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Analysis of the Multiple Roles of gld-1 in Germline Development: Interactions With the Sex Determination Cascade and the glp-1 Signaling Pathway

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ABSTRACT

The Caenorhabditis elegans gene gld-1 is essential for oocyte development; in gld-1 (null) hermaphrodites, a tumor forms where oogenesis would normally occur. We use genetic epistasis analysis to demonstrate that tumor formation is dependent on the sexual fate of the germline. When the germline sex determination pathway is set in the female mode (terminal fem/fog genes inactive), gld-1 (null) germ cells exit meiotic prophase and proliferate to form a tumor, but when the pathway is set in the male mode, they develop into sperm. We conclude that the gld-1 (null) phenotype is cell-type specific and that gld-1 (+) acts at the end of the cascade to direct oogenesis. We also use cell ablation and epistasis analysis to examine the dependence of tumor formation on the glp-1 signaling pathway. Although glp-1 activity promotes tumor growth, it is not essential for tumor formation by gld-1 (null) germ cells. These data also reveal that gld-1 (+) plays a nonessential (and sex nonspecific) role in regulating germ cell proliferation before their entry into meiosis. Thus gld-1 (+) may negatively regulate proliferation at two distinct points in germ cell development: before entry into meiotic prophase in both sexes (nonessential premeiotic gld-1 function) and during meiotic prophase when the sex determination pathway is set in the female mode (essential meiotic gld-1 function).

OOCYGENESIS in multicellular animals represents a complex developmental program in which the meiotic nuclear cycle and gametogenesis are coordinated to produce a functional oocyte. In the preceding paper, we describe the Caenorhabditis elegans gene gld-1 (FRANCIS et al. 1995). The genetic and phenotypic properties of gld-1 argue that it is a tumor suppressor gene that regulates oocyte development. Mutations that eliminate gld-1 function abolish oogenesis in the hermaphrodite and result in the formation of a germline tumor. Germ cells that give rise to the tumor complete the early stages of meiotic prophase but then exit pachytene and return to a mitotic cycle. These cells subsequently undergo repeated rounds of ectopic proliferation, giving rise to a tumor that fills much of the germline. Tumor formation is a sex-specific phenotype, as gld-1 (null) males show no abnormalities in germline development. Further, gld-1 has no essential function in the soma.

The sex specificity of the gld-1 tumorous phenotype has led to the proposal that gld-1 (+) may act as an important regulator of oocyte development (FRANCIS et al. 1995). Tumor formation would then result from a failure of oocyte determination and/or female meiotic prophase progression that allows germ cells to return to mitosis. Data available at present, however, do not exclude the possibility that tumors result from an intersexual mode of differentiation. Ovarian tumors in certain Drosophila mutants are comprised of germ cells with intersexual traits (BAE et al. 1994; J. HORABIN, personal communication). In this report, we investigate the basis of the sex-specific tumorous phenotype using genetic epistasis analysis. By constructing mutant combinations with gld-1 (null) and the sex determination genes, we ask whether tumor formation is specifically correlated with the female sexual fate in the germline. The cumulative results suggest that gld-1 (+) acts downstream of all known sex determination genes to either specify the oocyte fate or direct oocyte differentiation.

We also use genetic epistasis to investigate a second previously inferred role of gld-1 in germline development (FRANCIS et al. 1995). Although gld-1 has no essential role in male germline development, it acts to promote spermatogenesis in the hermaphrodite germline. For several reasons, we are unable to investigate this aspect of gld-1 function using a null gld-1 allele. Therefore epistasis tests are done with two classes of gain-of-function alleles that cause transformations in sexual fate in the hermaphrodite germline. The data obtained are consistent with the proposal that gld-1 (+) promotes spermatogenesis by assisting a set of sex determination loci that specify the male fate.

Finally, we examine whether germ cell proliferation in gld-1 (null) hermaphrodites is under the same controls that regulate proliferation in the wild-type germine. Previous work has shown that germ cell prolifer-
tion depends on the gene glp-1, which encodes a transmembrane protein belonging to the lin-12/Notch family of receptor molecules (Austin and Kimble 1987, 1989; Yokem and Greenwald 1989). glp-1 protein acts as the likely receptor for a somatically derived signal that induces germ cell proliferation (Austin and Kimble 1987; Crittenden et al. 1994). We examine the dependence of germ cell proliferation in gld-1 (null) mutants on the glp-1-mediated signaling pathway in two types of experiments: by ablating certain sets of somatic cells to eliminate the somatic signals and by analysis of mutant combinations to eliminate the germline receptor. These experiments confirm the meiotic prophase origin of the tumorous phenotype and indicate that gld-1 (+) has an additional, nonessential and/or redundant function in negatively regulating proliferation of germ cells before their entry into the meiotic pathway.

**MATERIALS AND METHODS**

**Nematode culture and strains**

General methods for *C. elegans* culture and genetic manipulation were as described (Brenner 1974; Sulston and Hodgkin 1988). Experiments were done at 20°C unless otherwise noted. *C. elegans* nomenclature follows Horvitz et al. (1979). If is used for loss-of-function, 0 is used for a null allele that has been shown to fail to produce a gene product, g is used for gain-of-function, glp-1(Tum) is used to identify alleles with a tumorous X Germ line (Tum) phenotype, glp-1 (Fog) is used to identify alleles with a feminization of the germ line (Fog) phenotype and glp-1 (Mog) is used to identify alleles with a masculinization of the germ line (Mog) phenotype. Maternal and zygotic genotypes are indicated using the notation m− or z−, where m represents the maternal genotype and z the zygotic genotype. All nematode strains used in this work are derived from the wild-type *C. elegans* var. Bristol isolate N2. The following genes and mutations, described in Hodgkin et al. (1988), the *C. elegans* genetic map (J. Hodgkin, R. Durbin and M. O’Callaghan, personal communication) or the cited references, were used:

**LGI:** fog-1(q180 and q187) (Barton and Kimble 1990), unc-11(e127), dpy-5(e61), dpy-14(e188), unc-13(e51 and e1091), glp-1 (all alleles) (Francis et al. 1995), fog-3(q443) (Ellis and Kimble 1995).

**LGII:** dpy-10(e128), tra-2(e1095), tra-2(q122g) (Schedl and Kimble 1988), unc-4(e120).

**LGIII:** fem-2(e2105), fog-1(q370) (Graham and Kimble 1998), unc-69(e587), tra-1(e1834) and tra-1(e1572g) (Hodgkin 1987), unc-32(e89), glp-1[see text and Table 4, all described in Austin and Kimble (1987) and/or Kodovanni et al. (1992)].

**LGV:** dpy-13(e458sd), fem-1(e1991, 2003ts), unc-5(e53), unc-24(e138), fem-3(e1996), fem-3(q20gf and q59gf) (Barton et al. 1987), dpy-20(e1282), tra-3(e107), tra-3(bn75) (E. Capowski, B. Brenza and S. Stromme, personal communication).

**LGX:** her-1(y101lu1), unc-42(e270), fog-2(q71).

**Rearrangements:** hT2(1)[il-4]; hT2(III)[dpy-18] (McKim et al. 1992), nDp4(1;V) (McKim et al. 1992).

**Construction of double mutants between gld-1 alleles and mutations in the sex determination pathway**

Tables 1 and 2 describe the phenotypes of double or triple mutants made between gld-1(Tum, Fog or Mog) alleles and mutations in the major sex determination loci. Except where noted below, all doubles requiring a gld-1(Tum) allele were made both with the null allele q485 and with the strong alleles q268; identical phenotypes were observed in double mutants containing these gld-1(Tum) alleles. In many constructions, gld-1 alleles were marked with unc-13, which lies ~0.2 map units to the left of gld-1 (Francis et al. 1995). In cases where the progeny segregating from a balanced strain were analyzed, the genotype of the balanced strain was verified by complementation tests. For mutations in the sex determination genes, we use + to indicate that the allele is putative null or strong loss-of-function. Other types of alleles are indicated. At least 50 animals of the appropriate genotype were examined for each double or triple mutant constructed.

**fog-1(If) gld-1(Tum or Mog):** Double mutants of fog-1(If) allele q180 were made using each of three gld-1(Tum) alleles (q268, q265 and q485), as well as each of three gld-1(Mog) alleles (e130, e30 and q93). To make recombinant fog-1 unc-13 gld-1 chromosomally, we picked female Unc-13 nonDpy-5 recombinants segregating from fog-1(q180) dpy-5 unc-13/unc-13 gld-1(Tum or Mog) hermaphrodites. The resulting fog-1 unc-13 gld-1 chromosomes were maintained balanced over hT2. Double mutants between a second fog-1 allele (q187) and two gld-1(Tum) alleles (q268 and q365) and the Mog allele q93 were constructed by picking nonUnc-11 female progeny segregating from fog-1 unc-11/unc-13 gld-1 hermaphrodites; the recombinant chromosome was balanced over hT2. fog-1 unc-13 gld-1 X0 males were generated by crossing fog-1 unc-13 gld-1 hT2 or + males to fog-1 unc-13 gld-1 hT2 hermaphrodites.

**glD-1(Tum or Mog) fog-3(If):** Double mutants with fog-3(If) were constructed using fog-3(q443) and the gld-1 tumorous allele q485 and the Mog allele q93. Recombinant unc-13 gld-1 fog-3 chromosomes were generated by picking recombinant nonUnc nonDpy females segregating from unc-13 gld-1 dpy-14 fog-3(If) hermaphrodites. Balanced unc-13 gld-1 fog-3 hT2 strains were used as the source of homozygous unc-13 gld-1 fog-3 animals. Males of the same genotype were generated by crossing unc-13 fog-3 hT2(1) [dpy-18] males with unc-13 gld-1(If) females (Barton and Kimble 1990).

**fog-1(If) glD-1(Tum) fog-3(If):** A balanced triply mutant strain of the genotype fog-1(If) q180 unc-13 gld-1(If) q485 fog-3(If) hT2 was constructed as follows. Self-progeny of heterozygous fog-1 dpy-5/unc-13 gld-1 fog-3 hermaphrodites were screened for female recombinants that were nonDpy-5 and nonUnc-13. To identify recombinant females of the desired genotype (fog-1 unc-13 gld-1 fog-3/dpy-5), resulting from recombination in the fog-1 dpy-5 interval), single females were crossed with unc-13/hT2 males. Only animals heterozygous for a recombinant fog-1 unc-13 gld-1 fog-3 chromosome produced X 0 Unc-13 male progeny (genotype fog-1 unc-13 gld-1 fog-3/unc-13) that display the semidominant fog-1+/+ male germine phenotype (production of sperm and then oocysts) (Barton and Kimble 1990). For these females that segregated such males, single XX L4 cross-progeny were picked on individual plates to identify candidate fog-1 gld-1 unc-13 fog-3/hT2 strains. Genotypes of these balanced strains were confirmed by using complementation tests to show that each was heterozygous for fog-1(If), gld-1(Tum) and fog-3(If).

**fog-1(If) fog-3(If):** X Animals of the genotype fog-1(If) q180 unc-13 fog-3(q443) were obtained from a balanced fog-1 unc-13 fog-3/hT2 hermaphrodite strain constructed as follows. NonUnc nonDpy female recombinants segregating from fog-1 dpy-5/unc-13 fog-3 hermaphrodites were picked and crossed individually to hT2/unc-13 males. Recombinant females of
the desired genotype (fog-1 unc-13 fog-3/fog-1 dpy-5) were identified based on their segregation of X0 Unc-13 male cross-progeny (genotype fog-1 unc-13 fog-3/unc-13) that display the semidominant fog-1/+ male phenotype (production of sperm and then oocytes). From such crosses, single non-Unc-13 XX cross-progeny were picked onto separate plates to identify candidate fog-1 unc-13 fog-3/HT2 animals. The genotypes of three independently isolated strains were then confirmed by showing that each carried mutations that fail to complement fog-1 and fog-3 mutations. Like fog-1 and fog-3 single mutants, XX and X0 fog-1 unc-13 fog-3 animals have germ lines that make only oocytes and show no obvious defects in proliferation or meiotic development.

gld-1 (Tum or Mog); fem-1 (e1991), an amber allele (DONACH and HODGKIN 1984), was used for the construction of double mutants with gld-1 (Tum) alleles (q268 and q268) and with gld-1(q93). Approximately 25% of the Unc-24 self-progeny of gld-1 (Tum)/+; fem-1 unc-24/+ hermaphrodites were Tum, indicating gld-1 (Tum) is epistatic to fem-1. Construction of unc-13 gld-1 (Mog); fem-1 unc-24 animals was facilitated by the property that fem-1 XX animals produced by fem-1/+ mothers are often self-fertile hermaphrodites owing to maternal rescue. Therefore, Unc-24 hermaphrodites segregating from unc-13 gld-1 (Mog)/+; fem-1 unc-24/+ mothers were picked onto separate plates. Some hermaphrodites segregated broods consisting of three females Unc-24 and one fourth sterile Unc-15 animals (unc-15 is epistatic to unc-24) of the genotype unc-13 gld-1 (q93)/fem-1 unc-24. Heterozygosity for gld-1 (q93) appears to increase the fraction of XX females (m+/+; z(+/−)) animals that make sperm, but this effect was not quantitated.

gld-1 (Tum or Mog); fem-2 (e1996) or female allele (HODGKIN 1986). Hermaphrodites segregating from unc-13 gld-1 (Tum or Mog)/+; fem-2/+ mothers were picked onto separate plates. Maternally rescued unc-13 gld-1/+; fem-2 hermaphrodites segregated a 3:1 ratio of nonUnc females and sterile Unc-15 progeny of the genotype unc-13 gld-1 (Tum or Mog); fem-2/+. Females were UnSexual, and in females, the unc-24 allele was essential.

gld-1 (Tum); fem-3 (e1996) or female allele (HODGKIN 1986; AHRINGER et al. 1992). Approximately one fourth of the Unc-24 progeny of gld-1 (Tum)/+; unc-24 fem-3 XX animals had a Tum germline. To generate X0 gld-1 (Tum)/+; fem-3 (e1996) single mutant, these animals were crossed to fem-1 unc-24 dpy-5 males with the property that fem-1 unc-24 dpy-5 animals make sperm, but these also are often self-fertile hermaphrodites owing to maternal rescue. Therefore, Unc-24 hermaphrodites segregating from fem-1 unc-24 dpy-5/+; fem-3 (e1996)/+ mothers were picked onto separate plates. Some hermaphrodites segregated broods consisting of three fourths female Unc-24 and one fourth sterile Unc-15 animals (unc-15 is epistatic to unc-24) of the genotype fem-3 (e1996)/fem-1 unc-24. Heterozygosity for fem-3 (e1996) appears to increase the fraction of XX fem-3 (m+/+; z(+/−)) animals that make sperm, but this effect was not quantitated.

gld-1 (Tum); tra-1 (e1984), a deletion allele that removes most of the tra-1 coding region (TRENT et al. 1991). To generate XX gld-1 (q485); tra-1 (e1834) heterozygous gld-1 (Tum)/+; tra-1 (e1834) hermaphrodites were made and allowed to self. Approximately one fourth of the Unc-42 self-progeny had a Tum germline. To make X0 gld-1 (q485); tra-1 (e1834) hermaphrodites, X0 males of the genotype gld-1 (Tum)/+; tra-1 (e1834) were crossed to gld-1 (Tum)/+; dpy-11 hermaphrodites. NonDpy-11 Unc-42 Lon-2 animals, which must be X0 crossover, were picked and scored for their germline phenotype. Approximately one fourth of the Unc-42 Lon-2 animals were Tum.

gld-1 (Tum); tra-2 (e1575gf), a deletion allele that removes most of the tra-1 coding region (ZARKOWER and HODGKIN 1992), was used to construct a gld-1 (q485); tra-1 (e1575gf) double mutant. unc-13 gld-1 (Tum)/+; tra-1 (e1575gf)/+ XX heterozygotes were constructed and their Unc-13 self-progeny with a male soma [of the genotype unc-13 gld-1 (Tum); tra-1 (e1575gf)] were examined. Like the tra-1 (e1575gf) single mutant, these animals have a completely male nongonadal soma and a gonadal soma that is sometimes male and sometimes morphologically abnormal. Germine phenotypes were scored only in animals whose somatic gonad showed no obvious morphologically abnormal.

gld-1 (Tum); tra-3 (e1984), a deletion allele that removes most of the tra-1 coding region (ZARKOWER and HODGKIN 1992), was used to construct a gld-1 (q485); tra-3 (e1984) double mutant. unc-13 gld-1 (Tum)/+; tra-3 (e1984)/+ XX heterozygotes were constructed and their Unc-13 self-progeny with a male soma [of the genotype unc-13 gld-1 (Tum); tra-3 (e1984)] were examined. Like the tra-3 (e1984) single mutant, these animals have a completely male nongonadal soma and a gonadal soma that is sometimes male and sometimes morphologically abnormal. Germine phenotypes were scored only in animals whose somatic gonad showed no obvious morphologically abnormal.

gld-1 (Tum); tra-1 (e1575gf); tra-2 (e1834), a deletion allele that removes most of the tra-1 coding region (ZARKOWER and HODGKIN 1992), was used to construct a gld-1 (q485); tra-1 (e1575gf); tra-2 (e1834) double mutant. unc-13 gld-1 (Tum); tra-1 (e1575gf); tra-2 (e1834)/+ XX heterozygotes were constructed and their Unc-13 self-progeny with a male soma [of the genotype unc-13 gld-1 (Tum); tra-1 (e1575gf); tra-2 (e1834)] were examined. Like the tra-1 (e1575gf); tra-2 (e1834) single mutants, these animals have a completely male nongonadal soma and a gonadal soma that is sometimes male and sometimes morphologically abnormal. Germine phenotypes were scored only in animals whose somatic gonad showed no obvious morphologically abnormal.
grown at 15°C usually was subtracted from 100 to estimate the percentage of which should be homozygous for sperm and oocytes (BARTON). To obtain an estimate (7%) of the fraction of animals grown at 25°C, we first generated with a female soma, one fourth had a Tum germline. In contrast, all X0 unc-4 tra-2(gf) animals had a normal male germline.

gld-1 (Tum);tra-3(gf): Double mutants of gld-1(q485) were constructed with two tra-3 alleles, el107 and bn75. el107 is an amber allele that transforms XX tra-3 [m(−/−) z(−/−)] animals grown at 25°C into pseudomales that have a partially masculinized soma and germline (HODGKIN 1980). bn75 is an unusual temperature-sensitive tra-3 allele; it has no major effect on the XX female soma but masculinizes the germline more strongly than do tra-3 amber alleles (E. CAPOWSKI, B. BRENDZA and S. STROME, personal communication). The phenotype of double mutants with both tra-3 alleles were analyzed at 25°C. We first generated XX unc-13 gld-1(q485)+/;tra-3 [m(−/−) z(−/−)] animals that, owing to maternal rescue by tra-3(+), activity, are self-fertile hermaphrodites. These segregated one fourth Unc-13 animals that are genotypically unc-13 gld-1(Tum);tra-3.

gld-1 (Tum);mog-1 (gf): The XX gld-1(q485);mog-1(q270) double mutant was examined at 25°C, the temperature at which the mog-1(gf) phenotype is strongest (GRAHAM and KIMBLE 1990). Starting with gld-1 (Tum)+;mog-1 unc-69/+ hermaphrodites, we scored all XX mog-1 unc-69 self-progeny, one fourth of which should be homozygous for gld-1 (Tum). For the data in Table 1, the percentage of total mog-1 unc-69 animals that showed ectopic germline proliferation was multiplied by four to obtain an estimate (7%) of the fraction of gld-1 (Tum);mog-1 unc-69 animals with ectopic proliferation. This number was subtracted from 100 to estimate the percentage gld-1 (Tum);mog-1 unc-69 animals with a Mog phenotype like that of the mog-1 single mutant (i.e., excess sperm, no ectopic proliferation).

gld-1 (Tum);fem-3(gf): The fem-3(gf) alleles q20gf and q95gf confer a temperature-sensitive Mog phenotype in which animals grown at 25°C produce only sperm, whereas animals grown at 15°C usually (q20gf) or sometimes (q95gf) make both sperm and oocytes (BARTON et al. 1987). Double mutants of fem-3(q20gf and q95gf) with gld-1(q485) and q365) were obtained from strains of the genotype unc-13 gld-1(Tum);fem-3(gf);ndp4/+ that were maintained at 15°C. These strains were made by first constructing unc-13 gld-1(Tum)+;fem-3(gf)/dpd-20;ndp4/+ heterozygotes at 15°C. Starting with these heterozygotes, we first identified unc-13 gld-1(Tum);ndp4/+ hermaphrodites based on their segregation of ~55% Tum animals. Animals homozygous for fem-3(gf) were identified by following elimination of dpd-20. For the data in Figure 1 and Table 1, unc-13 gld-1(Tum);fem-3(gf) XX animals were picked as newly hatched L1 larvae and grown for 58 hr at 25°C.

Dominant suppression of fog-2(gf) and tra-2(gf) mutations by a gld-1 (Mog) allele

The gld-1 (Mog) allele q93 was shown to dominantly suppress the female self-sterile phenotypes of XX fog-2(q71) and XX tra-2(q122gf) animals. For fog-2(q71), XX unc-13 gld-1(q93)+;fog-2(q71) rol-9 animals are hermaphrodites in contrast to fog-2(q71) animals, which are always female. However, XX unc-13 gld-1(q93);fog-2 rol-9 homozygotes have a Mog phenotype like that of XX unc-13 gld-1(q93) animals, showing that gld-1(q93) is epistatic to fog-2(gf). Therefore gld-1(q93) cannot masculinize the XX germline by acting through fog-2(+).

Dominant suppression of tra-2(gf) by gld-1(q93) was demonstrated by showing that XX unc-13 gld-1(q93)/+;tra-2(gf) animals are self-fertile hermaphrodites instead of females. These hermaphrodites segregate sterile unc-13 gld-1 (Mog);tra-2(gf) progeny that first make sperm and then undifferentiated germ cells.

Double mutants with the gld-1 fog allele q126

XX double mutants of the genotypes gld-1(q126);tra-1(e1832) and gld-1(q126);tra-2(e1095) were obtained as XX self-progeny from unc-13 gld-1(q126)/++;tra-1/+ or gld-1(q126)+;tra-2/+ hermaphrodites. XX Unc-13 Tra-2 pseudomales and XX Unc-13 Tra-1 males were picked and their germline and somatic phenotypes examined. The double mutant unc-13 gld-1 (q126);tra-3(e1107) was examined at 25°C. Unc-13 pseudomales segregating from unc-13 gld-1(q126)/++;tra-3 [m(−/−) z(−/−)] motile were examined for germline and somatic abnormalities. gld-1(q126) has no obvious effect on the male somatic phenotypes of XX tra-1, tra-2 or tra-3 mutants. Finally, a homozygous gld-1(q126);unc-24 fem-3(q20gf) dpy-20 hermaphrodite strain was constructed by virtue of the ability of gld-1(q126) to suppress the sterile Mog phenotype of fem-3(q20gf) animals grown at 25°C. Specifically, XX gld-1(q126)+;unc-24 fem-3(q20gf) dpy-20/+ heterozygotes grown at 25°C segregated many self-fertile Unc-24 Dpy-20 hermaphrodites. Several of these hermaphrodites were shown to contain both gld-1(q126) and fem-3(gf) by the independent segregation of both types of mutations after outcrossing with wild-type males.

Construction of strains mutant for gld-1 and gvp-1

gld-1 (Tum);gvp-1 double mutants: Table 4 and Figure 8 describe the different gld-1(Tum);gvp-1 (0 or if) genotypes examined in this work. For each, we constructed balanced heterozygous strains of the general genotype gld-1(Tum)/H72(1);unc-32 gvp-1/H72(III). Owing to h72(1) [bli-4]; h72(III) [dpy-18] induced pseudolinkage, these heterozygotes segregate Unc-32 self-progeny that are essentially always of the genotype gld-1 (Tum);unc-32 gvp-1. The gld-1 (+); gvp-1 (+) control animals used for comparison in all experiments were the Unc-32 self-progeny of unc-32 h72(III) hermaphrodites. During passing, the h72 chromosome l-III pseudolinkage was found to occasionally break down: if a single nonUnc tumorous animal or a nonDpy Bli-4 animal was observed, the plate was discarded.

To construct balanced strains heterozygous for gld-1 (Tum) and gvp-1 alleles, gld-1/h72 males were crossed with unc-32 gvp-1/h72 hermaphrodites. Of the resulting male progeny, one half were heterozygous for h72, whereas one quarter had the desired genotype of gld-1+/unc-32 gvp-1+. Single males were crossed with h72 [bli-4; dpy-18] hermaphrodites; sires that produced no Dpy-18 (h72) male cross-progeny were identified as being gld-1+/ unc-32 gvp-1+. From these crosses, 25 or more L4 XX cross-progeny were picked onto separate plates and their self-progeny inspected in the following generation. In most cases, balanced gld-1(Tum)/h72;unc-32 gvp-1 (0)/h72 strains were easily identified because their gld-1 (Tum);unc-32 gvp-1 (0 or if) progeny had a germline phenotype distinct from those of both gld-1 (Tum) and gvp-1 single mutants. The genotypes of many of these strains were confirmed by out-crossing or by complementation testing. In addition, because gld-1(Tum);unc-32 gvp-1 (q72) and gld-1(Tum);unc-32 animals have identical Tum germline phenotypes, we verified the presence of the gld-1 (q72) allele in double mutants by PCR analysis. PCR analysis was done using
primers that bracket the 260 bp of glp-1 sequence that is deleted by q172 (Kodovann et al. 1992). The glp-1 DNA fragment amplified from glp-1(Tum);unc-32 glp-1(q172) homozygotes showed the expected size reduction (compared with glp-1(Tum);unc-32 control animals), confirming that these animals were homozygous for q172.

gld-1(Tum);glp-1(0 or f) males and masculinized XX animals: Several balanced glp-1(q485);KT2:unc-32 gld-1(0 or f)/KT2 strains were maintained as X0 male/XX hermaphrodite strains to provide a source of X0 double mutants. The male germ line phenotypes of different glp-1(q485);glp-1(0 or f) double mutants varied depending on the allele, ranging from a Gip phenotype [for the glp-1(0) alleles q46 and q175 and the strong if allele q224] to essentially wild type [for the strong if allele q172]. In addition, we examined XX glp-1(q485);glp-1(q172 or q224) animals that were homozygous for fem-3(q20gf), a mutation that masculinizes the XX germ line (Barton et al. 1987). To construct these strains, glp-1(q485);KT2:unc-32 glp-1(q172 or q224)/KT2 males were crossed with KT2: fem-3(q20gf) hermaphrodites at 15°C. Single nonDpy-18 (non-hT2) cross-progeny were picked onto separate plates and the 31(gl/3) chromosomal time was made homozygous by testing different lines grown at 25°C for expression of the fem-3(gl) Mog phenotype (Barton et al. 1987). The glp-1 alleles q172 and q224 behaved differently in the XX glp-1(Tum);unc-32 glp-1;fem-3(gl) triple mutants; the triple mutant with q172 had a Mog phenotype (see RESULTS), whereas that with q224 had a glp-1 phenotype. gld-1(Tum);glp-1(0) triple mutants bearing f mutations in fog-1, fem-1 or fem-3: Table 4 lists the triple mutants that were constructed using a gld-1(Tum) allele, a glp-1(0) allele (q175 or q46) and one of the following f mutations: fog-1(q180), fem-1(e2003ts) or fem-3(e1996). In all cases, triple mutants were obtained from balanced heterozygous strains. To make triple mutants carrying fog-1(f), we first constructed a balanced fog-1 glp-1/hT2;unc-32/hT2 strain (as described above for the construction for gld-1/hT2;unc-32 glp-1/hT2). A cross of fog-1 glp-1/hT2;unc-32/hT2 hermaphrodites with unc-32 glp-1(0)/hT2 males was then used to generate hermaphrodites of the genotype fog-1 glp-1(Tum)/+;unc-32 glp-1(0)/unc-32. These were then crossed with hT2;unc-32 males, and wild-type hermaphrodite cross-progeny were picked onto individual plates. Hermaphrodites that were fog-1 glp-1/hT2;unc-32 glp-1/hT2 were initially identified based on the unique germ-line phenotype of fog-1 glp-1(Tum);unc-32 glp-1(0) segregants (see RESULTS). These strains were outcrossed to confirm they carried both glp-1(Tum) and glp-1(0).

Triple mutants containing fem-1(e2003ts) were obtained from a balanced strain of the genotype gld-1(Tum);KT2;unc-32 glp-1(0)/KT2;fem-1/dpy-13(e585sd) unc-5. Heterozygous gld-1(Tum);KT2;unc-32 glp-1(0)/hT2 males were first crossed to hT2;dpd-13 unc-5 hermaphrodites to generate males that were gld-1(Tum)/hT2;unc-32 glp-1(0)/hT2;dpd-13 unc-5+/++. These males were then crossed to KT2;fem-1 females. Cross-progeny that were partially Dpy-13, and hence dpy-13 unc-5/fem-1 in chromosome IV genotype, were picked onto separate plates. Self-progeny were inspected in the following generation to ensure segregation of all phenotypes expected for the balanced strain. Triple mutant gld-1(Tum);unc-32 glp-1(0)/fem-1 animals were identified as Unc-32 animals that failed to show the semidominant dpy-13 phenotype.

Triple mutants bearing fem-3(e1996) were obtained as segregants from a balanced strain with the genotype gld-1(Tum);KT2;unc-32 glp-1(0)/KT2;fem-3(e1996)/unc-24 fem-3(q20gf) dpy-20. These strains were constructed by a method analogous to that used for construction of a balanced triple mutant containing fem-1. Approximately one third of Unc-32 nonUnc-24 nonDpy-20 segregants are homozygous for fem-3(e1996).

Characterization of gld-1(Tum);glp-1 double mutants and feminized triple mutants

Quantitation of germ line proliferation: For assays of germ-line proliferation, the above described balanced strains were used as a source of hermaphrodites with the general genotypes gld-1(q485);unc-32 glp-1(+ or 0 or f) or the feminized triple mutants fog-1(f);glp-1(Tum);glp-1(0) and gld-1(Tum);unc-32 glp-1(0);fem-1 were also examined (see Figure 6). To obtain tightly staged animals, newly hatched L1 larvae were picked as described (Frances et al. 1995) and grown to the L4 stage or adulthood. At the times indicated in Figures 6 and 8, animals were fixed and stained with diamidino-phenolindole (DAPI) (Francis et al. 1995). For each timepoint, the number of germ cells per gonad arm was counted twice in 10 gonad arms, and the mean number of germ cells per gonad arm was determined. In experiments with nonconditional glp-1 alleles (Figures 6 and 8A), animals were grown at 20°C. Experiments with temperature-sensitive glp-1 alleles (q224, bn18, q415) were done using animals grown from hatching at 25°C.

Determination of when germ cells first enter meiotic prophase during larval growth: Data presented in the accompanying paper (Francis et al. 1995) showed that gld-1(q485) does not affect the timing with which germ cells first enter meiotic prophase in a glp-1(+) background. For the present work, it was important to determine when gld-1(Tum) germ cells in various fog-1(+ or f); glp-1(0 or f) backgrounds first reach pachytene of meiotic prophase. This was done as described (Frances et al. 1995) by examining DAPI-stained preparations of tightly staged larval for the presence or absence of pachyten-stage meiotic germ cells. For each genotype, the mean age (in hours after hatching) at which pachyten nuclei were first observed was determined using 10 animals. Results were as follows: unc-32 glp-1(0) (23 hr, L2 stage), fog-1;unc-32 glp-1(0) (23 hr), gld-1;unc-32 glp-1(0) (31 hr, L3), fog-1 gld-1;unc-32 glp-1(0) (32 hr, L3), unc-32 [46 hr, L4 (wild-type control)]; fog-1(f);unc-32 (47 hr), glld-1(Tum); unc-32 glp-1(0) (46 hr), fog-1 glld-1;unc-32 glp-1(0) (46 hr) and gld-1;unc-32 glp-1(0) (46 hr). Entry into meiotic prophase in fog-1(+ or f) gld-1(Tum); unc-32 glp-1(0) animals is delayed relative to a glp-1(0) single mutant suggesting that germ cells undergo the additional rounds of cell division before entering meiosis. Note that fog-1(+) has no effect on premeiotic proliferation by gld-1(Tum) germ cells nor does it increase the rate of tumor growth in gld-1(Tum) animals (Francis et al. 1995) (data not shown).

Ablation of somatic gonad cells: Ablations of specific cells of the hermaphrodite somatic gonad were performed using a nitrogen pulse laser (Laser Sciences Inc.) set up as described by Avery and Horvitz (1987). The laser was coupled to a Zeiss Axioplan microscope and beam intensity was adjusted by the use of neutral density filters. Somatic cells in L1 and L2 gonad primordia were identified by their position and morphology (Kimble and Hirsh 1979) and ablated using 30-80 pulses from the laser. Operated animals were reexamined within 2 hr to confirm killing of the target cell(s) and to assess collateral damage.

Previous results have shown that ablation of the distal tip cell (DTC) precursors (Z1a and Z4p) does not produce a perfect phenocopy of the glp-1(0) phenotype. In the ablated animals, all germ cells enter meiotic prophase at the normal time (Kimble and White 1981). By contrast, germ cells in unc-32 glp-1(0), gld-1(Tum);unc-32 glp-1(0) and the feminized gld-1(Tum);unc-32 glp-1(0) triple mutants enter meiotic pro-
which are considered to have a female soma and a hermaphrodite germ line. As a result, the terminal fem/fog genes. As a result, the terminal fem/fog genes are active continuously in males, and X0 germ cells form sperm throughout adulthood. In the hermaphrodite, the production of first sperm and then oocytes is achieved through a different mechanism. In place of her-1, which is not active in X0 animals (TRENT et al. 1991), the fog-2 gene (SCHEDL and KIMBLE 1988) may transiently repress tra-2 and/or tra-3 and thereby free the terminal fem/fog genes to direct a brief period of spermatogenesis. Later, increased tra-2 activity (DONIACH 1986; SCHEDL and KIMBLE 1988; GOODWIN et al. 1995) and/or activation of the mog-1 gene (GRAHAM and KIMBLE 1993) leads to negative regulation of one or more terminal fem/fog genes, and the germline switches to oogenesis.

Mutations in the sex determination genes allow the manipulation of germline and somatic sex independent of each other and of chromosomal sex. Therefore we have used epistasis analysis with gld-1(Tum) alleles and sex determination gene mutations to examine the effects of chromosomal, somatic and germline sex on tumor formation and to infer the relationship between the gld-1(+) function that directs oogenesis and the sex determination pathway. These data are summarized in Table 1 and detailed above. All experiments were done with the null gld-1(Tum) allele q485, and many were also performed with q268. Identical results were obtained with both alleles.

The gld-1 tumorous phenotype depends on germline sexual identity

Tumor formation in XX germlines is independent of the male fate: Tumor formation in X.X hermaphrodites that lack gld-1 activity might result from a failure to specify the female germ cell fate or a defect in an early step in oocyte differentiation (FRANCIS et al. 1995). A prediction of either hypothesis is that inactivation of any of the five genes required for spermatogenesis (fem-1, -2 and -3 and fog-1 and -3) should have no effect on tumor formation in XX gld-1(Tum) germlines. Analysis of XX double mutants (Table 1) shows that tumors still form when any one of the terminal fem/fog genes is inactivated by a null or strong If/allele or when both fog-1 and fog-3 are inactivated in the same animal. Further, quantitation of germline proliferation in a fog-1(If) gld-1(Tum) double mutant indicates that fog-1(If) has no effect on tumor growth (FRANCIS et al. 1995) (see below). These results are consistent with gld-1 being essential for oogenesis and also argue that tumor formation does not result from an intersexual mode of development that is dependent on the terminal fem/fog genes.

We also examined whether gld-1(Tum) is similarly epistatic to several other mutations that eliminate hermaphrodite spermatogenesis. These included (1) a fog-2(If) mutation (SCHEDL and KIMBLE 1988), (2) a tra-2(gf) allele (SCHEDL and KIMBLE 1988) and (3) a tra-
### TABLE 1

**Effect of sexual fate on the gld-1 tumorous phenotype**

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Somatic phenotype</th>
<th>Germline phenotype</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Wild type</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>XX</td>
<td>Female</td>
<td>Sperm, then oocytes</td>
</tr>
<tr>
<td>XO</td>
<td>Male</td>
<td>Sperm</td>
</tr>
<tr>
<td><strong>Feminizing mutations</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>fem-1(If), fem-2(If) or fem-3(If)</td>
<td>XX Female</td>
<td>Sperm, then oocytes</td>
</tr>
<tr>
<td>fem-3(If)</td>
<td>X0 Female</td>
<td>Oocytes</td>
</tr>
<tr>
<td>her-1(If)</td>
<td>XX Female</td>
<td>Sperm, then oocytes</td>
</tr>
<tr>
<td>X0 Female</td>
<td>Sperm, then oocytes</td>
<td>Tumorous</td>
</tr>
<tr>
<td>fog-1(If)</td>
<td>XX Female</td>
<td>Oocytes</td>
</tr>
<tr>
<td>X0 Male</td>
<td>Sperm, then oocytes</td>
<td>Tumorous</td>
</tr>
<tr>
<td>fog-2(If)</td>
<td>XX Female</td>
<td>Oocytes</td>
</tr>
<tr>
<td>X0 Male</td>
<td>Sperm</td>
<td>Tumorous</td>
</tr>
<tr>
<td>fog-3(If)</td>
<td>XX Female</td>
<td>Oocytes</td>
</tr>
<tr>
<td>X0 Male</td>
<td>Sperm</td>
<td>Tumorous</td>
</tr>
<tr>
<td>fog-1(If) fog-3(If)</td>
<td>XX Female</td>
<td>Oocytes</td>
</tr>
<tr>
<td>tra-1(gf)/+</td>
<td>XX Female</td>
<td>Oocytes</td>
</tr>
<tr>
<td>X0 Male</td>
<td>Oocytes</td>
<td>Tumorous</td>
</tr>
<tr>
<td>tra-2(gf)</td>
<td>XX Female</td>
<td>Oocytes</td>
</tr>
<tr>
<td>X0 Female</td>
<td>Oocytes</td>
<td>Tumorous</td>
</tr>
<tr>
<td>tra-2(gf); fem-3(If)</td>
<td>XX Female</td>
<td>Incomplete Male</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Sperm (43%)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Sperm plus ectopic proliferation (57%)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Sperm plus ectopic proliferation (71%)</td>
</tr>
<tr>
<td><strong>Masculinizing mutations</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Tra</td>
<td></td>
<td></td>
</tr>
<tr>
<td>tra-2(gf)</td>
<td>XX Incomplete Male</td>
<td>Sperm</td>
</tr>
<tr>
<td>tra-3(If)</td>
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<td>Sperm (46%)</td>
</tr>
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<td>tra-1(If)</td>
<td>XX Male</td>
<td>Sperm (63%)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Sperm (37%)</td>
</tr>
<tr>
<td><strong>Mog</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>fem-3(gf)</td>
<td>XX Female</td>
<td>Sperm (99%)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Sperm plus ectopic proliferation (1%)</td>
</tr>
<tr>
<td>mog-1(If)</td>
<td>XX Female</td>
<td>Sperm (96%)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Sperm plus ectopic proliferation (4%)</td>
</tr>
<tr>
<td>tra-3(Mog)</td>
<td>XX Female</td>
<td>Sperm (95%)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Sperm plus ectopic proliferation (7%)</td>
</tr>
</tbody>
</table>

*See MATERIALS AND METHODS for details. The phenotype is completely penetrant unless indicated. The genotypes of fem-1, fem-2, fem-3 and tra-3 were m(−/−) z(−/−) to eliminate maternal rescue effects associated with these genes.

*For fog-1(q180) gld-1(q485), 80% of tumorous germ lines make some sperm (see text). The percent of X0 males making sperm was not quantitated for fog-1(gf) gld-1(Tum) double mutants using different alleles.

*The amber allele e1107 was used as the putative tra-3 null mutation. Only animals with a normal male somatic gonad were scored. Not included were the ∼20% of animals with abnormal/intersexual somatic gonads. Not included were the ∼50% of animals with abnormal/intersexual somatic gonads.

*Only animals with a normal male somatic gonad were scored. Not included were the ∼20% of animals with abnormal/intersexual somatic gonads.

*tra-3(mn75) was used. In mn75 has a Mog phenotype at 25°C (E. CAPOWSKI, B. BRENDZA and S. STROME, personal communication).

1(gf) allele that results in constitutive tra-1 activity (HODGKIN 1987). None of these mutations have any obvious effect on tumor formation in XX gld-1 (Tum) germlines. This result was expected for tra-2(gf) and fog-2(If) because these mutations may lead to increased negative regulation of the terminal fem/fog genes in the XX germline (DONIACH 1986; SCHEDL and KIMBLE 1988; GOODWIN et al. 1993). The role(s) of tra-1 in germline sex determination are uncertain (HODGKIN 1987; SCHEDL et al. 1989).

Tumor formation is independent of the X chromosome dosage: gld-1(Tum) alleles disrupt germline de-
development in XX hermaphrodites but not in X0 males. To determine whether sex specificity is correlated with either the sexual phenotype of the animal or its chromosome dosage, we examined XX and X0 gld-1(Tum) animals whose sexual phenotype had been reversed by a mutation in the sex determination pathway. For this purpose her-1(If), fem-3(If) and tra-1(gf) mutations were each used to transform X0 animals into either hermaphrodites [her-1(If)] or females [fem-3(If) and tra-1(gf)] + . When also homozygous for a gld-1(Tum) allele, these X0 somatic females develop germ line tumors identical to those of XX gld-1(Tum) animals (Table 1). Thus tumor formation is not dependent on X chromosome dosage but is instead correlated with a female sexual phenotype. Although not tested, we presume that similar results would be obtained using fem-1(If) and fem-2(If) mutations. Because of these results, we have not examined mutant combinations with the upstream genes that regulate both sex determination and dosage compensation (Villeneuve and Meyer 1990).

The complementary experiments in which XX animals are transformed into phenotypic males were done using mutant alleles of tra-1, tra-2 and tra-3. Null and strong If mutations in each of the tra genes cause masculinization of both the soma and germ line of XX animals. However, none of these mutations completely masculinize all XX tissues (Table 1). For example, although tra-2(If) XX animals make only sperm, the soma is incompletely male. For tra-1(If), the soma is fully male, but the germ line often makes oocytes. Nonetheless, mutations in each of the tra genes were found to be fully [tra-2(If)] or partially [tra-1(If) and tra-3(If)] epistatic to gld-1(Tum) alleles (Table 1). In the case of tra-2, both tra-2(If) and gld-1(Tum);tra-2(If) XX animals have a male germline that never forms a tumor. As XX tra-2(If) animals have a completely normal male germline and somatic gonad, this result is consistent with the observation that gld-1(null) X0 males are unaffected (Francis et al. 1995). Because the normal function of tra-2 is to negatively regulate the fem genes, the suppression of the gld-1(Tum) phenotype in a tra-2(If) background should be dependent on fem gene activity. This expectation was confirmed by constructing a XX gld-1(Tum);tra-2(If);fem-3(If) triple mutant. XX animals of this genotype have a female soma and a tumorous germline, showing that fem-3 activity is required for suppression of tumor formation in a tra-2(If) background.

Although tra-1(If) and tra-3(If) alleles can also suppress tumor formation in XX gld-1(Tum) animals, these mutations are only partially epistatic to a gld-1(Tum) allele. A male germline is found in 43% of gld-1(Tum);tra-3(If) and in 29% of gld-1(Tum);tra-1(If) XX animals. The remaining animals make sperm but also have ectopically proliferating germ cells (Table 1). This phenotype most likely reflects the fact that tra-1(If) and tra-3(If) do not completely eliminate oogenesis in the XX germline (Hodgkin 1987; Schedl et al. 1989). Because of some, gld-1(Tum);tra-1(If) or tra-3(If) germ cells may fail to adopt the male fate and so proliferate ectopically.

**Suppression of tumor formation by germ line masculinizing mutations:** The above described results show that tumor formation is correlated with female development but do not address whether it is germ line or somatic sex that is important. We therefore examined whether certain mutations that masculinize only the germ line (Mog phenotype) are epistatic to gld-1(Tum) alleles. The Mog mutations used (Table 1) were (1) a fem-3(gf) allele that makes germ line fem-3 activity insensitive to negative regulation (Barton et al. 1987; Ahringer and Kimble 1991); (2) a If mutation in mog-1, a gene that may function in repressing the terminal fem/fog genes (Graham and Kimble 1993) and (3) a germine-specific tra-3(If) allele bn75 [designated tra-3(Mog)] (B. Capowski, B. Brendza and S. Strom, personal communication). The corresponding double mutants with gld-1(Tum) display a masculinized germ line phenotype [shown for gld-1(Tum);fem-3(gf) in Figure 1a] similar to that of each Mog single mutant. The germine makes excess sperm and usually displays no evidence of ectopic proliferation. Thus gld-1(Tum) XX germ cells that are forced to adopt the male identity differentiate as sperm rather than forming tumors. The tumorous phenotype is therefore correlated with germ line but not somatic sex. For all three double mutants, however, a small fraction of gonad arms (<10%) have ectopically proliferating germ cells in the most proximal region of the germine. As gld-1(Tum) alleles cause a partial feminization of the XX germine (Francis et al. 1995), we believe that the ectopic proliferation that sometimes occurs in these double mutants arises because some fem-3(gf), mog-1(If) and tra-3(Mog) germ cells fail to adopt a male fate in a gld-1(Tum) background. Consistent with this idea, we found that gld-1(q485 or q365) can dominantly suppress the Mog phenotype of fem-3(gf). In particular, unlike fem-3(gf) animals, which make only sperm at 25°, some gld-1(Tum)/ +;fem-3(gf) XX animals make both sperm and oocytes and are self-fertile (data not shown). Partial suppression of fem-3(gf) in gld-1(Tum) homozygotes may account for why some germ cells in a low percentage of animals proliferate instead of differentiate as sperm.

**Tumor formation is independent of somatic sexual environment:** As a final test of the sex and tissue specificity of tumor formation, we asked whether tumors form in X0 animals that have a female germline and a male soma. Mutations in the genes fog-1 and fog-3 feminize only the germ line (Barton and Kimble 1990; Ellis and Kimble 1995). As a result, fog-1(If) and fog-3(If) X0 animals have a normal male soma but possess a germ line that only makes oocytes. As described above, fog-1(If) gld-1(null), gld-1(null) fog-3(If) and fog-1(If) gld-1(null) fog-3(If) XX animals are somatic females that form germ line tumors. The corresponding X0 double
and triple mutants have a male soma, but these animals also develop germinal tumors [Table 1, and shown in Figure 1 for fog-1(1f) gld-1(Tum) X0 males]. Examination of DAPI-stained animals indicates that tumors form in these males by the same mechanism as in XX gld-1(Tum) germelines. In all cases, germ cells in meiotic prophase are first observed proximally in the L4 stage; these cells then appear to exit meiotic prophase and return to mitotic proliferation. In adults, more distal germ cells continue to enter meiotic prophase and may contribute to tumor growth by later returning to mitotic proliferation. Similar germinal phenotypes were observed by Ellis and Kimble (1995) for X0 fog-1 gld-1(Tum) and gld-1(Tum) fog-3(1f) double mutants. Based on these results, we conclude that tumor formation occurs independently of somatic sexual environment as long as the germ-line sex determination pathway is set in the female mode.

In the course of these experiments, we observed a surprising result: fog-1(1f) gld-1(Tum) X0 males usually make some sperm. As shown in Figure 2, these males have a tumorous germ-line containing sperm that can be recognized by their compact nuclei and their expression of a sperm-specific antigen (Ward et al. 1986). This is not an allele-specific interaction, as spermatogenesis was observed in mutant combinations of two fog-1 alleles (q180 or q187) with three different gld-1
alleles (q485, q268 or q365) (see MATERIALS AND METHODS). Although the two fog-1 alleles examined are not known to be null, both are strong if mutations (BARTON and KIMBLE 1990; ELLIS and KIMBLE 1995). Therefore it appears that in the absence of gld-1 function, X0 germ cells can develop as sperm by a pathway that requires little or no fog-1 activity. In contrast, sperm were never observed in XX fog-1(+/) gld-1(Tum) worms or in gld-1(Tum) fog-3(+/) and fog-1(+/) gld-1(Tum) fog-3(+/) animals of either chromosomal sex.

Summary of interactions between the sex determination genes and gld-1(Tum) mutations: These experiments demonstrate that the gld-1(null) tumorous phenotype is dependent on germline sexual identity but is not dependent on the chromosomal sex of the animal or on somatic sexual identity. For the germline, the ultimate effect of the sex determination gene mutations is to alter the activity of the terminal fem/fog genes. Because the gld-1(null) tumorous phenotype is responsive to the activity state of the terminal fem/fog genes, then gld-1(+/) must act downstream of these genes on the branch that directs oogenesis (see DISCUSSION and Figure 9).

Investigation of the role of gld-1 in promoting hermaphrodite spermatogenesis using two types of gld-1 gf mutations

The existence of a gld-1(+) activity that promotes hermaphrodite spermatogenesis was previously inferred from a gld-1 haplo-insufficiency phenotype: XX gld-1(null)/+ and Df(gld-1)/+ germlines make fewer sperm than normal (FRANCIS et al. 1995). This gld-1 function may also account for the existence of two classes of gld-1(gf) alleles that cause transformations in germline sexual fates. Alleles of the first type, the gld-1(Fog) mutations, feminize the germline of both sexes, so that XX animals usually make only oocytes and X0 males make both sperm and oocytes. Alleles of the second type, the gld-1(Mog) mutations, masculinize the XX germline, so that hermaphrodites make an excess of sperm. To learn how these gf alleles affect the sex determination pathway, we constructed double mutants between gld-1(Fog) or gld-1(Mog) and mutations in the major sex determination loci (results summarized in Table 2).

gld-1(Fog) alleles suppress germline masculinizing mutations: Genetic criteria indicate the gld-1(Fog) allele q126 produces a poisonous gld-1 product that acts to partially feminize both XX and X0 germlines. Because gld-1(null) males are unaffected, the q126 mutant product must interfere with another gene product involved in germline sex determination (FRANCIS et al. 1995). As indicated in Table 2, q126 is able to partially suppress the masculinized germline phenotypes conferred by a fem-3(gf) allele or by ifi alleles of each of the tra genes. Whereas each of these mutants makes only sperm [or some animals make sperm and then oocytes in the case of tra-1(+/) and tra-3(+) mutants], all XX double mutants with q126 make sperm and then oocytes. The suppression of tra-2(+/) and tra-3(+/) indicates that the q126 product cannot feminize the germline by affecting tra-2(+) and tra-3(+) activity. Instead gld-1(q126) is likely to interfere with a gene product that acts downstream or independently of tra-2 and tra-3.

gld-1(q126); fem-3(gf) XX animals are always self-fertile hermaphrodites, demonstrating that gld-1(q126) and fem-3(gf) mutually suppress one another. Mutual suppression has previously been reported for other combinations of gf mutations that affect germline sex determination and most likely represents a balance between the opposite effects of masculinizing and feminizing mutations (BARTON et al. 1987; SCHEDL and KIMBLE 1988).

Effects of gld-1(Mog) alleles on sex determination: gld-1(Mog) alleles that fall into three subclasses (C1, C2 and C3) were originally isolated as dominant suppressors of certain mutations that feminize the XX germline (FRANCIS et al. 1995). The C3 allele, ox10, retains gld-1 functions that are required for oogenesis. Homozygous ox10 XX animals make excess sperm but also can make oocytes late in adulthood and become self-fertile. In contrast, C1 and C2 gld-1(Mog) homozygotes never make oocytes and, as indicated by complementation data, these alleles disrupt gld-1 functions required for oogenesis (FRANCIS et al. 1995).

To determine whether gld-1(Mog) alleles can bypass the need for the fem genes or fog-1 and -3 in directing spermatogenesis, we constructed the XX double mutants described in Table 2. XX animals homozygous for the C3 allele ox10 and either a fem-3(+/) or fog-1(+/) mutation only make oocytes; fem-3(+/) and fog-1(+/) are thus epistatic to ox10 with regard to germline sex determination. Similarly, no sperm are made in double mutants between C1 or C2 gld-1(Mog) and mutations in the terminal fem/fog genes. Thus, like ox10, the C1 and C2 alleles do not bypass the need for the terminal fem/fog genes in directing spermatogenesis. However, unlike ox10, XX double mutants containing a C1 or C2 allele show no cytological signs of oogenesis. Instead, the proximal germline of each of the C1 and C2 gld-1(Mog) double mutants described in Table 2 fills with undifferentiated germ cells that have a nuclear morphology characteristic of germ cells at the pachytene stage of meiotic prophase (Figure 8). In all the double mutants analyzed, germ cells in adult animals usually remain arrested in meiotic prophase. In double mutants of certain genotypes, however, the germline occasionally becomes tumorous, probably because germ cells exit meiotic prophase and return to mitotic proliferation. These phenotypes are similar to the undifferentiated pachytene arrest phenotype conferred by class B gld-1 alleles (FRANCIS et al. 1995).

The absence of spermatogenesis in C1 and C2 double mutants indicates that mutations in the fem genes and
Multiple gld-1 Functions

Table 2

Interactions of gld-1 Fog and Mog alleles with sex determination gene mutations

<table>
<thead>
<tr>
<th>Genotype*</th>
<th>Soma</th>
<th>Germline</th>
</tr>
</thead>
<tbody>
<tr>
<td>gld-1(Fog)</td>
<td>XX</td>
<td>Female</td>
</tr>
<tr>
<td>gld-1(q126)</td>
<td>X0</td>
<td>Male</td>
</tr>
<tr>
<td>q126; tra-2(f)</td>
<td>XX</td>
<td>Incomplete male</td>
</tr>
<tr>
<td>q126; tra-3(f)</td>
<td>XX</td>
<td>Incomplete male</td>
</tr>
<tr>
<td>q126; tra-1(f)</td>
<td>XX</td>
<td>Male</td>
</tr>
<tr>
<td>q126; fem-3(gf)</td>
<td>XX</td>
<td>Female</td>
</tr>
<tr>
<td>gld-1(Mog)</td>
<td>XX</td>
<td>Female</td>
</tr>
<tr>
<td>C1</td>
<td></td>
<td>Germ cells arrested in meiotic prophase</td>
</tr>
<tr>
<td>q93; fem-1(f)</td>
<td>XX</td>
<td>Female</td>
</tr>
<tr>
<td>q93; fem-2(f)</td>
<td>XX</td>
<td>Male</td>
</tr>
<tr>
<td>q93; fem-3(f)</td>
<td>XX</td>
<td>Female</td>
</tr>
<tr>
<td>q93; fog-1(f)</td>
<td>XX</td>
<td>Female</td>
</tr>
<tr>
<td>q93; fog-2(f)</td>
<td>X0</td>
<td>Male</td>
</tr>
<tr>
<td>q93; tra-1(fg)+</td>
<td>XX</td>
<td>Female</td>
</tr>
<tr>
<td>q93; tra-2(gf)+</td>
<td>XX</td>
<td>Female</td>
</tr>
<tr>
<td>q93; tra-2(gf)</td>
<td>XX</td>
<td>Female</td>
</tr>
<tr>
<td>C2</td>
<td></td>
<td>Germ cells arrested in meiotic prophase</td>
</tr>
<tr>
<td>gld-1(oz30)</td>
<td>XX</td>
<td>Female</td>
</tr>
<tr>
<td>oz30; fem-3(f)</td>
<td>XX</td>
<td>Female</td>
</tr>
<tr>
<td>oz30; fog-1(f)</td>
<td>XX</td>
<td>Female</td>
</tr>
<tr>
<td>C3</td>
<td></td>
<td>Germ cells arrested in meiotic prophase</td>
</tr>
<tr>
<td>gld-1(oz10)</td>
<td>XX</td>
<td>Female</td>
</tr>
<tr>
<td>oz10; fem-3(f)</td>
<td>XX</td>
<td>Female</td>
</tr>
<tr>
<td>oz10; fog-1(f)</td>
<td>XX</td>
<td>Female</td>
</tr>
<tr>
<td>oz10; fog-1(f)</td>
<td>X0</td>
<td>Male</td>
</tr>
</tbody>
</table>

* See MATERIALS AND METHODS for details. Refer to Table 1 for the phenotype of sex determination single mutants. Animals were grown at 20°C and scored 1 and 2 days after L4 by Nomarski optics and in some cases also by DAPI staining. For tra-3, fem-1, -2 and -3, genotype was m(−/−) z(−/−).

† Phenotype is completely penetrant unless indicated. n > 100.

‡ Tumorous germ lines were observed in <1% of animals with these genotypes.

§ Oogenesis continues as in wild type (see FRANCIS et al. 1995).

fog-1 and -3 are epistatic to C1 and C2 alleles with regard to promotion of hermaphrodite spermatogenesis. This suggests that the germ cells in the double mutant develop along the female pathway. If so, germ cell arrest at the pachytene stage of meiotic prophase would simply reflect a disruption by C1 and C2 alleles of gld-1 functions that are required for oogenesis and progression through meiotic prophase (FRANCIS et al. 1995). We favor this hypothesis based on several findings. First, the C3 allele oz10 does not have a defect in oogenesis, and the fog-1(f) gld-1(oz10) and gld-1(oz10); fem-3(f) double mutants make functional oocytes. Second, complementation data show that C1 and C2 alleles are defective for oogenesis and that these alleles can cause germ cells to arrest at pachytene in certain combinations of gld-1 trans-heterozygotes (FRANCIS et al. 1995). Third, the pachytene arrested germ cells are not overtly intersexual as they do not express the sperm-specific antigens detected by the SP56 monoclonal antibody (data not shown) (WARD et al. 1986). Fourth, there is a parallel between the pachytene arrest phenotype of the C1 and C2 gld-1(Mog) double mutants and what
occurs in gld-1(Tum) germlines. In either genetic background, germ cells that do not develop as male are unable to progress beyond pachytene to later stages of female meiotic prophase. However, although germ cells return to mitosis in gld-1(Tum) single mutants, germ cells in the C1 and C2 double mutants for the most part remain arrested in meiotic prophase. This difference suggests C1 and C2 gld-1(Mog) alleles retain gld-1(+) functions that prevent germ cells from exiting meiotic prophase but cannot supply the gld-1(+) functions required for further meiotic progression and oogenesis.

**Dependence of tumor formation and premeiotic proliferation on the glp-1-mediated signaling pathway**

In wild type, proliferating germ cells are found throughout the gonad of early larvae but are limited to the distal region in late larvae and adults as more proximal germ cells have entered the meiotic pathway. Proliferation of these germline stem cells is promoted by the glp-1-mediated signaling pathway. When the distal tip cell (DTC) of the somatic gonad is ablated with a laser microbeam, distal germ cells divide a few times, then enter meiosis and subsequently produce gametes (KIMBLE and WHITE 1981). The germline receptor for the DTC signal is a transmembrane protein, encoded by the glp-1 gene, that belongs to the lin-12/Notch family of receptor molecules (AUSTIN and KIMBLE 1987, 1989; YOCHEN and GREENWALD 1989; CRITTENDEN et al. 1994).

In gld-1(Tum) hermaphrodites, germline proliferation in early larvae is apparently identical to wild type, and the proximal germ cells enter meiotic prophase at the normal time (FRANCIS et al. 1995). However, gld-1(Tum) germ cells exit meiotic prophase, return to the mitotic cell cycle and proliferate ectopically. The distal region of the late larval and adult gld-1(Tum) germline appears similar to wild type; a mitotic stem cell population is followed more proximally by a transition zone where germ cells enter meiotic prophase, which is in turn followed by a region of pachytene germ cells. In the mutant, the germline proximal to the pachytene zone is made up of ectopically proliferating cells that have exited meiotic prophase and returned to mitosis. As a result, gld-1(Tum) hermaphrodite gonads have two distinct populations of mitotically active germ cells: a distal premeiotic population, corresponding to the stem cell population in wild type, and a proximal population comprised of germ cells undergoing ectopic proliferation (Figure 4A). To distinguish between the two populations, we refer to mitotic germ cells in early larva and in the distal region of late larvae and adults as “premeiotic germ cells” and to the ectopically proliferating germ cells that are the result of exit from meiotic prophase as a “germline tumor” (Figure 4A). In the second half of this section, we investigate the role of the glp-1 signaling pathway in the control of premeiotic germ cell proliferation and tumor formation in gld-1(Tum) mutants.

**Premeiotic proliferation is dependent on the**
DTC: If the distal premeiotic germ cells in XX \textit{gld-1} (\textit{Tum}) mutants are similar to their wild-type counterparts, then their proliferation should depend on DTC signaling. To test this idea, we ablated the DTC in wild-type and \textit{gld-1} (\textit{Tum}) larvae (late L3/young L4 stage). Operated animals were allowed to develop for 24–48 hr, after which germlines were released by dissection and stained with DAPI to visualize nuclear morphology.

In ablated wild-type gonads, all distal germ cells enter meiotic prophase and reach the pachytene stage within 28–32 hr after DTC elimination; these cells later differentiate as oocytes (KIMBLE and WHITE 1981) (data not shown). Similarly, distal germ cells in operated \textit{gld-1} (\textit{Tum}) gonads also enter meiosis; by 28–32 hr all distal nuclei display a pachytene morphology (Figure 5, a and b). Therefore distal premeiotic proliferation in \textit{gld-1} (\textit{Tum}) hermaphrodites is signal dependent, indicating that it is under the same controls as in wild type. In contrast, proximal germ cells in the ablated gonads still form a tumor (Figure 5a), indicating that ectopic proliferation is not dependent on the DTC.

Further analysis of operated \textit{gld-1} (\textit{Tum}) gonads revealed that the distal meiotic germ cells fail to complete meiotic prophase and instead appear to return to mitosis. This is indicated by the later appearance (within 32–35 hr of DTC elimination) of dividing cells intermixed among the distal pachytene-stage germ cells (Table 3, Figure 5c). Because dividing cells display both a spindle pole morphology (data not shown) and metaphase plate configuration typical of mitotic germ cells, they appear to have returned to a mitotic cell cycle. Based on these results, we conclude the \textit{gld-1} (\textit{Tum}) germ cells enter the meiotic pathway in response to DTC ablation but then return to mitosis. This behavior is analogous to the \textit{gld-1} (\textit{Tum}) return to mitosis phenotype that occurs more proximally in the unoperated hermaphroditic gonad (FRANCIS et al. 1995).

Dependence of tumor formation on the somatic gonad: To further examine the dependence of premeiotic proliferation in \textit{gld-1} (\textit{Tum}) germlines on the somatic gonad, several additional ablation experiments were performed. As shown in Figure 4B, X X early L1 larvae contain two somatic precursor cells, Z1 and Z4, which give rise to the entire hermaphrodite somatic gonad (KIMBLE and HIRSH 1979). When Z1 and Z4 are ablated in wild type, the germ cell precursors, Z2 and Z3, divide one or two times but then fail to divide further or to form gametes (KIMBLE and WHITE 1981). The same result is observed when the daughters of Z1 and Z4 (Z1.a, Z1.p, Z4.a and Z4.p) are killed in wild type (data not shown). Similarly, when Z1 or Z4 (or their four daughters) are ablated in X X \textit{gld-1} (\textit{Tum}) L1 larvae, germ cells undergo one or two divisions but then cease dividing (data not shown). In a few cases, some germ cells in ablated \textit{gld-1} (\textit{Tum}) animals appeared to enter meiotic prophase, as judged from the appearance of pachytene-stage nuclei in DAPI-stained preparations, but a tumor was never formed. These results indicate that, as in wild-type, the initial proliferation in \textit{gld-1} (\textit{Tum}) early larvae is dependent on the somatic gonad.

We next attempted to determine whether specific lineages giving rise to different parts of the somatic gonad are important for promoting tumor formation by \textit{gld-1} (\textit{Tum}) XX germ cells. In wild-type L1 larvae, ablation of Z1.a and Z4.p—the precursor cells that give rise to two DTCs and parts of the sheath and spermatheca (refer to Figure 4B) —results in germ cells undergoing several rounds of division and then differentiating as sperm at the normal time during LA (KIMBLE and WHITE 1981). When the same ablation is done in \textit{gld-1} (\textit{Tum}) hermaphrodites, some germ cells differentiate as sperm but most go on to form a tumor (Table
TABLE 3

Ablations of somatic gonad cells in gld-1(Tum) hermaphrodites

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Larval stage</th>
<th>Precursor cell(s) ablated</th>
<th>Descendants of ablated precursors cell(s)</th>
<th>No. of animals</th>
<th>Adult germline phenotype</th>
</tr>
</thead>
<tbody>
<tr>
<td>gld-1(q268 or q485); unc-32</td>
<td>L3/L4</td>
<td>Z1.aa or Z4.pp</td>
<td>DTC</td>
<td>&gt;100</td>
<td>Enter meiosis, then return to mitosis$^a$</td>
</tr>
<tr>
<td></td>
<td>L1</td>
<td>Z1.a and Z4.p</td>
<td>DTC, one half of SH/SP</td>
<td>12</td>
<td>Ectopic proliferation$^b$</td>
</tr>
<tr>
<td></td>
<td>L1</td>
<td>Z1.p and Z4.a</td>
<td>AC, uterus, one half of SH/SP</td>
<td>9</td>
<td>Ectopic proliferation$^b$</td>
</tr>
<tr>
<td></td>
<td>L2</td>
<td>Z1.aa and Z4.pp</td>
<td>DTCs, one half of SH/SP</td>
<td>11</td>
<td>Ectopic proliferation$^b$</td>
</tr>
<tr>
<td></td>
<td>L2</td>
<td>Z1.pp and Z4.aa</td>
<td>AC, ventral uterus</td>
<td>12</td>
<td>Ectopic proliferation$^b$</td>
</tr>
<tr>
<td></td>
<td>L2</td>
<td>Z1.aaa and Z4.aaa</td>
<td>AC, ventral uterus</td>
<td>10</td>
<td>Ectopic proliferation$^b$</td>
</tr>
<tr>
<td></td>
<td>L2</td>
<td>Z1.aaa, Z1.pp, Z4.aaa</td>
<td>DTCs, AC, ventral uterus</td>
<td>3</td>
<td>Ectopic proliferation$^b$</td>
</tr>
<tr>
<td>gld-1(q268); unc-32</td>
<td>L3/L4</td>
<td>Z1.aa or Z4.pp</td>
<td>DTC</td>
<td>9</td>
<td>Enter meiosis, then return to mitosis$^a$</td>
</tr>
<tr>
<td>gld-1(q453); unc-32</td>
<td>L3/L4</td>
<td>Z1.aa or Z4.pp</td>
<td>DTC</td>
<td>8</td>
<td>Enter meiosis = all form sperm</td>
</tr>
<tr>
<td>gld-1(q172); fem-3(q20gf)</td>
<td>L3/L4</td>
<td>Z1.aa or Z4.pp</td>
<td>DTC</td>
<td>8</td>
<td>Enter meiosis, then return to mitosis$^a$</td>
</tr>
<tr>
<td>gld-1(q453); unc-32</td>
<td>L3/L4</td>
<td>Z1.aa or Z4.pp</td>
<td>DTC</td>
<td>8</td>
<td>Enter meiosis, then return to mitosis$^a$</td>
</tr>
</tbody>
</table>

DTC, distal tip cell; SH/SP, sheath and spermatheca lineage; AC, anchor cell.
$^a$ Distal premeiotic germ cells enter meiotic prophase after DTC ablation but then return to mitosis (see Figure 7, b and c and text). There is no obvious effect on ectopic proliferation.
$^b$ Proximal ectopic proliferation was unaffected by the ablation. Distal premeiotic proliferation was affected only when the DTC was eliminated; however, these distal germ cells were not examined for the return to mitosis phenotype.

3, also see MATERIALS AND METHODS). Tumors also form after ablation of Z1.p and Z4.a, the precursor cells that give rise to the anchor cell, uterus and part of the sheath/spermatheca lineage (Table 3). Finally, ablation of the two distal tip cells (Z1.aa and Z4.pp) and the precursors to the anchor cell (Z1.pp and Z4.aa) does not prevent tumor formation. Taken together, these results indicate that somatic factors that support ectopic proliferation (tumor formation) can be supplied both by descendants of Z1.a and Z4.p and by descendants of Z1.p and Z4.a.

Dependence of the gld-1 (Tum) phenotype on glp-1 function

Genetic and cytological evidence indicate that the glp-1 protein acts as the germline receptor for signaling by the DTC (AUSTIN and KIMBLE 1987; CRITENDEN et al. 1994) and potentially by other somatic gonad cells (SEYDOUX et al. 1990). Because somatic signaling is required for continued premeiotic proliferation in gld-1(Tum) germlines, it appeared likely that premeiotic proliferation would also be dependent on glp-1 (+) activity. This idea was tested by constructing a series of double mutants between gld-1 (Tum) alleles and two glp-1 molecular null alleles (KODOMANNI et al. 1992) [designated glp-1(0)].

Continued premeiotic proliferation is dependent on glp-1(+) function: The glp-1(0) molecular null alleles q46 and q175 are each associated with a nonsense mutation in the amino-terminal half of the glp-1 coding region (KODOMANNI et al. 1992) that abolishes accumulation of stable glp-1 protein (CRITENDEN et al. 1994). In each single mutant, the germline precursors Z2 and Z3 divide about two times to produce two to four germ cells in each hermaphrodite gonad arm and four to eight germ cells in the single male gonad arm (AUSTIN and KIMBLE 1987). In both sexes, these germ cells enter meiosis prematurely and differentiate as sperm by the L3 stage. Table 4 lists the double mutants constructed with glp-1(q46 or q175) and each of three gld-1(Tum) alleles (q485, q268 or q365). All double mutants, both as XX hermaphrodites and X0 males, have a glp-1(0) phenotype; germ cells divide several times but then enter meiotic prophase prematurely and form sperm. This suggests that premeiotic proliferation by gld-1(Tum) germ cells remains largely dependent on glp-1(+) activity (also see below).

Tumor formation is independent of glp-1(+) function: Because the results presented above indicate that
germline fate is eliminated by a pathway is set in the female mode (terminal gld-1(Tum);glp-1(0)
male mode. To overcome this situation, we constructed triple mutants (feminized double mutants)
to these triple mutants as feminized germ cells continue to proliferate throughout adulthood (Figures and
genes inactive, glp-1(Tum);glp-1(0) animals may fail to form tumors because all germ cells develop in the
tissues in which the male germline fate is eliminated by a mutation in one of three genes: fem-1, fem-3 or fog-1. For simplicity, we refer to these triple mutants as feminized glp-1(Tum);glp-1(0) animals or feminized triple mutants. As controls, fog-1(0);glp-1(0) and glp-1(0);fem-1(0) hermaphrodites were examined. These double mutants show the glp-1(0) germ cell proliferation defect, but germ cells differentiate as small oocyte-like cells rather than sperm. The same phenotype was observed previously for a fog-1(0) double mutant (KIMBLE 1990).

Table 4 describes nine different feminized glp-1(Tum);glp-1(0) triple mutants that were constructed. These triple mutants differ in their glp-1(q485, q268 or q365) and glp-1(q175 or q46) genotypes, and in the particular feminizing mutation they carry, but all display the same tumorous germline phenotype. Although the tumors are generally smaller than those in glp-1(Tum) single mutants, germ cells continue to proliferate throughout adulthood (Figures 6 and 7a). More detailed examination of one feminized triple mutant [fog-1(q180); glp-1(q485); glp-1(q175)] revealed that all germ cells in these animals enter meiotic prophase at the same time as do germ cells in glp-1(Tum);glp-1(0) double mutants (data not shown—see MATERIALS AND METHODS). However, instead of forming sperm as in unfeminized glp-1(Tum);glp-1(0) double mutants, many of these germ cells appear to exit meiotic prophase and return to mitosis. These results indicate that neither exit from meiotic prophase nor ectopic proliferation are absolutely dependent on glp-1(+) activity. Therefore tumor formation cannot result solely from a failure to downregulate glp-1 activity as germ cells progress through meiotic prophase. The finding that only feminized glp-1(Tum);glp-1(0) animals form tumors also reinforces the idea that the sex determination pathway must be set in the female mode for tumors to form.

Several properties of feminized glp-1(Tum);glp-1(0) triple mutants indicate that glp-1(+) activity, although not essential for tumor formation, is important for maximal tumor growth. First, as shown in Figure 6, tumors grow more slowly and variably in the triple mutants than in the corresponding glp-1(Tum) strains that are glp-1(+). Second, unlike tumors formed in a glp-1(+) background, which are comprised mainly of small germ cells with compact nuclei of relatively homogeneous morphology, those formed in feminized glp-1(Tum); glp-1(0) triple mutants display a wide range of nuclear morphologies. Some germ cells display a pachytene morphology, others stain intensely with DAPI and may

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Phenotype and number of germ cells/gonad arm</th>
</tr>
</thead>
<tbody>
<tr>
<td>XX unc-32 glp-1(q175 or q46)</td>
<td>~2-4 Pachytene germ cells = ~16 sperm</td>
</tr>
<tr>
<td>XO unc-32 glp-1(q175 or q46)</td>
<td>~4-8 Pachytene germ cells = ~32 sperm</td>
</tr>
<tr>
<td>XX glp-1(q485); unc-32 glp-1(q175 or q46)</td>
<td>~16 Pachytene germ cells = ~64 sperm</td>
</tr>
<tr>
<td>XX glp-1(q268); unc-32 glp-1(q175 or q46)</td>
<td>~16 Pachytene germ cells = ~64 sperm</td>
</tr>
<tr>
<td>XX glp-1(q365); unc-32 glp-1(q175 or q46)</td>
<td>~16 Pachytene germ cells = ~64 sperm</td>
</tr>
<tr>
<td>XO glp-1(q268 or q365); unc-32 glp-1(q46)</td>
<td>~32 Pachytene germ cells = ~128 sperm</td>
</tr>
<tr>
<td>XX glp-1(q485); unc-32 glp-1(q175); fem-1</td>
<td>~16 Pachytene germ cells = ectopic proliferation</td>
</tr>
<tr>
<td>XX glp-1(q365); unc-32 glp-1(q175); fem-1</td>
<td>~16 Pachytene germ cells = ectopic proliferation</td>
</tr>
<tr>
<td>XX glp-1(q268); unc-32 glp-1(q175); fem-1</td>
<td>~16 pachytene germ cells = ectopic proliferation</td>
</tr>
<tr>
<td>XX glp-1(q268 or q365); unc-32 glp-1(q175); fem-1</td>
<td>~16 pachytene germ cells = ectopic proliferation</td>
</tr>
</tbody>
</table>

* Self-progeny of unc-32 glp-1(q175 or q46)/H2 hermaphrodites.
* Described by AUSTIN and KIMBLE (1987).
* Self-progeny of glp-1(Tum)/H2; unc-32 glp-1(q175 or q46)/H2 hermaphrodites.
* Number of pachytene-stage germ cells/gonad arm counted in DAPI-stained XX hermaphrodites at the mid-1.3 larval stage. Most gonad arms contained 15-18 pachytene germ cells (average 16), but a few contained as many as 20.
* Determined by counting sperm in DAPI-stained L4 animals.
* Self-progeny of glp-1(Tum)/H2; unc-32 glp-1(q175)/H2; fem-1(e1996)/dpy-20 fem-3(q20gf) unc-24 hermaphrodites.
* Self-progeny of glp-1(Tum)/H2; unc-32 glp-1(q46); fem-1(e2003ts)/dpy-13 unc-5 hermaphrodites.
* Self-progeny of fog-1(q180) glp-1(Tum)/H2; unc-32 glp-1(q175 or q46); H2 hermaphrodites.
be polyploid and still others have 12 condensed chromosomes (possibly representing early mitotic prophase). These features suggest that an absence of glp-1 activity in _gld-I (Turn)_ germlines sometimes results in aberrant cell cycles and occasional arrest of germ cells in pachytene. Third, the germline in these strains lacks any evident distal/proximal polarity, as all germ cells appear to enter the meiotic pathway at about the same time during larval growth (data not shown). These results indicating that _gld-I (+)_ activity helps promote tumor formation are consistent with the finding of Crittenden et al. (1994) that _gld-I_ tumors express glp-1 protein at high levels.

__gld-I (Turn) mutations also affect premeiotic germ line proliferation:__ Because germ cells in _XX_ _gld-I (Turn)_ animals enter the meiotic pathway normally (Francis et al. 1995), there was no a priori reason to suspect that _gld-I_ regulates premeiotic germline proliferation. However, close examination of _gld-I (Turn);glp-1(0)_ double and feminized triple mutants revealed a weak effect of _gld-I (Turn)_ alleles on the proliferation of premeiotic germ cells. In _glp-1(0)_ single mutants, the germline precursor cells _Z2_ and _Z3_ divide about two times and then differentiate as sperm (Austin and Kimble 1987). In double mutants and feminized triple mutants, however, _Z2_ and _Z3_ undergo four premeiotic divisions to produce ~16 germ cells per hermaphrodite gonad arm and 32 cells in the single male gonad arm (Table 4). In both double and feminized triple mutants, germ cells enter meiosis in relative synchrony, so that all nuclei exhibit pachytene morphology by the mid-L3 stage (Figure 7, b and c). Increased premeiotic proliferation, in contrast to tumor formation, is not dependent on germline sexual fate; it occurs in animals that produce sperm _[gld-I (Turn);glp-1(0) XX X0]_ and in feminized triple mutants where the male fate is inactivated.

The small increase in premeiotic proliferation in the double and feminized triple mutants argues that _gld-I (+)_ inhibits this aspect of germline development. However, because _gld-I (null)_ mutations do not noticeably increase premeiotic germ cell proliferation in _glp-1(+)_ animals (Francis et al. 1995), the role of _gld-I_ in inhibiting premeiotic germline cell division must be relatively small. Because early larval germ cells do not appear to contain maternally supplied _glp-1(+)_ RNA or protein (Evans et al. 1994; Crittenden et al. 1994; Seydoux and Fire 1994), the elimination of _gld-I_ function in _glp-1(0)_ mutants cannot affect _glp-1_ activity. Therefore _gld-I_ may repress germline mitosis (or promote entry into the meiotic pathway) by a mechanism that is at least partially independent of _glp-1_ activity.

__gld-I (Turn) alleles are epistatic to certain glp-1 (lf) alleles:__ If _gld-I_ negatively regulates premeiotic proliferation (either by regulating a molecule other than _glp-1_ RNA or by regulating _glp-1_ and a _glp-1_-independent molecule), then elimination of _gld-I (+)_ activity might render germ cells more responsive to the _glp-1_-dependent mitotic signal. To test this idea, we examined whether _gld-I (null)_ can fully or partially suppress nonnull _glp-1 (lf)_ mutations. Double mutants of _gld-I (q485)_ were constructed with two classes of _glp-1 (lf)_ alleles. The first class includes three strong nonconditional _glp-1 (lf)_ mutations that affect the extracellular domain of the _glp-1_ protein (GLP-1) and the second class includes three

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**Figure 6.** — Comparison of germline proliferation in the _gld-I (q485) XX_ single mutant, _fog-1 (q180) gld-I (q485) XX_ double mutants and feminized _gld-I (q485);glp-1(0) XX_ triple mutants. Each data point represents the mean number of germ cells counted in a minimum of 10 gonad arms. Plus or minus one standard deviation is indicated with error bars. Each of the feminized _gld-I (Turn);glp-1(0)_ triple mutants describe in Table 4 forms a germline tumor. However, as shown here for two feminized triple mutants [using _glp-1 (q175)_ with either _fog-1 (q180)_ or _fem-1 (e2003)_], these tumors grow more slowly and variably than when _glp-1 (+)_ activity is present.
temperature-sensitive \textit{glp-1} alleles (diagrammed in Figure 8C).

Each nonconditional \textit{glp-1} mutation confers a strong \textit{glp-1(1)} phenotype similar to that of \textit{glp-1(0)} alleles (AUSTIN and KIMBLE 1987). \textit{q172} is an in-frame deletion that removes most of the three extracellular \textit{lin-12/Notch} (LN) repeats of GLP-1. \textit{q158} is a missense mutation in the second LN repeat and \textit{oa25} is a missense mutation in the seventh epidermal growth factor-like motif (KODOYANNI et al. 1992). Germline tumors form in all three \textit{XX glp-1(q485);glp-1(1)} double mutants. Germ cells in \textit{glp-1(q485);glp-1(q172)} mutants proliferate at essentially the same rate as those in the \textit{glp-1(q485)} single mutant, whereas proliferation in double mutants with \textit{glp-1(q158)} or \textit{oa25} is somewhat reduced and shows more variability between animals (Figure 8A). Thus \textit{glp-1(q485)} partially or completely suppresses the germline proliferation defects of these \textit{glp-1(1)} alleles. The \textit{glp-1(q485);glp-1(q172)} double mutant was chosen for more detailed analysis because robust proliferation was observed in every animal.

As was previously shown, \textit{glp-1(+) activity is required for continuous premeiotic proliferation in \textit{glp-1(1)/\textit{Tum))} germines but is dispensable for ectopic tumorous germ cell proliferation. However, because \textit{glp-1(q485)} is completely epistatic to \textit{glp-1(q172)}, we suspected that premeiotic proliferation in the double mutant may be close to normal. If correct, this idea would suggest that \textit{glp-1(q172)} is able to function essentially like a \textit{glp-1(+) allele when in a \textit{glp-1(1)/\textit{Tum)} background. Several observations indicate that this is the case. First, proximal germ cells in \textit{XX glp-1(q485);glp-1(q172)} mutants enter meiotic prophase at the same time as those in \textit{glp-1(null);glp-1(+) and wild-type hermaphrodites (data not shown). Second, the premeiotic \textit{glp-1(q172)} proliferative defect can be suppressed in germlines that show no ectopic tumorous proliferation. \textit{XX glp-1(q485);glp-1(q172)} males, for example, have a male germ line that appears normal in all respects; in contrast, \textit{glp-1(q172)} XO males have a Glp germline that makes only 20–32 sperm (AUSTIN and KIMBLE 1987). \textit{glp-1(1)/\textit{Tum)} mutations also suppress the \textit{glp-1(q172)} proliferative defect in \textit{XX} germlines that are exclusively undergoing male development. \textit{XX glp-1(q485);glp-1(q172);fem-3(gf)} hermaphrodites, like the \textit{XX glp-1(q485);fem-3(gf) double mutant (shown in Figure 1), exhibit a Mag phenotype. Third, we used ablation experiments to show that the premeiotic proliferation occurring in \textit{glp-1(q485);glp-1(q172)} germines depends on signaling by the DTC. When the DTC is ablated in the \textit{XX glp-1(null);glp-1(q172) double mutant or the \textit{glp-1(null);glp-1(q172);fem-3(gf) triple mutant, distal germ cells stop proliferating and enter meiosis (Table 3). This indicates that the \textit{glp-1(q172) product supports signal-dependent proliferation in \textit{glp-1(1)/\textit{Tum)} germines and therefore must retain some \textit{glp-1(+) activity. The premeiotic proliferation behavior of \textit{glp-1(q172)} in the \textit{glp-1(null) background does not result from a novel property of the \textit{glp-1(q172) allele; \textit{glp-1(q415) is also strongly suppressed by \textit{glp-1} (Table 3; Figure 8B). That \textit{glp-1(q172)} can support continued premeiotic proliferation in a \textit{glp-1(null) but not a \textit{glp-1(+) background is consistent with the proposal that \textit{glp-1(+) has a role in the negative regulation of premeiotic proliferation. This function of \textit{glp-1}, unlike that which prevents exit from meiotic prophase and a return to mitosis, is not sex-specific.

A second set of experiments was aimed at examining the role of the intracellular domain of the \textit{glp-1} protein in expression of the \textit{glp-1(1)/\textit{Tum)} phenotype. Recent work indicates that the GLP-1 intracellular domain, which contains six ankyrin repeats, is necessary and possibly sufficient for \textit{glp-1-mediated signaling (KODOYANNI et al. 1992; ROEHL and KIMBLE 1993). Double mu-
tants were constructed with two temperature sensitive (ts) glp-1(+/f) mutations that affect an ankyrin repeat: glp-1(q224), a missense mutation in ankyrin repeat 4 that results in a strong Glp-1 phenotype (Austin and Kimble 1987), and glp-1(bn18), a missense mutation at a different site in repeat 4 that results in a weak Glp-1 phenotype (Kodomyanni et al. 1992). For comparison, we also constructed a double mutant with glp-1(q415), a ts mutation in the extracellular domain of GLP-1 that alters the conserved cysteine residue (Figure 8C). Of the three gld-1(null); glp-1(ts) double mutants, the greatest effect on tumor growth was observed with glp-1(q224), the ankyrin repeat mutant with a strong Glp-1 phenotype (Figure 8B). In gld-1(null); glp-1(q224) hermaphrodites, some gonad arms fail to form a tumor (all germ cells differentiated as sperm by late L4), whereas others form tumors that grow more slowly and variably than in the other two double mutants. Thus glp-1(q224) has the strongest effect on tumor formation and growth of any nonnull glp-1(+/f) allele examined. This suggests that normal functioning of the intracellular ankyrin repeats is important for supporting both premeiotic proliferation in gld-1(Tum) germlines and subsequent tumor growth. Consistent with this idea, Figure 8C also shows that the other ankyrin repeat mutant, glp-1(bn18), promotes tumor growth to a lower level than does the extracellular domain mutant glp-1(q415). Because glp-1(bn18) confers a weaker Glp-1 phenotype than glp-1(q415) in a gld-1(+/+) background (Kodomyanni et al. 1992), this difference suggests the intracellular ankyrin repeats play an important role in promoting ectopic proliferation by gld-1(null) germ cells.

In summary, the analysis of gld-1(null); glp-1(0 or f) double mutants shows that glp-1(+) activity is important for two aspects of the gld-1(Tum) phenotype. First, it is required to maintain continued premeiotic...
proliferation by \( gld-1 (Tum) \) germ cells and second, it promotes a maximal level of ectopic proliferation among germ cells that have returned to mitosis. Non-null \( glp-1 (y) \) alleles can differ significantly in their ability to promote ectopic proliferation. In general, ectopic proliferation is promoted more strongly by mutant \( glp-1 \) receptors with an altered extracellular domain than by receptors with an altered intracellular domain.

**DISCUSSION**

The present work extends our understanding of the roles of \( gld-1 \) in germline development. We used epistasis analysis with \( gld-1 (Tum) \) alleles to show that the \( gld-1 \) function necessary for oocyte development acts downstream of (and in response to) the germline sex determination pathway. Therefore tumors are likely to result from a defect in oogenesis. These results do not distinguish between whether \( gld-1 \) functions to specify the oocyte fate or instead act to execute an early essential step in oocyte differentiation. We also address the role of \( gld-1 \) in promoting hermaphrodite spermatogenesis. Results from epistasis analysis using \( gld-1 (Fog) \) and \( gld-1 (Mog) \) alleles are consistent with the proposal that \( gld-1 (+) \) promotes hermaphrodite spermatogenesis by assisting the activities of the terminal \( fem/fog \) genes. Below, we consider a model for how \( gld-1 \) activity might accomplish the seemingly contradictory tasks of directing oogenesis and promoting hermaphrodite spermatogenesis. Finally, we address the role of the somatic gonad and the \( glp-1 \) signaling pathway in promoting tumor formation in \( gld-1 \) mutants.

The germline sex determination pathway controls the \( gld-1 \) function that directs oocyte development: Sexual fates in the \( C. elegans \) germline are determined through the control of five terminal regulators: \( fem-1, fem-2, fem-3, fog-1 \) and \( fog-3 \) (Figure 9) (for recent reviews see Kuwabara and Kimble 1992; Clifford et al. 1994). When the sex determination pathway is set in the male mode (terminal \( fem/fog \) genes active), oogenesis is repressed and germ cells are directed to adopt the male fate and differentiate as sperm. When the pathway is set in the female mode (by inactivation of at least one of the terminal \( fem/fog \) genes), germ cells adopt the female fate and differentiate as oocytes. The male mode is thought to be initially set by the \( fog-2 \) (XX hermaphrodite larvae) and \( her-1 \) (XX males) genes being active, whereas the female mode is initially set by both genes being inactive (XX adults). Previous work has not identified a gene(s) that acts downstream of the \( fem/fog \) genes to specify the female germline fate.

Based on the epistasis results with a null \( gld-1 (Tum) \) allele, Figure 9 shows \( gld-1 (+) \) acting downstream of the sex determination loci as part of the pathway for oogenesis. As this position implies, the behavior of \( gld-1 \) tumorous germ cells was found to depend on the activity state of the terminal \( fem/fog \) genes. When the terminal \( fem/fog \) genes are active, as occurs in the germ-lines of \( X0 \) males and certain \( XX \) mutants [\( tra-2 (f) \), \( tra-3 (f) \), \( tra-3 (Mog) \), \( mog-1 (f) \) and \( fem-3 (gf) \)], \( gld-1 (Tum) \) germ cells differentiate as sperm just as wild-type germ cells do. Conversely, when any one of the terminal \( fem/fog \) genes is inactivated by mutation, \( gld-1 (null) \) germ cells form a tumor regardless of either somatic sexual phenotype or \( X \) chromosome dosage. Feminized \( X0 \) \( gld-1 (null) \) germ cells, for example, form tumors when the soma is female, as in a \( fem-3 (f) \) background, and when the soma is male, as in a \( fog-1 (f) \) or \( fog-3 (f) \) background. Because \( X0 \) \( gld-1 \) tumors are observed in multiple mutant backgrounds, it appears unlikely that they arise from gene- or allele-specific interactions between \( gld-1 \) and genes in the sex determination pathway. Therefore tumor formation in \( gld-1 (Tum) \) animals appears to only require that the germline sex determination pathway is set in the female mode via inactivation of the terminal \( fem/fog \) genes. We place \( gld-1 (+) \) on a branch that directs oocyte development because it does not negatively regulate spermatogenesis.

Functioning at the end of the sex determination pathway, does \( gld-1 (+) \) directly oocyte development by acting to specify the oocyte (female) fate or by acting at an early step in the differentiation of a cell that is already specified as an oocyte (also see Francis et al. 1995)? Knowledge of the sexual identity of \( gld-1 \) tumors is key to distinguishing between these two models: if the tumorous germ cells are sexually uncommitted, then \( gld-1 (+) \) is likely to specify the oocyte fate, but if they are already specified as female, \( gld-1 (+) \) would function in oocyte differentiation. A third possibility, that \( gld-1 \) tumors are intersexual, is unlikely. As elimination of any of the terminal \( fem/fog \) genes has no effect on the \( XX \) tumorous phenotype, intersexuality of \( gld-1 (Tum) \) germ cells would have to result from the inappropriate activation of an as yet unidentified gene that acts downstream of the terminal \( fem/fog \) genes to promote male germ cell development. The genetic epistasis experiments presented here do not distinguish between the first two models as they only show that \( gld-1 \)'s role in oocyte development depends on the upstream sex determination genes being set in the female mode (terminal \( fem/fog \) genes inactive). The uncertainty role of \( gld-1 \) in oocyte development is indicated in Figure 9 by placing \( gld-1 \) in a shaded box that represents both specification of the oocyte fate and oocyte differentiation.

**Analysis of the \( gld-1 \) function that promotes hermaphrodite spermatogenesis:** Experiments discussed in the accompanying paper indicate that \( gld-1 (+) \) has a function in promoting hermaphrodite spermatogenesis. To determine the likely position of this activity in the germline sex determination pathway, we have investigated epistatic relationships between \( gf \) Fog and Mog \( gld-1 \) alleles and mutations in sex determination loci. Interpretation of epistasis data using \( gf \) mutations is less
straightforward than with null mutations because of uncertainties about the exact relationship between the g/l activity and wild-type activity. However, we were not able to use gld-1(null) mutations because the tumorous phenotype precludes us from determining the sexual identity of the germ cells.

Based on genetic studies, the g/l gld-1(Fog) alleles are likely to produce an abnormal gene product that interferes with specification of the male germline fate (Francis et al. 1995). In double mutants, gld-1(Fog) was found to be epistatic to putative null alleles of tra-2 and tra-3. Because the g/l gld-1(Fog) mutant product interferes with hermaphrodite spermatogenesis even in the absence of the tra-2 and -3 products, it must act on or poison the product of another gene that functions downstream or independently of tra-2 and -3. By extension, gld-1(+) is likely to act downstream or independently of tra-2 and -3. Any of the terminal fem/fog gene products are possible candidates for activities that might be poisoned by g/l gld-1(Fog) mutant products; poisoning of terminal fem/fog gene activity would explain why gld-1(Fog) alleles feminize the XO male germline whereas the gld-1(null) mutation does not.

gld-1(Mog) alleles masculinize the hermaphrodite germline by disrupting the switch from spermatogenesis to oogenesis (Francis et al. 1995). The g/l gld-1(Mog) mutations may masculinize the germline by interfering with negative regulation of the terminal fem/fog genes. This hypothesis predicts that spermatogenesis in gld-1(Mog) mutants should be dependent on the terminal
Double mutant analysis shows that male germine development in *gld-1* (Mog) mutants does require the activity of the terminal *fem/fog* genes (Table 2; also see RESULTS).

How does *gld-1* both promote spermatogenesis and provide functions essential for oogenesis? One speculative model to accommodate both functions is based on the idea that the *gld-1* product may exist in two forms, one that promotes spermatogenesis and another that is essential for oogenesis. When the terminal *fem/fog* genes are active, *gld-1* product/activity assumes a state that promotes hermaphrodite spermatogenesis. The altered *gld-1* product/activity might assist or enhance the terminal *fem/fog* genes, for example, and thereby form part of a positive feedback loop that promotes spermatogenesis. However, because spermatogenesis can occur in *gld-1* (null) hermaphrodites and males (Table 1) (FRANCIS et al. 1995), the altered *gld-1* product/activity is not essential for male germine development. When the terminal *fem/fog* genes are inactive, *gld-1* product exists in a state that directs oogenesis. The central feature of this model is that the activity state of terminal *fem/fog* genes determines whether *gld-1* functions to promote hermaphrodite spermatogenesis or to direct oocyte development. There is ample precedent from other systems for regulatory molecules that exist in distinct forms to perform different functions. For example, protein–protein interactions allow the yeast alpha2-alpha1 complex to repress haploid-specific genes, whereas alpha2 alone represses only a cell type specific genes (HERSKOWITZ et al. 1992). Similarly, chemical modification (phosphorylation) converts the *Escherichia coli* OmpR protein from a transcriptional activator to a transcriptional repressor (RAMPERSAUD et al. 1994).

Although it may seem paradoxical that *gld-1* has distinct functions in female and male germine development, a precedent is provided by the *C. elegans* sex determination gene *sxl-1*, which has distinct functions in the two sexes (MILLER et al. 1988). *sxl-1* has a major function in directing the male modes of sex determination and dosage compensation in *XO* animals and a minor function in promoting female development in *XX* animals.

**Etiology of tumor formation and role of the *glp-1* gene:** The *gld-1* (Tum) adult hermaphrodite contains two distinct populations of mitotic germine cells. The first, located at the distal end of the gonad, corresponds to the stem cell population in wild type; the second, which fills the proximal gonad, consists of ectopically dividing tumorous cells. Germ cells that have entered meiotic prophase separate the two populations of proliferative cells (Figure 4A). To distinguish the two groups of mitotically active cells, we refer to the normal mitotic population as "premeiotic germ cells" and the ectopically proliferating population as a "germline tumor" (see RESULTS). Our previous studies of *gld-1* (Tum) hermaphrodites suggested that tumors arise from germ cells that exit meiotic prophase and return to mitosis (FRANCIS et al. 1995). Several results presented here further support this idea, while also demonstrating that *gld-1* (Tum) alleles have no major effect on the controls that govern premeiotic proliferation. Two lines of investigation indicate that premeiotic proliferation in *gld-1* (Tum) hermaphrodites is, for the most part, dependent on the *glp-1*-mediated signaling pathway. First, when the DTC is killed in *XX gld-1* (Tum) larvae, distal germ cells stop proliferating and enter meiotic prophase (Figure 5). Therefore, as in wild type (KIMBLE and WHITE 1980), premeiotic proliferation by *gld-1* (Tum) germ cells is dependent on the signaling molecule produced by the DTC. Second, the *glp-1* gene, which encodes the likely receptor for the DTC signal, is also required for premeiotic proliferation in *gld-1* (Tum) mutants. In *XX gld-1* (Tum) larvae homozygous for a *glp-1* molecular null mutation [designated *glp-1*(0)] (KODOVANNI et al. 1992; CRITTENDEN et al. 1994), germ cells divide several times but then prematurely enter meiosis and form sperm (Table 4 and Figure 7b). Taken together, these results demonstrate that *gld-1* (Tum) alleles do not override the normal controls that make premeiotic proliferation dependent on the *glp-1* signaling pathway.

In contrast to its role in premeiotic proliferation, the *glp-1* signaling pathway is not required for the ectopic proliferation that accounts for tumor formation in *gld-1* (Tum) hermaphrodites. After DTC ablation in *LS/L4* larvae, distal germ cells enter meiotic prophase but then return to mitosis (Table 3 and Figure 4). Thus, in the absence of the DTC signal, germ cells can return to mitosis. Investigation of the role of *glp-1* activity in the return to mitosis phenotype is complicated by the fact that all germ cells in *gld-1* (Tum);*glp-1*(0) animals differentiate as sperm during larval growth. Therefore we examined *XX gld-1* (Tum);*glp-1*(0) triple mutants whose germine had been feminized by a *l(f2)* mutation in one of three genes (*fem-1*, *fem-3* or *fog-1*). As in the double mutants, all germ cells in the feminized triple mutants enter meiosis prematurely: by mid-L3, each hermaphrodite gonad arm contains only 15–18 germ cells, all of which reach pachytene at approximately the same time (Table 4 and Figure 7c). Because the germine sex determination pathway is set in the female mode, triple mutant germ cells do not form sperm but instead return to mitosis and give rise to a tumor (Figure 7a). The observation that all germ cells in the feminized triple mutants enter pachytene provides further evidence that tumors derive from meiotic prophase germ cells that return to mitosis. As tumor formation occurs in the absence of *glp-1*(+) activity, neither the initial exit from pachytene nor the subsequent ectopic proliferation can result solely from a failure to negatively regulate *glp-1*(+) activity during meiotic prophase.

Although *glp-1* activity is not essential for tumor for-
mation in glp-1 (Tum) animals, its elimination has quantitative and qualitative effects on tumor growth. Tumors grow more slowly and variably in the absence of glp-1 activity (Figure 6), and many tumorous germ cells exhibit abnormal nuclear morphologies that are not seen in a glp-1(+) background. These differences suggest glp-1 protein may be important for promoting the maximal level of cell cycling by germ cells undergoing ectopic proliferation. Indeed, CRITTENDEN et al. (1994) show that ectopically proliferating cells in glp-1 (Tum) germlines express glp-1 protein at high levels. Because glp-1 protein is not required for tumors to form, its expression by tumorous germ cells is likely to represent a secondary consequence of proliferation; in particular, ectopic proliferation may lead to a general upregulation of factors that drive mitosis, including glp-1. Because it is unclear whether proximal germ cells are exposed to glp-1 ligand, it is possible that ligand is not necessary for the promotion of ectopic proliferation by glp-1. The intracellular ankyrin repeats of glp-1, which mediate signaling (KODOMANNI et al. 1992; ROEHL and KIMBLE 1993), do seem to play a critical role in promoting glp-1 (Tum) ectopic proliferation, as glp-1 mutations affecting these repeats more severely diminish tumor growth than do mutations affecting the extracellular domain of the protein (see RESULTS).

**glp-1 functions as a sex nonspecific negative regulator of premeiotic proliferation:** An unexpected finding to emerge from these studies is that glp-1 (Tum) alleles can have a small effect on premeiotic proliferation. Elimination of glp-1 (+) function clearly does not override the need for the glp-1 signaling pathway because all germ cells in glp-1 (Tum); glp-1 (0) double mutants (both XX and XO) and feminized triple mutants enter meiosis prematurely. However, compared with glp-1 (0) single mutants, germ cells in the double and triple mutants undergo two extra rounds of division before entering meiosis (Table 4). Although slight, this effect suggests that glp-1 may play a nonessential role in either negatively regulating premeiotic proliferation or promoting entry into meiotic prophase. Because added premeiotic divisions occur in both double mutants (which produce sperm) and feminized triple mutants (which produce tumors), this effect of glp-1 (Tum) alleles is not dependent on germline sexual fate. This suggests that the glp-1 function regulating premeiotic proliferation is distinct from the sex-specific glp-1 function required for oogenesis.

Because glp-1 (Tum) and glp-1 (If) mutations have opposite effects on premeiotic proliferation, it is possible that glp-1 (+) might promote entry into meiotic prophase by acting as a negative regulator of glp-1 (+) activity. However, if this is the case, glp-1 cannot be the only negative regulator of glp-1, as germ cells enter meiotic prophase normally in the glp-1 (null); glp-1 (+) single mutant. Moreover, negative regulation of a molecule distinct from glp-1 must play a role in the inhibition of mitosis by glp-1. The two extra rounds of proliferation and entry into meiotic prophase observed in the glp-1 (null); glp-1 (0) double and feminized triple mutants are not dependent on glp-1 activity. Two lines of evidence argue that germlines of these animals completely lack glp-1 product. First, the two glp-1 (0) alleles used in this study make no detectable glp-1 protein (KODOMANNI et al. 1992; CRITTENDEN et al. 1994). Second, antibody staining and RNA in situ hybridization data (EVANS et al. 1993; CRITTENDEN et al. 1994; SEYDOUX and FIRE 1994) argue that glp-1 (0) mutant larval germ cells are unlikely to contain maternally derived glp-1 (+) RNA (or protein made from maternal RNA).

If glp-1 (+) inhibits premeiotic germ cell proliferation (either by negatively regulating a factor distinct from glp-1 or by negatively regulating glp-1 and a second molecule), we reasoned that an absence of glp-1 (+) function might lead to suppression of the proliferation defects found in nonnull glp-1 (If) mutants. In fact, glp-1 (null) is partially or completely epistatic to several glp-1 mutations that alter residues in the extracellular glp-1 domain (Figure 8). Because full epistasis was observed with glp-1 (q172), a strong If mutation, the combination of glp-1 (Tum) and glp-1 (q172) was examined in most detail. The strong epistasis of glp-1 (null) to glp-1 (q172) is the result of two effects. First, even though q172 is a strong glp-1 (If) allele, it appears to promote ectopic proliferation in tumors to approximately the same extent as does a glp-1 (+) allele (Figure 8A). Second, premeiotic proliferation in this double mutant also appears normal. This was initially indicated by examination of X0 glp-1 (Tum); glp-1 (q172) animals, which have a normal male germline, and confirmed by ablation results that show that the DTC is essential for premeiotic proliferation in the double mutant (Table 3). The DTC ablations indicate that glp-1 (q172) product must retain some residual glp-1 (+) receptor function. Apparently, glp-1 (null) mutants either increase residual glp-1 activity in the glp-1 (If) mutants or allow premeiotic proliferation to occur at a level of glp-1 activity that is not sufficient in a glp-1 (+) background.

Certain other glp-1 (If) mutations (e.g., q115 and q158; Figure 8) that affect the extracellular domain of glp-1 also show substantial suppression of the glp-1 (If) proliferation defect in a glp-1 (null) background. Like q172, these alleles probably retain some glp-1 (+) function. In contrast, glp-1 (q224), a mutation in one of the intracellular ankyrin repeats of glp-1, is only weakly suppressed by glp-1 (null).

Taken together, the various combinations of glp-1 and glp-1 mutations suggest that glp-1 (+) acts to negatively regulate germ cell proliferation before entry into the meiotic pathway. Because this glp-1 (+) function is not dependent on sexual fate, it must be distinct from the glp-1 function required for oogenesis. Because premeiotic glp-1 function is clearly not essential for the negative regulation of proliferation required for entry
into meiotic prophase, it is possible that this gld-1 (+) function is redundant with that of another gene (s). These results thus suggest that gld-1 acts to negatively regulate mitosis at two distinct stages of germ line development: premeiotically, in both sexes, and during the pachytene stage of meiotic prophase, when the upstream sex determination cascade is set in the female mode.

**gld-1 is a cell-type specific tumor suppressor gene:** Tumor formation in animals lacking gld-1 activity is not only restricted to a single tissue (the germ line) but is also dependent on sexual identity. A consequence of this sex specificity is that expression of the tumorous phenotype can be manipulated by changes in cell identity. In gld-1(Tum) hermaphrodites, X0 germ cells that would normally form a tumor can instead differentiate as sperm when the germ line is masculinized by a mutation in a second gene (e.g., fem-3(gf)). Thus differentiation along an alternative pathway (spermatogenesis) has the effect of suppressing tumor formation. X0 gld-1(Tum) males are unaffected, as mutant germ cells adopt the male fate and execute spermatogenesis normally. However, when the male germ line fate is inactivated by a mutation in a second gene (fog-1(ly) or fog-3(ly)), X0 gld-1(Tum) germ cells form a tumor by the same mechanism as do mutant X0 germ cells. Because fog-1 and fog-3 mutations by themselves cause X0 germ cells to develop as oocytes, the likely role of fog-1 and fog-3 mutations in generating male germ cell tumors is that they set the germ line sex determination pathway in the female mode. This change then generates a cell type that responds to the absence of gld-1 activity by exiting meiotic prophase and proliferating ectopically.

Could changes in cell identity play a role in multistep tumorigenesis in mammals? One example where an alteration in cell type may be important for tumor formation is the acute lymphoblastic leukemia caused by the t(10;14) (q24q11) translocation (Hatano et al. 1991). The translocation causes T cells to ectopically express the homeobox gene SPX (also called Hopx1), a locus required for spleen development (Hatano et al. 1992; Roberts et al. 1994). Ectopic expression of SPX presumably results in the expression of genes that are inappropriate for T cell development and may potentially generate a hybrid cell type that is susceptible to additional events leading to tumor formation.

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**LITERATURE CITED**


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