RESEARCH ARTICLE

A histone H4 lysine 20 methyltransferase couples environmental cues to sensory neuron control of developmental plasticity

Colin E. Delaney1, Albert T. Chen2, Jacqueline V. Graniel2, Kathleen J. Dumas2,3,* and Patrick J. Hu1,2,3,4,§

ABSTRACT

Animals change developmental fates in response to external cues. In the nematode Caenorhabditis elegans, unfavorable environmental conditions induce a state of diapause known as dauer by inhibiting the conserved DAF-2 insulin-like signaling (ILS) pathway through incompletely understood mechanisms. We have previously established a role for the C. elegans dosage compensation protein DPY-21 in the control of dauer arrest and DAF-2 ILS. Here, we show that the histone H4 lysine 20 methyltransferase SET-4, which also influences dosage compensation, promotes dauer arrest in part by repressing the X-linked ins-9 gene, which encodes a new agonist insulin-like peptide (ILP) expressed specifically in the paired ASI sensory neurons that are required for dauer bypass. ins-9 repression in dauer-constitutive mutants requires DPY-21, SET-4 and the FoxO transcription factor DAF-16, which is the main target of DAF-2 ILS. By contrast, autosomal genes encoding major agonist ILPs that promote reproductive development are not repressed by DPY-21, SET-4 or DAF-16/FoxO. Our results implicate SET-4 as a sensory rheostat that reinforces developmental fates in response to environmental cues by modulating autocrine and paracrine DAF-2 ILS.

KEY WORDS: C. elegans, Dauer, Dosage compensation, H4K20, Insulin-like peptides, FoxO

INTRODUCTION

To maintain evolutionary fitness, organisms must react appropriately to environmental cues. The free-living nematode Caenorhabditis elegans has evolved a developmental strategy to optimize survival in changing environments. Under replete conditions, larvae progress through four stages (L1-L4) to become reproductive adults. In adverse conditions such as overcrowding, heat or food scarcity, larvae arrest in an alternative stage known as dauer. Adapted for survival in harsh environments, dauer larvae are morphologically, metabolically and behaviorally distinct from the morphologically indistinguishable reproductive L3 larvae. Improvement of ambient conditions induces dauer exit and resumption of reproductive development.

Although genetic analysis has identified how components of the DAF-11, DAF-2/InsR, DAF-7/TGFβ and DAF-12 pathways interact to promote reproductive development in favorable conditions (Gottlieb and Ruvkun, 1994; Riddle et al., 1981; Thomas et al., 1993; Vowels and Thomas, 1992), the molecular nature of the upstream events that couple external cues to the activities of these pathways remains poorly understood. Laser ablation experiments demonstrated that the amphid sensory neurons are required for induction of dauer arrest by pheromone (Schackwitz et al., 1996; Vowels and Thomas, 1994). Indeed, the dauer-inhibitory ASI sensory neurons (Bargmann and Horvitz, 1991) are specific sites of expression of three insulin-like peptides (ILPs) that promote reproductive development through DAF-2/InsR (INS-4, INS-6 and DAF-28) (Chen and Baugh, 2014; Cornils et al., 2011; Hung et al., 2014; Li et al., 2003), as well as the DAF-7 TGFβ-like ligand that promotes reproductive development (Ren et al., 1996; Schackwitz et al., 1996). Furthermore, crude dauer pheromone reduces the expression of DAF-28 and DAF-7 in ASI (Li et al., 2003; Schackwitz et al., 1996), suggesting that pheromone induces dauer arrest at least in part by reducing the expression of agonist ligands in sensory neurons that regulate DAF-2/InsR and TGFβ-like signaling. How pheromone represses these ligands remains a mystery.

We have previously reported an unforeseen role for the C. elegans dosage compensation protein DPY-21 in promoting dauer arrest through inhibition of the DAF-2/InsR pathway (Dumas et al., 2013). DPY-21 is a component of the condensin-like dosage compensation complex (DCC) that equalizes X-linked gene expression between males and hermaphrodites by binding to both hermaphrodite X chromosomes during embryogenesis and repressing gene expression approximately twofold (Meyer, 2010; Yonker and
Meyer, 2003). Here, we show that the conserved histone H4 lysine 20 (H4K20) methyltransferase SET-4, which also influences dosage compensation (Kramer et al., 2015; Vielle et al., 2012; Wells et al., 2012), promotes dauer arrest in a sex-specific manner by synergizing with DAF-16/FoxO to repress ins-9, an X-linked gene that encodes an ILP expressed specifically in ASI neurons (Chen and Baugh, 2014; Pierce et al., 2001). These findings reveal a sexually dimorphic role for regulators of histone H4K20 methylation in broadening the dynamic range of sensory responses to environmental cues that control developmental plasticity.

**RESULTS**

**SET-4 acts through DAF-2 ILS to promote dauer arrest in a sex-specific manner**

DAF-2/InsR promotes reproductive development by activating a conserved phosphoinositide 3-kinase (PI3K)/Akt pathway to inhibit DAF-16/FoxO (Murphy and Hu, 2013). The conserved protein EAK-7 acts in parallel to AKT-1 to inhibit nuclear DAF-16/FoxO activity (Alam et al., 2010). In contrast to eak-7 and akt-1 single mutants, which develop reproductively, eak-7;akt-1 double mutant animals arrest as dayers in a DAF-16/FoxO-dependent manner (Alam et al., 2010). To identify new DAF-16/FoxO regulators, we performed a forward genetic screen for suppressors of the eak-7;akt-1 dauer-constitutive phenotype (seak). The first seak mutants characterized harbored loss-of-function mutations in the dosage compensation gene dpy-21 (Dumas et al., 2013). dpy-21 encodes a conserved component of the condensin-like dosage compensation complex (DCC) that binds to X chromosomes and represses X-linked gene expression (Meyer, 2010; Yonker and Meyer, 2003). One seak mutant strain contained a point mutation in set-4, which encodes a histone H4K20 methyltransferase homolog that influences dosage compensation (Vielle et al., 2012; Wells et al., 2012). set-4(dp268) is predicted to change the conserved SET domain catalytic residue serine 182 (Southall et al., 2014) to phenylalanine (Fig. 1A, Fig. S1A). In light of our findings on dpy-21 (Dumas et al., 2013), we tested the possibility that set-4(dp268) was the causative seak mutation in this strain. After outcrossing removing all but two closely linked single nucleotide variants, set-4(dp268) suppressed dauer arrest to a similar extent to two independently derived set-4 deletions, n4600 (Andersen and Horvitz, 2007) and ok1481 (Fig. 1B). Furthermore, an integrated single-copy HA::set-4 transgene rescued dauer arrest in set-4(n4600) animals (Fig. 1C and Fig. S1B). Therefore, SET-4 promotes dauer arrest.

DPY-21 enhances dauer arrest by activating DAF-16/FoxO, indicating that it acts in the DAF-2/InsR pathway to regulate dauer formation (Dumas et al., 2013). To determine whether SET-4 functions in the DAF-2/InsR pathway, we tested the effect of set-4 mutation on dauer-constitutive phenotypes caused by mutations in the daf-2/InsR, daf-7/TGFβ and daf-12 pathways. set-4 mutation suppressed the dauer-constitutive phenotypes of daf-2(e1368) mutants (Fig. 1C) as well as akt-1(ok325) and eak-7(tm3188) single mutants, which develop reproductively at 25°C but arrest as dauers at 27°C (Fig. S1C,D) (Ailion and Thomas, 2003; Alam et al., 2010; Hu et al., 2006). By contrast, set-4 mutation had no effect on the dauer-constitutive phenotypes caused by mutations in daf-1, which encodes a type 1 TGFβ receptor homolog (Georgi et al., 1990), or daf-8, which encodes a SMAD homolog (Park et al., 2010) (Fig. 1D and Fig. S1E). Similarly, set-4 mutation did not suppress dauer arrest in animals harboring mutations in daf-9 or daf-36, which encode DA biosynthesis pathway components (Fig. 1E and Fig. S1F) (Gerisch et al., 2001; Jia et al., 2002; Rottiers et al., 2006). Therefore, SET-4 acts specifically in the DAF-2/InsR pathway to promote dauer arrest.

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**Fig. 1. SET-4 promotes dauer arrest.**

(A) Schematic of the set-4 locus and three mutant alleles. Exons are indicated as boxes, separated by introns. Gray, green and yellow denote untranslated regions, coding sequence and SET domain coding sequence, respectively. Deletions are indicated by black bars. (B) set-4 mutations suppress the dauer-constitutive phenotype of eak-7;akt-1 mutants [n (left to right)=236, 627, 389, 521, 638]. (C) set-4(n4600) suppresses the dauer-constitutive phenotype of daf-2(e1368) mutants and is rescued by the single-copy set-4 transgene dpSi5 (n=913, 1668, 1568, 1785). (D,E) set-4 is dispensable for dauer arrest in (D) daf-7(n40) (n=2215, 2189, 1816, 1899) and (E) daf-9(dh6) mutants (n=1753, 1561, 2188, 2486). (F) set-4 and dpy-21 mutations suppress dauer arrest in XX hermaphrodites but not in XO males (n=567, 1330, 579, 1003, 1012, 700). (G) set-4 and dpy-21 mutations attenuate the response of wild-type animals to dauer pheromone [n (0 μl, 2 μl, 10 μl): wild type=542, 461, 544; set-4=413, 246, 387; dpy-21=334, 220, 275]. set-4 versus wild type: P<0.01 by two-way ANOVA.
As previous reports link H4K20 methylation status to dosage compensation (Vielle et al., 2012; Wells et al., 2012) and DPY-21 promotes dauer arrest through dosage compensation (Dumas et al., 2013), we hypothesized that SET-4 may also regulate dauer arrest through dosage compensation. To test this, we determined the effect of set-4 mutation on the dauer-constitutive phenotype of eak-7;akt-1 double mutant hermaphrodites and males. If SET-4 promotes dauer arrest through the same mechanism as dosage compensation, then set-4 mutation should suppress dauer in hermaphrodites but not in males, as the DCC is inactive in males (Meyer, 2010). dpy-21 and set-4 mutations suppressed the dauer-constitutive phenotype of eak-7;akt-1 hermaphrodites but did not affect dauer arrest in males (Fig. 1F). Therefore, SET-4 may act through dosage compensation to control dauer arrest. We verified the role of SET-4 in dosage compensation by showing that set-4 mutation suppressed lethality in xol-1 sex-1 mutant males, which die due to inappropriate activation of dosage compensation (Dawes et al., 1999) (Fig. S1G).

In order to determine whether SET-4 plays a role in regulating dauer entry in wild-type animals in response to physiologic stimuli, we tested the ability of dauer pheromone to induce dauer arrest in wild-type and set-4 mutant animals. Mutation of either set-4 or dpy-21 decreased the sensitivity of wild-type animals to pheromone (Fig. 1G). Therefore, SET-4 and DPY-21 promote dauer arrest in wild-type animals in response to increases in population density.

**SET-4 is a H4K20 methyltransferase**

The mammalian SET-4 ortholog SUV420H2 is a H4K20 methyltransferase (Schotta et al., 2004), and *C. elegans* SET-4 promotes H4K20 trimethylation (Vielle et al., 2012; Webster et al., 2013; Wells et al., 2012). We confirmed the requirement of SET-4 for H4K20 di- and trimethylation *in vivo* (Fig. 2A). Immunoblots showed no detectable SET-4 protein in set-4(n4600) and set-4(ok1481) backgrounds, consistent with these being strong loss-of-function alleles. SET-4 protein levels in set-4(dp268) are comparable with wild type (Fig. 2A). H4K20me2 and H4K20me3 levels are undetectable in all three set-4 mutant backgrounds (Fig. 2A), suggesting that the S182F substitution in the SET domain abrogates catalytic activity. To test this possibility directly, we purified recombinant wild-type and mutant GST-SET-4 fusion proteins and tested their ability to methylate modified H4 peptides (H4K20me0, H4K20me1 and H4K20me2) *in vitro*. Mass spectrometry analysis revealed that both wild-type GST-SET-4 and GST-SUV420H2 were capable of converting H4K20me1 to H4K20me2 (Fig. 2B,C). Consistent with *in vitro* experiments using human SET-4 orthologs SUV420H1 and SUV420H2 (Southall et al., 2014; Wu et al., 2013), methylation was not detected with unmethylated or dimethylated substrates, nor were trimethylated products detected in any assay (Fig. 2B,C). It is possible that an enzyme distinct from SET-4 catalyzes H4K20 trimethylation *in vivo*. Alternatively, conversion of H4K20me2 to H4K20me3 by SET-4 *in vivo* may require a co-factor that is absent from our *in vitro* reactions.

GST-SET-4(S182F) did not methylate H4K20me1, indicating that the S182F mutation abolishes catalytic activity (Fig. S2). Given that set-4(dp268) suppresses dauer to a similar extent to the two deletion alleles (Fig. 1B), these data are consistent with SET-4 influencing dauer arrest through its conserved role in methylating H4K20.

**Fig. 2. SET-4 is a histone H4K20 methyltransferase.** (A) SET-4 promotes H4K20 methylation *in vivo*. Anti-SET-4, H4K20me2, H4K20me3 and H3 immunoblots of lysates from wild-type and set-4 mutant animals are shown. SET-4 protein is indicated by the arrowhead. Images are representative of four biological replicates. (B) Recombinant GST-SET-4 fusion protein methylates H4K20me1 *in vitro*. Percentage methylation of H4K20 peptide substrates by GST proteins fused to wild-type SET-4, mutant SET-4(S182F) or human SET-4 ortholog SUV420H2 is shown. Data represent mean values from three biological replicates. (C) MALDI spectra illustrating conversion of H4K20me1 to H4K20me2 by GST-SET-4. Monoisotopic masses (protonated) of peptide substrates are indicated with arrowheads. Spectra are representative of three independent experiments.
SET-4 acts in neurons to promote dauer arrest

To determine where SET-4 is expressed, we generated strains expressing reporter genes under the control of set-4 regulatory elements. Because two independent C-terminal SET-4::GFP translational fusions failed to rescue dauer arrest in set-4 mutants, we generated strains expressing a set-4p::GFP promoter fusion to determine the spatiotemporal activity of the set-4 promoter. set-4p::GFP transgenic animals expressed GFP broadly in embryos (Fig. S3). Post-embryonically, we detected fluorescence predominantly in the head and tail regions of the animal, in a pattern consistent with neuronal expression. To confirm this, we established a transgenic strain that co-expressed set-4p::GFP and mCherry driven by the pan-neuronal rab-3 promoter (Nonet et al., 1997). At all developmental stages interrogated, we observed colocalization of green and red fluorescence (Fig. 3A), consistent with somatic expression. To test whether neuronal expression of set-4 is functionally important for dauer arrest, we generated tissue-specific set-4 transgenes and tested them for the ability to rescue dauer arrest in set-4 mutants. The neuronal rab-3p::set-4 transgene rescued dauer formation to a similar extent to a set-4 transgene driven by its native promoter (Fig. 3C). By contrast, intestine-, hypodermis- and muscle-specific set-4 transgenes did not rescue dauer arrest to a greater extent than a transgene expressing the set-4(dp268) mutant. Taken together, these data indicate that SET-4 functions in the nervous system to promote dauer arrest.

Transcriptome-wide influences of DPY-21 and SET-4 on dauer regulation

We previously showed that the DCC component DPY-21 promotes DAF-16/FoxO activity (Dumas et al., 2013). To gain broader insight into how DPY-21 and SET-4 control dauer arrest, we performed whole-transcriptome profiling to compare genome-wide regulatory influences (henceforth referred to as the ‘regulome’) of DPY-21 and SET-4 to those of the key transcription factors controlling dauer arrest in eak-7;akt-1 animals, DAF-16/FoxO and the nuclear receptor DAF-12 (Alam et al., 2010). We identified genes differentially expressed between wild-type and eak-7;akt-1 double mutant animals [fold change ≥1.5 and false discovery rate (FDR) <0.05]. We then compared the transcriptomes of eak-7;akt-1 double mutants with those of eak-7;akt-1 animals harboring mutations in dpy-21, set-4, daf-16/FoxO or daf-12, and identified genes that are differentially expressed in the opposite direction as in wild-type relative to eak-7;akt-1 (Table S1). Regulomes were validated by comparison with published data where possible (see below).

We defined the SET-4 dauer regulome by identifying 333 genes common to set-4(n4600) and set-4(dp268) regulomes (Table S1). Comparison of this gene set with SET-4-regulated genes identified in wild-type embryos and L3 larvae (Kramer et al., 2015) revealed minimal overlap [one gene (MTCE.34) among 94 regulated by SET-4 in embryos, and one gene (B0511.11) among 18 SET-4-regulated genes in L3 larvae]. This lack of concordance could be due to differences in genetic background (eak-7;akt-1 versus wild-type), developmental stage (early L2 larvae versus embryos/L3 larvae) and/or ambient temperature (25°C versus 20°C). A similar analysis with eak-7;akt-1 dpy-21 mutants revealed 2431 genes that comprise the DPY-21 dauer regulome (Table S1).
To validate the DPY-21 regulome, we found significant overlap between the set of 700 X-linked genes differentially expressed in 

\[ eak-7;akt-1 \] dpy-21 versus eak-7;akt-1 animals with the 374 X-linked genes subject to dosage compensation in embryos (Jans et al., 2009) (119 genes; Fig. S4A and Table S2; \( P=2.1e^{-26} \)). Three hundred and eight of the 333 genes that make up the SET-4 dauer regulome (92.5%) are also part of the DAF-21 dauer regulome (Fig. 4A and Table S1), suggesting that a functional relationship between DAF-21 and SET-4 may exist in post-embryonic dauer regulation.

The DAF-16/FoxO regulome consists of 2957 genes (Table S1). This gene set overlapped significantly with both the 469-gene young adult DAF-16/FoxO regulome (Chen et al., 2015) (203 common genes; Fig. S4B and Table S3, \( P=3.2e^{-115} \)) as well as the 1116-gene dauer regulome defined using daf-7 TGFβ-like pathway mutants (Liu et al., 2004) (522 common genes; Fig. S4C and Table S4, \( P=1e^{-100} \)). Furthermore, 65 of the 132 genes regulated by the DAF-7 TGFβ-like pathway that contained at least one upstream DAF-16/FoxO-binding motif (Liu et al., 2004) were part of the DAF-16/FoxO regulome (2282 of 2957 genes; 77.2%) are also regulated by DAF-12 (Fig. 4B and Table S1). Over two-thirds of genes that comprise both DAF-16/FoxO regulomes are concordantly regulated by DPY-21 and DAF-16/FoxO but not influenced by daf-12 mutation (Fig. 4B; Table S5).

Among these X-linked genes was ins-9, which encodes one of 40 C. elegans ILPs (Pierce et al., 2001). Transcriptome profiling revealed that ins-9 is silenced in eak-7;akt-1 animals in a manner that requires both daf-16/FoxO and dpy-21 (Table S2). We verified this by qPCR; ins-9 expression was reduced more than 30-fold in eak-7;akt-1 double mutants compared with wild-type animals (Fig. 5A). Full repression required DAF-16/FoxO as well as DPY-21 and SET-4, but was independent of daf-12. Notably, a daf-16/FoxO-null mutation did not restore ins-9 transcript levels to wild-type levels. Furthermore, mutation of either dpy-21 or set-4 increased ins-9 expression by substantially greater than twofold (Fig. 5A; 7.5-fold increase in set-4; eak-7;akt-1 versus eak-7;akt-1; 13.5-fold increase in eak-7;akt-1 dpy-21 versus eak-7;akt-1). Taken together, these observations suggest that DAF-16/FoxO and DPY-21/SET-4 act synergistically to repress ins-9.

ins-9 overexpression phenocopies dauer suppression caused by dpy-21 or set-4 mutation

INS-9 was an attractive candidate regulator of dauer arrest and DAF-2 ILS, as multiple ILPs have been shown to control dauer arrest through DAF-2/InsR (Cornils et al., 2011; Fernandes de Abreu et al., 2014; Hung et al., 2014; Li et al., 2003; Murphy et al., 2003; Pierce et al., 2001). If derepression of ins-9 contributes to suppression of eak-7;akt-1 dauer arrest in dosage compensation mutants, then ins-9 overexpression should phenocopy dauer suppression caused by set-4 or dpy-21 mutation. We tested this by establishing transgenic strains harboring a polycistronic construct that permitted expression of both ins-9 and mNeonGreen (Shaner et al., 2013) fused to an SL2 leader sequence (Blumenthal, 2005) under the control of native ins-9 3′ and 3′ regulatory elements (ins-9::SL2::mNG). In two independent transgenic lines, ins-9 overexpression (indicated by mNeonGreen detection) suppressed the dauer-constitutive phenotype of eak-7;akt-1 double mutants (Fig. 5B). Therefore, ins-9 overexpression recapitulated the phenotype caused by set-4 and dpy-21 mutations (Dumas et al., 2013) (Fig. 1B). These data are consistent with INS-9 acting as an agonist DAF-2/InsR ligand.

ins-9 is expressed specifically in a single pair of amphid neurons

Previous studies using reporters driven by the ins-9 promoter suggested that ins-9 is expressed in the ASI and ASJ amphid neurons, as well as in additional tissues (Chen and Baugh, 2014; Pierce et al., 2001; Ritter et al., 2013). By contrast, in transgenic L2 larvae expressing ins-9::SL2::mNG, we consistently observed green fluorescence solely in one pair of sensory neurons. In animals in
which neuronal morphology was discernible, we identified the fluorescent cells as the ASI amphid neurons (Fig. 5C). We did not observe fluorescence in more than one pair of amphid neurons in any animal, nor did we detect fluorescence in other neurons or tissues. As \textit{ins-9::SL2::mNG} contains genomic elements from the \textit{ins-9} locus that are missing from other reporters in the literature (Chen and Baugh, 2014; Pierce et al., 2001; Ritter et al., 2013), these observed patterns of expression are likely to be physiologically relevant.

\textbf{ins-9 and akt-2 are required for suppression of dauer arrest by set-4 mutation}

To determine the extent to which \textit{ins-9} derepression contributes to dauer suppression in \textit{set-4} mutants, we tested the ability of \textit{set-4} to suppress the dauer-constitutive phenotype of \textit{daf-2/InsR} mutants in wild-type and \textit{ins-9} loss-of-function backgrounds. We generated strong loss-of-function \textit{ins-9} alleles using CRISPR/Cas9 genome editing (Paix et al., 2015). Two probable null alleles, \textit{dp675} and \textit{dp677}, have nonsense mutations in the F-peptide region of \textit{ins-9} that lies N-terminal to the functional B and A peptides (Pierce et al., 2001) (Fig. S5). Although neither allele induced dauer arrest in a wild-type background, both \textit{ins-9(dp675)} and \textit{ins-9(dp677)} partially rescued dauer arrest in \textit{set-4;daf-2} double mutants (Fig. 5D), indicating that dauer suppression caused by \textit{set-4} mutation is due in part to de-repression of \textit{ins-9}.

We previously showed that the \textit{X-linked} gene \textit{akt-2} is required for dauer suppression caused by \textit{dpy-21} mutation (Dumas et al., 2013). We verified that \textit{akt-2} transcripts increase two-fold in \textit{eak-7;akt-1} double mutants when \textit{set-4} or \textit{daf-2} is mutated (Fig. S6A). Similar to \textit{ins-9} mutation, \textit{akt-2} mutation also partially rescued dauer arrest in animals lacking \textit{set-4} (Fig. 5E), and the phenotypic effects of \textit{ins-9} and \textit{akt-2} mutations on dauer arrest may be additive (Fig. 5E). However, \textit{set-4;daf-2;ins-9 akt-2} compound mutant animals still did not undergo dauer arrest to the same extent as \textit{daf-2} single mutant animals (Fig. 5E), indicating that regulation of additional genes may contribute to dauer arrest.

\textbf{The autosomal \textit{ins-7} gene contributes to suppression of dauer arrest by \textit{set-4} mutation}

As the only \textit{X-linked} \textit{ins} gene, \textit{ins-9} is the sole \textit{ins} gene subject to direct regulation by dosage compensation or other \textit{X}-chromosome-specific mechanisms of gene regulation. However, it is conceivable that other \textit{ins} genes could contribute to dauer regulation through indirect effects on their expression. Genes encoding three agonist ILPs, \textit{INS-4}, \textit{INS-6} and \textit{DAF-28}, are expressed in the ASI sensory neurons and have established roles in inhibiting dauer arrest and promoting reproductive development (Cornils et al., 2011; Hung et al., 2014; Li et al., 2003). To determine whether regulation of \textit{ins-4}, \textit{ins-6} and/or \textit{daf-28} contributes to dauer suppression in this context, we measured \textit{ins-4}, \textit{ins-6} and \textit{daf-28} transcript levels in wild-type, \textit{eak-7;akt-1} double mutant and \textit{eak-7;akt-1} triple mutants with reduced \textit{DPY-21} or \textit{SET-4} activity. None of these genes was repressed in \textit{eak-7;akt-1} double mutants compared with wild-type animals, nor did loss of \textit{set-4} or \textit{dpy-21} cause significant
increases in their expression (Fig. S6B-D). Therefore, neither DPY-21 nor SET-4 influences dauer arrest through regulation of ins-4, ins-6 and daf-28 expression.

To determine whether other ILPs could contribute to dauer regulation by DPY-21 or SET-4, we searched the set of genes common to DAF-16/FoxO and DPY-21 regulomes for ins genes. Seven ins genes are concordantly regulated by DAF-16/FoxO and DPY-21 based on FPKM counts from whole-transcriptome data (Table S6). Two genes encoding putative antagonist ILPs, ins-20 and ins-11 (Fernandes de Abreu et al., 2014), are repressed by DAF-16/FoxO and DPY-21; however, an increase in their expression in dpy-21 mutants would be expected to enhance, rather than suppress, dauer arrest. Similarly, two ins genes encoding agonist ILPs, ins-33 and ins-35 (Fernandes de Abreu et al., 2014; Michaelson et al., 2010), are induced by DAF-16/FoxO and DPY-21; a decrease in their expression in dpy-21 mutants would also be expected to enhance dauer arrest if changes in their expression were functionally important in dauer regulation. DAF-16/FoxO and DPY-21 induce the expression of two ins genes of unknown function, ins-16 and ins-29 (Fernandes de Abreu et al., 2014). Finally, ins-7, which encodes an agonist ILP (Murphy et al., 2007, 2003), is repressed by DAF-16/FoxO and DPY-21 (Murphy et al., 2007, 2003) (Table S6). As ins-7 and ins-9 both encode agonist ILPs, are concordantly regulated by DAF-16/FoxO and DPY-21, and have been shown to influence dauer arrest (Murphy et al., 2007, 2003) (Fig. 5C-E), we tested ins-7 for a role in promoting reproductive development in dpy-21 and set-4 mutants. We verified ins-7 repression by DAF-16/FoxO, SET-4 and DPY-21 using qPCR (Fig. S6E). The ins-7(tm1907) deletion allele partially rescued dauer in set-4;daf-2 animals and may have an additive effect with ins-9 mutation on dauer suppression (Fig. 5F). Thus, SET-4 may influence dauer arrest through both the direct repression of X-linked genes such as ins-9 and akt-2 and perhaps the indirect regulation of autosomal dauer regulatory genes such as ins-7.

**DISCUSSION**

Although much is known about the conserved signaling pathways that control *C. elegans* dauer arrest, how these pathways are regulated by upstream inputs is poorly understood. In the present study, we have established a framework for understanding how DPY-21 and SET-4 promote dauer arrest in the context of reduced DAF-2 ILS. Specifically, we have discovered that the conserved H4K20 methyltransferase SET-4 acts in the nervous system to arrest through activation of DAF-16/FoxO (Fig. 6).

Although ins-9 has been predicted to function as an agonist ILP based on structural models that indicate similarity to the agonist ILPs INS-4, INS-6 and DAF-28 (Pierce et al., 2001) and on expression changes upon starvation and feeding of larvae (Chen and Baugh, 2014), analysis of existing ins-9 mutants has not revealed phenotypes consistent with this (Fernandes de Abreu et al., 2014). This may be due to ins-9(tm3618) not being a strong loss-of-function allele. By contrast, our analysis of transgenic animals overexpressing ins-9 (Fig. 5B) and mutant animals harboring nonsense ins-9 alleles (Fig. 5D-F) provides the first experimental evidence demonstrating that INS-9 is an agonist ILP.

Several ILPs have been implicated in dauer regulation (Cornils et al., 2011; Fernandes de Abreu et al., 2014; Hung et al., 2014; Li et al., 2003; Murphy et al., 2003; Pierce et al., 2001). However, the
which INS-9 may function as a key node in an autocrine feed-forward loop in the ASI sensory neurons that reinforces levels of its own expression in response to changing environments, upstream of DA biosynthesis in the XXY cells and hypodermis. In replete conditions, ins-9 expression in ASI is expected to lead to activation of DAF-2 ILS and inhibition of DAF-16/FoxO. As DAF-16/FoxO inhibits ins-9 expression, decreased DAF-16/FoxO activity would lead to increased ins-9 expression, which would presumably lead to further activation of DAF-2 ILS and inhibition of DAF-16/FoxO, both in an autocrine fashion in ASI as well as in other cells that express DAF-2/InsR. In the context of increased population density, pheromone would promote ins-9 repression through DPY-21 and SET-4, and reduce autocrine and paracrine engagement of DAF-2/InsR, resulting in DAF-16/FoxO activation, further repression of ins-9 and dauer arrest (Fig. 6). The effect of DPY-21 and SET-4 would not be limited to sensory neurons, as they would also act in other cells responding to INS-9 to control their sensitivity to ILPs by repressing akt-2 (Dumas et al., 2013) (Fig. 6 and Fig. S6A). In addition, ins-9 regulation may also be amplified through other ILPs such as INS-7, which functions in a feed-forward loop in adults to coordinate DAF-16/FoxO activity throughout the animal (Murphy et al., 2007).

MATERIALS AND METHODS
C. elegans strains and maintenance
Mutant alleles are listed in the supplementary Materials and Methods. Compound mutants were generated using standard protocols. All animals were maintained on nematode growth media (NGM) plates seeded with E. coli OP50 using standard techniques. Strains are available upon request.

Dauer arrest assays
Dauer arrest assays were performed as previously described (Hu et al., 2006). daf-9(dh6) mutant animals were propagated on NGM plates supplemented with 10 mM D-β-mercaptoethanol, then transferred to NGM plates for egglay as previously described (Dumas et al., 2013). For male dauer assays, males were crossed to isogenic L4 hermaphrodites, and the gender of dauer progeny was determined after dauer exit.

Dauer pheromone assays
Dauer pheromone was prepared as previously described (Golden and Riddle, 1982; Schroeder and Flatt, 2014). Details are provided in the supplementary Materials and Methods.

Generation of transgenic strains
Details pertaining to the generation of reporter constructs and transgenic strains are provided in the supplementary Materials and Methods.

CRISPR/Cas9-based mutagenesis
ins-9(dp675) and ins-9(dp677) were generated using recombinant crRNA and tracrRNA (Dharmacon) and Cas9 (PNABio) as described previously (Paix et al., 2015). See Table S7 for sequences of guide RNAs and repair oligonucleotides.

RNA isolation
Greater than 200 gravid hermaphrodites were allowed to lay eggs for 6 h at 20°C and then removed. Eggs were transferred to 25°C for 24 h. Larvae were harvested, washed once in M9 buffer and once in water, and resuspended in TRIzol (Invitrogen). After five sequential freeze-thaws, RNA was extracted using chloroform. Extracted RNA was purified using a Direct-zol RNA Miniprep Kit (Zymo Research).

qPCR
cDNA was synthesized with oligo-dT priming using the SuperScript III First Strand Synthesis Kit (Invitrogen). The equivalent of 10 ng of starting RNA was used as template in a 15 µl reaction using the Quantitect SYBRgreen qPCR Kit (Qiagen). Reactions were performed in a RotorGene 6000 (Corbett Research) and results analyzed using RotorGene 6000 Software (version 1.7). Samples were normalized to pmp-3 expression prior to comparison between groups (Hoogewijs et al., 2008). See Table S8 for primer sequences. Relative expression was calculated as described (Nolan et al., 2006).

Confocal microscopy
Animals were mounted on slides layered with a thin 3% agarose pad containing 25 mM sodium azide. Images were captured on a Leica Inverted SP5X Confocal Microscope (Leica) using LAS AF software.

RNA-seq analysis
Whole-transcriptome profiling was performed by the University of Michigan DNA Sequencing Core as previously described (Chen et al., 2015) using 100 ng input RNA per sample. Samples were barcoded and multiplexed, and 100-nucleotide paired-end sequencing was performed using an Illumina HiSeq 2000 sequencer and Version 4 reagents. Five experimental replicates were analyzed. Correlation coefficients between replicates and genotypes are shown in Table S9.

Annotated gene expression data output from CushDiff v2.2.1 (Trapnell et al., 2013) was read into R version 3.2.1 (2015-06-18; The R Foundation for Statistical Computing; http://www.r-project.org/) for six comparisons: eak-7;akt-1 compared with: (1) wild type, (2) daf-16(mu86);eak-7;akt-1, (3) daf-12;eak-7;akt-1, (4) set-4(n4690);eak-7;akt-1, (5) set-4(dp266);eak-7;akt-1 and (6) dpy-21;eak-7;akt-1. We filtered genes using the following criteria: (1) status=’OK’ for wild type versus eak-7;akt-1, (2) fold change (FC) ≥1.5 or FC ≤1/1.5 for wild type versus eak-7;akt-1 and (3) FDR <0.05 for at least two separate comparisons.

DAF-16 targets were defined as those filtered genes that also met (1) status=’OK’ for eak-7;akt-1 versus daf-16;eak-7;akt-1 and (2) FC ≥1.5 for eak-7;akt-1 versus daf-16;eak-7;akt-1 in the opposite direction to wild type versus eak-7;akt-1. DPY-21, SET-4 and DAF-12 targets were determined in an analogous fashion. For SET-4, we generated a list of SET-4 targets that showed FC ≥1.5 or FC ≤1/1.5 for both set-4 alleles, and a list that showed these changes for either one or both set-4 alleles. Lists of overlapping targets were then generated from these target lists.

The significance of overlap with dosage-compensated X-linked genes (Jans et al., 2009), strongly regulated dauer genes (Liu et al., 2004) and DAF-16 targets in the daf-2(e1370) background (Chen et al., 2015) was calculated using a hypergeometric distribution, assuming 5863 X-linked transcripts and 46233 genome-wide transcripts in C. elegans detected in our RNA-seq analysis (by either the UCSCcvel0 reference transcriptome or de novo transcript assembly). If necessary, common WormBase Gene identifiers were downloaded from WormBase version WS250 (intermine. wormbase.org).

Immunoblotting and antibodies
To generate protein lysates, animals were washed in M9, then in sterile water. Pelleted animals were resuspended in equal volumes of worm lysis buffer (Webster et al., 2013), incubated at 85°C for 5 min, then sonicated on ice for two cycles of 30 s each at 70% power using a Sonic Dismembrator buffer (Webster et al., 2013), incubated at 85°C for 5 min, then sonicated on ice for two cycles of 30 s each at 70% power using a Sonic Dismembrator Model 100 (Fisher Scientific). Homogenates were quantified using a DC Protein Quantification Kit (BioRad). Protein (50 µg per lane) was loaded using Criterion systems (BioRad) and transferred to Immobilon P (Millipore). Details pertaining to antibodies are provided in the supplementary Materials and Methods. Membranes were blocked with 5% milk in TBS+0.5% Tween 20. Antibodies were diluted in West Blocking Solution (Sigma) prior to incubation with membranes. Blots were washed with TBS+0.5% Tween 20. Signal was detected by ECL (Pierce).

Histone methyltransferase assay
set-4 cDNAs were amplified from RNA isolated from wild-type or set-4(dp266) mutant animals. Human Suv420H2 cDNA was obtained from Origene. Clones were ligated into pGEX4T1 vector (GE Healthcare). Protein expression was induced overnight at 16°C with 0.1 mM IPTG in BL21-CodonPlus(DE3)-RIPL cells (Agilent Technologies) grown in LB-medium supplemented with 100 µg/ml ampicillin and 30 µg/ml chloramphenicol. After induction, cells were harvested by centrifugation at 10,000 g for 5 min, washed in wash buffer (50 mM HEPES pH 8.0, 10% glycerol, 300 nM NaCl, 1% Triton X-100) and resuspended in lysis buffer (50 mM HEPES pH 8.0, 300 mM NaCl, 10% glycerol, 40% NP-40, 10 µg/ml leupeptin and 10 µg/ml aprotinin). After 30 min on ice for two cycles of 30 s each at 70% power using a Sonic Dismembrator and clarified by centrifugation at 100,000 g for 90 min. Protein concentration was determined using a DC Protein Assay Kit (BioRad) and 30 µg of protein was loaded onto an 8% SDS-PAGE gel. A standard calibration was run on every gel to ensure a constant loading. After gel electrophoresis, proteins were transferred to an Immobilon P (Millipore) membrane, blocked in 5% non-fat dry milk in TBS+0.5% Tween 20, and incubated with a 1:2000 primary antibody overnight at 4°C. Protein expression was detected after 3 h with a 1:5000 dilution of goat anti-mouse antibody (Sigma) in TBS+0.5% Tween 20.
using a Sonic Dismembrator Model 100 sonicator (Fisher Scientific), with four cycles of ten 1 s on/off pulses of 10-30% intensity. Lysates were cleared by centrifugation at 20,000 g for 5 min and incubated with Glutathione-Sepharose beads (GE Healthcare) rotating overnight at 4°C. Expression of recombinant protein was confirmed by Coomassie staining and anti-GST immunoblot. Beads bound to recombinant protein were incubated in 10 mM Tris (pH 8.0), 2 μM β-mercaptoethanol, and 7 mM S-adenylylimidohydrolase (Sigma) in the presence of 2 mM substrate peptide corresponding to amino acids 8-30 of C. elegans histone H4 (AnaSpec) rotating for 4 h at 30°C. Reactions were analyzed using a Waters MicroMass MALDI-TOF mass spectrometer and analyzed with MassLynx software. Ratios of peak heights were calculated by integrating mass peaks using software, and error designations were ±10%.

**Male rescue assay**

Mated gravid hermaphrodites were placed on NGM plates to lay eggs for 24 h at 20°C. Egglayers were removed, and the numbers of hatchlings and eggs were counted. After 72 h, the adults were moved to 4°C to slow their movement. Male rescue was calculated as the ratio of live males to total eggs laid. Each experiment was performed in triplicate.

**Statistics**

Two-tailed Student’s t-test was used to measure significance in experiments unless otherwise noted. Data are presented as the average±standard error of the mean (s.e.m.) of at least three biological replicates, each replicate performed in triplicate. n values for male assays are listed from left to right.

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