# Coordinately and Differentially Mutable Activities of torpedo, the Drosophila melanogaster Homolog of the Vertebrate EGF Receptor Gene

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#### ABSTRACT

The torpedo (top) locus of Drosophila encodes the fruitfly homolog of the vertebrate epidermal growth factor receptor gene and the neu proto-oncogene. We have isolated 13 top alleles in a screen for mutations failing to complement the female sterility of  $top^{1}$ , a recessive maternal effect allele that disrupts the establishment of the dorsoventral pattern of the egg shell and embryo. Several alleles recovered in this screen are zygotic lethal mutations; genetic analysis of these alleles has demonstrated that top is allelic to the embryonic lethal locus faint little ball. The 13 mutations recovered in our screens and 19 previously isolated top alleles have been genetically characterized through complementation tests with a series of hypomorphic and amorphic alleles. Nearly every top allele fails to complement the maternal effect sterility of top'. Complementation tests show that the gene is required not only for oogenesis and embryogenesis, but also for pupal viability, for the growth of certain imaginal discs and for the patterning of specific ectodermal derivatives of the imaginal discs. Complementation analysis further demonstrates that the top lesions can be divided into general phenotypic categories: alleles affecting all gene activities in a coordinate manner, alleles preferentially affecting embryogenesis, alleles preferentially retaining oogenesis activity and alleles differentially affecting the development of specific imaginal disc, derivatives. Correlations observed between the various developmental defects produced by top lesions suggest that the gene possesses several differentially, though not independently, mutable activities.

 ${f R}^{
m ECEPTOR}$  tyrosine kinases play a central role in the regulation of cell proliferation and differentiation in vertebrates. This class of proteins includes the insulin receptor, receptors for a number of peptide growth factors and several of the known oncogenes. Biochemical and molecular studies using avian and mammalian cell lines have provided a wealth of information on the structure and function of these proteins. All receptor tyrosine kinases are structurally similar, consisting of an extracellular ligand binding domain, a hydrophobic membrane spanning region and an intracellular tyrosine kinase domain (reviewed in YARDEN and ULLRICH 1988). Although tissue culture studies have provided insights into the role these receptors play in the proliferation and differentiation of specific cell types, they have so far not proven useful for investigating the function of these genes in the development of the organism as a whole.

The molecular identification of Drosophila genes homologous to vertebrate receptor tyrosine kinases (reviewed in SHILO 1987) suggested that the fly can serve as a system for the genetic and developmental analysis of such transmembrane receptors. DER, the first receptor tyrosine kinase identified in Drosophila, was detected by LIVNEH et al. (1985) and WADS-WORTH, VINCENT and BILODAEU-WENTWORTH (1985) by virtue of its homology to v-erb-B, an avian oncogene derived from the epidermal growth factor receptor (DOWNWARD et al. 1984). Determination of the complete amino acid sequence of DER indicated that it is equally related to the EGF receptor gene and neu proto-oncogene (SCHECHTER et al. 1984; ULLRICH et al. 1984; SCHEJTER et al. 1986; SCHEJTER and SHILO 1989), while molecular studies have shown that the gene is expressed throughout the life of the fly in a variety of tissues (LEV, SHILO and KIMCHIE 1985; KAMMERMEYER and WADSWORTH 1987). PRICE, CLIF-FORD and SCHÜPBACH (1989) and SCHEJTER and SHILO (1989) have recently demonstrated that DER is encoded by the torpedo (top) locus. In the following work, we describe a genetic characterization of top intended to lay the foundation for a comprehensive analysis of the developmental role of this receptor in the fly.

The original top lesion,  $top^1$ , is a maternal effect lethal mutation isolated in a screen for recessive female sterile loci on the second chromosome of Drosophila. Females homozygous for this mutation produce eggs with ventralized egg shells that give rise to correspondingly ventralized embryos; these pattern alterations result from shifts in cell fate rather than localized cell death (SCHÜPBACH 1987). In Drosophila

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the egg shell is produced by the mesodermally derived follicle cells, while the establishment of the embryonic body plan is regulated by asymmetrically distributed determinants within the oocyte (a cell of germline origin). Since a mutation in top alters both patterns the gene must participate in a process by which the spatial pattern of the germline and somatic components of the egg chamber are coordinately established or maintained. top is unusual among the known female sterile loci affecting both the chorion and embryonic patterns, as top is required exclusively in the somatic tissues of the female (WIESCHAUS, MARSH and GEHR-ING 1978; WIESCHAUS 1979; FREY and GUTZEIT 1986; SCHÜPBACH 1987; MANSEAU and SCHÜPBACH 1989). Given the homology in predicted protein sequence, this suggests that the top product acts in the follicle cells as the receptor for an intercellular signal required for the establishment of polarity in the developing egg chamber.

This report presents a genetic demonstration that the *top* locus corresponds to the zygotic embryonic lethal gene *faint little ball*, first identified by NÜSSLEIN-VOLHARD, WIESCHAUS and KLUDING (1984). We further show that *top* is required not only for embryogenesis and oogenesis, but also for a variety of other developmental processes occurring throughout the life of the fly. Lesions in the gene lead to pupal lethality, disrupt the growth of certain imaginal discs and produce discrete pattern defects in the adult derivatives of the eye-antennal, humeral, wing, leg and genital imaginal discs. A phenotypic analysis of this gene indicates that several of these developmental processes can be preferentially, though not exclusively, affected by particular *top* lesions.

#### MATERIALS AND METHODS

**Stocks:** The mutations, chromosomal rearrangements and balancer chromosomes used in this study are described in LINDSLEY and GRELL (1968) or LINDSLEY and ZIMM (1985) unless otherwise noted.

CyO DTS-100 and CyO DTS-513 are CyO-derived balancer chromosomes bearing dominant temperature sensitive lethal mutations (Falke and Wright 1973). The lethal phase of CyO DTS-100 begins after embryogenesis and continues throughout the life cycle, while the temperature sensitive period of CyO DTS-513 is restricted to embryogenesis (STEW-ARD and NÜSSLEIN-VOLHARD 1986).

Fs(2)1 is a dominant second chromosomal female sterile mutation that does not affect male fertility. Females heterozygous for Fs(2)1 produce spindle-shaped eggs that never hatch (SZABAD, ERDÉLYI and SZIDONYA 1987).  $top^1$ ,  $gurken^{HK}$ and  $gurken^{WG}$  are described in SCHÜPBACH (1987);  $cappuccino^{RK}$  and  $spire^{RP}$  are described in MANSEAU and SCHÜPBACH (1989). 25.11 is a multiply marked tester chromosome bearing the female sterile mutations  $cappuccino^{RK}$ ,  $gurken^{WG}$ ,  $chalice^{WP46}$ ,  $spire^{RP}$  and  $torpedo^1$ , as well as the eye color mutations cn and bw.

faint little ball alleles (NÜSSLEIN-VOLHARD, WIESCHAUS and KLUDING 1984; O'DONNELL et al. 1989) were kindly provided by R. Boswell, C. Nüsslein-Volhard, J. O'Don-Nell and E. Wieschaus.

Fly food: Flies were grown on cornmeal agar medium described in CLINE (1978). Apple juice agar medium used for egg collections is described in WIESCHAUS and NÜSSLEIN-VOLHARD (1986).

**EMS mutagenesis:** To generate new *top* alleles, males homozygous for a lethal-free, previously isogenized, second chromosome marked with *b pr cn sca* were fed 50 mM EMS in 1% sucrose essentially as described by LEWIS and BACHER (1968). The males were starved on wet paper towels for 4 hr, then transferred to bottles containing five Kimwipes soaked with 12 ml of a 1% sucrose, 50 mM EMS solution. Alter 24 hr, mutagenized males were transferred to fresh medium, allowed to recover for 24 hr, then mated to *b Tft/ CyO DTS-100* virgin females (~50 males and ~150 females per bottle) at 18° as shown in Figure 1.

 $F_1$  (b pr cn sca)\* /CyO DTS-100 virgin females were mass mated to 25.11 /Fs(2)1 males at 18° for 3 days (Figure 1), then individually transferred to prewarmed vials at 29°. After 7 days, the females were discarded and the vials were maintained at 29°. Since CyO DTS-100 acts as a dominant lethal at temperatures above 25°, all F2 animals were either  $(b \ pr \ cn \ sca)^*/25.11 \ or \ (b \ pr \ cn \ sca)^*/Fs(2)1; \ as \ Fs(2)1 \ is \ a$ dominant female sterile mutation, the fertility of the (b pr  $cn \ sca$ )\*/25.11 females could be assayed by examining vials for the presence of first instar larvae 7-10 days after the eclosion of the  $F_2$  generation. The absence of  $F_3$  animals indicated either sterility of the F2 parents or, alternatively, the presence of a lesion on the mutagenized chromosome that is lethal when in trans to the 25.11 chromosome; such lethal mutations could then be recovered through the  $F_2$  (b  $pr \ cn \ sca$ )\*Fs(2)1 males. Putative top alleles were retested by crossing (b pr cn sca)\*/25.11 males to top' bw/CyO and gurken<sup>wG</sup> cn bw/CyO virgin females. The resulting (b pr cn sca)\*/top<sup>1</sup> bw and  $(b \ pr \ cn \ sca)*/gurken<sup>WG</sup> cn \ bw$  females were tested for fertility at 18° and 29°, and stocks were established by mating (b pr cn sca)\*/CyO males and virgin females inter se. Of 5222 mutagenized chromosomes screened in this manner, 9 carried top lesions.

An additional 3250 chromosomes were examined in a similar screen employing the Fs(2)D dominant female sterile mutation. In this screen, however, single mutagenized chromosomes were obtained from both F<sub>1</sub> males and females. A total of 1197 (*b* pr cn sca)\*/CyO DTS-100 F<sub>1</sub> virgin females were mated to 25.11/Fs(2)D males, and their progeny were screened for sterility as described above. In addition, 2053 (*b* pr cn sca)\*/CyO DTS-100 F<sub>1</sub> males were transferred to separate vials containing two 25.11/CyO DTS-100 females. The F<sub>1</sub> animals were allowed to mate in the vials for 1 week at 29°, then discarded. The F<sub>2</sub> generation, consisting solely of (*b* pr cn sca)\*/25.11 animals, was examined for fertility. This screen yielded 2 top mutations.

Two additional top alleles were isolated in a pilot screen of 267 b pr cn sca chromosomes mutagenized with 50 mM EMS and examined over a gurken<sup>HK</sup> cn top<sup>1</sup> bw tester chromosome. This mutagenesis screen involved mating individual  $F_1(b \ pr \ cn \ sIa)^*/CyO \ DTS-513$  males and virgin females to gurken<sup>HK</sup> cn top1 bw/CyO \ DTS-513 virgins or males in single vials at 29°. Because of the high frequency of CyO DTS-513 escapers in this screen the  $F_2(b \ pr \ cn \ sca)^*/gurken^{HK}$ cn top<sup>1</sup> bw females were hand selected and tested for sterility in egg laying blocks as described in WIESCHAUS and NÜS-SLEIN-VOLHARD (1986).

**Complementation tests and determination of lethal phenotypes:** Adult phenotypes of *top* heteroallelic combinations were determined in the following manner. Three to five  $top^*/CyO$  or  $top^*/SM1$  virgin females were crossed to an equal

number of top<sup>y</sup> /CyO or top<sup>y</sup>/SM1 males at 25°. Fifty top<sup>x</sup>/ top' progeny (unless otherwise noted) from each cross were scored for wing, eye and thoracic bristle defects at 25× under a Zeiss dissecting microscope, then placed in 70% ethanol for storage. To score cephalic structures, heads from an equal number of male and female flies of each genotype were dissected in 70% ethanol, bleached in 10% NaOH at 60° for 15-30 min, gently squeezed between the tips of a forceps to remove eye pigments, then washed in distilled H<sub>2</sub>O at 60° for at least 30 min. Bleached heads were mounted in a drop of Hoyer's mountant (WIESCHAUS and NÜSSLEIN-VOLHARD 1986) on a microscope slide, allowed to clear overnight at 40°, then flattened with weights. Head bristle, arista and ocellar defects were scored under a Zeiss compound microscope at 100×. The severity of compound eye defects were initially determined by examining the heads of 50 flies under a dissecting microscope, then verified by examining ten mounted heads at 400× using phase contrast optics. To avoid bias resulting from possible sex-specific differences in eye phenotypes, an equal number of male and female flies were examined whenever practicable. To examine the female sterile phenotype of the various top mutations, top females were transferred to egg laying blocks as described in WIESCHAUS and NÜSSLEIN-VOLHARD (1986). Eggs were examined at 25× under a Zeiss dissecting micro-

To determine whether the phenotypes observed in the complementation tests are reproducible, the  $top^{1}/top^{1}$ ,  $top^{1}/top^{co}$ , and  $top^{1}/top^{EB}$  complementation tests were repeated under the same conditions as the original complementation tests. In most cases, the frequency of bristle and wing vein defects observed in the repeat crosses differed by no more than 10% from the frequencies seen in the first round of tests, and the roughened eye and female sterile phenotypes also exhibited little variability.

To verify that the phenotypes seen over  $top^{1}$  accurately reflect each mutation's eye, wing, bristle and oogenesis activity rather than particular properties of or specific allelic interactions with the top' lesion, complementation tests were also performed between all top alleles and  $top^{CJ}$ ,  $top^{EE38}$  and  $top^{CA}$ . In general the mutant phenotypes correlated well with the severity of the tester allele used. The inconsistent behavior of some adult structures (e.g., the anterior crossvein) seen in comparisons between heteroallelic combinations employing different adult viable alleles (Figures 9 and 10) may reflect either region-specific variability in the expression of the mutant phenotype or allele-specific interactions between different mutations. Such variability, however, is exhibited only by a few structures and is rarely of great magnitude. In nearly every case, the regional specificities of each top allele's adult defects and the severity of its defects relative to those of other top alleles seen in complementation tests with  $top^{CJ}$ ,  $top^{EE38}$  and  $top^{CA}$  are in accord with those observed in combination with  $top^{1}$ .

To limit phenotypic variation due to genetic background, adult phenotypes of the *top* mutations were assayed, whenever possible, in combination with an adult viable allele induced in a different genetic background. The genetic background of *top*<sup>1</sup> differs from that of the other lesions examined in this study; thus all heteroallelic combinations involving *top*<sup>1</sup> satisfy the above condition. Most complementation tests involving  $top^{CJ}$ ,  $top^{EE38}$  and  $top^{CA}$  also meet this condition. When mutations derived from the same genetic background as  $top^{CJ}$ ,  $top^{EE38}$  or  $top^{CA}$  were examined over these adult viable alleles, a recombinant version of the chromosome carrying the adult viable tester allele was used for the complementation test. Since many of the *top* alleles examined in this study have not been extensively outcrossed, it is possible that some of the phenotypes are modified due to the effects of background mutations.

Embryonic cuticles were prepared as is described in WIE-SCHAUS and NÜSSLEIN-VOLHARD (1986) and examined under a Zeiss compound microscope at  $63\times$ ,  $160\times$ ,  $250\times$  and  $400\times$  with phase contrast optics. Chorions were prepared for photography by standard methods (WIESCHAUS and NÜS-SLEIN-VOLHARD 1986). Scanning electron micrographs of compound eyes and ocelli were made using live flies; animals were examined with a JEOL JSM 840-II scanning electron microscope at 3-5 kV.

**Determination of the** *torpedo* **postembryonic lethal phases:** The following scheme was employed to determine the lethal periods of postembryonic lethal *top* allelic combinations.  $Df(2R)top^{3F18}/CyO$  virgin females were mated to  $top^{*/Bc}$  males (where  $top^{*}$  represents the semiviable allele  $top^{CA}$  or the pupal lethal allele  $top^{EB}$  or  $top^{EC20}$ . No cross produced significant numbers of dead embryos. The larvae from each cross were divided into two groups, those possessing darkly pigmented cells  $(Bc/Df(2R)top^{3F18}$  and Bc/CyO) and those showing wild-type pigmentation  $(top^{*}/$  $Df(2R)top^{3F18}$  and  $top^{*}/CyO$ ). The lethal phase of each combination was determined from the number of larvae, pupae and eclosing adults in the latter group. Although each mating yielded approximately equal numbers of Bc and  $Bc^{+}$ pupae, only half of the  $Bc^{+}$  animals reached adulthood. All eclosing non-Bc animals were genotypically  $top^{*}/CyO$ .

**Determination of imaginal disc phenotypes:** To determine whether *top* mutants dying early in pupation show imaginal disc abnormalities at earlier stages of development, animals of a representative pupal lethal genotype,  $top^{EC20}/Df(2R)top^{3F18}$ , were examined. *cn*  $Df(2R)top^{3F18}$  bw sp/CyOfemales were crossed to *cn*  $top^{EC20}$  bw/CyO males. The adults were transferred to fresh vials daily. F<sub>1</sub> larvae were allowed to develop until they began crawling up the sides of the vials.  $top^{EC20}/Df(2R)top^{3F18}$  larvae (which are homozygous for *cn* and *bw* and possess unpigmented Malpighian tubules) could be distinguished from their genetically wild-type sibs (possessing yellow Malpighian tubules). Imaginal discs of mutant and wild-type larvae were dissected out in a drop of distilled H<sub>2</sub>O, fixed in 2.5% glutaraldehyde in phosphatebuffered saline for approximately 30 min, then mounted on microscope slides in a drop of distilled H<sub>2</sub>O and examined under the compound microscope.

#### RESULTS

#### Isolation of torpedo mutations

At the outset of this study, only one torpedo mutation,  $top^{1}$ , had been recovered. This lesion is homozygous viable and female sterile (SCHÜPBACH 1987). To identify new alleles of top, an ethyl methanesulfonate (EMS) mutagenesis was performed. Mutagenized chromosomes were tested for female sterility or lethality in trans to a tester chromosome carrying  $top^{1}$ . Thirteen top alleles were recovered from 8739 mutagenized chromosomes examined in our screens (see MATERIALS and METHODS and Figure 1). All 13 alleles are recessive, all are viable in combination with  $top^{1}$ and none is conditionally female sterile.

An examination of *top* alleles recovered in the EMS screens showed that seven of these 13 mutations, both in the homozygous state and in *trans* to  $Df(2R)top^{3F18}$  are required zygotically during embryogenesis and

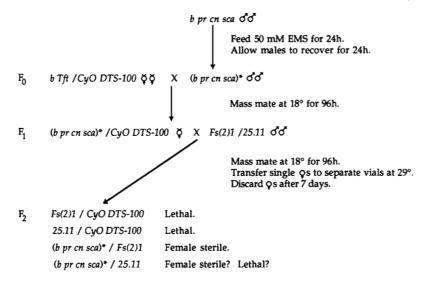


exhibit lethal phenotypes identical to those produced by lesions in the zygotic embryonic lethal locus faint little ball (flb, 2-101; NÜSSLEIN-VOLHARD, WIESCHAUS and KLUDING 1984) (Table 1). To demonstrate that top and flb mutations are allelic, 14 EMS-generated flb alleles isolated by NÜSSLEIN-VOLHARD, WIESCHAUS and KLUDING (1984), as well as a single ethylnitrosourea-induced and three EMS-induced flb mutations isolated by O'DONNELL et al. (1989) (Table 1) were crossed to  $top^{1}$  and  $top^{CJ}$  and scored for their ability to complement the oogenesis defects. All flb alleles fail to complement the two viable top mutations for female sterility (see below). By the same token,  $top^{CO}$ , isolated as a female sterile lesion over  $top^1$ , fails to complement the zygotic lethality of any *flb* mutation (data not shown). Therefore top and flb alleles are lesions in the same gene.

# Stage and spatial specificity of the torpedo phenotypes

To determine the temporal and tissue requirements for the *top* gene product, the 32 available *top* mutations were phenotypically examined in the homozygous state and in combination with selected alleles. This analysis revealed that lesions at the top locus produce four developmentally distinct defects: zygotic embryonic lethality, zygotic pupal lethality, imaginal disc pattern abnormalities and a maternal effect ventralization of the egg shell and embryo. Characterization of the mutant phenotypes has provided insights into the role *top* plays in development, and the correlations observed between the various defects have shed light on the functional organization of the gene. The phenotypes upon which these developmental and functional analyses are based are described below.

torpedo is required zygotically for embryonic development: Twenty-five of the 32 available top lesions exhibit embryonic lethality (Table 1). These muta-

FIGURE 1.-Mutagenesis screen for the isolation of torpedo mutations. CyO DTS-100 is a balancer chromosome that carries a dominant temperature-sensitive mutation that is lethal at  $29^\circ$ ; Fs(2)1 is a dominant female sterile mutation that has no effect on male fertility; 25.11 is a tester chromosome carrying the top<sup>1</sup> lesion. Single mutagenized chromosomes were recovered and balanced over the CyO DTS-100 chromosome in F1 females. Individual females were mated to Fs(2)1/25.11 males to establish lines of single mutagenized chromosomes. Progeny of these matings were raised at the restrictive temperature to kill flies carrying the balancer; consequently, the surviving flies were of either the  $(b \ pr \ cn \ sca)^*/Fs(2)I$  (female sterile) or  $(b \ pr \ cn \ sca)^*/25.11$  genotype. Vials containing F<sub>2</sub> lines derived from mutagenized chromosomes that are female sterile or lethal in combination with the 25.11 tester could be identified by the absence of F<sub>3</sub> progeny. Chromosomes carrying putative top mutations were recovered through (b pr cn sca)\*/25.11 or (b pr  $cn \ sca)^*/Fs(2)1$  males and retested over  $top^1$ .

tions show a range of "faint little ball" ("flb") lethal phenotypes that can be clearly arranged in order of severity: 14 lesions show a severe "flb" lethal phenotype, five a moderate "flb" phenotype and six exhibit a weak embryonic lethal phenotype. Animals homozygous for a deficiency of the locus or a strong top point mutation die as embryos that are tightly curled and folded back upon themselves, show anterior and posterior cuticular holes and possess few, if any, ventral setae (Figure 2D). Embryos of moderate phenotypes (Figure 2C) also show a large anterior hole, produce a poorly differentiated head skeleton and are curled upon themselves. These animals, unlike severe mutant embryos, often undergo partial germband retraction and possess nearly intact posterior cuticle. Weak embryonic lethal alleles (Figure 2B) produce an essentially intact cuticle and possess well-defined denticle belts. Mutant denticle bands are, however, composed of fewer and smaller ventral setae than wildtype denticle belts. Weak "flb" animals also exhibit reductions in the ventral plate and H-piece of the head skeleton and often show a "U-shaped" or "tail up" phenotype.

torpedo is required for pupal viability: Three top alleles allow homozygous embryos to develop normally but always cause lethality prior to eclosion of the adult (Table 1). To avoid possible obscuration of the terminal phenotypes of these postembryonic lethal alleles by background mutations, we determined their lethal phases over  $Df(2R)top^{3F18}$ . In combination with a deletion of the locus, two of these mutations die during early pupation. Animals homozygous for a fourth allele,  $top^{CA}$ , usually die during postembryonic development; the few  $top^{CA}$  homozygotes that do eclose survive poorly as adults. In *trans* to the deficiency,  $top^{CA}$ , too, exhibits pupal lethality (Table 1, see below).

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TABLE 1 torpedo alleles used in this study

Allele	Origin	Homozygous phenotype	Phenotype over Df	Reference <sup>a</sup>
top'	EMS	Viable	Viable	1
tob 38	EMS	Severe flb	Severe flb	2
top 101	EMS	Weak <i>flb</i>	Weak flb	2
top	EMS	Semiviable	Late pupal	2
top	EMS	Viable	Viable	2
topco	EMS	Severe flb	Severe flb	2
topEA	EMS	Postembryonic	Weak flb	2
topEB	EMS	Postembryonic	Early pupal	2
tob EC20	EMS	Postembryonic	Early pupal	2
tob ED16	EMS	Late embryonic	Late embryonic	2
tob <sup>ED26</sup>	EMS	Intermediate flb	Severe flb	2
tobEE38	EMS	Viable	Viable	2
tob <sup>EE39</sup>	EMS	Intermediate flb	Intermediate flb	2
tob EE42	EMS	Severe flb	Severe flb	2
top IF26kb	EMS	Weak flb	Weak flb	3
top1K35	EMS	Severe flb	Severe flb	3
tob 1P02	EMS	Severe flb	Severe flb	3
tob2082	EMS	Intermediate flb	Intermediate flb	3
tob2E07	EMS	Weak flb	Intermediate flb	3
tob2631	EMS	Intermediate flb	Intermediate flb	3
tob21.65	EMS	Severe flb	Severe flb	3
tob2W74b	EMS	Weak flb	Weak flb	3
tob2X51	EMS	Severe flb	Severe flb	3
tob 3B41	EMS	Severe flb	Severe flb	3
tob 3892	EMS	Severe flb	Severe flb	3
tob 3C81	EMS	Severe flb	Severe flb	3
tob 3C87	EMS	Severe flb	Severe flb	3
tob 3F18c	EMS	Severe flb	Severe flb	3
tobJEld	EMS	Severe flb	Severe flb	4
tob JE13e	EMS	Severe flb	Severe flb	4
tob JE14f	EMS	Intermediate flb	Not determined	4
top <sup>SH2b.g</sup>	ENU	Weak flb	Intermediate flb	4

<sup>a</sup> 1, Schüpbach (1987); 2, This work; 3, Nüsslein-Volhard, Wieschaus and Kluding (1984); 4, O'Donnell *et al.* (1989).

<sup>b</sup> These alleles are temperature-sensitive, exhibiting a more extreme "flb" phenotype at 29° than at 18°. No allele is, however, wildtype at 18°.

<sup>c</sup> This allele is a deficiency uncovering the 57D8,9-E1; 57F5-10 cytological interval (PRICE, CLIFFORD and SCHUPBACH 1989).

- <sup>d</sup> Designated l(2)57DEFa-1 in O'Donnell et al. (1989).
- Designated l(2)57DEFa-2 in O'Donnell et al. (1989).
- <sup>f</sup> Designated l(2)57DEFa-3 in O'Donnell et al. (1989).

<sup>g</sup> Designated l(2)57DEFa-4 in O'Donnell et al. (1989).

torpedo is required for the development of several imaginal discs: The role of top for pupal viability suggested that the gene may be needed for imaginal disc development. To investigate this possibility, imaginal discs from mature third instar larvae of the pupal lethal genotype  $top^{EC20}/Df(2R)top^{3F18}$  were examined. We have observed abnormalities in three imaginal discs in these animals. In  $top^{EC20}/Df(2R)top^{3F18}$  larvae, the portion of the eye-antennal disc that gives rise to the eye is reduced in size; on the other hand, the anterior lobe of the eye-antennal disc, which develops into the antenna, appears normal (Figure 3G). The development of the wing and haltere imaginal discs is also clearly altered in the mutant. Both discs are

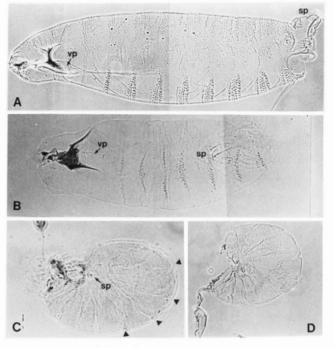


FIGURE 2.—Cuticular phenotypes of zygotic embryonic lethal torpedo alleles. (A) wild-type embryo. Anterior is to the left and dorsal is up. The ventral abdominal cuticle of the wild-type embryo is marked by eight prominent denticle belts, while the lateral and dorsal cuticle is covered by the dorsal hairs. The cephalopharyngeal skeleton, containing the ventral plate (vp), is clearly visible at the anterior of the embryo and the spiracles (sp) lie at the posterior end of the embryo. (B)  $top^{101}/top^{101}$  embryo: weak "faint little ball" phenotype. Mutant denticle bands are composed of fewer and smaller ventral setae than are wild-type denticle bands. The ventral plate (vp) of the top<sup>101</sup> homozygote is reduced in size. The spiracles (sp) of the mutant point anteriorly, as the animal has not fully completed germband retraction. (C) top<sup>2C82</sup>/top<sup>2C82</sup> embryo: moderate "faint little ball" phenotype. Only four denticle bands (arrowheads) are visible in the mutant, and cephalic structures are severely reduced. Germband retraction has not occurred in this animal; a rudimentary spiracle (sp) lies just behind the remnants of the head skeleton. As is evidenced by its small size, the top 2C82 embryo produces less cuticle than a wild-type embryo. (D) top<sup>CO</sup>/top<sup>CO</sup> embryo: severe "faint little ball" phenotype. This animal appears to lack all denticles and most head and thoracic cuticle. Germband retraction has not occurred. The severe mutant produces even less cuticle than the  $top^{2C82}/top^{2C82}$  animal.

severely reduced in size in  $top^{EC20}/Df(2R)top^{3F18}$  animals (Figure 3, E and F). In marked contrast to the eye-antennal, wing and haltere imaginal discs, the precursors of the prothoracic, mesothoracic and metathoracic legs appear to be morphologically normal in the mutant (Figure 3, E and F) (data not shown). We have not analyzed the labial, humeral or genital imaginal discs in the mutant.

Defects seen in mutant eye-antennal, wing and haltere imaginal discs indicate that *top* is necessary for the proliferation or maintenance of cells within these structures. The preferential size reduction of the eye portion of the eye-antennal disc demonstrates that a disc may show regional differences in its requirement for the *top* gene product.

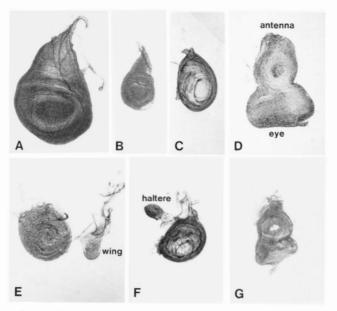


FIGURE 3.—torpedo is required for the growth of certain imaginal discs. Bright field micrographs of representative imaginal discs dissected from mature wild-type and  $top^{EC20}/Df(2R)top^{3F18}$  third instar larvae. (A) Wild-type wing disc. (B) Wild-type haltere disc. (C) Wild-type metathoracic leg disc. (D) Wild-type haltere disc. (C) Wild-type metathoracic leg disc. (D) Wild-type eye-antennal disc. The portion of the eye-antennal disc giving rise to the compound eye and the portion developing into the antenna are indicated. (E)  $top^{EC20}/Df(2R)top^{3F18}$  wing and metathoracic leg discs. (F)  $top^{EC20}/Df(2R)top^{3F18}$  haltere and metathoracic leg discs. (C) the mutant wing and haltere discs are severely reduced in size,  $top^{EC20}/Df(2R)top^{3F18}$  metathoracic leg discs appear to be of normal size and morphology. (G)  $top^{EC20}/Df(2R)top^{3F18}$  eye-antennal imaginal disc. The growth of the eye-antennal disc is nonuniformly disrupted in the mutant: the antennal half of the disc is nearly normal, while the region of the disc which develops into the compound eye is clearly reduced in size.

*torpedo* is required for the patterning of imaginal disc derivatives: The remaining *top* alleles are homozygous viable and survive to adulthood over a deficiency of the locus (Table 1). The adult viable *top* mutations, when homozygous or in *trans* to one another, exhibit adult cuticular pattern defects and female sterility. The severity of these defects are greatly intensified when the alleles are placed over a deficiency. Structures affected in mutant adults include the compound and simple eyes, certain wing veins, specific cephalic and thoracic macrochaetae, the aristae, the claws, the sex comb of the male and the female analia. The various pattern abnormalities are described below.

torpedo mutations disrupt compound eye and ocellus development: Mutations in top disrupt the development of the compound eye. In top mutants, the facets of the compound eye are often irregularly shaped and sometimes fused, while the interommatidial bristles are abnormally distributed (Figure 4B). These defects give the eye a rough appearance. In addition to a disorganization of the ommatidia and their associated bristles, severely affected eyes also exhibit prominent dark spots along their anterior margin (Figure 4B). Scanning electron micrographs of mutant eyes show that many facets located in the anterior portion of the eye possess defective corneas: whereas the cornea of a wild-type facet is convex, the cornea overlying these mutant ommatidia is concave (Figure 4D). Since the corneal material at the center of the ommatidium is produced by the cone cells (PERRY 1968), a concave cornea may result from a defect in cone cell development (R. CAGAN, personal communication).

Mutant animals also show defects in the ocelli, or simple eyes. Severely mutant animals may completely lack the ocelli. In these animals, a shallow depression is found in the place of the simple eye, suggesting that the ocellar precursor cells either have died or have failed to undergo differentiation. Less severe mutants possess ocelli that are reduced in size (Figure 4F).

torpedo is necessary for proper wing venation: Another adult structure whose differentiation is reproducibly altered in top mutants is the wing. The shape and size of the wing appears to be normal, but two veins, the anterior crossvein (acv) and fourth longitudinal vein (L4), are defective. Whereas the anterior crossvein is often completely removed, the fourth longitudinal vein is never completely absent in the top genotypes we have examined. Reductions in gene activity produce gaps of varying size in the portion of L4 extending from a point slightly proximal to the acv to a point lying between the posterior crossvein (pcv) and wing margin (Figure 5B).

torpedo mutations alter the distribution of macrochaetae: The adult cuticle of Drosophila melanogaster possesses a number of precisely located large sensory bristles, the macrochaetae (Figure 6A). The majority of bristles affected in top mutants are severely reduced in size or deleted. The macrochaetae most sensitive to elimination are the ocellar (OC), posterior supraalar (pSA), anterior supraalar (aSA), posterior postalar (pPA), dorsal humeral (dH) and ventral humeral (vH) bristles. Other bristles are absent only in some mutant animals (Figure 6A). In contrast to the other macrochaetae affected by top mutations, the anterior postalar (aPA) and postvertical (PV) bristles are duplicated rather than removed. The degree of duplication ranges from a bifurcation of the bristle shaft to the formation of a complete ectopic bristle shaft and socket (Figure 6, C-E).

torpedo is required for the development of the arista: Adults of certain heteroallelic top genotypes exhibit reduced or absent aristae. The arista, the fourth and distalmost segment of the antenna, is derived from the center of the anterior portion of the eye-antennal imaginal disc (BRYANT 1978).

torpedo lesions affect the development of the leg: Mutant adults also exhibit pattern defects in the leg. Male flies of several top genotypes show abnormalities in the

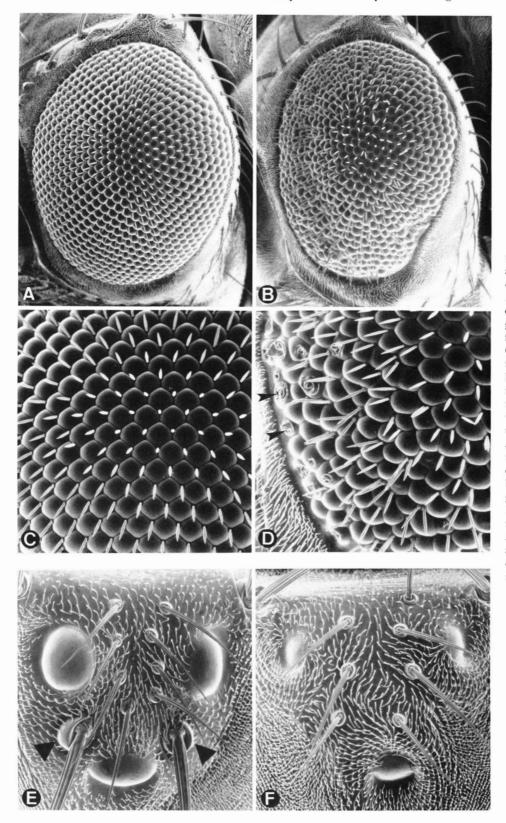
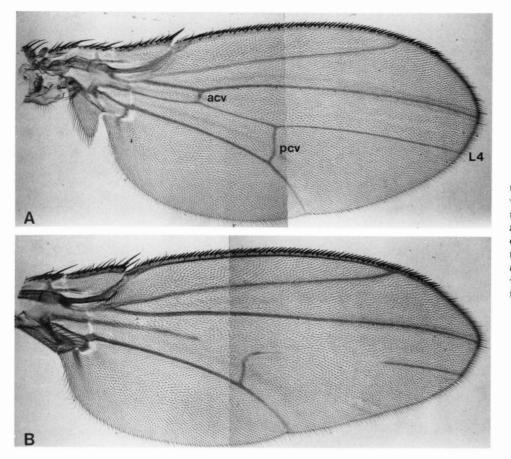
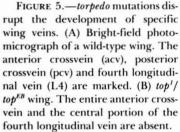


FIGURE 4.-torpedo is needed for the development of the compound eye and ocellus. (A) Scanning electron micrograph of a wild-type compound eye. Anterior is to the left. (B) Compound eye of a  $top^{1}/Df(2R)top^{18A}$  heterozy-gote;  $Df(2R)top^{18A}$  is a single-band deficiency removing the top locus (PRICE, CLIFFORD and SCHÜPBACH 1989). The facets of the mutant eye are of irregular shape and do not lie in straight rows. The interommatidial bristles are frequently clustered. (C) Detail of a wild-type compound eye. (D) Detail of the anterior margin of a  $top^{1}/$  $Df(2R)top^{18A}$  compound eye. Note that many facets along the edge of the eye exhibit corneal abnormalities (arrowheads). (E) Scanning electron micrograph of wild-type ocelli (simple eyes). Posterior is up. The ocellar bristles are marked by arrowheads. (F)  $top^{1/}$  $Df(2R)top^{3F18}$  ocelli. The mutant ocelli are reduced in size. Note also that the ocellar bristles are completely eliminated.

pattern of the sex comb. The sex comb, a male-specific structure located on the first tarsal segment of the foreleg, consists of a single anterior to posterior row of approximately 11 comb teeth. Mutant sex combs possess, on average, one additional tooth. Additionally, one or more teeth of *top* sex combs are displaced medially. A defect seen less frequently in the legs of *top* animals is the elimination of the tarsal claws, the distalmost leg structure; this abnormality occurs in flies of both sexes.

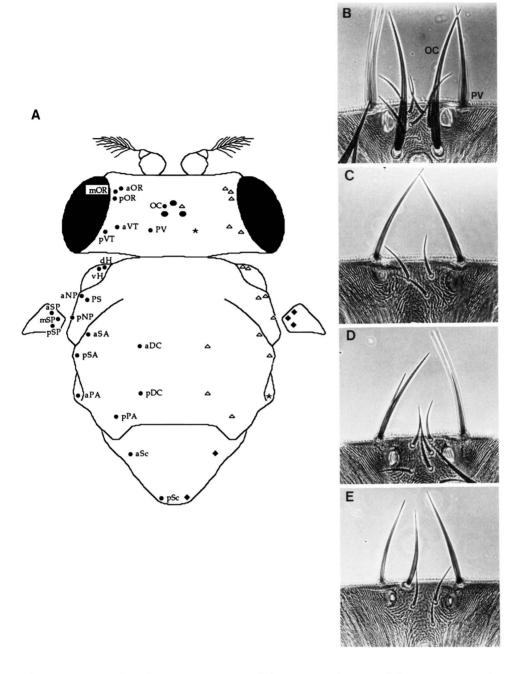




torpedo is needed for the development of the female genital disc: Severely mutant top females show defects in the anal plate, a derivative of the genital disc. The dorsal and ventral anal plates of affected females possess fewer bristles than wild-type analia and are correspondingly reduced in size. While the dorsal and ventral anal plates of a wild-type female contain roughly 20 and 18 bristles, respectively, the dorsal anal plate of a severely affected top female may entirely lack bristles and the ventral plate may possess as few as two bristles.

torpedo is required for oogenesis: All top alleles fail to complement the female sterility of  $top^1$  or  $top^{CJ}$ . Oogenesis defects of the heteroallelic combinations range from less severe to more severe than the  $top^{1}$ phenotype. As is described in SCHÜPBACH (1987) homozygous top<sup>1</sup> females produce eggs possessing a ventralized chorion (egg shell) that give rise to a correspondingly ventralized embryo. Eggs from top females have a characteristic chorion morphology: rather than possessing two dorsolaterally located dorsal appendages, as do wild type, these eggs bear fused dorsal filaments positioned on the dorsal midline of the egg (Figure 7C). Eggs laid by females of many heteroallelic genotypes exhibit a more extreme degree of ventralization than those produced by  $top^1$  homozygotes. These eggs show progressively greater reductions in the size of their dorsal appendages, with the most extreme chorions lacking all traces of dorsal filament material (Figure 7, E and F). This phenotype resembles that of extreme *gurken* alleles (SCHÜPBACH 1987), although *top* eggs never exhibit the posterior pole abnormalities seen in *gurken*. Like the most extreme *gurken* eggs, severely ventralized *top* eggs are rarely fertilized. Embryos developing within *top* eggs are also ventralized. The ventralmost embryonic tissue, the mesoderm, is expanded and the dorsalmost cells are correspondingly transformed to assume more ventral fates (SCHÜPBACH 1987). This leads to the embryonic cuticle phenotype shown in Figure 7D: the animal produces only ventral cuticle, which is recognizable by its denticles.

In general, the strength of the chorion defects and maternal effect ventralization of the embryo correlate well. In certain female sterile combinations, however, this correspondence is not absolute. For example  $top^{1}$  homozygotes occasionally lay eggs that possess two dorsal appendages but still produce ventralized embryos. On the other hand,  $top^{1}/top^{ED16}$  females can lay eggs with a single dorsal filament that develop into hatching embryos. Variation between the degree of follicle cell and embryonic defects might arise if one process is directly, and the other only indirectly, regulated by the *top* product. However, our observations



do not suggest that these two aspects of the oogenesis phenotype are functionally separable, since we have never observed strongly ventralized embryos in wildtype chorions or the converse.

## Genetic analysis of torpedo function

The phenotypes described above indicate that *top* is required for a variety of temporally and spatially distinct developmental processes. Complementation tests employing embryonic lethal, postembryonic lethal and adult viable *top* lesions as tester alleles have provided insights into the genetic nature of the *top* mutations and the functional organization of the locus.

All torpedo alleles analyzed in this study are loss

FIGURE 6.—torpedo is necessary for the development of the adult bristle pattern. (A) Schematic diagram of the cephalic and thoracic bristle pattern. The name of each bristle is indicated on the left and the manner in which the bristle is altered in top mutants is indicated on the right. Diamonds indicate unaffected bristles, triangles indicate eliminated bristles and stars indicate duplicated bristles. Abbreviations are as follows. aOR, anterior orbital bristle; mOR, median orbital bristle; pOR, posterior orbital bristle; OC, ocellar bristle; aVT, anterior vertical bristle; pVT, posterior vertical bristle; PV, postvertical bristle; dH, dorsal humeral bristle; vH, ventral humeral bristle; PS, presutural bristle; aNP, anterior notopleural bristle; pNP, posterior notopleural bristle; aSP, anterior sternopleural bristle; mSP, median sternopleural bristle; pSP, posterior sternopleural bristle; aSA, anterior supraalar bristle; pSA, posterior supraalar bristle; aPA, anterior postalar bristle; pPA, posterior postalar bristle; aDC, anterior dorsocentral bristle; pDC, posterior dorsocentral bristle; aSc, anterior scutellar bristle; pSc,posterior scutellar bristle. (B) Phase contrast photomicrograph of wild-type ocellar (OC) and postvertical (PV) bristles. Note that the anterior-posterior orientation of this panel is opposite that of panel A. (C) The ocellar region of a top<sup>1</sup>/top<sup>EB</sup> adult. The two postverticals appear normal, while the ocellar bristles are deleted. (D) Ocellar region of a  $top^{1}/$ top<sup>SH2</sup> animal. The postvertical bristle on the left is partially duplicated. The ocellar bristles are absent. (E) Ocellar region of a top1/top2G31 animal. An ectopic postvertical bristle lies between the two normal postverticals. The ocellar bristles are absent.

of function mutations: To assess the genetic nature of the available *top* alleles, all mutations were crossed to  $Df(2R)top^{3F18}$ . The majority of alleles in our collection are recessive zygotic embryonic lethal mutations. The phenotype of mutations exhibiting a severe "flb" embryonic lethal phenotype remains unchanged over the deficiency, suggesting that they represent amorphic (total loss of function) lesions. Alleles producing intermediate or weak "flb" phenotypes usually show a slightly enhanced phenotype in *trans* to  $Df(2R)top^{3F18}$ ; this argues that they are hypomorphic (reduced activity) mutations (Table 1). The semiviable allele  $top^{CA}$  and the three lesions that cause postembryonic lethality as homozygotes are all lethal in *trans* to a deletion of the locus. In combination with

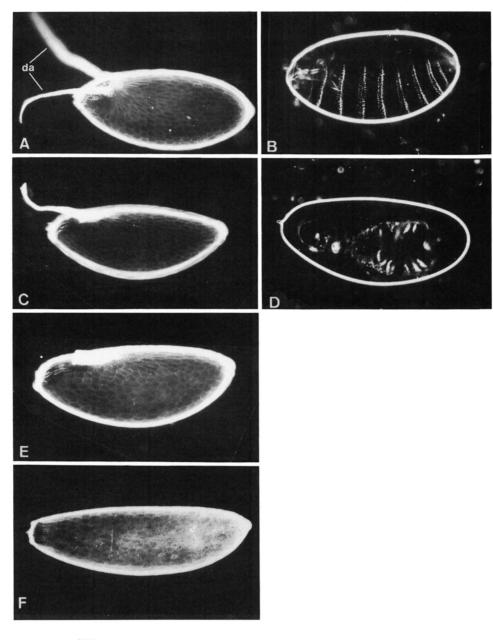


FIGURE 7.—torpedo is required for oogenesis. (A) Dark-field photomicrograph of a wild-type chorion (egg shell). The dorsal appendages (da) are positioned on either side of the dorsal midline of the egg and extend anteriorly. (B) Wild-type embryonic cuticle. The highly refractile denticle bands are located on the ventral surface of the embryo. (C) Egg laid by a  $top^1/top^{3C87}$  female. The egg shell is ventralized: the dorsal filaments are shifted dorsally onto the dorsal midline of the egg where they fuse into a single dorsal appendage. This chorion phenotype is identical to that seen in  $top^1$  homozygotes. (D) Cuticle of an embryo produced by a top1/top1 female. The embryo is ventralized. A patch of cuticle bearing ventral denticles overlies the dorsal surface of the animal. (E) Egg laid by a  $top^1/top^{3C81}$  female. The mutant egg shell shows a greater degree of ventralization than is seen in eggs produced by flies homozygous for the top' mutation. The dorsal appendages are fused and greatly reduced in size. (F) Egg laid by a  $top^{1}/top^{CO}$ heterozygote. This egg is severely ventralized. No dorsal appendage material is visible. The mutant chorion is also larger than a wild-type egg shell, as follicle cells that would have secreted the dorsal appendages assume more ventral fates and contribute to the production of the main body of the chorion.

 $Df(2R)top^{3F18}$ , two of the homozygous postembryonic lethal mutations exhibit early pupal lethality, while the third, top<sup>EA</sup>, shows a weak embryonic lethal phenotype. Animals *trans*-heterozygous for  $top^{CA}$  the semiviable allele, and the deficiency die late in pupal development as pharate adults (Table 1). The remaining three mutations,  $top^1$ ,  $top^{CJ}$  and  $top^{\hat{k}E38}$ , are viable in combination with  $Df(2R)top^{3F18}$ . All three lesions, however, exhibit much more severe adult pattern defects over the deletion than they do either in the homozygous state or in trans to one another (Figures 8 and 9). Thus  $top^{EA}$ ,  $top^{CA}$  and the adult viable alleles also appear to be loss of function mutations.  $Df(2R)top^{3F18}$  removes at least 15 polytene chromosome bands. To address the possibility that hemizygosity for genes flanking the top locus affects the mutant phenotypes observed in heteroallelic combinations involving this deficiency, all alleles were also examined over the apparent amorphic point mutation  $top^{CO}$ . The phenotypes observed in complementation tests with  $top^{CO}$  do not differ from those seen over  $Df(2R)top^{3F18}$  (data not shown).

torpedo possesses distinct embryonic and postembryonic vital activities: Results obtained in complementation tests with  $top^{CO}$  and  $Df(2R)top^{3F18}$  suggested that the top mutations can be ordered in a simple allelic series in which the severity of a given lesion's lethal phenotype corresponds to the amount of topactivity it retains. Amorphic mutations exhibit a strong "flb" embryonic lethal phenotype; as the amount of residual top activity is increased, the zygotic lethal phenotypes progress from a moderate embryonic lethal phenotype to a weak "flb" phenotype to pupal lethality. Alleles which result in the least reduc-

	Homozygous embryonic	over	7		Ad	ult pa	ittern	defe	cts ov	ver to	op1						phen	enesis 10type ver
Allele	phenotype	top CA	OC	pSA	aSA	L4	acv	pPA	oce	eye	dH	vН	PS	aNP	PV	t	top 1	ver topCJ
		C	lass I: Al	leles	Coor	dina	tely A	Affect	ing A	All Ge	ene A	ctivi	ties					
CJ	+	$\left[ + \right]$	•••	••	٠	+	••	•	•	٠	+	+	+	+	+	1	••	••
1	+	+	•••	•••	••	+	•	•	••	•	+	+	+	+	+		••	••
EC20		+	••	•••	•••	+	•••	•	••	••	•	۵	+	+	+		•••	•••
2 W74	•	••	•••	•••	•••	••	••	•••	•••	••	•	+	+	+	+		•••	•••
1F26	•	••	•••	•••		•••	••	••	••	••	•	+	+	+	+	1	•••	•••
2E07	•	•••	•••	•••	•••	•••	••	••	••	••	••	+	+	+	+		••	•••
EE39	••	•••	•••	•••	•••	•••	•••	•••	•••	••	•••	•	•	+			•••	•••
ED26		•••		•••	•••	•••	•		•••	•••		+		+ 0	+	1	••	••
2G31 3B41							•						•		+++	1		ne
3B92		•••										+	•	+	+	1	••	•••
1K35	•••	•••										+	+	+	+		ne	•••
EE42	•••	•••		•••								•	•	+	D			ne
3C81		•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•	•	+	+		•••	•••
CO	•••	•••		•••	•••	•••	•••	•••	•••	•••	•••	••	۵	+	+		•••	ne
1P02	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	•••	••	•	+	+		ne	••
3F18	•••	•••	•••	•••	•••	•••	••	•••	•••	•••	•••	••	•	+	+		•••	•••
			Class II:	Alle	les Pi	refere	ential	ly Af	fectin	g En	nbryo	gene	sis					
101		+	+	••	+	+	•	•	a	a	+	+	+	+	+		+	α
JE14	••	+	+	+	+	+	+	+	+	+	+	+	+	+	+		D	D
2C82	••	+	•	•	+	+	+	•	•	a	+	+	+	+	+	1	•	•
2L65	• • •	+	+	+	a	+	+	•	•	۵	+	+	+	+	+		•	•
L		Cla	ass III: A	lleles	Pref	erent	ially	Reta	ining	Oog	enesi	s Act	ivity			1	h	· · · ·
SH2		•••	•••	•••	•••	•••		•••		••	•••	•	+	+	+			•
3C87		•••	•••	•••			•••	•••	•••			••	ā	+	+			••
38	•••		•••	•••	•••	•••	•••	•••	•••	•••	••	••	•	+	D			••
		Class 1	V: Allel	es Di	ffere	ntiall	v Afi	fectin	g Im	agina	al Dis	c De	rivati	ves	L	1	<b></b>	L
<b>FE30</b>					a			•	•	•						1	•	•
EE38 CA	+ +	+		•••	•••	++	••	0	+	D	+	+ +	++	++	++		+	
2X51	•••							••	 ●●●	••		+	+	+	+ +		ne	
ED16	•	+	•		+	+	••	+	••	••	+	+	+	+	+	1	•	•
EA	a	•••		•••		••	•••		••	•	•••	•	ā	+	+		••	••
EB		•••	•••	•••	•••	••	•••	•••	••	••	•••	•••	•	+	+		•	••
JE13	•••	•••	•••	•••	•••	٠	•	•••	•••	••	•	+	+	+	+	1	••	••
JE1	•••	•••	•••	•••	•••	•	••	•••	•••	•••	••	+	+	+	+		•••	•••

FIGURE 8.—Phenotypic analysis of the torpedo alleles. Abbreviations are as follows. L4, fourth longitudinal wing vein; acv, anterior crossvein; oce, ocellus. Refer to Figure 6 for abbreviations of bristle names. Phenotypic quantifications are as follows. Homozygous embryonic phenotype: "+" = adult viable, "Ø" postembryonic lethal, "•" = weak "flb" embryonic lethal, "••" = moderate "flb" embryonic lethal, "••" extreme "flb" embryonic lethal. Lethality over topCA: "+"= 100-75% survival of trans-heterozygous adults, "•" = 74-50% survival, "•" = 49-25% survival, "••" = 4-0% survival. Oce: "+" = wild-type ocellar morphology, "O" = mild, variable size reduction of the ocelli, "•" = mild size reduction, "••" = moderate size reduction, "•••" = extreme size reduction. Eye: "+" = wild-type compound eye morphology, "D" = variable, slight eye roughness, "•" = mild eye roughness, "•" = moderate eye roughness, "••" = extreme eye roughness. Bristles and wing veins: = 0-14% frequency of defects, "□" = 15-24% frequency, "•" = 25-49% frequency, "•" = 50-74% frequency, "•" = 75-100% frequency. Oogenesis: "+" = produces wild-type eggs, "D" = occasionally produces eggs with fused dorsal appendages that give rise to mostly normal embryos, "•" = usually produces eggs with fused dorsal appendages that give rise to normal and some weakly ventralized embryos, "•" = produces eggs with fused dorsal appendages that give rise to ventralized embryos, "••" = produces eggs with fused dorsal appendages that give rise to strongly ventralized embryos and eggs with severely reduced or absent dorsal appendages that are rarely fertilized, "ne" = no eggs laid.

tion of top function survive to adulthood over a deficiency and are female sterile.

However, complementation tests performed between  $top^{CA}$  and all other top alleles indicate that certain mutations do not fit into a simple allelic series.  $top^{CA}$  is a semiviable lesion exhibiting pupal lethality in trans to a deficiency of the locus. If all alleles in the collection can be arranged in a simple series, muta-

Genotype	00	pSA	aSA	L4	acv	pPA	eye	dH	vН	PS	aNP	pNP	aPA	aDC	pDC	Egg	_
CJ / EC20		••	+	+	••	+	+	+	+	+	+	+	+	+	+	••	
1 / EC20	••	•••	••	+	•••	•	+	•	+	+	+	+	+	+	+		
EE38 /EC20		• • • •		••	•••	•	+	•••	••	•	+	+	+	+	+	•	
CA / EC20	••		•	•	••	••	+	••	+	+	+	+	+	+	+	•	
		1															1
CJ / ED16	••	••	+	+	+	+	•	+	+	+	+	+	+	+	+	•	
1 / ED16	•	•••	+	+	•	+	••	+	+	+	+	+	+	+	+	•	
EE38 / ED16	••	•••	+	+	•	+	+	+	+	+	+	+	+	+	+	+	
CA / ED16	•••	• • • •	•	D	•	•	۵	+	+	+	+	+	+	+	+	ND	1
											1						L
CJ / ED26	•••	• • • •	•••	•••	•••	•	•••	••	+	•	+	+	+	+	+		L
1 / ED26	•••	• • • •	•••	•••	•	•••	•••	••	+	•	+	+	+	+	+		L
EE38 / ED26		• • • •	•••	•••	•••	•	•	•••	•••	••	+	+	+	+	+	•	
																	L
CJ / EB	•••	• • • •	•••	••	•••	••	••	•••	•	•	+	+	+	+	+	ND	
1 / EB	•••		•••	••	•••	•••	••	•••	•••	•	+	+	+	+	+	+	
EE38 / EB	•••	•••	•••	•••	•••	•••	•	•••	•••	•••	•	•	+	+	+	ND	
CJ / 38	•••	••••	•••	•••	•••	•	•••	••	+	••	+	+	+	+	+	••	
1/38	•••	••••	•••	•••	•••	•••	•••	•••	••	•	+	+ 1	+	+	+	••	
EE38 / 38	•••	••••	•••	•••	•••	•	•	•••	•••	••	+	+	+	+	+	ND	
01/2510																	
CJ / 3F18	•••	•••	•••	•••	•••	•••	••	•••	•••	•	+	+	+	+	+	•••	
1 / 3F18	•••	••••	•••	•••	••	•••	•••	•••	••	•	+	+	+	+	+	•••	
EE38 / 3F18	•••	•••	•••	•••	•••	••	•	•••		•	•	•	D	+	+	•	

FIGURE 9.—The adult viable torpedo mutations show qualitative phenotypic differences. Adult phenotypes of  $top^{CJ}$ ,  $top^{FE38}$  and  $top^{CA}$  in combination with representative tester alleles.  $top^{CA}/top^{FE2}$ ,  $top^{CA}/top^{FB}$ ,  $top^{CA}/top^{38}$  and  $top^{CA}/top^{3F18}$  animals do not survive to adulthood. Abbreviations are the same as in Figure 8, with the addition of the following: "IND" = phenotype not determined.

tions showing a severe embryonic lethal phenotype (presumptive amorphic alleles) should die over  $top^{CA}$ , lesions showing moderate "flb," weak embryonic lethal and pupal lethal phenotypes might show intermediate viability that increases with decreasing allelic strength and the adult viable alleles should survive well in combination with  $top^{CA}$ . This prediction was not entirely borne out. Although most alleles behave as expected, four embryonic lethal mutations with different terminal phenotypes ranging from weak to strong  $(top^{101}, top^{2CS2}, top^{JE14}, top^{2L65})$  are fully viable over  $top^{CA}$  (Figures 8 and 10). Thus these four mutations do not appear to fit into a simple allelic series based on quantitative differences in top activity; rather, it appears that these alleles retain a top activity needed for pupal survival while they reduce a gene activity required for embryonic development.

To demonstrate that this complementation does not reflect a specific interaction with  $top^{CA}$ , the four exceptional alleles were also crossed to the pupal lethal lesions  $top^{EB}$  and  $top^{EC20}$ . As controls,  $top^{EB}$  and  $top^{EC20}$  were also crossed to three embryonic lethal alleles showing the expected severely reduced viability over  $top^{CA}$ . Both  $top^{EB}$  and  $top^{EC20}$  die in *trans* to the control mutations; however, both pupal lethal mutations survive to adulthood over  $top^{101}$ ,  $top^{2C82}$ ,  $top^{JE14}$  and  $top^{2L65}$  (Table 2). Since these four embryonic lethal lesions

complement the pupal lethality of several *top* mutations, it is unlikely that complementation is due to allele-specific interactions. Rather, the exceptional lesions, while clearly deficient for *top*'s embryogenesis activity, still retain gene activity needed for pupal viability. As  $top^{101}$ ,  $top^{2C82}$ ,  $top^{JE14}$  and  $top^{2L65}$  all show some reduction in viability in combination with  $top^{EB}$ , they are not completely wild-type for pupal activity (Table 2). Thus these mutations preferentially, but not exclusively, affect a gene function required for embryogenesis.

The adult viable torpedo alleles show qualitative differences in their effects on imaginal disc patterning and oogenesis: To assess the nature and severity of the imaginal disc and oogenesis phenotypes of the top lesions, and to elucidate how the adult defects of each mutation correlate with one another and with the mutation's embryonic lethal and pupal lethal phenotypes, the top alleles were examined in trans to top<sup>1</sup>, top<sup>CJ</sup> and top<sup>EE38</sup>, mutations which are viable over  $Df(2R)top^{3F18}$ . In addition, we have determined the adult phenotypes of the viable  $top^{CA}$  heteroallelic combinations (Figures 8, 9 and 10).

Over a given top allele,  $top^{CJ}$  generally produces the weakest imaginal disc pattern defects,  $top^{I}$  shows a more severe phenotype and  $top^{EE38}$  and  $top^{CA}$  exhibit the most extreme overall phenotypes (Figures 9 and

# **Drosophila EGF Receptor Homolog**

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CJ*	50	•••	••	••	+	••	•	•	+	•	+	+	+	+	+	+	+	+	+	+
1 1	50		•••	••	+	•	+	+	D	+	+	+	+	+	+	+	+	+	+	+
EC20*	50	••	•••	•	•	••	••	•	D	••	+	+	+	+	+	+	+	+	+	+
2 W74	30	•••	•••	•••	•••	•••	•••	•••	••	•••	•••	•	••	0	+	+	+	+	D	+
1F26	40	•••	•••	•••	•••	•••	•••	•••	••	•••	•••	••	•	•	•	+	+	+	•	+
2E07	18	•••	•••	•••	•••	•••	••	•••	•••	•••	•••	•	•••	••	•	+	+	+	+	+
3B41	5	•••	•••	•••	•••	•••	•••	•••	•••	•••		•••	••	•••	•••	••	•••	•	+	+
				(	Class	[]: All	eles I	Prefer	ential	ly Aff	ecting	g Emb	oryog	enesis						
101*	50	•••	•••	•	+	•••	••	•	+	•	+	+	•+	+	+	+	+	+	+	+
JE14	50	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
2C82	50	•••	•••	•••	+	••	••	•	+	•••	+	+	+	+	+	+	+	+	+	+
2L65	50	•••	•••	•••	+	••	•	•	α	a	+	+	+	+	+	+	+	+	+	+
			C	lass I	V: A1	leles 1	Differ	entia	lly Af	fectin	g Ima	iginal	Disc	Deri	vative	es				
EE38*	50	•••	•••	+	+	+	•	+	+	••	+	+	+	+	+	+	+	+	+	+
CA*+	24	•••	•••	•••	•	•••	•••	••	+	•••	•••	••	+	+	+	+	••	+	•	+
ED16*	50	•••	•••	•		•	•	••	••‡	+	+	+	+	+	+	+	+	+	+	+
2X51	7	•••	•••	•••	•••	•••	•••	•••	••	•••	•••	•••	+	•••	••	+	o	•	+	•

Allele	n=	OC pSA aSA	L4	acv pPA or	æ eye	dH vH	PS	aDC aOR pOR pDC aNP pN	IP PV	AR
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FIGURE 10.—Phenotypes of the torpedo alleles in combination with  $top^{CA}$ . Abbreviations are the same as in Figures 8 and 9, with the addition of the following: "n" = the number of adults examined for each genotype; AR, arista. "\*" = the allele was tested over a b pr cn top<sup>CA</sup> recombinant chromosome rather than the original b pr cn sca top<sup>CA</sup> chromosome; "†" = the cross was performed at room temperature rather than 25°;  $top^{CA}/top^{EDI6}$  females exhibit more extreme eye roughening than  $top^{CA}/top^{EDI6}$  males.

#### TABLE 2

Certain embryonic lethal torpedo mutations complement pupal lethal alleles

	Cross		<u>mutant</u> balancer	<u>mutant</u> mutant	Survival rate of trans- heterozygote (%)
top <sup>CA</sup>	×	top <sup>2W74</sup>	216	35	32
to $\boldsymbol{b}^{CA}$	×	to 2E07	219	19	17
tob <sup>CA</sup>	×	top <sup>3892</sup>	201	1	1
tob <sup>CA</sup>	×	tob101	278	154	111
to $b^{CA}$	×	top <sup>2C82</sup>	271	171	126
top <sup>CA</sup>	×	tob JE14	205	110	107
top <sup>CA</sup>	×	top <sup>2L65</sup>	241	129	107
top <sup>EC20</sup>	×	top <sup>2W74</sup>	124	0	<2
tob <sup>EC20</sup>	×	to 2E07	123	0	<2
tob <sup>EC20</sup>	×	top <sup>3892</sup>	135	0	<2
tob <sup>EC20</sup>	×	top <sup>101</sup>	137	43	63
top <sup>EC20</sup>	×	to 0 <sup>2C82</sup>	139	80	115
toh <sup>EC20</sup>	×	tob <sup>JE14</sup>	125	97	155
top <sup>EC20</sup>	×	top <sup>2L65</sup>	154	77	100
top <sup>EB</sup>	×	top <sup>2W74</sup>	49	0	<5
tob	×	ton <sup>2E07</sup>	139	0	<2
top <sup>EB</sup>	×	top <sup>3B92</sup>	172	0	<2
top <sup>EB</sup>	×	tob <sup>101</sup>	111	6	11
top <sup>EB</sup>	×	tob <sup>2C82</sup>	116	13	22
top <sup>EB</sup>	×	tob <sup>JE14</sup>	120	52	87
top <sup>F.B</sup>	×	top <sup>2L65</sup>	120	15	25

top<sup>2W74</sup>, top<sup>2E07</sup> and top<sup>3B92</sup> are class I alleles with weak, weak and severe embryonic lethal phenotypes, respectively.

top<sup>101</sup>, top<sup>2C:82</sup>, top<sup>IE14</sup> and top<sup>2L65</sup> are class II alleles with weak, moderate, moderate and strong embryonic lethal phenotypes, respectively.

10) (data not shown). Since  $top^{CA}$  is lethal over a deficiency of the locus and in combination with many embryonic lethal top lesions, it represents the most severely affected adult viable allele. Systematic exceptions to this ordering do exist.  $top^{CJ}$  combinations exhibit higher frequencies of ocellar bristle defects than do the corresponding  $top^1$  heterozygotes and often show more extreme oogenesis phenotypes (Figures 8 and 9), while  $top^{EE38}$  and  $top^{CA}$  heteroallelic animals usually exhibit substantially weaker eve and oogenesis abnormalities and more extreme wing and bristle defects than do the corresponding  $top^1$  or  $top^{CJ}$ trans-heterozygotes (Figures 9 and 10). As these differences between the adult viable lesions are observed over a variety of tester mutations, they are more likely due to qualitative differences between  $top^{1}$ ,  $top^{CJ}$ ,  $top^{EE38}$  and  $top^{CA}$  than to allele-specific interactions between the adult viable and tester alleles or to differences in genetic background. Thus the overall phenotype of a given adult viable allele becomes more extreme as the residual activity of the tester allele decreases, and the regional specificities of its defects are reflected in each heteroallelic combination.

Complementation tests with the adult viable alleles allow us to measure how each *top* mutation affects the development of the imaginal disc derivatives and oogenesis. These phenotypes also provide a means of confirming the classification of *top* alleles based on zygotic lethal phenotypes and the ability to complement the pupal lethality of  $top^{CA}$ . The most easily scored adult pattern defects (eye roughening, dis-

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rupted wing venation, bristle abnormalities and female sterility) were used for the phenotypic analysis.

torpedo mutations can be divided into phenotypic classes: By comparing each allele's zygotic lethal phenotype (an indicator of its embryogenesis activity) to its rate of survival in trans to  $top^{CA}$  (a measure of its pupal vital activity), the severity of its adult defects over  $top^{1}$  (a measure of its imaginal disc activities) and its ability to complement the female sterility of  $top^{1}$ and  $top^{cj}$  (an indicator of its oogenesis activity), the top mutations can be divided into four classes (Figure 8). Most lesions fall into one of three allelic series (I-III). Within each series alleles may be ranked according to the amount of top activity they retain; however, the series are distinguished by apparent qualitative differences in the degree to which their member alleles affect the various top activities. Members of the fourth class of mutations, in contrast, cannot be ordered in an allelic series.

The 17 class I mutations  $(top^{CJ}-Df(2R)top^{3F18})$  appear to reduce all gene activities in a uniform manner. When these mutations are ordered by the severity of their homozygous zygotic lethal phenotypes, it can be seen that an allele's ability to complement  $top^{CA}$  (which should be proportional to the amount of pupal vital activity an allele possesses), the strength of adult morphological defects produced in *trans* to  $top^1$  and the ability to complement the female sterility of  $top^{1}$  and top<sup>CJ</sup> correspond fairly well to the severity of its homozygous lethal phenotype. This ordering further indicates that the relative sensitivities of eight macrochaetae, the fourth longitudinal vein, the anterior crossvein, the compound eye and the ocellus fall into a fairly consistent hierarchy (Figure 8). Since  $Df(2R)top^{3F18}$  by all criteria falls into this class of top lesions, class I presumably represents mutations that reduce all gene activities more or less uniformly.

The class II lesions,  $top^{101}$ ,  $top^{JE14}$ ,  $top^{2C82}$  and  $top^{2L65}$ , preferentially exhibit defects in embryogenesis. Although these alleles are embryonic lethals, they survive in *trans* to  $top^{CA}$ ,  $top^{EB}$  and  $top^{EC20}$ ; they therefore retain considerably more pupal vital activity than would be predicted from their homozygous embryonic lethal phenotypes (Table 2, Figure 8). These four mutations also exhibit very mild adult pattern and oogenesis abnormalities over  $top^{1}$ , and can be ordered in their own allelic series.

Class III mutations,  $top^{SH_2}$ ,  $top^{38}$  and  $top^{3C87}$ , differ from alleles of the first class by preferentially retaining oogenesis activity. These three lesions show significantly weaker female sterile phenotypes—both in combination with  $top^{I}$  and  $top^{CJ}$ —than do class I alleles showing equivalent homozygous lethal phenotypes, survival over  $top^{CA}$  and adult pattern defects. The three lesions can be ordered in a hypomorphic series, with  $top^{SH2}$  and  $top^{3C87}$  representing the weakest and strongest alleles, respectively.

Class IV mutations  $(top^{EE38}-top^{JE1})$  exhibit phenotypes suggesting that they preferentially lack or retain gene activity required for particular developmental processes.  $top^{EE38}$  and  $top^{CA}$  (see Figures 9 and 10) exhibit milder eye defects than would be expected from the severity of their wing and bristle abnormalities, whereas  $top^{ED16}$  shows the converse phenotype, enhanced eye defects.  $top^{EE38}$  and  $top^{CA}$  also appear to retain significant oogenesis activity. top<sup>EA</sup> and top<sup>EB</sup> preferentially produce bristle defects and show enhanced lethality in *trans* to  $top^{CA}$ . On the other hand,  $top^{2X51}$  seems to preferentially retain eye and bristle activity. When compared to class I mutations producing eye and bristle defects of equivalent severity,  $top^{JE13}$  and  $top^{JE1}$  exhibit an enhanced zygotic embryonic lethal phenotype and a decreased disruption of wing venation (Figure 8).

Thus a phenotypic examination of the *top* alleles reveals that several developmental processes dependent upon *top* are differentially, though not exclusively, affected by lesions in the gene. These include the functions required for embryonic development, the differentiation of the eye, wing and bristles and oogenesis This phenomenon may reflect the differential mutability of regulatory or structural elements of the *top* locus, cell type-specific stability of mutant gene products, cell type-specific reduction of mutant protein activity or some combination of the above.

# DISCUSSION

It has recently been shown that the torpedo (top) gene of Drosophila encodes the fruitfly homolog of the vertebrate EGF receptor and neu proto-oncogene, DER (PRICE, CLIFFORD and SCHÜPBACH 1989; SCHEJTER and SHILO 1989). Previous molecular studies have shown that two alternately spliced mRNAs are transcribed from this locus throughout the life of the fly (LEV, SHILO and KIMCHIE 1985; WADS-WORTH, VINCENT and BILODAEU-WENTWORTH 1985; SCHEJTER et al. 1986; KAMMERMEYER and WADS-WORTH 1987). Both transcripts are expressed in all tissues of the embryo, in the developing eye-antennal, wing and genital imaginal discs of the larvae, in the adult nervous system and in the follicle cell epithelium of the ovary (SCHEJTER et al. 1986; KAMMERMEYER and WADSWORTH 1987). We have genetically analyzed 32 top mutations. This analysis has allowed us to assay the spatial and temporal requirements for top activity and has revealed the functional complexity of the gene.

Based on a comparison of their phenotypes, the *top* alleles can be divided into several broad categories: those affecting all gene activities uniformly, those preferentially affecting embryogenesis, those affect-

ing oogenesis to a lesser degree than other developmental processes and those differentially affecting the development of specific imaginal disc derivatives. This analysis suggests that *top* possesses differentially, though not independently, mutable functions regulating processes required for oogenesis, embryogenesis, pupal development, wing venation, the formation of the compound eye and ocellus and the development of sensory bristles.

The phenotypes of the top alleles argue against the idea that the gene possesses independent functional domains. If, for example, there existed an independently mutable domain required only for oogenesis, we should have found top lesions causing only female sterility. No allele of this kind has been isolated. The absence of mutations exclusively affecting oogenesis is not due to the mutagenesis protocols, since the 14 alleles isolated in our screens were selected as female sterile lesions. All proved to affect imaginal disc development, and many are zygotic lethals. By the same token, 18 alleles were selected as zygotic lethals, yet all affect oogenesis (Figure 8). A similar argument can be made against the existence of an independent domain encoding the embryonic vital activity. None of the top alleles selected as zygotic lethal mutations exclusively affects embryogenesis (Figure 8). Thus, although the oogenesis and embryogenesis activities of top can be preferentially affected by lesions at the top locus, they were not mutated independently of the remaining gene activities in any allele in our sample.

Given the expression pattern of top and the homology of its product to the vertebrate EGF receptor, the phenotypic complexity exhibited by top alleles can be explained in various ways. One possible basis for the gene's differentially mutable activities is that it encodes multiple products. Sequence analysis of cDNA clones corresponding to the two top transcripts has shown that the predicted products of the two mRNAs differ at their amino termini (LEV, SHILO and KIMCHIE 1985; SCHEITER and SHILO 1989). If each protein functions primarily in a subset of the developmental process requiring top but also acts in a secondary capacity in all remaining top-dependent processes, point mutations in the locus can preferentially, but not exclusively, affect gene functions. This model further predicts that there will exist one more class of top point mutations than there are gene products: a class of alleles specific to each alternate form of the protein and an additional class of mutations altering the region of the gene common to both products. Our collection of alleles does contain lesions affecting all top activities (the class I alleles) and lesions that preferentially affect embryogenesis (the class II alleles). Other alleles appear to preferentially disrupt the development of the compound and simple eyes  $(top^{ED16})$ or the bristles ( $top^{EA}$  and  $top^{EB}$ ). The existence of more

than three classes of *top* lesions argues that this explanation for differential mutability is not sufficient to account for *top*'s phenotypic diversity.

Another possible source of phenotypic complexity is that one or both products of the *top* locus may interact with several tissue-specific ligands or substrates. By functional analogy to the mammalian EGF receptor, the extracellular domain of a *top* protein might interact with a variety of tissue-specific signal molecules, and its intracellular tyrosine kinase domain may phosphorylate a variety of cellular proteins. Lesions in *top* could then alter the conformation of one or both domains so that binding to one ligand or substrate is severely disrupted while the remaining interactions are affected to lesser extents.

A third possibility is that some top mutations interfere with the stability or activity of the gene products in a tissue- or cell-specific manner: certain mutant mRNAs or proteins may be differentially destabilized in a subset of the tissues in which they are expressed and the activity of mutant proteins may vary in a cellspecific fashion. A final source of phenotypic complexity may be genetic background. Background mutations in some top stocks may modify the expression or activity of the mutant gene at specific stages of development or in specific tissues of the fly. These mechanisms for the gene's functional complexity are not mutually exclusive, and the genetic data does not favor any particular explanation. The molecular analysis of specific top mutations may provide insight into this question.

The high degree of structural similarity existing between the predicted *top* protein products and the vertebrate epidermal growth factor receptor argues that *top* is involved in the reception of extrinsic signals during Drosophila development. The nature of the defects seen in *top* mutants provide insight into how tissues in the developing fly respond to these signals.

Analysis of the oogenesis defect of *top* suggests that this gene mediates intercellular communication in the ovary leading to the establishment or maintenance of cellular identities. During oogenesis *top* activity is required to promote dorsal follicle cell fate; maternally expressed *top* product also acts through the *dorsal-Toll* group of genes to regulate the dorsoventral pattern of the embryo (SCHÜPBACH 1987; PRICE, CLIF-FORD and SCHÜPBACH 1989).

The zygotic function of *top* in the embryo is very different from its role in oogenesis: early zygotic gene activity is not required for the initial establishment of the embryonic body pattern. The head and thoracic segments of embryos homozygous for severe zygotic lethal *top* alleles appear to form normally, but they degenerate during later development (SCHEJTER and SHILO 1989; R. J. CLIFFORD and T. SCHÜPBACH, unpublished results). This defect is associated with extensive cell death (PRICE, CLIFFORD and SCHÜPBACH 1989; R. J. CLIFFORD and T. SCHÜPBACH, unpublished). Thus the zygotic embryonic activity of *top* is required for the viability of particular embryonic tissues.

The postembryonic defects of top argue that the gene is required for the growth of the imaginal discs during larval development and the subsequent patterning of cuticular structures derived from the discs during pupation. The absence or duplication of particular bristles on the head and thorax, the production of supernumerary sex comb teeth, the elimination of the tarsal claw, the deletion of specific wing veins and a disruption of the compound eye pattern are seen in animals of viable top genotypes. These position-specific defects suggest that reductions or alterations in top activity may cause cells to assume incorrect identities by interfering with intercellular communication, which is known to play an important role in the patterning of bristles on the cuticle (GARCIÀ-BELLIDO 1981; MOSCOSO DEL PRADO and GARCIÀ-BELLIDO 1984), the patterning of the compound eye (TOMLIN-SON and READY 1987a, b; HAFEN et al. 1987; REINKE and ZIPURSKY 1988) and in wing venation (GARCIÀ-BELLIDO 1977; RIPOLL et al. 1988). Defects observed in animals of more severe top genotypes are consistent with this gene mediating the reception of signals required for cellular proliferation or viability in the imaginal discs. Larvae of the early pupal lethal genotype  $top^{EC20}/Df(2R)top^{3F18}$  suffer severe reductions in the size of the wing and haltere imaginal discs and a moderate size reduction in the portion of the eyeantennal disc that gives rise to the eye, ocellus and head capsule.

There apppears to be a correspondence between the growth and differentiation abnormalities of the imaginal discs. In the mutant genotype examined, wing and haltere discs are nearly absent, while the eye portion of the eye-antennal disc is somewhat reduced in size and the leg imaginal disc and the region of the eye-antennal disc giving rise to the antenna appear morphologically normal. In the adult, pattern of the wing is more sensitive to disruption by reductions in or alterations of the top product than is the patterning of the eye; the development of the compound eye, in turn, is more sensitive to disruption than the development of the antenna or leg. In addition, a top allele's ability to complement the pupal lethality of  $top^{CA}$ , which presumably corresponds to the severity of its imaginal disc growth defects, always correlates with the overall strength of its adult pattern defects. This correlation holds true for lesions of all phenotypic classes. This correspondence lends further support for the idea that top participates in a process through which the growth and pattern formation of the imaginal discs are intimately linked.

The good correlation seen between the imaginal disc growth and patterning abnormalities of top mutants can be explained in several ways. First, spatially restricted adult pattern defects may arise from localized defects in cell proliferation or viability. Since the adult defects presumably result from a less severe reduction or alteration of the top product than do the imaginal disc growth defects, the adult pattern abnormalities would occur in regions of the disc showing the greatest requirement for the putative proliferation or maintenance signal transduced by top. Another possibility is that the growth defects of the imaginal discs are the consequence of alterations in cell identities. The loss of certain cell fates in the disc could lead to a reduction in cell proliferation and a concomitant reduction in the final size of the imaginal disc. A third possiblity is that growth and patterning of the discs are unrelated processes that both require the top gene product.

In summary, the range of defects seen in *top* mutants suggests that the gene participates in a variety of developmental processes. In the ovary, *top* is required for the establishment or maintenance of cellular identities, in the embryo, it is needed for the viability of certain tissues and, in the imaginal disc, the gene is necessary for growth and patterning. Further genetic and biochemical analysis of *top* should shed light on the functional relationships of these diverse physiological processes and the nature of the signals that trigger them.

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