endocrine signaling systems can be co-opted by the cancer cells to promote their own proliferation; an account of all of these is beyond the scope of this review.

THE NEED FOR NEW MODEL SYSTEMS

In the last two decades, genetic studies using very short-lived model organisms including flies, worms, and yeast (which have not been discussed here due to their lack of “endocrine” signaling) have revealed a wealth of new knowledge about the molecular basis of aging. The advantage of short-lived models is that they are amenable to “lifespan extension experiments,” that is, experiments in which a genetic manipulation or intervention is tested with the hypothesis that it will extend the lifespan. An extension of maximum lifespan, coupled with a retardation of demographic senescence, and a delay in aging-related disease incidence, is one of the most robust ways to demonstrate the involvement of the manipulated process or mechanism in normal aging. Conversely, when only reductions in levels of markers associated with aging, or a reduction in lifespan is reported, it is difficult to know whether these effects are truly due to changes in aging rate.

Short-lived models also have the disadvantage that it is impossible to know whether any given mechanism that is demonstrated to be at work in a short-lived organism is also present in longer-lived organisms such as humans. Many short-lived organisms are distant from humans on the tree of life and differ in certain aspects of their biology. One way to address this problem is to study each process in multiple different short-lived organisms from different phyla and confirm broad evolutionary conservation. *C. elegans* and *Drosophila* alone may be insufficient for this due to their phyla belonging to the same superphylum of ecdysozoa (Mallatt and Winchell, 2002; Dunn et al., 2008). Another approach would be to study long-lived organisms and focus on the differences between young and old individuals. This may be necessary in order to uncover ways to extend the lifespan of already long-lived humans.

It is clear that new model systems will be a useful addition to aging research (see **Table 1**). The honey bee as a social insect and the naked mole rat as a relatively long-lived mammal as discussed above are now being studied more extensively (Buffenstein, 2005; Munch and Amdam, 2010). In addition, extremely long-lived mollusks (bivalves) that live hundreds of years are beginning to be studied (Philipp and Abele, 2010). Some fish can also live more than 200 years and continue reproduction into advanced age (De Bruin et al., 2004; Mangel et al., 2007). Zebrafish are now being studied as a gradually aging fish model system (Gerhard et al., 2002). Zebrafish can live up to 4–5 years and thus, despite their many advantages (small size, genetic tractability, etc.), they cannot be used for the same kinds of rapid aging experiments as *Drosophila* and *C. elegans*.

Another fish model that is gaining traction is the exceptionally short-lived annual killifish *Nothobranchius furzeri*. *N. furzeri*

has the advantages of being both short-lived, with a maximum lifespan of around 3 months in the shortest-lived strain (Valdesalici and Cellerino, 2003; Terzibasi et al., 2008), and being a vertebrate and therefore sharing many biological features with humans that are not shared by lower organisms (Valdesalici and Cellerino, 2003; Austad, 2004b). An initial characterization of the *N. furzeri* genome has been published (Reichwald et al., 2009), and a number of vertebrate aging genes have been cloned (Genade et al., 2005). The appearance of aging-related biomarkers and aging pathology have been characterized, and they suggest that the aging process in *N. furzeri* follows a normal pattern but is highly accelerated (Genade et al., 2005; Di Cicco et al., 2011).

CONCLUDING REMARKS

Our current understanding of the endocrinology of aging is still incomplete and many open questions exist. Mutants that are deficient in a particular endocrine signaling pathway throughout life have provided most of the evidence that endocrine signaling is involved in regulating aging. It is generally unknown whether hormones actively influence the rate of the aging process or are simply required during a certain period to stimulate a developmental progression that later influences aging. Another major open question is, to what extent will the findings on the endocrine regulation of aging in model organisms be applicable to humans, and will hormone replacement or modulation therapies be effective

in treating or delaying aging-related diseases? Further research should increase our understanding of the endocrine pathways that regulate aging and the molecular mechanisms by which hormones affect the aging rate in different species.

A major lesson from studies in comparative endocrinology is that IIS signaling is involved in regulating longevity in many different species. This is logical considering its role as a highly conserved pathway that promotes growth and is regulated by nutritional status. IIS genes are good candidates for antagonistically pleiotropic genes because IIS signaling usually promotes fecundity in addition to aging. However, in many cases, aging and fecundity have been shown to be decoupled, indicating that a simple trade-off between reproduction and longevity is not necessarily sufficient to explain the causes of aging. Caloric restriction promotes longevity in virtually all species that have been examined and IIS signaling is likely at least partially involved in this phenomenon in some species. Further studies on the comparative endocrinology of aging may provide more evidence to link steroids and other hormones more concretely to longevity regulation in mammals.

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