Inhibition of germline proliferation during \textit{C. elegans} dauer development requires PTEN, LKB1 and AMPK signalling

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In \textit{C. elegans}, reduced insulin-like signalling induces developmental quiescence, reproductive delay and lifespan extension. We show here that the \textit{C. elegans} orthologues of LKB1 and AMPK cooperate during conditions of reduced insulin-like signalling to establish cell cycle quiescence in the germline stem cell population, in addition to prolonging lifespan. The inactivation of either protein causes aberrant germline proliferation during diapause-like ‘dauer’ development, whereas the loss of AMPK uncouples developmental arrest from lifespan extension. Reduced TGF-\(\beta\) activity also triggers developmental quiescence independent of the insulin-like pathway. Our data suggest that these two signalling pathways converge on the \textit{C. elegans} PTEN orthologue to coordinate germline proliferation with somatic development during dauer formation, via the regulation of AMPK and its upstream activator LKB1, rather than through the canonical insulin-like signalling cascade. In humans, germline mutations in TGF-\(\beta\) family members, PTEN or LKB1 result in related tumour-predisposing syndromes. Our findings establish a developmental relationship that may underscore their shared, characteristic aetiology.

\textbf{KEY WORDS: Insulin, TGF-\(\beta\), AMPK, PTEN, LKB1, Cell cycle, Lifespan, Dauer, Germ line, \textit{C. elegans}}

\section*{INTRODUCTION}

Following embryogenesis in \textit{C. elegans}, the first stage (L1) larvae emerge with a gonad primordium that contains four progenitor cells referred to as Z1, Z2, Z3 and Z4. In the hermaphrodite, the somatic gonad precursors Z1 and Z4 will undergo multiple divisions to give rise to the tissues that will make up the two U-shaped arms of the adult somatic gonad, which are delineated distally by the distal tip cells (DTCs) and proximally by a shared uterus (Hubbard and Greenstein, 2000). The other two cells present in the primordium (Z2, Z3) are the germ cell precursors and, unlike the divisions of the somatic gonadal precursors, which are essentially invariant from one animal to another, Z2 and Z3 do not demonstrate the same stereotypic division pattern and/or division timing as they proliferate to form the germ lineage (Kimble and Hirsh, 1979).

Even though the \textit{C. elegans} germ line develops as a syncytium, individual germline nuclei and their surrounding cytoplasm can be referred to as germ cells (Hubbard and Greenstein, 2000). Sustained proliferation of the germ cell precursors and their daughters during larval development requires signalling through a Notch receptor. The Notch ligand (LAG-2) is expressed in the somatic DTCs, and through the activation of a Notch receptor (GLP-1) present in the germ cells it inhibits them from executing their alternative meiotic pathway, while instructing them to proliferate (Kimble and Crittenden, 2005). Initially, owing to the influence of a nearby DTC, the germline stem cell population expands until the late L3 larval stage. At this point, however, the proximal-most germ cells no longer receive the Notch-dependent proliferative signal provided by the DTCs, and therefore they execute the alternative meiotic pathway. In hermaphrodite animals, a transient period of spermatogenesis is initiated, followed by a switch to oogenesis in the L4 larval stage (Ellis and Schedl, 2006).

Germline proliferation therefore proceeds uninterrupted in the distal germ line during post-embryonic development, but can be pre-empted when environmental conditions are sensed to be inappropriate to sustain reproductive development during the L1 larval stage. Three parallel signals, including reduced insulin-like signalling, can independently generate a neuro-endocrine signal that triggers a developmental switch, instructing the larva to execute an alternative diapause-like stage referred to as ‘dauer’. In anticipation of initiating the dauer pathway, the second larval (L2) stage is extended (L2d), allowing the larva to prepare for nutrient deprivation by slowing development and metabolism, while storing energy (Riddle and Albert, 1997). One important feature of this developmental switch is the progressive establishment of a generalized cell cycle arrest that is maintained thereafter, presumably to conserve resources, thus rendering the dauer larva specialized for long-term survival.

The transcriptional targets of the downstream effectors that mediate dauer development identified to date include genes involved primarily in metabolic, antimicrobial and stress-response pathways (McElwee et al., 2003; Murphy et al., 2003; Shostak et al., 2004). Although much interest has been focused on the regulation of adult lifespan by some of these factors, the key to the extreme longevity and developmental quiescence of the dauer juvenile remains largely unclear. Most importantly, how the three parallel signalling pathways (insulin-like, TGF-\(\beta\), cGMP) that control dauer formation interact and presumably converge on the same downstream targets in order to specify the behavioural, morphological, physiological and metabolic changes associated with this stage is not well understood.

Through our analysis of the mechanisms involved in controlling germ cell divisions during the establishment of developmental quiescence, we found that the independent signals that promote dauer formation converge to control the activity of the tumour suppressor gene \textit{daf-18}/PTEN, an upstream component of the insulin-like signalling pathway. The regulation of germline proliferation, however, diverges from the canonical insulin-like targets Akt/PKB and \textit{daf-16}/FOXO, but requires the tumour
suppressor par-4/LKB1 and its downstream target AMP-activated kinase (aak-1, aak-2/AMPK) to appropriately arrest proliferation of the germline stem cell population in response to the environmental signals that induce dauer development.

MATERIALS AND METHODS

C. elegans genetics

All nematode strains were maintained at 15°C and grown on standard NGM plates seeded with E. coli (HB101) (Brenner, 1974), unless otherwise stated. The Bristol (N2) strain was used as wild type throughout. The following alleles, rearrangements and transgenes were used. LGI: daf-16(muD947, megD950), rrf-1(pk1417), szT1([lon-2(e678)]). LGF: daf-2(e1370), daf-2(rk23), unc-32(e1899), glp-1(oz112, q175, e2141), unc-36(e251), pha-1(e2123), LGIV: daf-18(e1375, ok480), LGV: q566(lag-2::GFP; unc-119(+)), akt-1(m144), him-5(e1467), par-4(id147, id57), LGX: aak-2(rk48, ok524), unc-1(e719), unc-7(e5), mec-4(u52), lin-15(n765), ydF1, szT1, qEx308(lag-2::LAG-2::GFP; rol-6(su1006), arEx645[pha-1(+)]; lag-2::GFP::lucZ; ceb-22::GFP) (Horvitz et al., 1979).

aak-2(ok524) is a predicted molecular null allele in which part of the catalytic domain is deleted; this introduces a premature stop codon shortly after the breakpoint, thus eliminating the conserved regulatory domain (Apfeld et al., 2004). The deletion in daf-18(ok480) is predicted to remove part of the C-terminal regulatory domain, while introducing a premature stop codon after the breakpoint.

Genetic screen for regulators of germ cell proliferation during dauer development
daf-2(e1370) is a temperature-sensitive hypomorphic allele of the C. elegans insulin-like receptor, which allows reproductive development constitutively at the permissive temperature (15°C), but induces dauer formation constitutively at the restrictive temperature (25°C) (Albert and Riddle, 1988; Kimura et al., 1997). The F1 progeny of EMS mutagenized daf-2(e1370); qfs56 L4 larvae were reared at 15°C until the adult stage, at which point they were distributed five per plate and up-shifted to 25°C. F2 dauer larvae were subsequently screened for gonad enlargement using lag-2::GFP; the DTC expression of which delineated the distal extremes of the dauer gonad. Using this approach, we screened 3800 haploid genomes and isolated one mutant (rr48) that demonstrated dauer germline hyperplasia and dauer lethality. This mutant was outcrossed five times prior to any subsequent analysis.

Mapping and cloning of rr48

Using conventional linkage analysis, followed by three-factor crosses, rr48 was mapped to the far right of LGX. After crossing daf-2; rr48 males into daf-2; unc-7 mec-4 hermaphrodites, we found 0/59 Mec non-Unc F2 recombinants that produced rr48 F3 progeny, whereas 15/15 Unc non-Mec produced rr48 F3 animals, indicating that rr48 is tightly linked to, or to the right of, mec-4, at the far right of LGX. The rr48 map position was refined using transformation rescue. The YAC clone Y53B5, which is covered by three overlapping pools of three, and the second and third pools both rescued rr48. The cosmids T01C8 was common to both pools, and contains five open reading frames. T01C8.1, a predicted C. elegans orthologue of the mammalian α2 catalytic subunit of AMP-activated kinase (aak-2), was an obvious candidate as its yeast and mammalian orthologues have been implicated in cell cycle/growth control (Hardie, 2005). From T01C8, we sub-cloned an 11.1 kb fragment (Ncol/PstI) containing aak-2 into pgEM-T and injected it (10 ng/μl) into daf-2; rr48 hermaphrodites, rescuing the dauer lethality phenotype. To identify the molecular lesion in rr48, we cloned and sequenced aak-2 cDNA from mutant animals. In three different clones obtained from two independent RT-PCR reactions, we found a typical EMS-induced G/C to A/T transition at position 1 of the predicted codon 208. This mutation is predicted to substitute a conserved histidine with a tyrosine residue in a highly conserved region of the catalytic domain. Furthermore, aak-2(ok524) and aak-2(RNAi) phenocopied the dauer germline hyperplasia and dauer lethality of rr48 mutants, confirming our positional cloning results.

Staining

For whole worm DAPI (4′,6-diamidino-2-phenylindole) staining, animals were washed off plates and soaked in Carnoy’s solution (60% ethanol, 30% acetic acid, 10% chloroform) on a shaker overnight. Animals were then washed twice in PBST (1× PBS + 0.1% Tween 20), and stained in 0.1 mg/ml DAPI solution for 30 minutes. Finally, larvae were washed four times (20 minutes each) in PBST, and mounted in Vectashield (Vector Laboratories) medium.

For extruded dauer gonad staining, gonads were dissected, fixed and stained as described elsewhere (Arduengo et al., 1998). Primary rabbit polyclonal anti-GLP-1, rabbit polyclonal anti-P-granule (anti-PGL-1) and mouse monoclonal 1CB4, and secondary anti-rabbit FITC and anti-mouse Texas-Red-conjugated (Invitrogen) antibodies were used. DAPI was used as a counterstain.

Germ cell nuclei counts

DAPI staining was performed on a synchronized (by hatching in the absence of food) population of L1 larvae plated and grown at 25°C until the appropriate stage/time was reached, except for RNAi experiments, where adult animals were allowed to lay eggs at 15°C overnight before the plate was transferred to 25°C, and the adults killed. The total number of germ cell nuclei per hermaphrodite gonad was then determined, based on their position and nuclear morphology. Animals in which the proximal germ cells had developed into spermatids were excluded from this analysis.

Dauer longevity assay

Because dauer larvae have a tendency to crawl off the bacterial lawn, and often desiccate on the edges of the plate, we developed a novel method to monitor the survival of individual dauer larva. Briefly, C. elegans were synchronized and plated at 25°C. Three days later, ~10 dauer larvae were randomly picked into a 20 μl drop of double-distilled H2O suspended under a Petri dish cover. We refer to this system as ‘the dauer trap’. A wet tissue was placed in the bottom of the dish to maintain humidity, and the plate was sealed with Parafilm. Dauer longevity was monitored daily, and survival was scored as moving response upon exposure to a focused beam of 425-440 nm light. For the ablation experiments, unc-1(e719) was introduced in the background of each strain to prevent dauer larvae from crawling off the agar and survival was scored daily as response to prodding.

Dauer recovery assay

Worms were synchronized and plated at 25°C for ~50 hours. Dauer larvae were then picked fresh, pre-acclimated plates at 25°C in cohorts of 100 individuals. Recovery was monitored daily. In Fig. 2B, him-5(e1467) was in the background of daf-7(e1372); aak-2(ok524).

All other techniques, such as microscopy (Kostic et al., 2003), adult longevity and dauer formation assays (both at 25°C) (Hertweck et al., 2004), laser ablation, aak-1 RNAi (Kostic et al., 2003), and aak-2 RNAi (Kamath and Ahringer, 2003), were performed as previously described.

RESULTS

Dauer-dependent germ cell cycle quiescence is mediated by aak-2

Paradoxically, we noticed that the expression of the Notch ligand remains strong in the DTCs during the dauer stage (Fig. 1A,B), whereas GLP-1 protein is present in the germ line of the dauer larvae (Fig. 1C). Notch should therefore be activated and, with meiosis being repressed, the germ cells would be predicted to still be proliferating during this stage. However, ongoing cellular divisions are never observed in the germ line of dauer larvae, even in glp-1(oz112)gf mutants (data not shown) in which Notch signalling is constitutively active (Berry et al., 1997). Hence, we reasoned that mitosis must be inhibited in the germ line downstream of, or in parallel to, lag-2, by signals that promote dauer formation.

To better understand how the dauer-associated cell cycle quiescence is established in the germline stem cell population through compromised insulin-like signalling, we performed a genetic screen to isolate mutants defective in regulating germline...
Fig. 1. aak-2 larvae are defective in establishing germline quiescence under compromised insulin-like signalling. (A) Open arrowheads delineate the distal extremities of the gonad of daf-2(e1370) dauer larvae. (B) An integrated lag-2p::GFP transgene (q565) is strongly expressed in the DTCs throughout the dauer stage. A lag-2p::CFP transgene (arEx645) containing the full 6.2 kb promoter (Chen and Greenwald, 2004) was also strongly expressed in the DTCs of dauer larvae (data not shown). We similarly found strong GFP expression in the DTCs of qEx308 dauer larvae (data not shown), which contain a functional lag-2p::LAG-2::GFP lag-2(q411) rescuing construct (S. Crittenden and J. Kimble, personal communication). (C) Extruded daf-2(e1370) dauer gonad stained with DAPI (blue) and anti-GLP-1 antibodies (red). (D) Enlarged gonad of daf-2(e1370); aak-2(rr48) dauer larvae. (E) aak-2 is required to progressively suppress germline proliferation during L2/dauer formation. (F-H) In both daf-2(e1370) and daf-7(e1372) larvae, germ cells arrest in mitotic interphase during dauer (arrowhead), as shown in a DAPI-stained, extruded daf-7(e1372) dauer gonad. (G) In daf-2(e1370) gfp-1(e2141) dauer larva, germ cell nuclei arrest in late stage meiotic prophase I, the nuclear size and chromosome morphology being consistent with the pachytene stage (inset). (H) Germ cells often (26/30 animals) progress further through meiosis in daf-2(e1370) gfp-1(e2141); aak-2(rr48) dauer larvae, and their chromosomal morphology closely resembles that of spermatids (arrow). Similar defects were observed in daf-2(e1370) gfp-1(e2141); aak-2(ok524) (19/40 animals) and in daf-2(e1370) gfp-1(e2141); par-4(it57) (25/30 animals) dauer larvae. (I-L) Extruded daf-2(e1370) gfp-1(e2141); aak-2(rr48) dauer gonad. Asterisks indicate germ cells undergoing spermatogenesis. Cells were stained with (I) DAPI (blue); (J) anti-P-granule (green), a germ cell marker that is lost during spermatogenesis (Gruidl et al., 1996); (K) anti-membranous organelle (1CB4; red), a sperm marker (Arduengo et al., 1998). A merged image is shown in L. Images in B,C,F-H are single focal planes; condensed z-stacks are shown in I-L. Scale bars: 50 μm in A,B,D; 10 μm in C,F-H,J-L.

Proliferation during dauer development triggered by reduced insulin-like signalling. We isolated one mutation (rr48) that causes pronounced germline hyperplasia in insulin-like receptor (daf-2) (Kimura et al., 1997) mutant dauer larvae (Fig. 1D). Although pharyngeal and body radial constriction are partially incomplete, daf-2; rr48 mutant dauer larvae demonstrate all of the morphological and behavioural characteristics associated with this stage, including SDS resistance (Cassada and Russell, 1975) (data not shown). By contrast, rr48 animals show no obvious morphological, behavioural or reproductive phenotype during reproductive development (data not shown).

Meiotic mapping, followed by transformation rescue indicated that rr48 affects an orthologue of the α2-catalytic subunit of the mammalian AMP-activated kinase (AMPK): aak-2 (AMP-activated kinase α2) in C. elegans. Biochemical studies have shown that AMPK exists as a heterotrimeric complex composed of one catalytic α-subunit, and two regulatory subunits (Carling, 2004). The EMS-induced point mutation in aak-2(rr48) is predicted to disrupt the catalytic activity of the α2-subunit, without altering the regulatory domain. aak-2(rr48) heterozygous animals display a dauer germline phenotype that is intermediate between the wild-type and homozygous mutant situations, and this is not due to haplo-insufficiency (Table 1, rows A-D). Furthermore, aak-2(RNAi) partially suppresses the germline phenotype of aak-2(rr48) mutants (Table 1, row E). Our analysis therefore suggests that aak-2(rr48) behaves semi-dominantly in the germ line because of a dominant-negative effect that most likely arises through interference with the activity of the second C. elegans AMPK catalytic subunit: aak-1 (AMP-activated kinase α1). Consistent with this, our experiments indicate that aak-1 acts additively with aak-2 to inhibit germline proliferation during dauer development (Table 2, rows F,J,L).
Table 1. aak-2(rr48) acts in a dominant-negative manner in the germ line

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Number of germ cell nuclei in dauer* (n)</th>
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<tbody>
<tr>
<td>(A) daf-2(e1370)</td>
<td>35.44±3.85 (25)</td>
</tr>
<tr>
<td>(B) daf-2(e1370); aak-2(rr48)/+</td>
<td>50.97±5.71 TA (35)</td>
</tr>
<tr>
<td>(C) daf-2(e1370); aak-2(+)/yDf1</td>
<td>34.93±4.14 TA (27)</td>
</tr>
<tr>
<td>(D) daf-2(e1370); aak-2(rr48)</td>
<td>96.16±18.06 TA (25)</td>
</tr>
<tr>
<td>(E) daf-2(e1370); aak-2(rr48); aak-2(RNAi)</td>
<td>69.35±9.96 TD (26)</td>
</tr>
</tbody>
</table>

* Mean values±s.d.
1 Statistical significance using the one-tailed t-test with unequal variance (P=0.0005), versus row 'X'.
2 As above, but P=0.64.
3 Genotype includes qIs56+.
4 Complete genotype is: +/szT1[lon-2(e678)] I; daf-2(e1370) II; lin-15(n765)/yDf1; szT1 X (yDf1 uncovers aak-2).

Dauer germline hyperplasia could result from over-proliferation during dauer formation, and/or from ongoing divisions after the dauer moult. To distinguish between these possibilities, we examined germline proliferation prior to, and during, the dauer stage. In contrast to what we observed in daf-2 mutants alone, the germline proliferation rate does not decrease appropriately during L2d/dauer formation in daf-2; aak-2 double mutants (Fig. 1E). Germline proliferation did, however, finally cease in the daf-2; aak-2 dauer larvae (Fig. 1E), suggesting that additional mechanisms may cooperate with aak-2 to establish dauer-associated germ cell cycle quiescence. Our data therefore indicate that aak-2 is required to appropriately decrease the rate of mitotic proliferation in the germ line during preparation for dauer in response to reduced insulin-like signalling, to coordinate the growth of the germline stem cell population with developmental status.

In both daf-2 and daf-7 [TGF-β mutant (Ren et al., 1996)] dauer larvae, germ cells arrest in interphase of the mitotic cell cycle (Fig. 1F). The intensity of DAPI-stained germ cell nuclei in daf-2 dauer animals is twofold greater than that of the DTC (data not shown), suggesting a 4C DNA content, consistent with a G2/M-phase arrest. Hence, during the dauer stage, germ cells are not only mitotically quiescent, they are also allogenaically blocked from initiating their alternative meiotic program. During reproductive development, inactivating mutations in the core components of the Notch signalling pathway limit mitotic divisions in the germ line and cause premature meiotic entry, resulting in the production of only a small number of sperm (Austin and Kimble, 1987). To test whether aak-2 also regulates the execution of the meiotic program, we first examined whether germ cells could undergo meiosis if the Notch-dependent meiotic block was removed from the germ line of dauer larvae. The germ cells of daf-2 glp-1 larva enter meiosis prematurely during L2d, but arrest nonetheless in late stage meiotic prophase I in dauer (Fig. 1G), indicating that meiotic progression is blocked independently of Notch signals during this stage. Remarkably, in daf-2 glp-1; aak-2 mutants, germ cells progress through the entire meiotic program, including both meiotic divisions, during dauer development and in fact, undergo spermatogenesis (Fig. 1H-L). This suggests that under these conditions, aak-2 ensures that gametogenesis is appropriately coordinated with somatic development, and, in its absence, germ cells can differentiate to sperm prematurely. We therefore conclude that aak-2 contributes to mitotic and meiotic cell cycle regulation to ensure quiescence of the germ cells under compromised insulin-like signalling conditions during dauer formation.

Table 2. Regulation of dauer formation and germline proliferation

<table>
<thead>
<tr>
<th>Genotype</th>
<th>% Dauer arrest (n)</th>
<th>Number of germ cell nuclei in dauer* (n)</th>
</tr>
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<tbody>
<tr>
<td>(A) N2</td>
<td>0 (124)</td>
<td>39.92±4.58 (25)</td>
</tr>
<tr>
<td>(B) aak-2(ok524)</td>
<td>0 (148)</td>
<td>60.36±3.0 AT (25)</td>
</tr>
<tr>
<td>(C) daf-2(e1370)</td>
<td>100 (293)</td>
<td>35.44±3.85 (25)</td>
</tr>
<tr>
<td>(D) daf-2(e1370); aak-2(rr48)</td>
<td>100 (156)</td>
<td>96.16±18.06 TA (25)</td>
</tr>
<tr>
<td>(E) daf-2(e1370); aak-2(ok524)</td>
<td>100 (290)</td>
<td>69.96±9.08 TA (25)</td>
</tr>
<tr>
<td>(F) daf-2(e1370); aak-1(RNAi)</td>
<td>100 (95)</td>
<td>47.77±5.26 TA (30)</td>
</tr>
<tr>
<td>(G) daf-2(e1370); daf-18(e1375)</td>
<td>99.48 (763)</td>
<td>98.17±13.61 TA (30)</td>
</tr>
<tr>
<td>(H) daf-2(e1370); akt-1(1444)gf; aak-2(rr48)</td>
<td>97.7 (607)</td>
<td>50.82±6.57 TA (28)</td>
</tr>
<tr>
<td>(J) daf-2(e1370); akt-1(1444)gf; aak-2(ok524)</td>
<td>77.4 (1387)</td>
<td>126.60±18.95 TA (15)</td>
</tr>
<tr>
<td>(K) daf-2(e1370); akt-1(1444)gf; akt-1(RNAi)</td>
<td>ND</td>
<td>165.00±36.13 TA (28)</td>
</tr>
<tr>
<td>(L) daf-2(e1370); akt-1(1444)gf</td>
<td>67.7 (653)</td>
<td>85.33±12.40 TA (15)</td>
</tr>
<tr>
<td>(M) daf-2(e1370); akt-1(1444)gf; aak-2(ok524)</td>
<td>ND</td>
<td>152.64±32.51 TA (25)</td>
</tr>
<tr>
<td>(N) daf-2(e1370); akt-1(1444)gf; aak-1(RNAi)</td>
<td>85.13 (316)</td>
<td>189.53±23.71 TA (15)</td>
</tr>
<tr>
<td>(O) daf-2(e1372); akt-1(1444)gf</td>
<td>100 (182)</td>
<td>33.19±4.07 TA (26)</td>
</tr>
<tr>
<td>(P) daf-2(e1372); akt-2(ok524)</td>
<td>100 (201)</td>
<td>80.12±6.44 TA (26)</td>
</tr>
<tr>
<td>(Q) daf-2(e1372); aak-1(RNAi)</td>
<td>100 (311)</td>
<td>44.60±10.68 TA (25)</td>
</tr>
<tr>
<td>(R) daf-7(e1372); akt-18(e1375)</td>
<td>99.8 (376)</td>
<td>87.24±14.41 TA (25)</td>
</tr>
<tr>
<td>(S) daf-7(e1372); akt-18(e1480)</td>
<td>92.8 (377)</td>
<td>177.48±21.48 TA (25)</td>
</tr>
<tr>
<td>(T) daf-7(e1372); akt-1(1444)gf</td>
<td>100 (423)</td>
<td>32.15±2.60 TA (26)</td>
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<tr>
<td>(U) daf-16(mgDF50); daf-7(e1372)</td>
<td>98.7 (234)</td>
<td>39.68±9.89 TA (25)</td>
</tr>
<tr>
<td>(V) daf-16(mgDF50); daf-7(e1372); aak-2(rr48)</td>
<td>32.0 (222)</td>
<td>95.24±10.65 TA (25)</td>
</tr>
<tr>
<td>(W) daf-16(mgDF50); daf-7(e1372); aak-2(ok524)</td>
<td>50.5 (497)</td>
<td>82.93±10.14 TA (15)</td>
</tr>
</tbody>
</table>

* Mean values±s.d.
1 Statistical significance using the one-tailed t-test with unequal variance (P=0.0005), versus row ‘X’.
2 As above, but P=0.14.
3 Dauer formation (>90% daf-c) was induced using dauer pheromone preparation.
4, sample size.
5 ND, not determined.

ND, not determined.

§, Genotype includes qIs56+.
1, Complete genotype is: +/szT1[lon-2(e678)] I; daf-2(e1370) II; lin-15(n765)/yDf1; szT1 X (yDf1 uncovers aak-2).

n, sample size.

§, Dauer formation (>90% daf-c) was induced using dauer pheromone preparation.
‡, As above but, P=0.64.
†, Statistical significance using the one-tailed t-test with unequal variance (P=0.0005), versus row ‘X’.
*, Mean values±s.d.
**aak-2 couples developmental arrest to lifespan extension**

In addition to the observed germline hyperplasia, *daf-2; aak-2* dauer larvae die within 12-14 days (Fig. 2A), unlike wild-type dauer larvae, which are non-ageing and can survive beyond 70 days (Klass and Hirsh, 1976). The lethality of *daf-2; aak-2* dauer larvae was not suppressed by ablation of the germline precursors, or of the somatic gonad, or of both (Fig. 3), suggesting that this effect is independent of the germ line defect. Therefore, our data suggest that the extreme lifespan extension characteristic of the *C. elegans* dauer larva does not directly or solely result from the generalized cell cycle/developmental arrest associated with this larval stage, but largely requires *aak-2* activity.

Conversely, compared with *daf-7* mutants, which form dauer larvae constitutively as a result of compromised TGF-β function, *daf-7; aak-2* larvae exhibit a marked increase in recovery from dauer (Fig. 2B). Because *aak-2* dauer larvae display both germ line and dauer longevity defects when induced by either reduced cGMP, TGF-β or insulin-like signalling, or by crowding/starvation, or dauer pheromone (Table 2, rows A-E,N-P; Fig. 2A,B; data not shown), *aak-2* is likely to be required downstream of each of these pathways to ensure appropriate dauer development. Furthermore, because insulin-like signalling is necessary for dauer recovery (Kimura et al., 1997; Ogg et al., 1997), and because reducing *aak-2* function causes premature recovery in *daf-7* dauer larvae, insulin-like signalling may negatively regulate *aak-2*, which would act to promote dauer maintenance. In most organisms examined to date, reduced insulin-like signalling causes adult lifespan extension (Kenyon et al., 1993; Kimura et al., 1997; Lin et al., 1997; Ogg et al., 1997). As the genes involved in the regulation of dauer longevity may additionally affect adult lifespan, we verified whether *aak-2* mutations could also antagonize the extension of adult lifespan in insulin-like mutants. Consistent with this, *aak-2* mutations suppress the lifespan extension of *daf-2* mutants considerably (Fig. 2C), indicating that *aak-2* is required to potentiate the effect of reduced insulin-like signalling on adult lifespan.

**TGF-β and insulin-like signalling converge on the tumour suppressor PTEN to mediate germ cell cycle arrest**

The severity of the phenotypes that result from reduced insulin-like signalling, such as constitutive dauer formation and increased adult lifespan, are generally dependent on dosage (Kenyon et al., 1993; Kimura et al., 1997; Ogg and Ruvkun, 1998; Paradis and Ruvkun, 1998). To directly test whether the level of insulin-like signalling regulates germline proliferation through *aak-2* in a dose-dependent manner, we verified whether mutations that are known to activate this signalling pathway downstream of the insulin-like receptor (*daf-2*) could phenocopy the effect of *aak-2* mutations on germ cell proliferation at the onset of dauer. We therefore introduced a hypomorphic mutation in the *C. elegans* PTEN orthologue *daf-18* (Ogg and Ruvkun, 1998), or a gain-of-function mutation in an Akt/PKB orthologue, *akt-1* (Paradis and Ruvkun, 1998), to partially upregulate insulin-like signalling in *daf-2* mutant larvae. *daf-2; daf-18* and *daf-2; akt-1(gf) animals form dauer larvae that have 164.9% and 43.4% more germ cell nuclei than *daf-2* animals, respectively (Table 2, rows G,H), indicating that efficient inhibition of germline proliferation by reduced insulin-like receptor function occurs via the proper activation of *daf-18*, inactivation of *akt-1*, as well as the activation of *aak-2*. Interestingly, the effects of *daf-18(lf) or akt-1(lf)*, and *aak-1/aak-2* inactivation on dauer formation and germline proliferation are additive (Table 2, rows L,K,M), suggesting that these pathways work in parallel, or that other factors, in addition to *aak-1/aak-2*, function downstream of *daf-18* and *akt-1* to regulate dauer formation and insulin-dependent cell cycle quiescence in the germ line.

Activity of the FOXO-like forkhead transcription factor *daf-16*, a direct Akt/PKB target (Lee et al., 2001), is believed to be responsible for all of the phenotypes of reduced insulin-like receptor function
suggesting that larvae when compared with wild-type or daf-16(mgDf50); daf-7(0) larvae (Fig. 4), 72.0% of daf-16(0); daf-7 dauer larvae had germ cell nuclei counts that were below/equal to the maximum observed in daf-7 dauer larvae (41), suggesting that daf-16, in contrast to daf-18 and aak-2, is not absolutely required for the appropriate downregulation of germline proliferation during dauer formation. Moreover, the effect of daf-16(0) on dauer formation and germline proliferation in daf-7 mutants is enhanced by aak-2 mutations (Table 2, rows V,W), indicating that daf-16 is not required for aak-2 activity during dauer formation triggered by compromised TGF-β signalling. Consistent with previous observations (Ogg et al., 1997), however, several daf-16(0); daf-7 dauer larvae did not maintain germ cell cycle quiescence and resumed reproductive development (data not shown). Our data therefore suggest that reduced TGF-β signalling downregulates germline proliferation during dauer development primarily through the activation of daf-18 and aak-7, whereas the inactivation of akt-1 and the subsequent activation of daf-16 appear to be required to ensure the proper maintenance, rather than the establishment, of germ cell cycle quiescence in larvae with compromised TGF-β signalling.

**TGF-β and insulin-dependent signals target aak-2 to regulate proliferation cell autonomously**

Because the insulin-like and TGF-β pathways demonstrate both cell autonomous and cell non-autonomous functions (Ihse and Thomas, 2000; Wolkow et al., 2000), we determined whether aak-2 activity is required for germ cell cycle regulation in the tissues where these signalling pathways function to regulate dauer formation, or within the germ line proper. To address this question, we studied the response of rrf-1 mutants to aak-2(RNAi). rrf-1 mutants are resistant to dsRNA-mediated interference in the soma, whereas they remain RNAi-sensitive in the germ line (Sijen et al., 2001). aak-2(RNAi) performed in both rrf-1; daf-2 and rrf-1; daf-7 animals recapitulated the germline hyperplasia typical of daf-2; aak-2(RNAi) and daf-7; aak-2(RNAi) dauer larvae (Table 3, rows A-H), indicating that aak-2 is required cell autonomously (within the germ cells) to regulate germline proliferation in response to compromised insulin-like and TGF-β signalling, during dauer development.
par-4 mediates TGF-β and insulin-dependent control of cell cycle

Recently, it has been shown that AMPK itself is activated by LKB1/STK11, the major AMPK-activating kinase (Hong et al., 2003; Woods et al., 2003). In humans, inactivating mutations in LKB1 are responsible for most cases of Peutz-Jeghers Syndrome, a rare dominantly inherited disorder characterised primarily by predisposition to benign and malignant tumours in many organ systems (Hemminki et al., 1998; Jenne et al., 1998). We reasoned that if LKB1 was required for optimal AMPK function, inactivating mutations in the C. elegans LKB1 orthologue par-4 (Watts et al., 2000) should phenocopy the effect of reduced aak-1/aak-2 activity. par-4 mutations indeed phenocopy the dauer germline hyperplasia caused by the inactivation of both aak catalytic isoforms (Table 2, rows J, L; Table 4, rows D-G), indicating that par-4 is required to suppress proliferation of the germline stem cell population in response to reduced insulin-like or TGF-β signalling levels. If the germline hyperplasia in par-4 mutant dauer larvae results from defective aak activation, the loss of aak-1 and/or aak-2 activity should not enhance the effect of a strong par-4(i57) inactivating mutation (Watts et al., 2000). However, only aak-1(RNAi) was not significantly additive to par-4(i57) (Table 4, rows J, L). In fact, while daf-2; par-4 dauer larvae are long-lived when compared with daf-2; aak-2 animals (Table 4, rows A-E), par-4 enhances the dauer germline and lifespan phenotypes of aak-2 mutants (Table 4, rows H, J-K), suggesting that par-4 and aak-2 function, at least in part, in an additive manner, and that aak-2 activity may not absolutely rely on par-4 to control germ cell cycle and lifespan during compromised insulin-like signalling conditions. Moreover, our data suggest that par-4 may target other factors along with aak-1/aak-2 to control germline proliferation under these dauer-promoting conditions.

DISCUSSION

Our analysis of aak-2 function in C. elegans reveals that it is required for the characteristic long-term survival of the developmentally arrested juvenile dauer larva and thereby complements and further supports the recent finding that it is required for the adult lifespan extension associated with reduced insulin-like signalling (Apfeld et al., 2004). In plant, yeast and mammalian systems, the AMPK orthologues act as ‘metabolic master switches’ to appropriately reset gene expression for survival on alternative energy sources (Carling, 2004; Hardie et al., 1998). The lifespan extension that is associated with developmental arrest and/or compromised insulin signalling in most organisms is therefore likely to require a substantial switch to alternative metabolic pathways, which is triggered predominantly through the activation of AMPK.

We have demonstrated that daf-18/PTEN, par-4/LKB1 and aak-1, aak-2/AMPK are crucial factors commonly required for the regulation of germline proliferation in response to the neuroendocrine signal generated as a result of compromised insulin-like and/or TGF-β signalling (Fig. 5), whereas daf-16/FOXO appears, at least in part, dispensable. Our data is therefore consistent with a model in which par-4 and aak-1/aak-2 function together with daf-18, and partially in parallel with daf-16. Namely, the efficient suppression of germ cell cycle progression during early larval development requires either compromised TGF-β signalling or daf-16 activity. Although we provide evidence that aak-2 is required in the germ line to control proliferation in response to these signalling pathways, it would be of great interest to determine the cellular requirement of each of the players that link the insulin-like and/or TGF-β-dependent neuroendocrine signals to the regulation of aak-2 activity within a target tissue.

Table 3. aak-2 is required cell autonomously for germ cell cycle regulation

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Number of germ cell nuclei in dauer* (n)</th>
</tr>
</thead>
<tbody>
<tr>
<td>(A) daf-2(e1370)</td>
<td>35.44±3.85 (25)</td>
</tr>
<tr>
<td>(B) daf-2(e1370); aak-2(RNAi)</td>
<td>65.29±8.09 (35)</td>
</tr>
<tr>
<td>(C) daf-2(e1370); aak-2(ok524)</td>
<td>35.37±3.66 (30)</td>
</tr>
<tr>
<td>(D) daf-2(e1370); par-4(it47)</td>
<td>55.93±7.25 (28)</td>
</tr>
<tr>
<td>(E) daf-2(e1372)</td>
<td>33.19±4.07 (26)</td>
</tr>
<tr>
<td>(F) daf-2(e1372); aak-2(RNAi)</td>
<td>66.90±8.02 (10)</td>
</tr>
<tr>
<td>(G) daf-2(e1370); aak-2(i57)</td>
<td>34.90±4.36 (10)</td>
</tr>
<tr>
<td>(H) daf-2(e1372); par-4(it47)</td>
<td>57.40±9.70 (10)</td>
</tr>
</tbody>
</table>

* Statistical significance using the one-tailed t-test with unequal variance (P=0.0005, versus row ‘X’).
†, As above, but P=0.15.
§, As above, but P=0.035.

Table 4. Regulation of germline proliferation and dauer lifespan

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Number of germ cell nuclei in dauer* (n)</th>
<th>Dauer lifespan (days)* (n)</th>
</tr>
</thead>
<tbody>
<tr>
<td>(A) daf-2(e1370)</td>
<td>35.44±3.85 (25)</td>
<td>&gt;15 (100)</td>
</tr>
<tr>
<td>(B) daf-2(e1370); aak-2(rr48)</td>
<td>96.16±18.06 (25)</td>
<td>8.64±1.77 (98)</td>
</tr>
<tr>
<td>(C) daf-2(e1370); aak-2(ok524)</td>
<td>69.96±9.08 (25)</td>
<td>8.18±2.41 (60)</td>
</tr>
<tr>
<td>(D) daf-2(e1370); par-4(i57)</td>
<td>109.00±28.42 (25)</td>
<td>&gt;15 (50)</td>
</tr>
<tr>
<td>(E) daf-2(e1370); par-4(it57)</td>
<td>148.28±30.90 (25)</td>
<td>&gt;15 (60)</td>
</tr>
<tr>
<td>(F) daf-7(e1372)</td>
<td>33.19±4.07 (26)</td>
<td>ND</td>
</tr>
<tr>
<td>(G) daf-7(e1372); par-4(i57)</td>
<td>160.20±29.99 (25)</td>
<td>ND</td>
</tr>
<tr>
<td>(H) daf-2(e1370); par-4(147); aak-2(rr48)</td>
<td>187.53±16.60 (15)</td>
<td>6.97±2.12 (60)</td>
</tr>
<tr>
<td>(I) daf-2(e1370); par-4(it57); aak-1(RNAi)</td>
<td>155.95±25.21 (25)</td>
<td>ND</td>
</tr>
<tr>
<td>(J) daf-2(e1370); par-4(it57); aak-2(rr48)</td>
<td>213.10±38.87 (10)</td>
<td>5.83±1.16 (60)</td>
</tr>
<tr>
<td>(K) daf-2(e1370); par-4(it57); aak-2(ok524)</td>
<td>202.65±24.14 (17)</td>
<td>6.85±1.83 (59)</td>
</tr>
<tr>
<td>(L) daf-2(e1370); par-4(it57); aak-2(ok524); aak-1(RNAi)</td>
<td>215.87±17.65 (15)</td>
<td>ND</td>
</tr>
</tbody>
</table>

* Mean values±s.d.; all strains were ~100% dauer constitutive at 25°C.
†, As above, but P=0.18.
‡, As above, but P=0.035.
n, sample size.
ND, not determined.
Together, these results complement/modify our current model of cell cycle/growth control, in which growth factors are believed to function through Akt/PKB (which is negatively regulated by PTEN), while intracellular energy stress is thought to work in parallel, activating AMPK through LKB1, then converging on the TSC/mTOR pathway to cell autonomously regulate growth and division (Corradetti et al., 2004; Shaw et al., 2004). Our work indicates that the insulin and TGF-β signalling pathways independently converge on both tumour suppressors, PTEN and LKB1, which then mediate cell cycle control under stress conditions.

Finally, we have shown that inactivating mutations in par-4/LKB1 partially phenocopy and enhance the defects associated with reduced aak-2/AMPK activity in insulin-like-compromised animals, linking metabolic status, through insulin-like signalling, to the regulation of the germline stem cell divisions and lifespan. Previous work has suggested that LKB1 functions as a tumour suppressor through its role in controlling both cell polarity (Boudeau et al., 2003) and AMPK (Corradetti et al., 2004; Shaw et al., 2004); however, evidence that mutations in AMPK recapitulate the proliferative defects associated with LKB1 mutations has up to now been lacking. Our findings provide strong genetic evidence that the aberrant cell cycle regulation associated with Juvenile Polyposis Syndrome, Cowden’s Disease and Peutz-Jeghers Syndrome, which are caused by mutations in genes involved in TGF-β signal transduction, in PTEN and in LKB1, respectively (Waite and Eng, 2003; Wirtzfeld et al., 2001), may result from defects at different levels of a single genetic pathway that unifies general growth factor levels to the regulation of cell proliferation via AMPK regulation.

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