
Dauer*

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Abstract

In response to harsh environmental conditions, *C. elegans* larvae undergo dauer arrest at the second molt. The past decade has yielded many insights into the signaling pathways and the molecular mechanisms

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that govern this developmental transition. Dauer pheromone, the major physiologic signal promoting dauer arrest, has been purified, identified, and synthesized. The molecular identities of the vast majority of dauer regulatory genes isolated in initial genetic screens are now known. Physiologic ligands for **DAF-12**, a nuclear receptor that is the final common target of dauer regulatory pathways, have been identified. The discovery of the **Hid** (**h**igh temperature induction of **d**auer) phenotype and the results of enhancer screens have greatly expanded the repertoire of dauer regulatory genes. Genomic analysis of dauer arrest has highlighted the role of pathway crosstalk in dauer regulation. Nonetheless, critical questions remain about the mechanistic underpinnings of dauer arrest.

1. Introduction

In 1975, Cassada and Russell described the dauerlarva, an arrested developmental variant of *C. elegans* that forms at the second molt in response to environmental duress. Dauer larvae exhibit morphological and behavioral characteristics distinct from those of larvae developing in replete environments (Cassada and Russell, 1975). Since that discovery, the transition to dauer arrest has been a fertile area of investigation in the *C. elegans* field, both as a model for regulatory mechanisms governing morphological change during organismal development as well as a parallel to obligate dauer-like developmental stages in parasitic nematodes. In recent years, the molecular identities of genes mutated in various mutants exhibiting dysregulation of dauer arrest (*daf* mutants) have revealed the critical roles of evolutionarily conserved guanylyl cyclase, transforming growth factor- β (TGF β)-like, insulin-like, and hormonal signaling pathways in the regulation of dauer arrest.

2. Environmental influences on dauer arrest

The dauer developmental decision occurs late in the L1 larval stage and hinges on the integration of three environmental parameters: population density, food supply, and ambient temperature. Population density is the major influence on dauer arrest and is conveyed by a constitutively synthesized pheromone that induces dauer arrest and prevents dauer recovery. Conversely, a heat-stable, hydrophilic “food signal” that provides information about food availability inhibits dauer arrest and promotes dauer recovery. The relative amounts of pheromone and food signal, rather than absolute levels, are critical in determining whether an animal undergoes dauer arrest (Golden and Riddle, 1982). Increased temperature enhances pheromone-induced dauer arrest (Golden and Riddle, 1984a), and some temperature-sensitive dauer-constitutive mutants are suppressible by an amber nonsense suppressor (Golden and Riddle, 1984b), suggesting that dauer arrest is intrinsically dependent upon ambient temperature.

3. Dauer morphology

Dauer larvae are morphologically distinct from larvae that develop in replete conditions. Dauers are radially constricted and possess a specialized cuticle with alae (Cassada and Russell, 1975). Their oral orifices are closed by an internal plug (Riddle et al., 1981), and their pharynxes are constricted (Vowels and Thomas, 1992) and do not pump (Cassada and Russell, 1975). Dauers are easily distinguishable from L3 larvae under a dissecting microscope. The dauer-specific cuticle and the lack of pharyngeal pumping confer resistance to many environmental insults, including 1% SDS (Cassada and Russell, 1975). SDS resistance provides a convenient method for isolating dauers and has greatly facilitated the genetic analysis of dauer formation.

4. Dauer metabolism

C. elegans undergoes a metabolic shift between L1 and L2 stages; embryos and L1 larvae use the glyoxylate cycle to generate carbohydrates from lipid stores, whereas L2 and later stages shift toward aerobic respiration and exhibit a relative increase in TCA cycle activity. Dauers do not undergo this shift toward aerobic respiration (Wadsworth and Riddle, 1989). Relative to growing larvae, dauers also appear to be transcriptionally quiescent but have elevated levels of mRNA encoding the heat shock protein Hsp90 (Dalley and Golomb, 1992; Snutch and Baillie, 1983) and elevated superoxide dismutase (Larsen, 1993; Vanfleteren and De Vreese, 1995) and catalase (Vanfleteren and De Vreese, 1995) activities. This suggests that dauers are adapted to resist metabolic stress and is consistent with the observation that they are long-lived (Klass and Hirsh, 1976).

5. Pheromone

Dauer pheromone has recently been purified from *C. elegans* extracts and molecularly characterized. Paik and colleagues first demonstrated that the ascaroside (-)-6-(3,5-dihydroxy-6-methyltetrahydropyran-2-yl)oxy heptanoic

acid has dauer pheromone activity (Jeong et al., 2005). Recently, Jon Clardy's group has identified three distinct ascarosides in *C. elegans* extracts with dauer pheromone activity (including the molecule identified by Paik's group). The two ascarosides distinct from that initially isolated by Paik's group, 5-O-ascarylosyl-5*R*-hydroxy-2-hexanone and an ascaroside derivative of 8*R*-hydroxy-2*E*-nonenoic acid, are two orders of magnitude more potent than (-)-6-(3,5-dihydroxy-6-methyltetrahydropyran-2-yl)oxy heptanoic acid at inducing dauer arrest (Butcher et al., 2007). These discrepancies may be a consequence of differences in the purification steps used by the two groups (Jeong et al., 2005; Butcher et al., 2007). Furthermore, during purification, one group followed activity using a dauer formation assay (Jeong et al., 2005), whereas the other followed activity using a dauer recovery assay (Butcher et al., 2007).

Little is known about how dauer pheromone is synthesized *in vivo* and released into the environment. Culture medium and organic extracts of a dauer-defective mutant, *daf-22(m130)*, do not contain dauer pheromone activity, suggesting that *daf-22(m130)* is defective in dauer pheromone synthesis (Golden and Riddle, 1985). Furthermore, exogenous dauer pheromone rescues the *daf-22(m130)* dauer-defective phenotype (Jeong et al., 2005). Interestingly, aqueous extracts of *daf-22(m130)* animals have measurable dauer pheromone activity (Golden and Riddle, 1985), suggesting that these animals may have a defect in a late step in dauer pheromone synthesis that results in the accumulation of a hydrophilic precursor or precursors that possess dauer pheromone activity. The molecular identity of *daf-22* is not known.

The mechanisms underlying direct cellular responses to dauer pheromone have not been elucidated. It has been assumed that dauer pheromone binds to a specific cell surface receptor expressed in amphid neurons; however, the molecular identity of such a receptor has remained elusive. The demonstration that active dauer pheromone consists of multiple compounds (Butcher et al., 2007) suggests that each compound may bind to a distinct receptor that transduces a dauer-promoting signal. This may explain why candidate dauer pheromone receptors have not emerged from the extensive genetic analysis of dauer development that has been performed to date. The availability of synthetic pheromone components should facilitate the search for their cognate receptors.

Consistent with the possibility that dauer pheromone binds to and activates a G-protein-coupled seven-transmembrane domain receptor, the G-protein α -subunits GPA-2 and GPA-3 promote dauer arrest when activated, suppress pheromone-induced dauer arrest when deleted, and are expressed in amphid neurons (Zwaal et al., 1997). The ability of cyclic GMP (cGMP) analogs to suppress pheromone-induced dauer arrest (Birnbay et al., 2000) suggests that dauer pheromone may cause dauer arrest at least in part by antagonizing a guanylyl cyclase. Many transmembrane guanylyl cyclase receptors are expressed in amphid neurons (Birnbay et al., 2000; Yu et al., 1997) and could potentially regulate responses to dauer pheromone.

6. Molecular characterization of signaling pathways regulating dauer arrest

Genetic analysis of dauer-constitutive (Daf-c) and dauer-defective (Daf-d) mutants has defined four distinct pathways that regulate dauer arrest (Gerisch et al., 2001; Gottlieb and Ruvkun, 1994; Jia et al., 2002; Riddle et al., 1981; Thomas et al., 1993; Vowels and Thomas, 1992). In the past decade, components of these and other pathways have been cloned and characterized, revealing the complex interplay of at least four evolutionarily conserved signal transduction pathways in regulating dauer formation.

6.1. Guanylyl cyclase pathway

The Daf-c gene *daf-11* defines a pathway that inhibits dauer arrest in parallel (at least in part) to a pathway defined by the genes *daf-1*, *4*, *7*, *8*, and *14* (Thomas et al., 1993). *daf-11* mutants also have defects in chemosensation (Vowels and Thomas, 1994). *daf-11* encodes a transmembrane guanylyl cyclase that is expressed in the chemosensory neurons ASI, ASJ, ASK, AWB, and AWC (Birnbay et al., 2000). 8-bromo-cGMP rescues the Daf-c phenotype of *daf-11* mutants, suggesting that the Daf-c phenotype of *daf-11* mutants is secondary to a reduction in cGMP synthesis. The inability of 8-bromo-cGMP to rescue dauer arrest in most other Daf-c mutants suggests that DAF-11 functions proximally in the regulation of dauer arrest (Birnbay et al., 2000).

Components of a cGMP-gated ion channel are candidate downstream effectors of DAF-11. *tax-2* and *tax-4* encode subunits of a cGMP-gated ion channel that regulates thermosensation, chemosensation, and neuronal development (Coburn and Bargmann, 1996; Coburn et al., 1998; Komatsu et al., 1996). Both *tax-2* and *tax-4* are expressed in sensory neurons and have overlapping expression patterns with *daf-11*, indicating that they may function together in the same cells. The *tax-4* dauer arrest phenotype is not rescued by 8-bromo-cGMP (Birnbay et al., 2000), suggesting that TAX-4 is a target of DAF-11-dependent cGMP signaling. These data suggest that

DAF-11 inhibits dauer arrest at least in part by activating TAX-2 and TAX-4 through increased cGMP synthesis. *tax-4* mutants have a weaker Daf-c phenotype than *daf-11* mutants (Coburn et al., 1998), indicating that DAF-11 probably activates multiple downstream effectors that contribute to inhibition of dauer arrest.

The *daf-21* gene was defined by a single allele, *p673*, that has genetic interactions and chemosensory pleiotropies similar to those of *daf-11* mutants (Thomas et al., 1993; Vowels and Thomas, 1994). Detailed genetic analysis of *daf-21(p673)* indicates that it is a recessive gain-of-function allele and that its phenotypes may be a consequence of allele-specific inhibition of DAF-11 function. Consistent with this finding, a null allele of *daf-21* does not have a dauer arrest phenotype and is larval lethal. *daf-21* encodes a Hsp90 homolog (Birnby et al., 2000).

6.2. TGF β -like pathway

The TGF β -like pathway that regulates dauer arrest is defined by the Daf-c genes *daf-1*, 4, 7, 8, and 14 and the Daf-d genes *daf-3* and *daf-5* (Patterson and Padgett, 2000). TGF β family ligands bind to and activate heteromeric cell surface receptors with serine/threonine kinase activity, resulting in the phosphorylation and activation of SMAD transcription factors that translocate to the nucleus to regulate transcription (Shi and Massague, 2003). Previous reviews (Riddle and Albert, 1997) described the molecular characterization of homologs of TGF β (DAF-7; Ren et al., 1996; Schackwitz et al., 1996) and Type I (DAF-1; Georgi et al., 1990) and Type II (DAF-4; Estevez et al., 1993) TGF β receptors. Since then, cloning of the remaining genes in this pathway has defined downstream transcription factors that are targets of DAF-7/TGF β -like signaling. This and other *C. elegans* TGF β -like signal transduction pathways are described in detail in another section of WormBook (see TGF β signaling). With the exception of DAF-7, which is expressed primarily in the ASI amphid neuron (Ren et al., 1996; Schackwitz et al., 1996), all components of this pathway are widely expressed (Da Graca et al., 2004; Gunther et al., 2000; Inoue and Thomas, 2000b; Patterson et al., 1997; Tewari et al., 2004). Mosaic analysis and rescue experiments with tissue-specific translational fusions indicate that DAF-4 functions non-autonomously to regulate dauer arrest (Inoue and Thomas, 2000b).

daf-3, *daf-8*, and *daf-14* encode SMAD transcription factors (Estevez, 1997; Inoue and Thomas, 2000b; Patterson et al., 1997), and *daf-5* encodes a Sno/Ski oncoprotein homolog that binds to DAF-3 (Da Graca et al., 2004; Tewari et al., 2004). Consistent with the role of mammalian SMADs as positive effectors of TGF β -like signaling (Shi and Massague, 2003), DAF-8 and DAF-14 are required for DAF-7/TGF β -mediated inhibition of dauer arrest (Inoue and Thomas, 2000b). However, in contrast, DAF-3 appears to be inhibited upon activation of the DAF-7/TGF β pathway (Patterson et al., 1997).

Recent findings indicate that the role of DAF-3 in the regulation of dauer arrest may be more complex than initially appreciated. Although *daf-3* loss-of-function mutations are Daf-d at 25°C (Thomas et al., 1993), they are Daf-c at 27°C (Ailion and Thomas, 2000), indicating that temperature may influence DAF-3 activity. Furthermore, although *daf-3* mutants suppress 25°C dauer arrest in the Daf-c mutants *daf-1*, 4, 7, 8, and 14 (Thomas et al., 1993), they enhance the weak 25°C dauer arrest phenotype of some Daf-c mutants (Gerisch et al., 2001; Ohkura et al., 2003). Thus, DAF-3 can function to promote or to inhibit dauer arrest depending upon environmental and genetic context. The mechanisms underlying these observations remain obscure.

A genetic screen to identify suppressors of the dauer arrest phenotype of *daf-1*, *daf-8*, and *daf-14* mutants identified three novel genes, *scd-1*, *scd-2*, and *scd-3* (Scd: suppressors of constitutive dauer arrest) that have weak Daf-d phenotypes when mutated (Inoue and Thomas, 2000a). *scd-1* and *scd-2* appear to be novel components of the TGF β pathway, whereas *scd-3* suppresses both DAF-7/TGF β pathway mutants as well as *daf-11* mutants and may function downstream of both pathways (Inoue and Thomas, 2000a). *scd-1* encodes a glutamine-rich protein, and *scd-2* encodes a homolog of the mammalian anaplastic lymphoma kinase (WormBase website, <http://www.wormbase.org>, release WS170, February 10, 2007). SCD-2 inhibits synaptic differentiation and is antagonized by the F-box-containing synaptic protein FSN-1 (Liao et al., 2004). The molecular identity of *scd-3* is not known.

egl-4 encodes a cGMP-dependent protein kinase that regulates chemosensation, locomotion, and body size (Daniels et al., 2000; Fujiwara et al., 2002; L'Etoile et al., 2002; Stansberry et al., 2001). *egl-4* mutants are hypersensitive to dauer pheromone (Golden and Riddle, 1984b) and have a weak dauer arrest phenotype (Daniels et al., 2000). Although the molecular identity of *egl-4* suggests that it may function in the guanylyl cyclase pathway to inhibit dauer arrest, genetic analysis indicates that *egl-4* functions primarily in the TGF β pathway to regulate dauer formation (Daniels et al., 2000).

BRA-1, a protein that binds to **DAF-1/TGF β RI**, appears to inhibit TGF β signaling proximally, as a *bra-1* deletion allele partially suppresses the dauer arrest phenotype of *daf-1* mutants but does not suppress *daf-14/SMAD* dauer arrest (Morita et al., 2001). *kin-8*, which encodes a homolog of the ROR family of tyrosine kinases, promotes dauer bypass and is required for full expression of **DAF-7/TGF β** in the ASI amphid neuron (Koga et al., 1999).

6.3. Insulin-like pathway

A third pathway regulating dauer formation was originally defined by the Daf-c genes *daf-2* and *daf-23* (allelic to *age-1*) and the Daf-d gene *daf-16* and functions in parallel to the guanylyl cyclase and TGF β -like pathways (Gottlieb and Ruvkun, 1994; Riddle and Albert, 1997; Thomas et al., 1993). Mutations affecting this pathway are phenotypically distinct from other Daf-c mutations in that strong alleles of *daf-2* and *age-1* arrest as dauers non-conditionally and do not recover (Gems et al., 1998; Morris et al., 1996). Furthermore, unlike guanylyl cyclase pathway and TGF β pathway mutants, *daf-2* pathway mutants exhibit extended lifespans (Friedman and Johnson, 1988; Hertweck et al., 2004; Kenyon et al., 1993; Morris et al., 1996; Paradis et al., 1999; Wolkow et al., 2002). The impact of this pathway on *C. elegans* longevity is described in detail in another WormBook chapter and will not be discussed further here.

Cloning and characterization of these and other genes in this pathway have defined a conserved insulin-like pathway that inhibits dauer arrest through activation of the **DAF-2** insulin receptor homolog, **AGE-1** phosphoinositide 3-kinase (PI3K), and the protein kinases **PDK-1**, **AKT-1**, and **AKT-2** (Kimura et al., 1997; Morris et al., 1996; Paradis et al., 1999; Paradis and Ruvkun, 1998). **AKT-1** phosphorylates and inhibits the FoxO transcription factor **DAF-16** by promoting its sequestration in the cytoplasm (Hertweck et al., 2004; Lee et al., 2001; Lin et al., 1997; Lin et al., 2001; Ogg et al., 1997). Cytoplasmic retention of **DAF-16** requires the 14-3-3 proteins **PAR-5** and **FTT-2** (Berdichevsky et al., 2006; Li et al., 2007). **DAF-18**, the *C. elegans* ortholog of the phosphoinositide 3-phosphatase **PTEN**, antagonizes **AGE-1/PI3K** (Gil et al., 1999; Mihaylova et al., 1999; Ogg and Ruvkun, 1998; Rouault et al., 1999). The E3 ubiquitin ligase **RLE-1** catalyzes polyubiquitination and proteasomal degradation of **DAF-16** (Li et al., 2007; see Figure 1). As is the case for TGF β pathway components, most of these genes are expressed throughout the animal. Mosaic analysis (Apfeld and Kenyon, 1998) and rescue experiments with tissue-specific translational fusions (Wolkow et al., 2000) indicate that **DAF-2/InsR** and **AGE-1/PI3K** function non-autonomously to inhibit dauer arrest.

Although most mutants with reduced insulin-like signaling have both Daf-c and extended longevity phenotypes, recent studies illustrate that dauer arrest and lifespan regulation by insulin-like signaling are decoupled by spatiotemporal compartmentalization. Intriguingly, although studies on **DAF-2/InsR** suggest that it functions primarily in the nervous system to regulate lifespan as well as dauer arrest (Apfeld and Kenyon, 1998; Wolkow et al., 2000), similar studies on the major target of insulin-like signaling, **DAF-16/FoxO**, suggest that dauer arrest and lifespan may be regulated by **DAF-16/FoxO** activity in distinct tissues. **DAF-16/FoxO** in the nervous system has stronger influences on dauer arrest than on lifespan, whereas intestinal **DAF-16/FoxO** plays a greater role in regulating lifespan than in regulating dauer arrest (Libina et al., 2003). Thus, **DAF-16/FoxO** activation in different tissues may have distinct phenotypic consequences. Furthermore, insulin-like signaling during larval development regulates dauer arrest without significantly impacting lifespan, whereas insulin-like signaling during adulthood suffices to regulate longevity (Dillin et al., 2002), indicating that temporal specificity also determines (at least in part) the biological output of insulin-like signaling.

Strikingly, the *C. elegans* genome is predicted to encode 40 insulin-like (INS) molecules (Pierce et al., 2001; WormBase website, <http://www.wormbase.org>, release WS170, February 10, 2007). Studies on *ins* genes are complicated by the potential functional redundancy of these genes as well as the possible indirect effects of INS protein overexpression on the processing of other INS family members. Notwithstanding these caveats, there is substantial evidence to indicate that *ins* genes regulate dauer arrest.

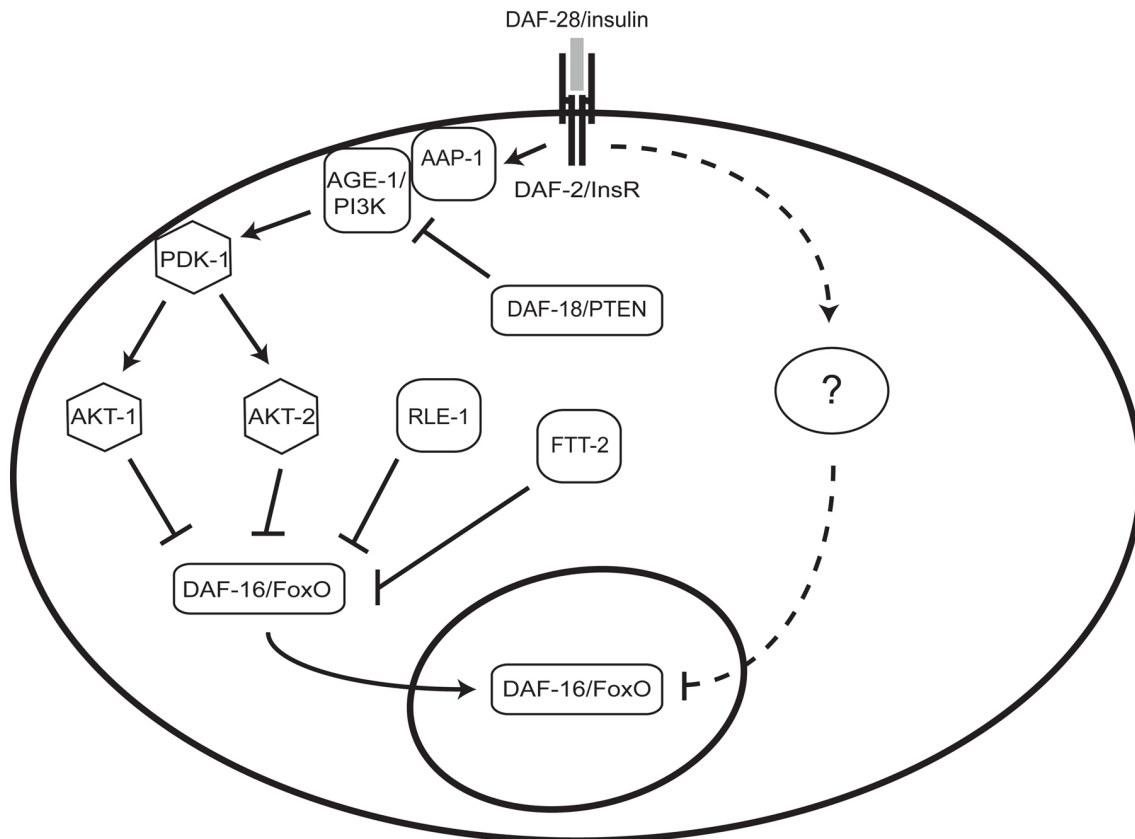


Figure 1. An insulin-like signaling pathway that regulates dauer arrest in *C. elegans*. See text for details.

ins-1 encodes an INS protein that is most similar to human insulin among *C. elegans* INS proteins. An *ins-1* deletion mutant does not have a dauer arrest phenotype. However, overexpression of *ins-1* or a cDNA encoding human insulin enhances dauer arrest, both in wild-type and *daf-2/InsR* mutant backgrounds. This suggests that INS-1 and human insulin antagonize DAF-2/InsR signaling. Although it remains unclear whether this effect is direct or indirect, there is some specificity among INS family members, as overexpression of *ins-18* also enhanced dauer arrest, whereas overexpression of *ins-9*, *ins-22*, *ins-19*, or *ins-31* did not. It is noteworthy that INS-1 and INS-18 are the only *C. elegans* INS proteins predicted to have C-peptides, which are proteolytically cleaved from proinsulin during normal insulin processing. Promoter::GFP fusions of many of these genes are expressed in amphid neurons, suggesting that dauer-regulatory environmental inputs could regulate expression and/or secretion of insulins (Pierce et al., 2001).

The *Daf-c* gene *daf-28* encodes an INS family member that promotes insulin-like signaling. It is the only *ins* mutant that has emerged from forward genetic screens and is defined by a single semidominant allele (Li et al., 2003; Malone and Thomas, 1994). Strikingly, a *daf-28p::GFP* transgene is expressed in the amphid neurons ASI and ASJ and is downregulated in response to pheromone and starvation. The related INS proteins INS-4 and INS-6 appear to function similarly to DAF-28 to promote insulin-like signaling (Li et al., 2003). INS-6 can bind directly to and activate the human insulin receptor *in vitro* (Hua et al., 2003). A *daf-28* deletion mutant does not undergo dauer arrest at 25°C (Weiqing Li, personal communication).

INS-7 may also promote reproductive development, as *ins-7* RNAi enhances dauer arrest in a *daf-2(e1370)* mutant background (Murphy et al., 2003). Recently it has been shown that the ATPase ASNA-1 potentiates DAF-2/InsR signaling by promoting the secretion of INS peptides such as DAF-28 (Kao et al., 2007). The biological role of most of the other insulin-like proteins remains to be elucidated.

Orthologs of components of the conserved target-of-rapamycin (TOR) pathway that is activated by insulin-like molecules (Oldham and Hafen, 2003) also promote reproductive development in *C. elegans*. TOR is a protein kinase activated by insulin that couples global mRNA translation to nutrient availability. It exists in at least two heteromeric complexes, TORC1 and TORC2, which have distinct subunit compositions and biological

functions. TORC1, which is sensitive to inhibition by rapamycin and contains the TOR binding partner Raptor, is required for activation of the ribosomal S6 kinase, whereas TORC2, which is insensitive to rapamycin and contains the TOR binding protein Rictor, phosphorylates and activates Akt (Inoki and Guan, 2006). *let-363* and *daf-15* encode orthologs of TOR and Raptor, respectively (Jia et al., 2004; Long et al., 2002). In contrast to loss-of-function mutants of *daf-2*, *age-1*, and other upstream components of insulin-like signaling, which arrest as complete dauers, *let-363/TOR* and *daf-15/Raptor* mutants arrest as dauer-like larvae that lack cuticular and intestinal characteristics of full dauers (Jia et al., 2004). This larval arrest phenotype is epistatic to *daf-16/FoxO* loss-of-function mutations, suggesting that *LET-363/TOR* and *DAF-15/Raptor* act downstream of or parallel to *DAF-16/FoxO*. In replete environments, insulin-like ligands may activate *LET-363/TOR* and *DAF-15/Raptor* to promote reproductive development. Inactivation of *LET-363/TOR* and *DAF-15/Raptor* suffices to induce developmental arrest, but other effectors of insulin-like signaling must also be inactivated in order for full dauer morphogenesis to take place.

Genetic evidence supports the existence of additional *DAF-2* outputs that function in parallel to *AGE-1/PI3K* (see Figure 1). Activating mutations in *akt-1* and *pdk-1* suppress dauer arrest in *age-1* null mutants but do not efficiently suppress dauer formation in *daf-2(e1370)* mutants (Inoue and Thomas, 2000a; Paradis et al., 1999; Paradis and Ruvkun, 1998), and the weak loss-of-function allele *daf-18(e1375)* suppresses dauer arrest in *age-1* null mutants but not in *daf-2(e1370)* mutants (Gil et al., 1999; Gottlieb and Ruvkun, 1994; Inoue and Thomas, 2000a; Ogg and Ruvkun, 1998; Vowels and Thomas, 1992). Also, *DAF-16/FoxO* localized to the nucleus by virtue of either *AKT-1* inactivation, inactivation of the 14-3-3 protein *FTT-2*, or mutation of consensus *AKT-1* phosphorylation sites is not fully active unless *daf-2* is also mutated (Berdichevsky et al., 2006; Hertweck et al., 2004; Lin et al., 2001). These results suggest that *DAF-2* also inhibits the activity of nuclear *DAF-16/FoxO* in an *AKT*-independent manner. Candidate components of this parallel pathway have been isolated recently (described below in the section on modifier screens).

6.4. Guanylyl cyclase regulation of TGF β -like and insulin-like ligand expression

Although genetic analysis is consistent with *DAF-7/TGF β* and *DAF-11* pathways functioning in parallel (Thomas et al., 1993), *DAF-11* likely also functions upstream of TGF β -like and insulin-like signaling. Ohshima and colleagues isolated a *daf-11* allele in a genetic screen for mutants exhibiting enhanced dauer arrest and reduced *daf-7::GFP* expression. Specific expression of *DAF-11* in the ASI neuron rescued both dauer arrest as well as *daf-7::GFP* expression, indicating that *DAF-11* functions cell autonomously to promote *daf-7* transcription (Murakami et al., 2001). Intriguingly, the insulin-like molecule *DAF-28* is also expressed in ASI, and expression of a *daf-28::GFP* promoter fusion is significantly reduced in *daf-11* mutants (Li et al., 2003). Thus, *DAF-11* may promote reproductive growth at least in part by promoting cell-autonomous expression of insulin-like and TGF β -like ligands in sensory neurons.

6.5. Steroid hormone pathway

The *Daf-c* gene *daf-9* and the *Daf-d* gene *daf-12* function downstream of most other proteins that regulate dauer arrest (Albert and Riddle, 1988; Gerisch et al., 2001; Jia et al., 2002; Riddle et al., 1981; Thomas et al., 1993). *daf-9* and *daf-12* mutants have similar pleiotropies in gonadal migration that are unique among *Daf* mutants; alleles of both were isolated in a genetic screen for mutants with distal tip cell migration defects (Antebi et al., 1998). Thus, *daf-9* and *daf-12* define a regulatory module distinct from the guanylyl cyclase, TGF β -like, and insulin-like pathways.

Multiple lines of evidence are consistent with a model whereby *DAF-9* and *DAF-12* participate in a steroid hormone pathway that regulates dauer arrest. First, cholesterol deprivation phenocopies *daf-9* mutants (Gerisch et al., 2001). Furthermore, *DAF-9* functions non-autonomously to inhibit dauer arrest (Gerisch and Antebi, 2004; Mak and Ruvkun, 2004), consistent with its effects being mediated by a hormone. Most strikingly, cloning of *daf-9* and *daf-12* revealed that *daf-9* encodes a cytochrome P450 similar to steroid hydroxylases (Gerisch et al., 2001; Jia et al., 2002), and *daf-12* encodes a nuclear receptor homolog with highest similarity in its DNA binding domain to vertebrate pregnane X and vitamin D receptors and in its ligand binding domain to vertebrate thyroid hormone receptors (Antebi et al., 2000). The expanded family of nuclear receptors in *C. elegans* is described in detail in WormBook (see Nuclear hormone receptors in *C. elegans*).

Dauer arrest in *daf-9* mutants requires *DAF-12* (Gerisch et al., 2001; Jia et al., 2002), indicating that *DAF-9* normally inhibits *DAF-12* function. Also, *daf-12* ligand binding domain mutants have a *Daf-c* phenotype, suggesting that these mutants are insensitive to *DAF-9* inhibition by virtue of their reduced ability to bind ligand (Antebi et al., 2000). Recently, endogenous steroids that are metabolites of *DAF-9* and high-affinity ligands for

DAF-12 have been identified. DAF-9 is a 3-keto-sterol-26-monooxygenase that synthesizes the DAF-12 ligands Δ^4 -dafachronic acid and Δ^7 -dafachronic acid (Motola et al., 2006; see Figure 2).

Daf-c mutants whose phenotypes are exacerbated by cholesterol deprivation may define other components of this pathway (Li et al., 2004; Ohkura et al., 2003; Rottiers et al., 2006). *daf-36* encodes a Rieske oxygenase that functions upstream of DAF-9 in dafachronic acid synthesis (Rottiers et al., 2006). Intriguingly, although *daf-9* is expressed in the hypodermis, somatic gonad, and XXX cells (Gerisch et al., 2001; Jia et al., 2002; Ohkura et al., 2003), *daf-36* is expressed primarily in the intestine and is not present in the XXX cells (Rottiers et al., 2006). It is not clear whether intestinal DAF-36 metabolites are actively transported to DAF-9-expressing tissues or whether they diffuse into neighboring tissues. Mutants of the Niemann-Pick C (NPC) homologs *ncr-1* and *ncr-2* are weakly Daf-c, but a *ncr-2;ncr-1* double mutant has a strong Daf-c phenotype (Li et al., 2004; Sym et al., 2000). The NPC genes encode proteins thought to be involved in intracellular cholesterol trafficking (Chang et al., 2005). NPC1 mutant mice exhibit decreased levels of neurosteroids (Griffin et al., 2004). Analogously, *ncr-2;ncr-1* double mutants may undergo dauer arrest as a consequence of reduced dafachronic acid synthesis. Mutations in *sdf-9*, a gene identified in a synthetic dauer formation screen, cause weak dauer arrest phenotypes that are rescued by overexpression of wild-type *daf-9* (Ohkura et al., 2003).

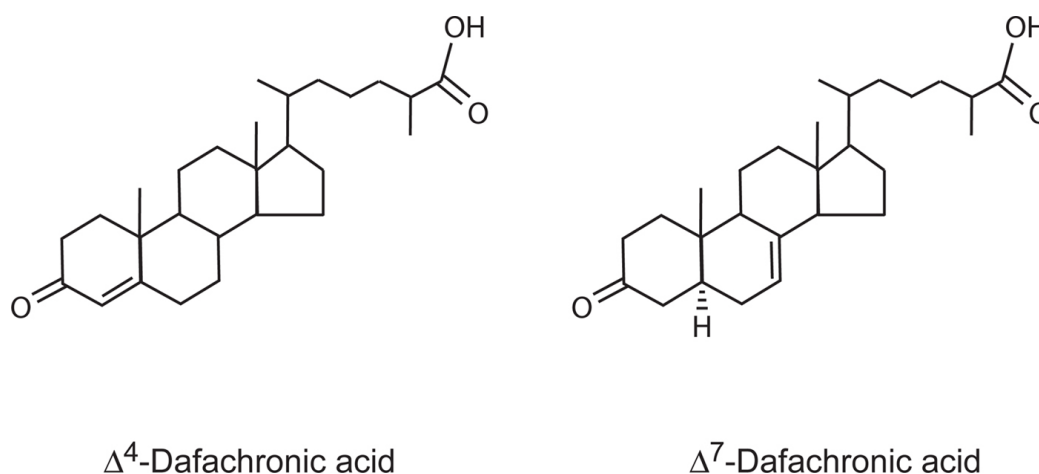


Figure 2. Structure of dafachronic acids. Adapted from Motola et al. (2006).

7. Amphid neuron mutants

Three mutants initially isolated based on defects in dauer arrest have structural abnormalities in the cilia of chemosensory neurons (see *The sensory cilia of C. elegans*, and *Chemosensation in C. elegans*). These ciliary structure abnormalities prevent the amphid neurons from taking up lipophilic dyes, resulting in a Dyf (for abnormal dye filling) phenotype (Perkins et al., 1986; Starich et al., 1995). One of them, *daf-10(e1387)*, was originally isolated as a mutant that did not form dauers in response to starvation (Albert et al., 1981). *daf-10* and most other Dyf mutants suppress the dauer arrest phenotype of *daf-11* mutants (Starich et al., 1995; Vowels and Thomas, 1992), indicating that cilium structure abnormalities prevent sensory neurons from promoting dauer arrest in the absence of DAF-11 guanylyl cyclase signaling. This may be due in part to excessive activation of insulin-like signaling, as Dyf mutants exhibit enhanced *daf-28::GFP* expression (Li et al., 2003). *daf-10* encodes a protein with several WD repeats that is homologous to IFT122, a component of the intraflagellar transport particle in *Chlamydomonas* (Bell et al., 2006; Qin et al., 2001).

daf-6(e1377) was also identified based on its inability to form dauers under starvation conditions (Albert et al., 1981). However, in contrast to most Dyf mutants, which have primary defects in sensory neuron ciliary structure (Perkins et al., 1986), dye-filling abnormalities in *daf-6* mutants appear to be secondary to defects in the amphid channel that is formed by the glial sheath and socket cells (Albert et al., 1981; Perens and Shaham, 2005; Perkins et al., 1986). These defects prevent the amphid neurons from coming into direct contact with the external environment (Albert et al., 1981; Perens and Shaham, 2005). *daf-6* mutants are also unique among Dyf mutants in their inability to suppress the *daf-11* dauer arrest phenotype (Vowels and Thomas, 1992), indicating that dauer arrest due to an absence of DAF-11 guanylyl cyclase activity does not require proper formation of amphid channels. The

The ability of both *daf-12* and *daf-16/FoxO* loss-of-function mutations to suppress dauer arrest caused by XXX ablation (Ohkura et al., 2003) was the first indication that the XXX cells couple to both steroid hormone and insulin-like pathways. This was underscored by the discovery that three *eak* genes are also specifically expressed in the XXX cells and function upstream of *daf-12* and *daf-16/FoxO* (Hu et al., 2006). Specific expression of *akt-1* in XXX suppresses the dauer arrest phenotype of *eak-4;akt-1* double mutants (Hu et al., 2006), suggesting that insulin-like signaling in XXX can promote dauer bypass, perhaps by potentiating the synthesis and/or secretion of daftachronic acids. Thus, in one model for how insulin-like and steroid hormone signaling are integrated in the XXX cells, insulin-like molecules secreted from amphid neurons (Li et al., 2003; Pierce et al., 2001) could engage DAF-2/InsR on the XXX cell surface, activate AKT-1, and promote daftachronic acid synthesis by DAF-9/CYP27A1.

It remains to be seen whether *daf-2/InsR* is expressed in the XXX cells, as well as whether DAF-7/TGF β -like signals converge on the XXX cells. Furthermore, how XXX outputs regulate DAF-16/FoxO nonautonomously (Ohkura et al., 2003) is not understood. One obvious hypothesis is that the XXX cells may secrete insulin-like molecules as well as steroid hormones. It will be of great interest to determine the expression profile of the XXX cells.

It should be noted that, although the XXX cells clearly play a role in regulating dauer development, the relative weakness of the XXX laser ablation dauer arrest phenotype (Ohkura et al., 2003) compared to the dauer arrest phenotype observed in strong *daf-2/InsR*, *daf-7/TGF β* , and steroid hormone pathway mutants indicates that other cells and tissues besides XXX likely play major roles in the dauer decision.

11. Expression profiling of dauers

Gene expression profiles have been generated using serial analysis of gene expression (SAGE; Jones et al., 2001) and microarray-based profiling (Wang and Kim, 2003) to identify gene expression changes that correlate with dauer arrest. Marra and colleagues performed SAGE on wild-type dauers generated by starvation and mixed-stage animals (both grown in liquid culture; Jones et al., 2001). This mixed-stage culture was highly enriched in L1 larvae. They identified 358 dauer-specific and 533 mixed-stage-specific transcripts ($P = 0.05$). The most abundant dauer transcript was the non-coding transcript *tts-1*. *tts-1* was enriched 20-fold in dauers compared to mixed-stage animals. The most highly expressed dauer-specific transcript corresponded to the small heat shock protein *hsp-12.6*. Enrichment of the variant histone H1 *hil-1* and the nucleosome assembly protein D2096.8 in dauers suggests that dauer chromatin structure may differ from that of growing animals (Jones et al., 2001).

To obtain a picture of the dynamics of gene expression accompanying exit from dauer arrest, Wang and Kim performed a 12-hour time course of microarray-based expression profiles on dauers after recovery was triggered by refeeding on plates (Wang and Kim, 2003). To control for gene expression changes induced by refeeding *per se*, they compared these profiles to those generated after refeeding of starved L1 larvae as well as to a mixed-stage sample. They clustered 2430 genes that change expression during dauer exit ($P \leq 0.001$) into five groups based on time course kinetics.

Although genes such as *hsp-12.6* and *sod-3* were identified as dauer-enriched transcripts by both SAGE and microarray-based profiling, there was strikingly little overlap in the expression profiles generated using the two different approaches (Jones et al., 2001; Wang and Kim, 2003). The biological significance of these expression changes remains to be determined.

Using the same platform as Wang and Kim (Wang and Kim, 2003), Garth Patterson and his colleagues compared gene expression profiles of *daf-7/TGF β* pathway mutants undergoing dauer arrest to profiles of wild-type early L3 larvae (Liu et al., 2004). They identified over 1200 genes whose expression was regulated strongly in the *daf-7/TGF β* pathway mutants undergoing dauer arrest ($P = 0.01$). Notably, *daf-2/InsR* and *daf-9* are downregulated and *daf-12* is upregulated in *daf-7/TGF β* pathway mutants, suggesting that DAF-7/TGF β signaling feeds forward to promote insulin-like and steroid hormone signaling during larval development in replete environments. *daf-9* expression increases early and remains elevated during dauer exit (Wang and Kim, 2003), suggesting that modulation of steroid hormone signaling is an important aspect of dauer recovery as well as dauer bypass in replete environments.

16. References

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