Germ-line tumor formation caused by activation of \textit{glp-1}, a \textit{Caenorhabditis elegans} member of the \textit{Notch} family of receptors

Laura Wilson Berry, Bethany Westlund and Tim Schedl*  
Department of Genetics, Campus Box 8232, Washington University School of Medicine, 4566 Scott Ave, St Louis MO 63110, USA  
*Author for correspondence (e-mail: ts@sequence.wustl.edu)

SUMMARY

\textit{Caenorhabditis elegans} germ-line proliferation is controlled by an inductive interaction between the somatic distal tip cell and the germ line. GLP-1, a member of the Notch family of transmembrane receptors, is required continuously in the germ line to transduce the proliferative signal. In the absence of GLP-1, all proliferative germ cells exit the mitotic cell cycle and enter meiotic prophase. We have characterized an activating mutation in \textit{glp-1 (oz112gf)}, that has the opposite phenotype. Homozygous \textit{glp-1 (oz112gf)} hermaphrodites and males have a completely tumorous germ line in which germ cells never leave the mitotic cycle. In \textit{glp-1 (oz112gf)} heterozygotes, germ-line polarity is established correctly, but as adults age, the distal proliferative population expands leading to a late-onset tumorous phenotype. The mutant receptor is constitutively active, promoting proliferation in the absence of ligand. The normal distal-proximal spatial restriction of GLP-1 expression is lost in tumorous and late-onset tumorous animals; ectopically proliferating germ cells contain membrane-associated GLP-1. The correlation between proliferation and expression, both in wild-type where \textit{glp-1} signalling is limited by localized ligand and in \textit{glp-1 (oz112gf)} where signalling is ligand-independent, suggests that \textit{glp-1} signalling positively regulates GLP-1 expression. In addition to germ-line defects, \textit{glp-1 (oz112gf)} causes inappropriate vulval cell fate specification. A missense mutation in a conserved extracellular residue, Ser642, adjacent to the transmembrane domain, is sufficient to confer the \textit{glp-1 (oz112gf)} mutant phenotypes. Two mammalian Notch family members, TAN-1 and \textit{int-3}, are proto-oncogenes. Thus, activating mutations in both invertebrate and vertebrate Notch family members can lead to tumor formation.

Key words: germ line, tumor, proliferation, meiosis, cell fate, oncogene, \textit{glp-1}, Notch

INTRODUCTION

During metazoan development, tissues are formed by the coordination of proliferative and differentiative decisions. Such cell fate decisions are often controlled by signalling between nearby cells and, in many cases, the signal transduction pathways employed are evolutionarily conserved (Greenwald and Rubin, 1992). A number of vertebrate proto-oncogenes are components of conserved signal transduction pathways (Bishop, 1991). During tumor formation, the activity of signalling pathways can be deregulated, leading to inappropriate proliferative and differentiative decisions.

The Notch family of transmembrane receptors function in cell signalling during vertebrate and invertebrate development (Artavanis-Tsakonas et al., 1995). Certain mammalian Notch family members are proto-oncogenes; activating mutations in the human \textit{TAN-1} and mouse \textit{int-3} loci are associated with \textit{T}-cell leukemia and mammary epithelial tumors, respectively (Ellisen et al., 1991; Robbins et al., 1992; Jhappan et al., 1992). The \textit{Drosophila Notch} gene and the \textit{C. elegans} Notch family members \textit{glp-1} and \textit{lin-12} function in cell fate decisions; loss-of-function (\textit{lf}) mutations cause inappropriate cell fate specification resulting in abnormal differentiation (Lambie and Kimble, 1991a; Greenwald and Rubin, 1992). Previously described gain-of-function (\textit{gf}) activating mutations/transgenes for \textit{Notch}, \textit{glp-1} and \textit{lin-12} can cause cell fate alterations that are opposite those of loss-of-function mutations but do not lead to tumor formation (Greenwald, 1994). In this paper, we describe an activating gain-of-function mutation in \textit{glp-1} that causes both germ-line tumor formation and a somatic multi-vulva phenotype.

GLP-1 functions in several cell fate decisions during \textit{C. elegans} development (Bowerman, 1995; Lambie and Kimble, 1991a). Here we focus on the function of GLP-1 in the decision between germ-line proliferation versus entry into the meiotic pathway.

GLP-1 is the germ-line receptor for an inductive signal from the somatic gonadal distal tip cell (DTC). The signalling molecule produced by the DTC, LAG-2, is related to the transmembrane protein Delta, a ligand for Notch (Tax et al., 1994; Henderson et al., 1994). Killing the DTC with a laser microbeam (Kimble and White, 1981) and loss-of-function mutations in \textit{glp-1} (Austin and Kimble, 1987) and \textit{lag-2} (Lambie and Kimble, 1991b) result in essentially identical phenotypes: all proliferative germ cells enter meiosis. The DTC-GLP-1 signalling pathway thus acts to specify the pro-
liferative germ cell fate (or inhibit entry into meiotic prophase).

Germ-line polarity observed in wild-type late larval and adult worms (Fig. 1A,C) is generated by the DTC-GLP-1 signalizing pathway. At the distal end of the gonad, capped by the DTC, is a population of proliferating germ-line stem cells that extends ~24 cell diameters from the distal tip (Crittenden et al., 1994). As germ cells move proximally, they exit the mitotic cycle, enter meiotic prophase and progress through pachytene. Gametogenesis and further meiotic progression occur as germ cells move through the proximal germ line. By localizing the source of ligand to the DTC (Henderson et al., 1994), GLP-1 signaling, and thus proliferation, is spatially restricted. Although the exact mechanism is unclear (see Crittenden et al., 1994; Fitzgerald and Greenwald, 1995), it appears that at increasing distance from the DTC, the level of ligand falls, GLP-1 signaling decreases and germ cells exit the mitotic cycle and enter meiosis. Consistent with this model, transgenic animals that produce a secreted form of ligand, which presumably can diffuse to more proximal regions of the gonad, display ectopic germ-line proliferation (Fitzgerald and Greenwald, 1995).

In this paper, we present characterization of a novel activating mutation in glp-1. The glp-1(oz112gf) mutation causes inappropriate specification of the proliferative germ-line stem cell fate, leading to tumor formation, and inappropriate specification of the vulval secondary cell fate, leading to abnormal differentiation in the ventral epidermis. A positive feedback model is presented to explain the observed correlation between proliferation and GLP-1 expression in wild-type and oz112gf mutants.

MATERIALS AND METHODS

General methods and strains

Standard methods were used for maintaining and manipulating Caenorhabditis elegans (Brenner, 1974). All strains were derived from the wild-type C. elegans var. Bristol strain N2 (Brenner, 1974), except for glp-1(oz112gf) which was derived from CB4855 (natural isolate) (Hodgkin and Barnes, 1991). Mutations used in this study are listed in Tables 1-6 and described in Hodgkin et al. (1988) unless indicated. Experiments were done at 20°C unless otherwise indicated.

Isolation of glp-1(oz112gf) and intragenic revertants

glp-1(oz112gf) was isolated as a tumorous mutant in a screen for dominant hermaphrodite steriles following ethyl methanesulfonate (EMS) mutagenesis of CB4855. oz112gf was placed in the Bristol background by repeated backcrossing to N2-derived strains followed by recombining linked markers (unc-56 and dpy-18) on and off the oz112gf chromosome.

To determine the loss-of-function phenotype of the gene identified by the glp-1(oz112gf) mutation, we screened for eo-intragenic revertants unc-32(e189) oz112gf(e171) let-505(e2165) (Rosenbluth et al., 1983). hermaphrodites were mutagenized with EMS, shifted to 25°C as adults and non-tumorous F1 hermaphrodites with eggs were cloned. F2 progeny were analyzed for phenotypes as lethality or sterility. From 1500 mutagenized genomes, three revertants, oz112oz120, oz112oz132 and oz112oz134 were obtained with a recessive glp-1(lf) phenotype. Both glp-1(oz112oz132) and glp-1(oz112oz134) mutants have a strong Glp phenotype similar to glp-1(q721) (Kodoyianni et al., 1993). The oz120 lesion is identical to that of glp-1(q231ts) (Fig. 3; Kodoyianni et al., 1992) and both have similar temperature-sensitive Glp phenotypes (Austin and Kimble, 1987).

Identification of glp-1 missense mutations

Both strands of the glp-1 coding region, 5′ and 3′ untranslated regions were sequenced from N2, CB4855, glp-1(oz112gf), glp-1(oz112oz120) and glp-1(oz112oz132) as described in Jones and Schied (1995) using primers kindly provided by S. Crittenden, J. Kimble and E. Main (Kodoyianni et al., 1992; Lissemore et al., 1993). In addition to the oz112gf missense mutation, two silent polymorphisms were found in the ~5000 bases of CB4855 glp-1 DNA that was sequenced.

Transgenic studies

Plasmid pPD25.47 (provided by Andy Fire) contains glp-1(+e) in pBlueScript.KS (numbering refers to this plasmid). A 300 bp fragment that spans the oz112gf point mutation at bp 7081 was PCR amplified from two unc-32(glp-1(e304gf)) homozygotes (Williams et al., 1992) using the primers em9 and vl1 (Lissemore et al., 1993). The fragment was ligated into a pGLP1(+e) plasmid lacking this region to form pGLP1.S642N. Individual clones of this plasmid were sequenced through the oz112gf region to confirm the presence of the point mutation and three independent clones were selected for microinjection.

Either pPD25.47 or pGLP1.S642N (50-100 μg/ml) was coinjected into adult N2 hermaphrodites along with prf-4 (75-200 μg/ml) as a dominant roller transformation marker (Mello et al., 1991). 55 F1 Rol hermaphrodites, including seven heritable lines, were generated from the pPD25.47 injections. Four F1s were Glp sterile and three lines segregated Glp steriles, but no progeny with Muv or tumorous germ-line phenotypes were observed. It is not uncommon to obtain Glp sterile phenotypes from injection of pPD25.47, but Muv and tumorous phenotypes are never observed (K. Fitzgerald, personal communication). The pGLP1.S642N injections yielded 89 F1 Rol hermaphrodites and six heritable lines. Two F1s were Glp sterile, three were Muv and one had a tumorous germ line. Three of the six lines segregated Glp steriles, one of these also segregated Muv and that same line gave rise to a single animal with one tumorous gonad arm.

Characterization of glp-1(oz112gf) tumorous phenotype

Synchronization of animals, dissection, fixation and staining with DAPI, nuclear counts, and laser ablations are basically the same as described in Francis et al. (1995a,b). For staining with α-GLP-1 antibodies (kindly provided by S. Crittenden and J. Kimble), dissected animals were fixed and stained essentially as described by Crittenden et al. (1994) except Chemicon alkaline phosphatase goat anti-rat IgG secondary antibody was used to visualize GLP-1 staining.

RESULTS

Identification of glp-1(oz112gf), a tumorous germ-line mutant

We have isolated a mutation, oz112gf, with a tumorous germ-line phenotype. The term ‘tumorous’ describes germ lines with three characteristics: (1) a vast excess of germ cells compared to wild-type, (2) ectopic proliferation and (3) little or no germ cell differentiation (Figs 1B,D, 2). The oz112gf phenotype is temperature sensitive (ts) and dose sensitive in both hermaphrodites and males (Tables 1, 3; see below).

Genetic and phenotypic characterization indicates that oz112gf is a novel allele of glp-1. First, oz112gf maps genetically to a two centimorgan interval containing glp-1 (data not shown). Second, the dominant oz112gf tumorous phenotype is opposite to that of the recessive Glp-1(lf) phenotype (premature entry of germ cells into the meiotic pathway). Third, three tightly linked (intragenic) revertants of oz112gf were identified.
glp-1(oz112gf) causes germ-line tumors

(Materials and Methods) which have a recessive Glp-1(lf) phenotype and fail to complement canonical glp-1(lf) alleles.

Identification of the glp-1(oz112gf) molecular lesion
To define the molecular lesion, the glp-1 coding region (Yochem and Greenwald, 1989) was sequenced in oz112gf and the parental strain, CB4855 (Hodgkin and Barnes, 1991). CB4855-derived glp-1(+) was sequenced to identify any polymorphisms differing from the reference strain N2. Sequence analysis revealed a single missense mutation (S642N) located

Fig. 1. Morphology of wild-type and glp-1(oz112gf) tumorous germ lines. Surface view of dissected gonads stained with DAPI to visualize nuclear morphology. (A) wild-type young adult hermaphrodite and (C) male; (B) homozygous (25°C) glp-1(oz112gf) adult hermaphrodite and (D) young adult male. Wild-type germ lines show distal-proximal polarity: proliferation is limited to the distal mitotic region; germ cells enter the meiotic pathway in the transition zone and progress through the pachytene region; late stages of meiotic prophase and gametogenesis occur in the proximal germ line. glp-1(oz112gf) germ lines lack polarity. Proliferation is found throughout (arrows indicate nuclei in mitosis) and there is no evidence of nuclei in meiotic prophase or gametogenesis. Although most of the wild-type germ line is syncytial, each nucleus, its surrounding cytoplasm and membranes is called a germ cell (Austin and Kimble, 1987). Scale bar, 10 μm.
extracellularly in a region between the third LNG repeat and the transmembrane domain (Fig. 3). An alignment of this region (data not shown) with invertebrate Notch homologs and mammalian Notch 1 homologs (Maine et al., 1995) indicates that this serine residue is conserved in these Notch family members. Gain-of-function mutations in both lin-12 and Notch are also located in this general area (Greenwald and Seydoux, 1990; Lyman and Young, 1993), although the oc112gf molecular lesion is novel.

To verify that the identified oc112gf molecular lesion was responsible for the observed glp-1(gf) mutant phenotypes, the S642N change was introduced into a glp-1(+), pPD25.47 (provided by A. Fire). Following microinjection into wild type, transgenic animals were observed with somatic multivulvae and low penetrance tumorous phenotypes, indicating the S642N lesion is sufficient to confer the glp-1(oz112gf) mutant phenotypes (see Materials and Methods).

glp-1(oz112gf) hermaphrodites and males have germ-line tumors

Two tumorous germ-line phenotypes are observed in glp-1(oz112gf) animals. Expressivity of the defects varies with gene dosage and temperature. At higher temperatures, homozygous oc112gf germ lines are completely tumorous (contain only proliferating germ cells); at lower temperatures, heterozygous and hemizygous oc112gf animals exhibit a late-onset tumorous phenotype. Table 1 summarizes a systematic analysis of the dose and temperature dependence of the tumorous phenotypes.

All glp-1(oz112gf/oz112gf) and glp-1(oz112gf/oz112gf(+)) hermaphrodites at 25°C are sterile, with a completely tumorous germ line (Fig. 1B). Proliferation occurs throughout the gonad and there is no evidence of entry into the meiotic pathway (see below). Thus, the distal-to-proximal germ-line polarity that is normally observed in late larvae and adults is completely absent (Fig. 1), a novel C. elegans phenotype.

Hemizygous and heterozygous oc112gf hermaphrodites grown at 15°C and 20°C are initially fertile, but develop a late-onset tumorous phenotype. Normal germ-line polarity is initially established, but over time the distal mitotic region expands and eventually fills the entire gonad arm. The late-onset tumorous phenotype results in an ~4-fold reduction in brood size compared to wild type (from ~300 to ~75), probably because proliferation is occurring at the expense of oocyte development. Additionally, less than a quarter of the progeny of oc112gf hemizygous or heterozygous hermaphrodites are viable (Table 2). Crosses using oc112gf/+ males indicate this lethality is due to a dominant maternal effect. Maternally derived GLP-1 is necessary for specifying cell fates in the embryo (reviewed by Bowerman, 1995). We have not investigated the basis of the embryonic lethality.

Hemizygous and heterozygous oc112gf hermaphrodites grown at 25°C and homozygotes grown at 15°C and 20°C are sterile. Some gonad arms are filled with proliferating cells while the remaining display limited germ cell differentiation prior to the appearance of the late-onset tumorous phenotype. Elevated glp-1 dose and temperature causes both the late-onset tumorous phenotype to appear at a younger age and the per-

---

**Fig. 2.** Comparison of germ-line proliferation in wild-type and glp-1(oz112gf) hermaphrodites. The number of germ-line nuclei per gonad arm is plotted versus developmental time for wild-type (unc-32) and unc-32 glp-1(oz112gf). oc112gf germ lines produce a significantly greater number of germ cells than wild-type. In older adults, extragonadal germ cells are found in the pseudocelom, presumably because of rupture of the somatic gonad/basement membrane, and in the spermatheca and uterus. Nuclei were counted from four or more gonad arms per time point. Error bar represents ± one standard deviation.

**Fig. 3.** Molecular lesions for glp-1(oz112gf) and intragenic revertants. The positions and amino acid changes are shown on a schematic diagram of GLP-1. The extracellular domain contains two cysteine-rich regions, ten EGF-like repeats and three LNG repeats. The cytoplasmic domain contains six ankyrin (cdc10/SW616) motifs. The glp-1(oz112gf) missense mutation (S642N) is located extracellularly, between LNG-3 and the transmembrane domain. The oc132 lesion in the intragenic revertant oc112oc132 is C248T, a conserved Cys residue in the fifth EGF-like repeat. oc120 in oc112oc120 is G1057E in the fourth ankyrin repeat, indicating that at least one ankyrin repeat is required for oc112gf activity.
The indicated genotypes or temperatures show over proliferation defects that have been classified as tumorous or late-onset tumorous defects. Rodites have 105 meiotic germ cells. In contrast, per temperature dependent (Table 1).

The dose dependence of the tumorous phenotype (Table 1) suggests that \textit{oc112gf} acts as a genetic hypermorphic (Muller, 1932). To quantitatively test this idea, the number of germ cells in the meiotic pathway was determined in strains with differing copies of \textit{glp-1} (Table 3). If \textit{glp-1(oc112gf)} is hypermorphic, the addition of \textit{glp-1(+/+)} should result in a more tumorous phenotype (i.e. smaller number of germ cells in the meiotic pathway).

Wild-type young adult hermaphrodites (56 hours after hatching, 20°C) have approximately 400 germ cells in the meiotic pathway/gonad arm. Homozygous \textit{oc112gf} hermaphrodites have 105 meiotic germ cells. In contrast, \textit{oc112gf/oc112gf+/+} have only ~23 germ cells (Table 3). Thus, the number of germ cells in the meiotic cell cycle decreases as \textit{glp-1(+/+)} activity is added, consistent with \textit{glp-1(oc112gf)} acting as a hypermorphic lesion.

\textbf{Tumors arise from a failure of germ cells to exit from the mitotic cell cycle}

Since \textit{glp-1(oc112gf/oc112gf+/+)} germ lines lack polarity and \textit{glp-1(+/+)} functions to promote proliferation, we hypothesized that tumors arose from a failure of germ cells to leave the mitotic cycle and enter meiosis. To test this possibility, germ lines were examined for entry into the meiotic pathway at different times during late larval development in \textit{glp-1(oc112gf/oc112gf+/+)} and control hermaphrodites at 25°C (Fig. 4). In wild-type animals 32 hours after hatching (L4), 100% of the gonad arms have proximal germ cells in pachytene. By contrast, proximal pachytene nuclei are never observed in \textit{glp-1(oc112gf/oc112gf+/+)} animals, even 48 hours after hatching (adult). Instead, proximal germ cells continue

## Table 1. \textit{glp-1(oc112gf)} hermaphrodites and males exhibit a dosage-sensitive and temperature-sensitive tumorous germ-line phenotype

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Temperature</th>
<th>Self-fertile</th>
<th>% Late-onset tumorous</th>
<th>% Tumorous</th>
<th>(n=)</th>
<th>% Late-onset tumorous</th>
<th>% Tumorous</th>
<th>(n=)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Control*</td>
<td>15, 20, 25°C</td>
<td>Yes</td>
<td>0%</td>
<td>0%</td>
<td>(&gt;100)</td>
<td>0%</td>
<td>0%</td>
<td>(&gt;100)</td>
</tr>
<tr>
<td>\textit{oc112gf/oc112gf}</td>
<td>15°C</td>
<td>Yes</td>
<td>100%</td>
<td>0%</td>
<td>(&gt;200)</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>\textit{oc112gf/oc112gf}</td>
<td>15°C</td>
<td>No*</td>
<td>71%</td>
<td>29%</td>
<td>(&gt;100)</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>\textit{oc112gf/oc112gf}</td>
<td>20°C</td>
<td>Yes</td>
<td>100%</td>
<td>0%</td>
<td>(&gt;300)</td>
<td>58%</td>
<td>42%</td>
<td>(&gt;100)</td>
</tr>
<tr>
<td>\textit{oc112gf/oc112gf}</td>
<td>20°C</td>
<td>No*</td>
<td>39%</td>
<td>61%</td>
<td>(&gt;100)</td>
<td>2%</td>
<td>98%</td>
<td>(50)</td>
</tr>
<tr>
<td>\textit{oc112gf/oc112gf}</td>
<td>20°C</td>
<td>No*</td>
<td>26%</td>
<td>74%</td>
<td>(&gt;100)</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>\textit{oc112gf/oc112gf}</td>
<td>25°C</td>
<td>No*</td>
<td>16%</td>
<td>84%</td>
<td>(&gt;100)</td>
<td>24%</td>
<td>76%</td>
<td>(50)</td>
</tr>
<tr>
<td>\textit{oc112gf/oc112gf}</td>
<td>25°C</td>
<td>No*</td>
<td>0%</td>
<td>100%</td>
<td>(&gt;200)</td>
<td>0%</td>
<td>100%</td>
<td>(20)</td>
</tr>
<tr>
<td>\textit{oc112gf/oc112gf}</td>
<td>25°C</td>
<td>No*</td>
<td>0%</td>
<td>100%</td>
<td>(&gt;100)</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
</tbody>
</table>

*Germ-line phenotypes were analyzed using Nomarski microscopy and DAPI staining (Francis et al., 1995a,b). 100% of \textit{glp-1(oc112gf)} gonad arms (for any of the indicated genotypes or temperatures) show overproliferation defects that have been classified as tumorous or late-onset tumorous defects.

The percentage of gonad arms that are not completely tumorous. Gonad arms initially have normal distal-to-proximal polarity of proliferation, meiotic prophase progression and gametogenesis. Over time the distal mitotic zone expands proximally, often filling the entire gonad with proliferating cells and thus abolishing germ-line polarity (see text). See Fig. 5A.

1Non-Unc hermaphrodites self-progeny from \textit{unc-32(e189)/unc-36(e251) glp-1(q175) and him-8(e1489)} male self-progeny. 2Non-Unc-32 male self-progeny from \textit{unc-32(e189)/unc-36(e251) glp-1(q175) and him-8(e1489)}. 3Unc-32 female self-progeny from \textit{unc-32(e189)/unc-36(e251) glp-1(q175) and him-8(e1489)}. 4Unc-32 male self-progeny from \textit{unc-32(e189)/unc-36(e251) glp-1(q175) and him-8(e1489)}.

5Non-Dpy hermaphrodites from \textit{dpy-19(e1259)/unc-32(e189) glp-1(q177);qDp3} contains \textit{unc-32(e189)} and wild-type alleles of \textit{dpy-19} and \textit{glp-1} (Austin and Kimble, 1987). 6Proximal proliferation observed in 1% of examined gonad arms. 75% of observed gonad arms have 1-2 germ cells in the meiotic pathway (pachytene). 8Sterility is the result of limited gametogenesis and excess proliferation.
Table 2. glp-1(oz112gf) exhibits semi-dominant maternal effect lethality

<table>
<thead>
<tr>
<th>Parental genotype</th>
<th>% Embryonic lethality</th>
<th>% L4 larval lethality</th>
<th>% Viable adults</th>
</tr>
</thead>
<tbody>
<tr>
<td>oz112gf</td>
<td>83%</td>
<td>2%</td>
<td>14%</td>
</tr>
<tr>
<td>null</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>oz112gf</td>
<td>72%</td>
<td>5%</td>
<td>23%</td>
</tr>
<tr>
<td>+</td>
<td>3%</td>
<td>5%</td>
<td>92%</td>
</tr>
</tbody>
</table>

*Single L4 or young adult hermaphrodites (genotype: dpy-19(e1259) unc-32(e189) glp-1(oz112gf)/unc-32(e189) glp-1(q175); or dpy-19(e1259) unc-32(e189) glp-1(oz112gf)/hm-3(rb169)) were placed on agar plates at 20°C. Animals were transferred every 12 hours to fresh plates. Embryonic viability was determined 24-36 hours after embryos were laid. Larvae were counted every 24 hours after hatching. The number of viable adults was determined after progeny had achieved at least the fourth larval stage. mau-3(rb169) was provided by J. Plenefisch.

The percentage of embryonic lethality was calculated for each brood as the number of dead embryos/total number of laid embryos (brood size).

The percentage of larval lethality was calculated for each brood as the number of dead L1 larvae/total number of laid embryos (brood size). Percentages are averages of >10 broods. See Table 3 for brood sizes.

The percentage of viable adults was determined as the number of viable adults/total number of laid embryos and is the average of >10 broods. Expected percentages of F1 genotypes were observed in each brood.

-Self-progeny from dpy-19(e1259) unc-32(e189) glp-1(oz112gf)/unc-32(e189) glp-1(q175) (n=15).

-Self-progeny from dpy-19(e1259) unc-32(e189) glp-1(oz112gf)/unc-32(e189) mau-3(rb169) (n=13).

-Cross progeny generated from mating single oz112gf/+ males to fog-3(q443) females (n=13) (Ellis and Kimble, 1995). Brood sizes were determined as described in footnote "a" except single L4 unc-32(e189) glp-1(oz112gf)+/+ males (generated from outcrossing unc-32(e189) glp-1(oz112gf)/unc-32(e189) glp-1(q175) hermaphrodites to N2 males) were mated to single adult fog-3 females. The oz112gf/+ male parental phenotype can be distinguished by dissecting scope. Embryos were picked to fresh plates every 12 hours. Embryonic, larval and adult viabilities were determined as described in "a".

Progressive expansion of the distal mitotic region results in a late-onset tumorous phenotype

In glp-1(oz112gf) hemizygous hermaphrodites grown at 15°C and 20°C, 100% of gonad arms (n=500) develop a late-onset tumorous germ-line phenotype (Fig. 5A). We suspected that the late-onset tumorous phenotype might arise from a progressive enlargement of the distal mitotic region caused by a failure of germ cells in the adult to exit the mitotic cell cycle. We therefore determined the size of the distal mitotic region as a function of time in both wild-type and glp-1(oz112gf) hemizygotes. In wild-type adult hermaphrodites, the distal mitotic zone is maintained at ~24 cell diameters in length (Crittenden et al., 1994). Normal distal/proximal germ-line polarity is initially established in glp-1(oz112gfnull) hermaphrodites (data not shown) with the distal mitotic zone averaging ~26 cell diameters in length at 45 hours after hatching (late L4, 20°C). However, the distal mitotic zone expands to ~37 cell diameters by 50 hours (young adult), and to more than 65 cell diameters by 70 hours after hatching (Fig. 5B). In older adults, to proliferate as evidenced by mitotic figures. This result supports the idea that glp-1(oz112gf) tumors arise from a failure of germ cells to exit from the mitotic cycle.

Table 3. glp-1(oz112gf) acts as a genetic hypermorph

<table>
<thead>
<tr>
<th>Genotype</th>
<th>No. of germ cells in meiotic pathway</th>
<th>Range</th>
<th>ab</th>
<th>Brood size</th>
</tr>
</thead>
<tbody>
<tr>
<td>a</td>
<td>396±12*</td>
<td>384-408</td>
<td>7</td>
<td>ND</td>
</tr>
<tr>
<td>b</td>
<td>206±19*</td>
<td>187-238</td>
<td>7</td>
<td>77±26*</td>
</tr>
<tr>
<td>c</td>
<td>180±28*</td>
<td>142-210</td>
<td>6</td>
<td>48±30*</td>
</tr>
<tr>
<td>d</td>
<td>105±11*</td>
<td>92-121</td>
<td>6</td>
<td>6 Sterile</td>
</tr>
<tr>
<td>e</td>
<td>23±10*</td>
<td>10-47</td>
<td>7</td>
<td>Sterile</td>
</tr>
</tbody>
</table>

*Young adults (56 hours after hatching at 20°C) were fixed and stained with DAPI as described by Francis et al. (1995a). The number of nuclei in the meiotic pathway were calculated as the total number of sperm (divided by four), primary spermatocytes, oocytes and nuclei in pachytene of meiosis. Each arm was counted two times and the numbers averaged.

-Number of gonad arms examined. One gonad arm/animal was counted.

-Brood size is the number of laid eggs and is the average of 15 broods. L4 hermaphrodites (genotype: dpy-19(e1259) unc-32(e189) glp-1(oz112gf)/unc-32(e189) glp-1(q175); or dpy-19(e1259) unc-32(e189) glp-1(oz112gf)/unc-32(e189) mau-3(rb169)) were cloned on Petri plates at 20°C. Hermaphrodites were transferred every 12 hours and the number of laid eggs were counted.

-Brood size was used as another measure of the tumorous phenotype, since ectopic proliferation occurs at the expense of gamete formation. For oz112gfnull and oz112gf+/+ strains, there was a significant difference in brood sizes supporting the hypothesis glp-1(oz112gf) acts as a genetic hypermorph.

-Unc-32 self-progeny from unc-32(e189) unc-36(e251) glp-1(q175).

-Unc-32 non-Dpy self-progeny from dpy-19(e1259) unc-32(e189) glp-1(oz112gf)/unc-32(e189) glp-1(q175).

-Unc non-Dpy self-progeny from dpy-19(e1259) unc-32(e189) glp-1(oz112gf)/unc-32(e189) mau-3(rb169).

-Unc-32 self-progeny from unc-32(e189) glp-1(oz112gf)/unc-36(e251) glp-1(q175).

-Unc non-Dpy self-progeny from dpy-19(e1259) unc-32(e189) glp-1(oz112gf)/dpypy-19(e1259) glp-1(q172); qDp3.

-nnn For the indicated pairs, values are significantly different (>95%, t-test).

Fig. 4. glp-1(oz112gf/oz112gf+/+) germline cells never leave the mitotic cell cycle. Synchronized wild-type (unc-32) and dpy-19 unc-32 glp-1(oz112gf); qDp3 hermaphrodite larvae were examined at 1-2 hour intervals by DAPI staining for the presence of proximal pachytene nuclei. The ordinate represents the fraction of gonad arms at each time point with pachytene nuclei (n=8).
germ-line tumors arises by a progressive expansion of the distal mitotic region. (A) Dissected gonad stained with DAPI shows the late-onset tumorous phenotype (surface view). Note the distal mitotic zone is expanded to approximately 50 cell diameters (arrows indicate mitotic nuclei) which is followed by the transition zone (Trans), the pachytene region and germ cells undergoing spermatogenesis. Scale bar, 10 μm. (B) Plot of the size of the distal mitotic region as a function of time. Gonad arms (n=20) from synchronized wild-type [unc-32; unc-36; glp-1(q175)] and hemizygotes [unc-32; glp-1(oz112gf); unc-36; glp-1(q175)] were dissected and stained with DAPI at the indicated time. The relative distal-proximal position of mitotic figures, the transition zone and the pachytene region was determined. The size of the distal mitotic zone was the average position (cell diameters from the DTC) of the most proximal mitotic figure (only gonad arms with continuous mitotic regions are included). Error bar represents ± one standard deviation.

the germ line can consist solely of proliferating cells. The expansion of the distal mitotic zone in adult oz112gf hemizygotes is consistent with a progressive failure of germ cells to exit the mitotic cycle after distal-mitotic/proximal-meiotic germ-line polarity is initially established.

While 100% of glp-1(oz112gf) null animals have the late-onset tumorous phenotype, only 1% display proximal proliferation (where the most proximal germ cells fail to enter meiotic prophase during larval development while more distal germ cells enter meiosis normally (Table 1; Seymour et al., 1990)). This preferential disruption of the decision to proliferate versus enter meiotic prophase during adulthood rather than during larval development suggests that downregulation of glp-1 signalling in larval and adult germ cells may differ qualitatively.

GLP-1(oz112gf) receptor signals constitutively

Two methods were used to examine whether the GLP-1(oz112gf) receptor requires ligand to promote proliferation. First, a laser microbeam was used to ablate the DTC, the somatic cell that produces the ligand (Kimble and White, 1981). Second, double mutants were constructed with lag-2, the gene that encodes the DTC proliferative signal (Tax et al., 1994; Henderson et al., 1994). If the oz112gf receptor acts independently of the DTC ligand, then removal of the signal will not affect the tumorous phenotype. In contrast, if the oz112gf receptor requires ligand, then removal of the signal should eliminate the tumorous phenotype.

Germ cells continue to proliferate in glp-1(oz112gf), but not wild-type, following ablation of either the DTC during the L3 stage (Fig. 6) or the DTC precursors during L1 (Table 4). glp-1(oz112gf) is epistatic to lag-2(q420) [a germ-line proliferation defective, glp-1(0)]-like phenotype] and the putative null lag-2(q411) [L1 lethal phenotype] (Lambie and Kimble, 1991b; Henderson et al., 1994); both double mutants are tumorous
Table 5. Constitutively active glp-1(oz112gf) suppresses mutations in lag-2, but not lag-1

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Phenotypea</th>
</tr>
</thead>
<tbody>
<tr>
<td>lag-2(q420)</td>
<td>Glp(1f)-like sterile</td>
</tr>
<tr>
<td>glp-1(e122gf); lag-2(q420)</td>
<td>Tumorous</td>
</tr>
<tr>
<td>lag-2(q411f)</td>
<td>L1 lethal</td>
</tr>
<tr>
<td>glp-1(e122gf); lag-2(q411f)</td>
<td>Tumorous</td>
</tr>
<tr>
<td>lag-1(q416 or q420)</td>
<td>Glp(1f)-like sterile</td>
</tr>
<tr>
<td>glp-1(e122gf); lag-1(q416 or q426)</td>
<td>L1 lethal</td>
</tr>
<tr>
<td>lag-1(q585f)</td>
<td>L1 lethal</td>
</tr>
<tr>
<td>glp-1(e122gf); lag-1(q585f)</td>
<td>L1 lethal</td>
</tr>
</tbody>
</table>

*Phenotypes were analyzed at 25°C where the glp-1(oz112gf) tumorous phenotype is most severe. Phenotypes were determined using a dissecting scope and vented by Nomarski optics. Genotypes of the parental strains were confirmed by outcrossing and recovering the appropriate phenotypes.

1 Unc-32 self-progeny from unc-32(e189)y(t1; lag-2(q420); eT1) 100% of examined unc-32 glp-1(oz112gf); lag-2(q420) animals were tumorous (n=25).
3 Unc-32 self-progeny from unc-32(e189) glp-1(e122gf); eT1; lag-2(q420); eT1 100% of examined unc-32 glp-1(oz112gf); lag-2(q420) animals were tumorous (n=25).
4 Described by Henderson et al. (1994) as putative lag-2-null.
5 Dpy-unc self-progeny from dpy-19(e1259) unc-32(e189) glp-1(e122gf) glp-1(oz112gf); eT1; lag-2(q420); eT1 100% of examined dpy-unc animals (genotype: dpy-19 unc-32 glp-1(e122gf); lag-2(q411f)) were tumorous (n=25).
6 Germ line phenotype was analyzed at 20°C.
7 Unc-32 unc-24 self-progeny from unc-32(e189) unc-36(e251); unc-24(e133) lag-1(q416 or q420); f(h6); eT1.
8 Unc-32 unc-24 self-progeny from unc-32(e189) glp-1(oc112gf) unc-36(e251); unc-24(e133) lag-1(q416 or q420); f(h6); eT1. The double Unc-32 unc-24 phenotype was difficult to distinguish from Unc-24 alone. Thus germ line phenotypes of all Unc-32-like progeny were examined with 25% expected to have the desired genotype: unc-32(e189) glp-1(oc112gf); unc-24(e133) lag-1(q416 or q420). Of the 95 examined animals, 27% had a Glp(lf)-like sterile phenotype while 73% were tumorous.
9 Self-progeny from unc-44(e1260) lag-1(q585f); deb-1(st385) (Williams et al., 1992).
10 Self-progeny from glp-1(oz112gf) unc-36(e251); unc-44(e1260) lag-1(q585f); deb-1(st385).
11 Presumed lethal since no viable unc-44 [glp-1(oc112gf); unc-44(e1260) lag-1(q585f)] animals were observed in >100 broods.

*Fig. 6. DTC (ligand) independence of germ-line proliferation in glp-1(oz112gf). One DTC per wild-type (unc-32) or unc-32 glp-1(oz112gf) hermaphrodite was ablated with a laser microbeam at 21-22 hours post-hatching (mid-L3). The ablated gonad arms were examined at the indicated times by DAPI staining for the presence of distal pachytene nuclei. The ordinate represents the fraction of ablated gonad arms at each time point with distal pachytene nuclei (n=77).

Fig. 7. Ectopic expression of GLP-1 in glp-1(oz112gf) germ lines. Dissected gonad arms from (A) a wild-type adult (unc-32) and (B) a homozygous unc-32 glp-1(oz112gf) young adult (grown at 25°C) were stained with anti-GLP-1 antibody (Crittenden et al., 1994). Alkaline-phosphatase-conjugated secondary antibody was used to visualize GLP-1 staining. GLP-1 is spatially restricted to the distal mitotic region of wild type, but found throughout the tumorous germ line in glp-1(oz112gf). The spermathecal (Sp) staining, which outlines cell boundaries, is also seen in control animals incubated with the alkaline-phosphatase-conjugated secondary antibody alone. Scale bar, 10 μm.
GLP-1 is ectopically expressed in glp-1(oz112gf)

hermaphrodites

In wild-type animals, Crittenden et al. (1994) demonstrated GLP-1 accumulation correlates with proliferation (Fig. 7A). Consistent with this observation, we find that GLP-1 accumulates throughout the tumorous germ lines of glp-1(oz112gf) animals (Fig. 7B). In addition, hemizygous glp-1(oz112gf) hermaphrodites were also stained with anti-GLP-1 antibody to determine whether GLP-1 accumulates in an expanded region in animals with enlarged distal mitotic zones. GLP-1 accumulation is expanded but remains correlated with proliferation in the late-onset tumors (data not shown).

glp-1(oz112gf) hermaphrodites have a somatic

multivulva phenotype

In addition to a tumorous germ line, glp-1(oz112gf) hermaphrodites and males exhibit a semi-dominant multivulva (Muv) phenotype (Greenwald et al., 1983). The Muv phenotype is incompletely penetrant; 71% of homozygous and 3% of heterozygous glp-1(oz112gf) hermaphrodites have at least one pseudovalve, while 44% of homozygous males have at least one pseudovalve (20°C). To establish the cellular basis of the Muv phenotype, we determined the vulval lineage of three glp-1(oz112gf) hermaphrodites.

Briefly, six vulval precursor cells (VPCs, P3.p-P8.p) all have the potential to give rise to vulval structures. However, due to a complex set of cell-cell interactions that culminate in the specification of the 1°, 2° and 3° cell fates, a vulva is normally formed from the descendants of just three VPCs (P5.p, P6.p and P7.p, Sternberg and Horvitz, 1986). By observing the pattern of cell divisions for each of the VPCs, we found that ectopic 2° lineages were specified in glp-1(oz112gf) hermaphrodites (Table 6).

glp-1 has no essential function in vulval development (Austin and Kimble, 1987), although it appears to be expressed at a low level in the VPCs (Mango et al., 1991). In contrast, the related LIN-12 receptor is required for specification of the vulval lineages (Sulston and Horvitz, 1977).

Table 6. glp-1(oz112gf) vulval cell lineages

<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Wild-type</td>
<td>S</td>
<td>S</td>
<td>L</td>
<td>T</td>
<td>N</td>
<td>TT</td>
</tr>
<tr>
<td>glp-1(oz112gf)</td>
<td>L</td>
<td>L</td>
<td>T</td>
<td>N</td>
<td>TT</td>
<td>TT</td>
</tr>
<tr>
<td></td>
<td>S</td>
<td>S</td>
<td>L</td>
<td>T</td>
<td>N</td>
<td>TT</td>
</tr>
<tr>
<td></td>
<td>S</td>
<td>S</td>
<td>TT</td>
<td>TT</td>
<td>N</td>
<td>TT</td>
</tr>
</tbody>
</table>

*The complete vulval lineage (Sulston and Horvitz, 1977) of three homozygous unc-32(e189) glp-1(oz112gf) hermaphrodites grown at 25°C was determined. Animals were recovered after lineageing and maintained at 25°C to verify that P5.p, P6.p and P7.p differentiated normally. Similar results were obtained from partial lineages of additional animals. Specification of the P8.p lineage as secondary was also observed, but less frequently (data not shown). 

**Nomenclature adapted from Sternberg and Horvitz (1986, 1989). S (joins hypodermal syncytium), L (longitudinal division), T (transverse division) and N (no division) refer to vulval cell types. Vulval cells are generated by both the 1° lineage (LTTT) and the 2° lineage (LTTNT) or (NNTL), sometimes (LTTT) and (TTLT) are generated and are equivalent; L adherence to the ventral cuticle is an important criterion for distinguishing 2° vulval cell types. [S] S differentiates as 3°.

2° cell fate. Moreover, ligand-independent lin-12(gf) mutations cause inappropriate specification of secondary cell fates and a multivulva phenotype (Greenwald et al., 1983) similar to glp-1(oz112gf). The GLP-1 and LIN-12 receptors are interchangeable in all developmental decisions that have been analyzed to date (Mango et al., 1991; Fitzgerald et al., 1993; Roehl and Kimble, 1993). Therefore, ligand-independent hyperactive glp-1(oz112gf) is likely to be activating signal transduction machinery in the VPCs that would normally respond to LIN-12.

**DISCUSSION**

We have characterized a novel glp-1 gain-of-function mutation, oz112gf, that produces tumorous germ-line and multivulva phenotypes. The oz112gf mutation is temperature and dose sensitive and appears to result in constitutive activation of the GLP-1 receptor; germ-line proliferation still occurs in oz112gf mutants following elimination of its ligand. Genetic experiments indicate that the glp-1(oz112gf) mutation results in hyperactive signalling. Increasing the gene dose of glp-1(+) increases the penetrance of the tumorous phenotype, consistent with the hypothesis that the oz112gf mutation causes an elevation of essentially wild-type GLP-1 signalling. Our analysis thus provides strong support for the proposal that the GLP-1 receptor acts as a binary switch (Austin and Kimble, 1987) for the decision between germ-line proliferation versus entry into meiotic prophase: loss of glp-1 activity eliminates germ-line proliferation, while a mutation that activates glp-1 causes proliferation to occur independent of the somatic inductive signal.

**Mutational activation of Notch family receptors**

The molecular lesion responsible for the glp-1(oz112gf) phenotypes is a missense mutation (Ser642Asp) located in the extracellular domain of the Notch receptor (Gröger et al., 1993). The molecular lesion responsible for the glp-1(oz112gf) phenotypes is a missense mutation (Ser642Asp) located in the extracellular domain of the Notch receptor (Gröger et al., 1993). The molecular lesion responsible for the glp-1(oz112gf) phenotypes is a missense mutation (Ser642Asp) located in the extracellular domain of the Notch receptor (Gröger et al., 1993). The molecular lesion responsible for the glp-1(oz112gf) phenotypes is a missense mutation (Ser642Asp) located in the extracellular domain of the Notch receptor (Gröger et al., 1993). The molecular lesion responsible for the glp-1(oz112gf) phenotypes is a missense mutation (Ser642Asp) located in the extracellular domain of the Notch receptor (Gröger et al., 1993). The molecular lesion responsible for the glp-1(oz112gf) phenotypes is a missense mutation (Ser642Asp) located in the extracellular domain of the Notch receptor (Gröger et al., 1993). The molecular lesion responsible for the glp-1(oz112gf) phenotypes is a missense mutation (Ser642Asp) located in the extracellular domain of the Notch receptor (Gröger et al., 1993). The molecular lesion responsible for the glp-1(oz112gf) phenotypes is a missense mutation (Ser642Asp) located in the extracellular domain of the Notch receptor (Gröger et al., 1993). The molecular lesion responsible for the glp-1(oz112gf) phenotypes is a missense mutation (Ser642Asp) located in the extracellular domain of the Notch receptor (Gröger et al., 1993). The molecular lesion responsible for the glp-1(oz112gf) phenotypes is a missense mutation (Ser642Asp) located in the extracellular domain of the Notch receptor (Gröger et al., 1993). The molecular lesion responsible for the glp-1(oz112gf) phenotypes is a missense mutation (Ser642Asp) located in the extracellular domain of the Notch receptor (Gröger et al., 1993). The molecular lesion responsible for the glp-1(oz112gf) phenotypes is a missense mutation (Ser642Asp) located in the extracellular domain of the Notch receptor (Gröger et al., 1993). The molecular lesion responsible for the glp-1(oz112gf) phenotypes is a missense mutation (Ser642Asp) located in the extracellular domain of the Notch receptor (Gröger et al., 1993).
points in the TAN-1 gene which appear to result in the expression of truncated molecules that lack much of the extra-cellular domain (Ellisen et al., 1991). By analogy to the glp-1(oz112gf) germ-line phenotype, activated forms of int-3 and TAN-1 may disrupt the choice between a proliferative cell fate and a more differentiated cell fate. It is noteworthy that the Notch receptor family is the first evolutionarily conserved gene family in which oncogenic activating mutations occur in both vertebrates and invertebrates.

**The cellular origin of the glp-1(oz112gf) tumors**

The glp-1(oz112gf) tumorous phenotype appears to arise from a defect in the proliferative germ cell population. In animals showing a completely tumorous phenotype, proximal germ cells fail to enter the meiotic pathway at the normal time during larval development and distal germ cells greater than 24 cell diameters from the DTC fail to exit the mitotic cell cycle in late larvae and adults. Furthermore, the late-onset tumorous phenotype (hemizygotes and heterozygotes at 20°C) is characterized by a failure of distal germ cells to exit the mitotic cycle in adults after distal-mitotic/proximal-meiotic polarity is established.

The cellular origin of tumors in glp-1(oz112gf) is distinct from that of tumors in the C. elegans gld-1 mutant. Germ cells enter the meiotic pathway normally in gld-1(null) hermaphrodites. However, gld-1(null) germ cells exit pachytene and return to the mitotic cycle resulting in ectopic proliferation (Francis et al., 1995a,b). The difference in cellular origin is reflected in the adult germ-line phenotype: glp-1(oz112gf) homozygotes have germ lines that lack polarity, while gld-1(null) mutants display normal polarity in the distal germ line. Additionally, the glp-1(oz112gf) mutation causes both hermaphrodite and male germ-line tumors, while the gld-1(null) mutation only causes tumors when the germ line is undergoing female development. The sex specificity is consistent with glp-1 functioning to control proliferation in both sexes (Austin and Kimble, 1987) and gld-1 functioning in oocyte development.

Analogous to glp-1(oz112gf), certain germ cell tumors in humans may arise from a defect in the proliferative (premeiotic) germ cell population. Most testicular germ cell tumors are thought to arise from proliferative germ cells (gonocytes), while a low percentage of ovarian teratomas may arise from proliferative germ cells (Skakkebaek et al., 1987; Surti et al., 1990). Currently, the genetic/molecular mechanisms for germ-line tumorigenesis in humans are unknown.

**GLP-1 signalling and the control of GLP-1 expression**

Expression studies have revealed that GLP-1 is spatially restricted to the distal proliferative region in wild-type adult hermaphrodites (Crittenden et al., 1994). Membrane-associated GLP-1 is found at high levels in the proliferating germ cell population (1 to 20 cell diameters from the DTC) then decreases as germ cells stop proliferating and enter meiotic prophase (transition zone) and is virtually absent in the pachytene region. Localization of GLP-1 to the proliferative germ cell population in wild-type hermaphrodites appears to be due in large part to translational control; glp-1 mRNA is found throughout the germ line and reporter RNAs carrying the glp-1 3'UTR are not translated in the proximal germ line (Crittenden et al., 1994; Evans et al., 1994).

GLP-1 protein is expressed ectopically, although still concordant with proliferation, in glp-1(oz112gf) mutants. In fully tumorous homozygotes at 25°C, membrane-associated GLP-1 and proliferating cells are found throughout the germ line while, in adult hemizygotes at 20°C, membrane-associated and GLP-1 is found in an extended region that corresponds to the expanded mitotic zone. How does the oz112gf mutation override the normal spatial control of GLP-1 expression? We do not think that the residue altered in the oz112gf missense mutation has a direct effect on glp-1 transcription or translation. Rather, we believe ectopic GLP-1 accumulation is a secondary effect of ligand-independent signalling and reveals a positive feedback mechanism between GLP-1 signalling (or proliferation) and glp-1 expression.

We propose that the distal proliferative region is maintained in wild-type hermaphrodites by a positive feedback of GLP-1 signalling on glp-1 expression (Fig. 8). Since the spatial restriction of GLP-1 accumulation appears to result from a translational control mechanism, the feedback loop may function at this level. Initially, ligand binding activates GLP-1 signalling, leading to proliferation and increased glp-1 mRNA translation. Increased glp-1 mRNA translation provides more receptor which can respond to ligand. As germ cells move away (proximally) from the localized source of ligand, GLP-1 signalling decreases, leading to reduced receptor production. When signalling by GLP-1 falls below a certain threshold, germ cells exit the mitotic cycle to enter meiotic prophase and glp-1 mRNA translation ceases.Previously, a feedback loop that maintains glp-1 in an active state has been proposed to explain the all-or-none phenotype of certain glp-1(oz1) alleles (Kodoyianni et al., 1992).

A feedback mechanism provides a simple explanation for the correlation of proliferation with ectopic GLP-1 accumulation in both tumorous and late-onset tumorous oz112gf mutants (Fig. 8). In oz112gf mutants, receptor signalling is no longer limited by ligand. In fully tumorous homozygous larvae and adults (25°C), GLP-1 signalling is never down regulated, so proliferation continues and glp-1 mRNA is always translated. As continued translation produces more of the mutationally activated receptor, proliferation is stimulated further.

Since glp-1 mRNA is found throughout the hermaphrodite germ line (Crittenden et al., 1994), the positive feedback loop would appear to act post-transcriptionally. However, it is formally possible that germ-line glp-1 transcription is controlled by two distinct mechanisms, one in proliferative germ cells and a second in meiotic prophase germ cells undergoing oogenesis. A positive transcriptional feedback loop could then function in proliferative germ cells, where glp-1 mRNA translation would be unregulated. In meiotic prophase germ cells, feedback (signalling) independent glp-1 transcription would presumably supply maternal glp-1 mRNA necessary for embryogenesis, while repression of glp-1 translation would be initiated immediately following entry into the meiotic pathway. Ectopic GLP-1 accumulation in tumorous germ lines would occur because germ cells never enter meiotic prophase and would continue to transcribe and translate glp-1 mRNA. Transcriptional feedback loops that amplify the activity of the LIN-12 and GLP-1 pathways have been proposed (Wilkinson et al., 1994; Christensen et al., 1996).

We can not rule out the possibility that the positive feedback loop functions at the level of receptor stability or subcellular...
Localization. However, if the feedback loop did not involve new protein synthesis, one would expect that proximal germ cells in *glp-1(oz112gf)* animals, which are continuing to proliferate, should contain less GLP-1 than distal mitotic cells. In contrast to this prediction, we see uniform high levels of GLP-1 staining throughout the tumorous germ line.

**Implications of cell-type-specific *glp-1(oz112gf)* phenotypes for tumorgenesis in mammals**

In the germ line, mutational activation of GLP-1 causes tumor formation by inappropriate specification of a proliferative stem cell and/or preventing entry into the meiotic pathway. In the ventral epidermis, activated GLP-1 causes a multivulval phenotype by inappropriate specification of a differentiative fate (2° VPC; see Results). Signalling by the GLP-1(oz112gf) receptor is likely to be identical in both cell types since GLP-1 and LIN-12 are interchangeable between cell types (Fitzgerald et al., 1993; Roehl and Kimble, 1993). Thus, other cell-type-specific factors must exist to account for the different phenotypic outcomes.

Certain proto-oncogenes and tumor suppressor genes in mammals are implicated in a somewhat restricted set of tumor types (Bishop, 1991). *glp-1(oz112gf)* may provide a useful model for one of the possible explanations for tissue/cell-type specificity of oncogenic mutations. During multistep tumor formation in mammals, a mutationally activated proto-oncogene may, in one cell type, cause inappropriate specification of a stem cell fate or prevent stem cell differentiation. Such an excess of proliferative stem cells would likely contribute to tumor formation (Sawyers et al., 1991), and is analogous to the excess germ-line proliferation in *glp-1(oz112gf)*. In another cell type, the same activating mutation may cause inappropriate specification of a differentiative fate, analogous to *glp-1(oz112gf)* in VPCs. However, such a change in cell fate would lead to inappropriate differentiation and thus be less likely to have a predisposing effect for tumor formation.

We thank the Kimble lab and Eleanor Maine for *glp-1* primers and especially thank Sarah Crittenden for anti-GLP-1 antibodies. We thank Eleanor Maine, Sarah Crittenden, Sioux Christensen, Kevin Fitzgerald, Andy Fire, Eric Lambie, Kimberly Van Aken and Fran Tax for strains/constructs and communication of data prior to publication; Allan Jones for help with the sequencing; Ross Francis and Jim Waddle for help with the Figures and photography; and Bob Clifford, Sarah Crittenden, Jane Hubbard and Iva Greenwald for comments on the manuscript. The initial phase of this research was funded by a institutional grant from the American Cancer Society, MIN-36-34. This work was funded by US Public Health Service grant HD25614. B. W. was supported by a Lucille P. Markey Special Emphasis in Human Pathobiology postdoctoral fellowship. Some strains used were provided by the Caenorhabditis Stock Center, which is supported by the National Institutes of Health Center for Research Resources.

**REFERENCES**


(Accepted 7 November 1996)