**INTRODUCTION**

Imaginal discs are the progenitors of adult integument in holometabolous insects. They consist of a single-cell layer epithelium that arises as an infolding of the embryonic ectoderm. After exponential increase in cell number during the three larval instars, cell division slows and the discs evaginate (Bryant and Levinson, 1985; Madhavan and Schneiderman, 1977). Cessation of cell division occurs in a spatially and temporally defined pattern across the disc (Schubiger and Palka, 1987; O’Brochta and Bryant, 1987), and is controlled by a disc autonomous mechanism that is dependent on intercellular contact (Bryant and Schmidt, 1990; Bryant and Simpson, 1984).

Mutants in seven loci have been found that interfere with cessation of cell division in imaginal discs (Bryant and Schmidt, 1990; Mechler et al., 1991). These have been called tumor suppressor genes because of the resulting overgrowth of discs, which occurs during an extended larval period. Tumor suppressor genes have been divided into two groups based upon the type of disc overgrowth. Mutations in one group lead to neoplastic overgrowth. In these mutants, the discs lose their single-layer epithelial organization and their ability to differentiate. The genes in this group are *discs large-1 (dlg)* (Woods and Bryant, 1989; Stewart et al., 1972) and *lethal(2) giant larvae (lgd)* (Gateff and Schneiderman, 1974). Mutations in the second group lead to hyperplastic overgrowth. In these mutants, the discs retain their single-layer epithelial structure and their ability to differentiate adult cuticular structures. The genes in this group are *discs overgrown (dco)* (Jursnich et al., 1990), *lethal(2)fat (fat)* (Bryant et al., 1988), *lethal(2) giant discs (lgd)* (Bryant and Levinson, 1985), *lethal(3)c43 (c43)* (Martin et al., 1977; Shearn, 1977), and *tumorous discs (tud)* (Gateff and Mechler, 1989). In addition to causing disc overgrowth, mutants in the tumor suppressor genes also cause some cell death. The most extreme example of degeneration occurs in *dco* mutants, in which certain allelic combinations lead to complete degeneration, while others lead to overgrowth of discs (Jursnich et al., 1990).

The Fat protein is a member of the cadherin superfamily (Mahoney et al., 1991). Vertebrate cadherins are calcium-dependent cell adhesion molecules, indicating Fat may be involved in cell adhesion. The Fat protein also contains four epidermal growth factor repeats and is a transmembrane protein. The Lgl protein is also somewhat similar in sequence to cadherins (Lützelschwab et al., 1987; Klambt et al., 1989) and is membrane associated (Strand et al., 1991). *dlg* encodes a guanylate kinase that is localized in a lateral belt near the apical cell surface (Woods and Bryant, 1991). Mutations in *dco* and *c(43)* reduce the number of gap junctions on cell membranes (Jursnich et al., 1990; Ryerse and Nagel, 1984a,b). The net function of these genes is to inhibit cell proliferation, possibly via cell-cell communication mechanism.

Here we provide evidence that the *expanded (ex)* gene affects the growth of imaginal discs. The original *ex* mutation (Stern and Bridges, 1926) causes wide wings. Waddington (1940) characterized the *ex* phenotype in greater detail and concluded that the wing defect was probably due to effects on cell division. We have isolated an enhancer-trap transposon insertion in the *ex* gene, and...
used it to generate an allelic series of \textit{ex} mutations that cause varying degrees of hyperplastic overgrowth of discs. We have also cloned \textit{ex}, determined the sequence of its predicted protein product and characterized its expression pattern with antibodies raised against an Ex fusion protein. \textit{ex} encodes a protein with three potential SH3-binding sites and may therefore interact with SH3-containing proteins such as Dlg, \textit{Drosophila Abl} (Dabl) or \textit{Drosophila Src} (Dsrc).

**MATERIALS AND METHODS**

**Fly stocks**

Flies were reared on standard cornmeal molasses medium at room temperature. \textit{ lethal(2)eyeless (l(2)ey)} a mutant isolated in an EMS screen by Huettner and Bryant (1988), and \textit{l(3)dco} were provided by P. Bryant. \textit{Df(2)al} was provided by J. Kennison. \textit{ds^{3k}} and \textit{ds^{13k}} were provided by A. Dingwall. (Complementation tests were done using both alleles.) In the text, \textit{ush} refers to the allele \textit{ush^{1012}}. Complementation tests with \textit{al} were done with alleles \textit{al} and \textit{al^2}. \textit{ush} and \textit{al} stocks were obtained from the Bloomington Stock Center. Canton S (CS) and balancer chromosomes were laboratory stocks. Except the new \textit{ex} mutants described in the text, all mutants used here are described in Lindsley and Zimm (1992).

**Enhancer-trap insertion characterization**

A new set of \textit{P}[\textit{lacW}] insertions on the 2nd and 3rd chromosome was generated by the mobilization of an \textit{X}-chromosome insert as described by Bier et al. (1989). The starting \textit{X}-chromosome \textit{P}[\textit{lacW}] insert was generously provided by E. Bier. New inserts on the autosomes were selected on the basis of \textit{w^+}. Lines containing inserts were screened for \textit{\beta}-gal activity in imaginal discs.

Polytene chromosome squashes and in situ hybridizations were performed according to the protocol of Ashburner (1989). The probes were labelled with digoxigenin-dATP (Boehringer Mannheim) using random primers.

**Isolation of \textit{ex} clones**

Screening of recombinant DNA libraries, subcloning, Southern and northern blot analysis was performed according to Sambrook et al. (1989). Genomic DNA clones were isolated from the \textit{Drosophila} genomic library of Maniatis et al. (1978) using an amplified aliquot provided by B. Ganetzky. 50,000 plaques were plated in each round of screening. cDNAs were isolated from a third instar imaginal disc library kindly provided by G. Rubin. 300,000 plaques from this library were plated in each round of screening. All probes used to screen libraries were labelled with \textit{\alpha}{\textsuperscript{32P}}dATP using the random primer method to a specific activity of at least 10\textsuperscript{8} cts/minute/\mu g of DNA. 500,000 cts/minute/ml of the labelled probe was used for each hybridization.

**Sequencing**

Nested deletion series for DNA sequencing were created using an Erase-a-base kit (Promega) following the manufacturer’s recommended procedures. DNA templates were prepared by the small-scale alkaline lysis method (Sambrook et al. 1989). Sequencing was done using Sequenase version 2.0 (US Biochemicals) following the manufacturer’s recommended procedures. Compressions and premature terminations were resolved using deaza-dGTP with Sequenase and high temperature reactions with Pfu DNA polymerase (Stratagene), respectively. Deletion series constructs and several relevant subclones were sequenced to span the 6.1 kb of cumulative cDNA. Except for 253 bases in the 3’ untranslated region, all sequence was determined for both strands.

**Antibody production and staining**

A 2405 bp \textit{PstI-BamHI} fragment from cDNA pL3 was cloned into a T7 expression vector (Rosenberg et al., 1987). Cells carrying this construct were induced, harvested and lysed. Inclusion bodies were spun down and washed four times with RIPA buffer (150 mM NaCl, 1% Tween, 0.5% deoxycholate, 0.1% SDS, 50 mM Tris pH 7.5), resuspended in PBS (10 mM KPO\textsubscript{4}, 150 mM NaCl, pH 7.2) and 2 mg were injected intradermally into New Zealand White Rabbits. Monthly subcutaneous boosts were given. Antibodies were affinity purified on an Ex-Actigel (Sterogene) affinity column according to the supplier’s instructions. Staining was done as follows. Fixed imaginal discs were blocked with PBS supplemented with 3% BSA for 1 to 4 hours, and incubated with a 1:8000 dilution of anti-Ex in PBTw (PBS + 0.1% Tween) with 0.3% BSA for 4 hours. The material was washed in PBTw and then incubated overnight in a 1:500 dilution of horseradish peroxidase-conjugated goat anti-rabbit IgG (Fischer-Biotech). The discs were washed and equilibrated in reaction buffer. Detection was done following the manufacturer’s recommendations.

**Comparative analysis of wings**

Photographs of mounted wings were traced by hand then scanned and imported into a drawing program. Wings were rotated about the vertex of veins L2 and L3 to align veins L2 or L3. After wings were aligned, they were scaled so the aligned veins were the same length from the vertex to the margin. To obtain an average wing shape the three flattest wing mounts for each genotype were aligned and scaled along vein L2, printed and retracted. Tracings of wing hairs were taken from photographs of the dorsal and ventral wing surfaces between veins L4 and L5. The dorsal and ventral images were coded so their identities were unknown until after the analysis was complete.

**Database searches**

The predicted protein was used in searches of NBRF-PIR release 33 and SwissProt release 22 using Prosran software (DNASTar) with PAM matrices. PATMAT version 2.21 was used to search the Blocks database (release 4.1) for matches with conceptual proteins translated from all six frames of the cDNA sequence. The Prosite database was also searched to identify any matches to known protein motifs.

**RESULTS**

**Isolation of \textit{ex} mutant alleles**

In a search for genes involved in imaginal disc development, a collection of \textit{P}[\textit{lacW}] enhancer-trap transposon insertions was generated and screened for \textit{\beta}-galactosidase expression in discs. Insert 697 expresses \textit{lacZ} throughout discs and also disrupts disc development, causing overgrown, missing, or improperly differentiated adult limbs. The most obvious defect in 697 mutants is broad, arced wings. A single \textit{P}[\textit{lacW}] insert at 21C1-4, \textit{P}[\textit{lacW}]/\textit{21C1-4}, was detected in polytene chromosomes squashes prepared from the 697 stock after probing with \textit{P}[\textit{UC}] sequences contained in \textit{P}[\textit{ucW}]. A deficiency spanning this region, \textit{Df(2L)al21B8-C1:21C8-D1}, failed to complement the 697 defect, confirming the cytological mapping. \textit{Df(2L)al} uncovers mutations in several known genes: \textit{al}, \textit{ex}, \textit{l(2)ey}, \textit{ds}, and \textit{ush}. 697, \textit{ex} and the previously identified mutant \textit{l(2)ey} fall into one complementation group. Since \textit{ex} was the first allele named, it will be referred to as \textit{ex}\textsuperscript{1}, and 697 and \textit{l(2)ey} will be called \textit{ex}\textsuperscript{697} and \textit{ex}\textsuperscript{[2]ey}, respectively.
Southern blot analysis confirmed the existence of a single insert in the ex697 stock. To test whether the ex697 phenotype was due to P[lacW](21C1-4), 100 independent lines were created by transgenic crosses that lacked the white+ marker contained in P[lacW]. As expected, most of the lines (89) retained the ex697 phenotype. These presumably contained an internal excision of the enhancer-trap that disrupts the white marker and were therefore discarded. Five were full phenotypic revertants, providing evidence that insert 697 causes the ex697 phenotype. Six gave a more severe phenotype, which may have arisen due to excision of DNA flanking the insert. These were designated exl-exe6, and were tested inter se and against al, ds, ush. exl through exe6 fall into a single ex complementation group. We have further characterized exl, exe2 and exe6.

exe1-exe6 were originally classified as recessive lethals because no homozygous progeny were recovered among at least 100 scored. However, during routine stock maintenance escapes in the exe6 and exe2 stocks were observed, implying that exe2 and exe6 retain some ex function. Escapees have not been observed in Df(2L)al, exl or exe2 stocks. The allele strength was estimated by viability, eclosion rate and penetrance of the ex phenotype (Table 1). All the data are consistent with the following ranking (from most to least severe): Df(2L)al= exe1>exe2>exe6>exe697. exe1 is a small deficiency that removes S sequences of the expanded transcription unit (see below) and behaves like Df(2L)al in all heteroallelic tests, and is therefore classified as a genetic null allele.

ex mutants phenotypes

The ex mutant phenotype is incompletely penetrant and expressive (Table 1). Weak mutant alleles, such as exl, generally show only a broad wing phenotype, which occasionally have an upward or downward arc. Intermediate mutants such as ex697 or mutant combinations such as exe2/exe697 display phenotypes affecting legs, thorax, head and wings. Occasionally, entire legs are missing, but more commonly, legs are kinked or have swollen distal tarsal segments, with completely separated internal vesicles of unknown origin and composition (Fig. 1G). In intermediate mutant combinations such as exe2/exe697, about 50% of the individuals display leg defects. In these flies, only one or two legs are typically affected. The thoracic defects include duplication of scutellar bristles and sensilla on the wing. Defects in the head capsule are variable. Eyes are reduced in size and occasionally split. Duplicated antennae or vibrissae occur in about 50% of exe2/exe697 heterozygotes, apparently at the expense of peripheral eye tissue. In addition to being broad, the wings are arced down and have incomplete crossveins (Fig. 1C). The wing phenotype of intermediate mutants will be discussed in detail below.

Compared to the intermediate alleles, exe1 pharate adults display a highly penetrant and expressive phenotype. exe1 mutants survive until the pharate adult stage and show massive head, wing and leg defects (Fig. 1D, G). All exe1 pharate adults have leg defects and usually all legs of an individual are defective (Fig. 1F). Some legs are entirely missing, but the most common defect is missing distal tarsal segments including the claw organs. The legs usually terminate beyond the second tarsal segment. The remaining proximal tarsal segments have supernumerary bristles. The antennae are enlarged and are missing aristae, but otherwise appear normal (Fig. 1D). The reduction of eye tissue seen in intermediate mutant alleles is exaggerated in exe1 pharate adults, such that eyes fail to differentiate ommatidia (Fig. 1D). Unlike intermediate mutants, antennal duplications do not generally occur.

To understand better the function of ex, the phenotype of null mutants was examined at earlier stages. No visible defects were seen in exe1 mutant embryos and they hatched at a rate comparable to wild type (data not shown). The first obvious defects occur in the imaginal discs at about mid-third instar, by which time the wing disc is noticeably enlarged (data not shown). The wing disc continues to grow, mainly in the presumptive wing pouch region and, by day

<table>
<thead>
<tr>
<th>Table 1. Summary of inter se crosses with ex mutants</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
</tr>
<tr>
<td>--------</td>
</tr>
<tr>
<td>Df(2L)al</td>
</tr>
<tr>
<td>el</td>
</tr>
<tr>
<td>l(2)ey</td>
</tr>
<tr>
<td>e2</td>
</tr>
<tr>
<td>e6</td>
</tr>
<tr>
<td>697</td>
</tr>
<tr>
<td>ex</td>
</tr>
</tbody>
</table>

†stocks maintained as homozygotes; other stocks maintained over SM6

*fraction homozygous viable progeny (total scored)

nt - viability not scored

b - broad wings

cv - greater than 10% of the mutant progeny have incomplete posterior cross vein

ea - greater than 10% of the mutant progeny have defects in eye-antennal disc derivatives

l - greater than 10% of the mutant progeny have swollen or missing leg segments
Fig. 1. Adult ex phenotype. (A) Wing from Canton S fly. (B) Canton S head capsule showing normal eyes and antennae with aristae (arrowhead). (C) Wing from ex697 fly. Arrowhead points to incomplete crossvein. (D) An ex1 pharate adult head capsule with missing eyes and aristae. (E) Canton S with tarsal segments numbered. (F) SEM of ex1 pharate adult showing 2 missing legs and 4 legs with truncated tarsal segments. The remaining tarsal segments are bracketed. (G) ex697 tarsal segments with characteristic swelling and internal vesicles. Tarsal segments are numbered in panels E and G.
**Fig. 2.** *ex* null phenotype in wing imaginal discs. All photos are at the same magnification. (A) Wild-type wing disc at day 5. (B) *ex* mutant at day 5 showing enlarged wing pouch and extra fold. (C) *ex* mutant at day 8, grown to about double the size of wild type and with a prominent extra fold (arrow) near the anterior-posterior compartment boundary.

**Fig. 3.** Wing shape phenotype in *ex* mutants. (A) Average CS wing with veins labelled (L1-L5). (B) Average *ex* mutant wing, solid black line, showing the hyperplasia between L1 and L2 and between L4 and L5 (shaded regions). *ex* pharate adult wings, dashed lines, showing additional hyperplasia between L5 and the margin. Panels C-F show position of hairs at intersections of diagonal lines. Dorsal (C) and ventral (E) wing surfaces of wild-type (taken from region near boxed region in A) are well organized compared to the dorsal (D) and ventral (F) surfaces of mutant wing. C and E show that cells in the wild-type wing are elongated in the long axis of the wing, while B shows cells elongated predominantly in the broad axis of the wing. D shows both types of elongation, above region a is more similar to wild-type than above region b. The difference in dorsal and ventral cell shapes may account for the downward arc of the wing seen in intermediate *ex* alleles.
five, begins to form an extra fold approximately at the anterior-posterior compartment boundary (Fig. 2B). Growth continues during an extended larval period (2-3 extra days in uncrowded conditions), usually until the wing disc reaches double the wild-type size (Fig. 2C), although occasionally continuing until they are many times the size of wild type. Overgrowth also occurs in the haltere disc (data not shown). In the eye-proper and the leg discs, degeneration is visible (data not shown). The eye region of the eye-antennal disc is largely atrophied, presumably due to a lack of ommatidial development, as evidenced by the lack of a morphogenic furrow or organized photoreceptor cells and by the missing eye in pharate adults (Fig. 1D). The presumptive head capsule is still intact (data not shown). The leg discs appear to be lacking distal segments (data not shown). All discs examined retained a single-cell layer epithelium.

**ex affects the number, size and shape of cells in the wing**

Since each cell in the wing blade is associated with a single hair, the hairs can serve as markers for cell number and position (Dobzhansky, 1929). An examination of ex hypomorphic mutant wings revealed that the increased size of the wing is due to hyperplasia in two regions of the wing. In one of these regions, there is an increase in cell density, an elongation of cells in the broad axis of the wing and a greater elongation in dorsal surface than ventral surface.

The wing phenotype of a viable ex mutant is shown in Fig. 3. To analyze their shape, the wings were aligned along a wing vein and scaled to the same size. After scaling, all mutant wings were essentially superimposable (as are wild type), showing that the mutant wing phenotype is highly reproducible. This was true regardless of the heteroallelic combinations tested, allowing a comparison of wing shape to be made between scaled mutant and wild-type wings. Moreover, the overgrowth phenotype is completely recessive, indicating that overgrowth is not due to dominant allele-specific affects. The shape of ex mutant wings is broader than wild type, and rounder at the tip. The distal tip of wild-type wings occurs where L3 meets the margin, whereas the distal tip of ex wings is at the margin between L3 and L4 (Fig. 1A, C). The sizes of intervein regions were compared separately between wild-type and ex mutant wings. This analysis revealed that only specific regions of the wing are larger in expanded mutants. The area between L1 and L2, and between L4 and L5 are increased the most (shaded regions in Fig. 3B). The area bounded by L3, L4 and the anterior crossvein is not significantly different in the mutant. Although the figure shows ex697 wings, essentially identical results were obtained for ex1, ex2, ex697, ex1/697, ex2/697 and ex697 mutant wings. The posterior crossvein is about the same length in mutants and wild type and does not span the intervein region in ex mutants. Thus, it is possible that the overgrowth is limited to a region anterior to the incomplete crossvein. From this analysis, it cannot be determined whether overgrowth is limited in the proximal distal axis. To determine whether overgrowth is spatially limited in null mutants, adult wings were dissected from pharate adults and carefully flattened. There was considerably more variation in shape among mutant pharate wings. The mutant pharate wings were generally larger than wild type with excessive growth between L1 and L2, and between L4 and the margin (dotted lines in Fig. 3B). These results indicate that regional hypertrrophy occurs in complete as well as partial loss-of-function ex mutations.

Hair distribution was used to examine the shape and distribution of cells in wild type and ex697 in the most severely affected region, between L4 and L5 (Fig. 3D,F). The density of hairs on mutant wings is increased and the hairs are more disorganized than on wild-type wings. The ratio of the average distance between hairs in the broad and long axis of the wing is larger in the mutant than in wild type. The ratio in wild-type wings is the same for the dorsal and ventral wing blade surfaces, 0.53±0.05 (n=20) and 0.53±0.07 (n=24), respectively. However, in mutants the...
Fig. 5. ex and protein sequence. Genomic sequence is in capital letters followed by the cDNA sequence in lowercase. The \( P[lacW](21C1-4) \) is at position −1. Below the cDNA sequence is a conceptual translation in single letter amino acid code starting at the ATG at position 892. The 9 upstream ATGs are underlined. The 697 insert is at position −1 in this figure. Three basic regions 306-408, 840-879, 1194-1270 are separated by neutral or slightly acidic regions. Homopolymeric runs, and QA and LX repeat regions are in bold underlined text. Three putative SH3-binding domains are boxed.
ratio is larger on the dorsal surface than on the ventral surface (1.59±0.22 (n=15) and 0.90±0.41 (n=42), respectively). The abnormal hair distribution indicates that, in this region, the cells in ex mutants are elongated along the broad axis of the wing. This type of cell elongation does not occur in the region between L5 and the margin in ex<sup>4697</sup> mutants (data not shown).

An estimate of the number of extra cell divisions occurring between L4 and L5, \( N_e \), was made using the formula \( N_e = \ln R / \ln 2 \), where \( R \) is the ratio of cell densities in mutant versus wild-type wings. This calculation assumes that wild-type and mutant wing discs start with the same number of cells and that the amount of cell death is unchanged in the mutant. \( R \) was estimated as 1.7 for the region between L4 and L5 in ex<sup>4697</sup> mutants, yielding an \( N_e \) of 0.7. According to this estimate, an average increase of 0.7 cell divisions per cell occurs in the region between L4 and L5. This is a minimum estimate, since it is quite possible that increased cell death occurs in ex mutants, as has been described for other tumor suppressor mutants (Jursnich et al., 1990). Also, ex<sup>4697</sup> is a viable allelic combination, and a qualitative difference in size exists between mutant wing discs from this allelic combination and null alleles. Based on visual examination of mutant wing discs from null mutants and not accounting for possible cell death, we estimate that the \( N_e \) is slightly greater than 1.

**Molecular characterization of ex**

The ex gene was unambiguously identified by the position of the P[<i>lacW</i>]/21C1-4) and by a small deletion, ex<sup>e1</sup>, that removes part of the ex transcript. Genomic DNA flanking one side of the ex<sup>697</sup> P[<i>lacW</i>] insert was recovered by plasmid rescue. The resulting plasmid, p697, contained 2.8 kb of flanking DNA and was used as a probe to polytene chromosomes from salivary glands of wild-type larvae. A single band was detected at 21C1-4, confirming the identity of the rescued plasmid. p697 was then used as a probe to polytene chromosomes from salivary glands of wild-type larvae. A prominent band at 6.9 kb (data not shown). This same probe was used to retrieve cDNAs from a larval disc cDNA library. Eight cDNAs, which together span 6.1 kb, were analyzed by restriction mapping and sequencing. No differences were found in the overlapping regions and thus appear to be derived from a single species of transcript.

The composite sequence of the three ex cDNAs was determined (Fig. 5). There is a single large open reading frame of 4287 bases, encoding a predicted protein of 1429 amino acids. A good in-frame match to the Drosophila consensus translational start (Cavener, 1987) is present at base 892. There are nine other ATGs present upstream. The longest potential protein encoded by an upstream ORF is relatively short, 137 amino acids in length. We conclude that the 1429 amino acid protein is the major ex product.

The approximate positions of the ex exons were determined by hybridization of cDNAs to genomic DNA fragments on Southern blots. The precise locations of intron-exon junctions were determined from comparison of cDNA and genomic DNA sequences at those junctions (Fig. 5). Southern blots of ex<sup>e1</sup> mutant DNA shows that a small deletion is associated with a partial excision of the P element. This deletion removes at least the rightmost 1.9 kb of the P[<i>lacW</i>] insert plus 3-12 kb of flanking genomic DNA, including the first exon. The deletion does not extend as far as the second exon (Fig. 4). Because no other transcripts are affected by the deletion, the 6.9 kb transcript belongs to ex. Absence of the first exon is consistent with genetic evidence that ex<sup>e1</sup> is a null allele.

**Ex protein contains potential SH3-binding sites**

Comparisons of the predicted Ex protein sequence to protein databases and translated DNA databases reveals no striking similarities to known proteins. A lack of hydrophobic segments suggests that the Ex protein is probably not secreted or membrane spanning. Overall the predicted protein is basic, with three positively charged amino acid segments (isoelectric point greater than 9.0) separated by neutral or slightly acidic regions. The C-terminal half of the protein contains many short homopolymeric runs of proline, serine, alanine, histidine and glutamine. Three consensus binding sites for Src homology 3 (SH3) domains, defined as PXXPPPXXP (Ren et al., 1993), are boxed in Fig. 5. SH3-binding sites have also been found in 3BP1, a mammalian protein that also has homology to GAP-rho outside the SH3-binding site (Cicchi et al., 1992), in forms, which are products of the limb deformity gene in mice (Woychik et al., 1990), and in the muscarinic acetylcholine receptor genes (Bonner et al., 1987). HomopolymERIC runs of glutamine, proline and histidine have been associated with

![Fig. 6. ex protein expression.](image-url)

(A) Staining of a third instar wing disc with anti-ex shows the appearance of more intense staining in folds.

(B) Longitudinal section of an anti-ex-stained third instar wing disc showing that the ex protein is tightly localized to the apical cell surface. wp marks the wing pouch and b marks the basal cell surface.
DISCUSSION

The phenotypes seen in the ex mutants resemble those in some tumor suppressor mutants. To date, seven tumor suppressor gene affecting imaginal discs have been identified (Bryant and Schmidt, 1990). Five of these, when mutant, cause hyperplastic growth of discs during an extended larval period. Based on the disc overgrowth phenotype, we propose that ex be assigned to the hyperplastic group of tumor suppressor genes. The discs of these tumor suppressor mutants, including ex, continue to grow during an extended larval period. Overgrowth in the previously characterized tumor suppressor mutants is not due to the extended larval period, but rather has been interpreted to be due to a disruption of a signal normally required to limit growth (Bryant and Schmidt, 1990). The hyperplastic phenotype suggests that ex may also be required to generate or respond to growth-limiting signals. Overgrowth of mid-third instar discs suggests that ex must be needed before this time (as are other tumor suppressor genes). This overgrowth could be due to extra cell divisions or decreased cell death. Since there is normally little cell death during development of the wing disc (James and Bryant, 1981), we infer that the increase in cell number is due primarily to extra cell divisions starting before mid-third instar and continuing throughout an extended larval period.

Degeneration, instead of overgrowth, occurs in distal tarsi, aristae and eyes of ex null mutants. This may reflect a varying sensitivity to reduced ex activity rather than different functions of ex in these discs. It is possible that loss of ex function causes cell death in these structures, as seen in dpp, vg and scalloped mutants (James and Bryant, 1981), or simply a failure to grow, as has been postulated for wg mutants (Cousso et al., 1992). In either case, these defects may be mechanistically related to the hypertrophy seen in wing discs.

The ex phenotype closely resembles the phenotype of dco mutants. Both phenotypes include duplications of head structures, bulged leg segments and disc overgrowth and degeneration (Jursnich et al., 1990; this work). There is also a striking similarity in the abnormal folding pattern of wing discs from ex and dco mutants, whereas all the other tumor suppressor mutants have distinctly different abnormal disc morphologies. Therefore, we suggest that ex and dco may impinge on the same growth control pathway. Although the molecular function of dco is unknown, dco mutants have a reduced number of gap junctions. By extension, ex may be involved in gap junction formation or may be part of a signalling pathway dependent on gap junctions.

Recently, a consensus peptide was defined that binds to SH3 regions (Ren et al., 1993; Cicchetti et al., 1992). Analysis of the Ex protein sequence revealed three such SH3-binding sites. SH3 domains have been found in proteins involved in signal transduction pathways, including non-receptor tyrosine kinases and proteins in Ras signalling pathways (for review see Pawson and Gish, 1992; Clark et al., 1992). The SH3 domain has been shown to have a negative regulatory effect on the Abl and Src tyrosine kinases (Seidel-Dugan et al., 1992; Franz et al., 1989), and to be necessary for signal transduction involving guanosine triphosphatase activating protein (GAP) (Duchesne et al., 1993). Thus Ex may function by binding to proteins that are directly involved in a signal transduction pathway.

The SH3-containing proteins, Drosophila Abl (Dabl) (Bennet and Hoffman, 1992) and Dsrc29A (Katzen et al., 1990), are expressed in imaginal discs. Moreover, the Dabl protein, like Ex, is localized to the apical surface of cells in imaginal discs. p66, a product of Dsrc29A, is localized to the plasma membrane in embryonic cells, and may be membrane localized in imaginal disc cells as well. However, genetic analysis of dabl in flies has yet to reveal any connection to growth control in imaginal discs.

Another potential interaction is with the SH3-containing product of the tumor suppressor gene dlg, which encodes a guanylate kinase, and has therefore been postulated to affect growth by regulating the GTP:GDP ratio in the cell. A high GTP:GDP ratio is known to activate Ras and it was therefore postulated that Dlg could affect this pathway. The Dlg protein is expressed in a lateral belt at the apical end of the cell (Woods and Bryant, 1991) and may make some direct contact with Ex.

Overgrowth of wing tissue is limited to certain regions of the wing blade of ex mutants depending on the allelic combination, implying that multiple growth control mechanisms operate across the wing disc. An initial examination of other wing shape mutants indicates that different regions of the wing can also be affected. For example, Broad and fat^Gull seem to cause an increase in the area between L2 and L3 (unpublished data). Multiple growth control mechanisms may have provided a simple evolutionary mechanism accounting for differences in wing shape in Drosophila species. Since the Ex protein expression is not limited to the overgrown regions, it seems likely that an unidentified localized signal is directly responsible for regionalized growth control.

It remains to be determined whether region-specific overgrowth in ex mutants is related to compartment boundaries (Garcia-Bellido et al, 1973, 1976; Lawrence and Morrata, 1976; Blair, 1992), regions of neuronal competence (Simpson and Carteret, 1986), or patterns of gene expression, which run parallel to the proximal-distal axis (Kornberg et al., 1985; Brower, 1986; Orenic et al., 1990;
Cousso et al., 1993; Williams et al., 1993). Another possibility is that an redundant growth control system may be active in the presumptive medial wing blade, which could compensate for effects of ex mutations in this region. dpp, for example, is expressed in a proximal-distal stripe centered in the wing disc (Massucci et al, 1990; Blair, 1992), and, although dpp is needed throughout the wing disc, the region most sensitive to loss of dpp is where dpp expression is highest. Consistent with this idea is the observation that the regions sensitive to ex levels flank the regions of high dpp expression.

We thank Duane Price for his participation in carrying out the enhancer-trap screen. We thank Peter Bryant, Andy Dingwall, Jim Kennison and Matthew Scott for generously providing stocks and for valuable discussion of unpublished results. We appreciate helpful comments on the manuscript from Jim Williams, Brian Florence and Duane Price. We thank Bill Engels for use of a 4x objective. This work was supported by a grant to A. L. from the NSF and by an NIH predoctoral training grant (GM07133). This is publication number 3351 from the Laboratory of Genetics, University of Wisconsin, Madison.

REFERENCES


Bennet, R. L. and Hoffman, F. M. (1992). Increased levels of the wingless signalling gene for example, is expressed in a proximal-distal stripe centered in the wing disc (Massucci et al, 1990; Blair, 1992), and, although dpp is needed throughout the wing disc, the region most sensitive to loss of dpp is where dpp expression is highest. Consistent with this idea is the observation that the regions sensitive to ex levels flank the regions of high dpp expression.

We thank Duane Price for his participation in carrying out the enhancer-trap screen. We thank Peter Bryant, Andy Dingwall, Jim Kennison and Matthew Scott for generously providing stocks and for valuable discussion of unpublished results. We appreciate helpful comments on the manuscript from Jim Williams, Brian Florence and Duane Price. We thank Bill Engels for use of a 4x objective. This work was supported by a grant to A. L. from the NSF and by an NIH predoctoral training grant (GM07133). This is publication number 3351 from the Laboratory of Genetics, University of Wisconsin, Madison.

Bryant, P. J. and Simpson, P. (1992). Increased levels of the wingless signalling gene for example, is expressed in a proximal-distal stripe centered in the wing disc (Massucci et al, 1990; Blair, 1992), and, although dpp is needed throughout the wing disc, the region most sensitive to loss of dpp is where dpp expression is highest. Consistent with this idea is the observation that the regions sensitive to ex levels flank the regions of high dpp expression.

We thank Duane Price for his participation in carrying out the enhancer-trap screen. We thank Peter Bryant, Andy Dingwall, Jim Kennison and Matthew Scott for generously providing stocks and for valuable discussion of unpublished results. We appreciate helpful comments on the manuscript from Jim Williams, Brian Florence and Duane Price. We thank Bill Engels for use of a 4x objective. This work was supported by a grant to A. L. from the NSF and by an NIH predoctoral training grant (GM07133). This is publication number 3351 from the Laboratory of Genetics, University of Wisconsin, Madison.
Identification of a ten-amino acid proline-rich SH3 binding site. Science 259, 1157-1161.


(Accepted 3 May 1993)