Mutations in *Drosophila myb* lead to centrosome amplification and genomic instability

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**SUMMARY**

We have previously established that the single *myb* gene in *Drosophila melanogaster*, *Dm myb*, which is related to the proto-oncogene *Myb*, is required for the G2/M transition of the cell cycle and for suppression of endoreduplication in pupal wing cells. We now report that studies of the abdominal phenotype in loss-of-function *Dm myb* mutants reveal additional roles for *Dm myb* in the cell cycle, specifically in mitosis. Abdominal epidermal cells that are *Dm myb* in the cell cycle, reveal additional roles for *Dm myb* abdominal phenotype in loss-of-function mutants of pupal wing cells. We now report that studies of the cell cycle and for suppression of endoreduplication in their lack of the tumor suppressor proteins *p53* (TP53 – Human Gene Nomenclature Database), BRCA1 or BRCA2 (Fukasawa et al., 1996; Tutt et al., 1999; Xu et al., 1999).

The vertebrate Myb gene family consists of three closely related members, *Myb* (c-*myb*), *Mybl1* (A-*myb*) and *Mybl2* (B-*myb*). Myb genes encode DNA-binding proteins that regulate transcription and have been implicated in regulatory decisions affecting cell proliferation, differentiation and apoptosis (Oh and Reddy, 1999; Weston, 1998). Mutant versions of *Myb* have been implicated in the genesis of neoplastic disease in chickens, mice and humans (Oh and Reddy, 1999). *Drosophila melanogaster* possesses a single *myb* gene (*Dm myb*; *Myb* – FlyBase), which contains four regions of homology with the vertebrate Myb genes (Bishop et al., 1991; Katzen et al., 1985; Peters et al., 1987). The *Dm myb* gene product, DMyb (Myb – FlyBase), shares several biochemical properties with the vertebrate family of Myb proteins, including binding to a similar consensus sequence and the ability to activate transcription from a reporter construct regulated by vertebrate Myb proteins (Jackson et al., 2001).

We have previously reported the isolation of temperature-sensitive, recessive lethal mutations in *Dm myb*. Mutant phenotypes revealed a requirement for *Dm myb* in diverse cellular lineages throughout development (Katzen and Bishop, 1996). Even when mutants are raised at temperatures permissive for viability, adults display abnormalities, including cuticular defects in wings and abdomens. Analysis of the wing phenotype demonstrated that *Dm myb* is required for both and/or failure to complete cell division are common in the later cell cycles of mutant cells. Resulting nuclei are often aneuploid and/or polyploid. Similar defects have also been observed in loss-of-function mutations of the tumor suppressor genes *p53*, *Brca1* and *Brca2*. These data demonstrate that in abdominal epidermal cells, *Dm myb* is required to sustain the appropriate rate of proliferation, to suppress formation of supernumerary centrosomes, and to maintain genomic integrity.

Key words: *Drosophila, myb*, Transcription factor, Mitosis, Centrosomes, Genomic instability

**INTRODUCTION**

Failure to precisely regulate chromosome duplication and segregation leads to genomic instability, a term encompassing an assortment of genomic alterations including loss or gain of entire chromosomes, and other chromosomal abnormalities, such as rearrangements, translocations, amplifications and deletions. Genomic instability can result in cell or organismal death (Chester et al., 1998; Gao et al., 2000; Reed, 1999), is associated with premature aging disorders (Karow et al., 2000), and is considered to be a primary driving force of multistep carcinogenesis (Nowell, 1976; Solomon et al., 1991).

Genomic integrity is maintained by cell cycle checkpoints that monitor DNA replication and detect cellular/DNA damage (Hartwell et al., 1994). Centrosomes organize the poles of the mitotic bipolar spindle and play a key role in genomic stability by ensuring balanced chromosome segregation (Sluder and Hinchcliffe, 1999). When a mitotic cell contains more than two functional centrosomes, a multipolar spindle can be formed that either randomly distributes chromosomes into multiple daughter cells or results in failure to complete cell division (Fukasawa et al., 1996; Sluder and Hinchcliffe, 1999). Either way, the consequence is genomic instability, a hallmark of many aggressive tumors (Pihan et al., 1998; Salisbury et al., 1999). Abnormally high numbers of centrosomes have been detected in many human tumor cells, an anomaly ascribed to their lack of the tumor suppressor proteins *p53* (TP53 – Human Gene Nomenclature Database), BRCA1 or BRCA2 (Fukasawa et al., 1996; Tutt et al., 1999; Xu et al., 1999).

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We have previously reported the isolation of temperature-sensitive, recessive lethal mutations in *Dm myb*. Mutant phenotypes revealed a requirement for *Dm myb* in diverse cellular lineages throughout development (Katzen and Bishop, 1996). Even when mutants are raised at temperatures permissive for viability, adults display abnormalities, including cuticular defects in wings and abdomens. Analysis of the wing phenotype demonstrated that *Dm myb* is required for both
promotion of the G2/M transition and suppression of endoreduplication in pupal wing cells (Katzen et al., 1998).

The abdominal phenotype in Dm myb mutants, which includes missing bristles and patches of undifferentiated and unpigmented cuticle, is also suggestive of a proliferation defect. However, there are notable differences between wing and abdominal phenotypes (see Results), which may reflect the fact that the post-embryonic program for the development of abdominal epidermis is distinct from that of the rest of the adult epidermis (Cohen, 1993; Fristrom and Fristrom, 1993). The epidermis of the thorax (including the wing) and head is formed from imaginal discs, which contain diploid cells that proliferate throughout larval development, completing only their final one or two cell divisions during early pupation. By contrast, the abdominal epidermis is formed from small nests of imaginal cells, called abdominal histoblasts, which do not divide during larval development, but undergo rapid proliferation after pupariation (Madhavan and Madhavan, 1980).

The differences in Dm myb mutant phenotype between wings and abdomens at the cuticular level, together with the divergences in developmental programs, suggested that an analysis of the cellular basis of the abdominal phenotype might reveal more about Dm myb function. We now report distinct differences between the cellular defects in mutant Dm myb wing and abdominal cells, and we provide evidence that in proliferating abdominal epidermal cells, Dm myb is required to sustain the appropriate rate of proliferation, to suppress formation of supernumerary centrosomes and to maintain genomic integrity.

MATERIALS AND METHODS

Drosophila stocks
Generation of mutant Dm myb alleles, myb1 and myb2, on a white chromosome; construction of lines carrying a wild-type Dm myb rescue transgene, P[w*;myb+]; and the Df(1)sd72b62 chromosome, which deletes a region including Dm myb, have been described previously (Katzen and Bishop, 1996). Dp(1;Y)sht+Y3 is a specialized Y chromosome that carries a region of the X chromosome, including Dm myb (13F1-4 to 14F4-6) (Poodyr, 1980). The only apparent difference between Df(1)sd72b62 and Dp(1;Y)sht+Y3 (13F1-14B1) (Craymer and Roy, 1980) chromosomes is that the latter carries a recessive lethal mutation which is not completely linked with the deleted region (A. L. K., unpublished). Therefore, Df(1)sd72b62, but not Dp(1;Y)sht+Y3, is rescued by the Dp(1;Y)shs+Y3 chromosome. Stocks carrying exg3, exg58, Df(2L)TE35D-2 (which deletes exg), and bsp70-Gal4 provided by S. Hayashi; UAS-RBF provided by Bruce Edgar; and exgr1006, RpS31 and M(3)65F1 obtained from Bloomington Stock Center.

Adult abdomen preparation
Matings were performed at 18°C, and female white prepupa were collected and shifted to indicated temperatures. For mutants shifted to non-permissive temperatures, pharate adults were dissected out of pupal cases. Viable and pharate adults were preserved in 100% isopropanol. Abdomens were dissected and immersed in mineral oil for imaging using a Zeiss LSM 550 microscope. DAPI staining was used to determine the number of abdominal epidermal cells in control and mutant Dm myb animals (see Results and Table 1). BrdU labeling was performed as described by Shermoen (Shermoen, 2000), with the only modification being that samples were incubated with BrdU for 1 hour. Samples were imaged either by confocal microscopy (Zeiss LSM 550) or by wide-field microscopy (Zeiss Axioplan2) using a Princeton Instruments Micromax cooled CCD camera.

Fluorescent in-situ hybridization
The probe representing a 359 bp repeat present in X-chromosome heterochromatin was generously provided by Tin Tin Su. Fluorescent in-situ hybridization (FISH) was carried out as described by Dernburg (Dernburg, 2000) with the following modifications: hybridization solution contained 35% formamide, 1× SSC, 100 μg/ml tRNA and 0.1% Tween; probe and chromosomal DNA were denatured for 3 minutes at 92°C; samples were incubated for annealing at room temperature for 3 hours; samples were incubated with PH3 antibodies overnight, after which anti-DIG-rhodamine (Boehringer Mannheim, 1:10) and anti-rabbit-FITC were added together and samples were incubated for 2 hours at room temperature.

Quantitation of DNA content
Abdominal epidermal samples were fixed in 4% paraformaldehyde for 30 minutes and then stained with rhodamine-conjugated phalloidin (Molecular Probes, 5 U/ml) for 30 minutes and DAPI (0.5 μg/ml) for 10 minutes. After mounting in Vectashield, cover slips were sealed and samples were immediately imaged by confocal microscopy (Zeiss LSM 550) under identical conditions, set such that the DAPI fluorescence was within a linear range. Stacks of optical sections were collected at 2/3 μm intervals. Relative DNA contents of mutant and wild type nuclei were determined using a method similar to those described by others (Euling and Ambros, 1996; Hayashi and Yamaguchi, 1999). Briefly, the public domain NIH Image program 1.61 (http://rsb.info.nih.gov/nih-image/) was used: images were stacked, and the mean fluorescence value of each nucleus for each layer was determined and then multiplied by the area of the nucleus. Total values were obtained for each nucleus by summing the values for each layer. Background levels of signal were measured for all samples. They were low and did not differ significantly between samples.

Preparation and fluorescent staining of the abdominal epidermis from larvae and pupae
The enhancer trap insert exg3, which expresses β-galactosidase in larval abdominal histoblasts (Hayashi et al., 1993) was used to identify these cells. Wandering third instar larvae were fixed in 4% paraformaldehyde, 0.1% deoxycholic acid, and 0.1% Tween-20 in phosphate-buffered saline (PBS). Samples were then incubated with mouse anti-β-galactosidase antibodies (Promega, 1:1000), followed by an anti-mouse secondary conjugated to rhodamine (Boehringer Mannheim, 1:10). Finally, samples were stained with DAPI (4′-diamidino-2-phenylindole) at 0.5 μg/ml, rinsed, and mounted in Vectashield (Vector).

To prepare pupal samples from females of appropriate genotype (see figure legends), control (w), myb1 or myb2 virgin females were mated with myb1, myb2 or Df(1)sd72b62/Dp(1;Y)sht+Y3 males at 18°C. Female progeny were selected as larvae and maintained at 18°C until pupariation. White prepupa (0 hours after puparium formation (APF)) were picked and shifted to indicated temperatures for specified times. Pupae were then treated for abdominal epidermal preparation as previously described (Kopp et al., 1997) before fixation. Fixation conditions varied, depending upon the antiser: for PH3 and Bub1 antibodies, 4% paraformaldehyde for 30 minutes at room temperature; and for CP60, CP190 and β-tubulin antibodies, 37% formaldehyde for 5 minutes at room temperature. Immunostaining was performed as previously described (Audibert et al., 1996; Theurkauf, 1994) with the following dilutions for primary antibodies: 1:20 for β-tubulin (Harlan); 1:500 for CP60 and CP190; 1:1000 for Bub1 and PH3 (Upstate Biotech); and 1:10,000 for γ-tubulin (Sigma). Secondary antibodies conjugated to either FITC or rhodamine were purchased from Boehringer Mannheim and used at recommended dilutions. After immunostaining, samples were treated with DAPI at 0.5 μg/ml for 10 minutes, rinsed and mounted. DAPI staining was used to determine and compare the number of abdominal epidermal cells in control and mutant Dm myb animals (see Results and Table 1). BrdU labeling was performed as described by Shermoen (Shermoen, 2000), with the only modification being that samples were incubated with BrdU for 1 hour.

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Abdominal epidermal samples were fixed in 4% paraformaldehyde for 30 minutes and then stained with rhodamine-conjugated phalloidin (Molecular Probes, 5 μg/ml) for 30 minutes and DAPI (0.5 μg/ml) for 10 minutes. After mounting in Vectashield, cover slips were sealed and samples were immediately imaged by confocal microscopy (Zeiss LSM 550) under identical conditions, set such that the DAPI fluorescence was within a linear range. Stacks of optical sections were collected at 2/3 μm intervals. Relative DNA contents of mutant and wild type nuclei were determined using a method similar to those described by others (Euling and Ambros, 1996; Hayashi and Yamaguchi, 1999). Briefly, the public domain NIH Image program 1.61 (http://rsb.info.nih.gov/nih-image/) was used: images were stacked, and the mean fluorescence value of each nucleus for each layer was determined and then multiplied by the area of the nucleus. Total values were obtained for each nucleus by summing the values for each layer. Background levels of signal were measured for all samples. They were low and did not differ significantly between samples.
Abdominal cuticular defects in adult Dm myb mutants resemble those observed in esg and cdc2 mutants

In addition to the previously characterized wing phenotype (Katzen et al., 1998), myb1 and myb2 mutants raised at temperatures permissive for viability (18°C and 24°C, respectively) also displayed abdominal cuticular defects, including missing and misoriented bristles, and patches of undifferentiated and unpigmented cuticle (Fig. 1B,C,F). The expressivity of the abdominal phenotype varied at viable temperatures, but was stronger and more consistent in pharate adults raised at temperatures restrictive for viability (Fig. 1D,G).

Abdominal and wing phenotypes in myb mutants differ in several respects. Mutant wings are the appropriate size, but contain approximately half the number of hairs as wild type. Mutant hairs are considerably larger than normal and often misoriented. Bristles are never missing on mutant wings or elsewhere on the thorax and head, but the mutant bristles are larger and less uniform in orientation (Katzen et al., 1998). By contrast, the remaining abdominal bristles (and hairs) in Dm myb mutants appear to be wild type in size, although they are often misoriented (Fig. 1B-D,F,G). Phenotypic distinctions may reflect differences in post-embryonic developmental programs (see Introduction). Indeed, the abdominal phenotype is characteristic of situations in which there are not enough adult epidermal cells to replace all larval cells (Poodry, 1975), and is therefore suggestive of a defect in cell proliferation.

The abdominal phenotype in Dm myb mutants resembles those reported for certain mutant alleles of escargot (esg), which encodes a zinc-finger transcription factor, and for Drosophila cdc2 (Hayashi et al., 1993; Stern et al., 1993) (Fig. 1H). These defects have been attributed to a failure to suppress endoreduplication in abdominal histoblasts during larval development, thereby producing polyploid abdominal histoblasts that are no longer capable of dividing after puparium formation (Hayashi, 1996; Hayashi et al., 1993). Given the similarity of the phenotypes and our previous finding that when mutant Dm myb wing cells were arrested in G2 of their final cell cycle, they entered into an endoreduplication cycle, it seemed likely that the cellular basis of the myb phenotype would be the same as it is in esg and cdc2 mutants.

We used the enhancer trap line esgP3 (Hayashi et al., 1993) to identify abdominal histoblasts in third instar larvae of wild type, mutant Dm myb, and mutant esg animals (Fig. 1I-L). As expected, abdominal histoblast nuclei of esg mutant larvae were much larger than wild type (Fig. 1L). By contrast, no abnormalities were observed in either the number or appearance of the abdominal histoblasts of mutant Dm myb larvae (Fig. 1I,K), indicating that despite similarities in the adult cuticular phenotypes, the cellular basis of these defects in Dm myb mutants is different than in esg and cdc2 mutants.

Fig. 1. Dm myb mutants have missing and improperly oriented abdominal bristles, and patches of undifferentiated tissue. (A-H) Comparison of wild-type and mutant abdomens. Dorsal (A-D,H) and ventral (E-G) cuticles from female adult abdomens: control w/Df(1)sd27a (A,E) flies raised at 24°C; myb2 (B,F) flies raised at 24°C; (C) myb1 raised at 18°C; (H) esg mutant (esgk0060/Df(2L)TE35D-2) raised at 24°C; pharate adults of myb2/Df(1)sd27a raised at 24°C (D); and pharate adults of myb1 raised at 28°C (G). (I-L) Comparison of wild-type and mutant abdominal histoblast nuclei in third instar larvae raised at 24°C. All nuclei within the field were visualized by DAPI staining. (I’-L’) Abdominal histoblast nest cells were identified by using β-galactosidase antibodies and the enhancer trap insert esgP3. (I) Control w; esgP3+/+; (J) myb2; esgP3+/+; (K) myb2/Df(1)sd27a; esgP3+/+; (L) esgVS8/esgP3. Scale bars: in A, 0.5 mm for A-H; in I’, 0.05 mm in I’-L’.
Fig. 2. Abdominal development is delayed in Dm myb mutants. At specified timepoints (hours after puparium formation), the abdominal epidermis was dissected from females that had been raised at 18°C until puparium formation and then shifted to 24°C for continued development. Samples were stained with DAPI to visualize nuclei. Large nuclei represent larval polyplody cells; small nuclei correspond to the diploid nuclei of abdominal histoblast cells. (A-C) w/Df(1)sd^{72a} controls at 13 (A), 30 (B), and 42 (C) hours APF; (D-F) myb^2 at 18 (D), 42 (E) and 51 (F) hours APF; (G) myb^2/Df(1)sd^{72a} at 42 hours APF; (H) myb^2/Df(1)sd^{72a}; P(w^+, myb^*) at 30 hours APF; and (I) myb^1 at 36 hours APF. Arrowheads indicate small histoblast nests. Scale bar: 0.05 mm.

Abdominal histoblasts that are mutant for Dm myb proliferate more slowly than wild-type cells

As no defects were apparent in the larval abdominal histoblasts of Dm myb mutants, we examined their proliferation during pupal development. Female animals were staged as white prepupae and incubated at 24°C (unless otherwise indicated) for specified time periods. Wild-type controls carried the parental white (w) chromosome from which the Dm myb mutants were generated, over a deficiency chromosome (Df(1)sd^{72a}) that deletes the Dm myb gene. The deficiency chromosome was used experimentally to reduce the Dm myb activity of the hypomorphic alleles. No significant differences were observed between w homozygotes and w/Df(1)sd^{72a} females (not shown).

Several types of defects were observed in this analysis. When abdominal epidermal cells were treated with the DNA stain DAPI, it was apparent that abdominal epidermal development was considerably slower in Dm myb mutants than in wild-type controls (Fig. 2). For example, myb^2 abdomens were less developed at 42 hours APF than were control abdomens at 30 hours APF (Fig. 2B,E). When compared with controls at 18 and 24 hour APF, there were approximately half the number of histoblast nuclei in myb^2 mutants, indicating that mutant cells were about one cell division cycle behind. The delay was more pronounced when Dm myb activity was further reduced by either carrying myb^2 over Df(1)sd^{72a} (non-permissive for viability at 24°C; Fig. 2G) or by shifting myb^2 homozygotes to 28°C (not shown). At 18 and 24 hours APF, myb^2/Df(1)sd^{72a} animals had an average of one-sixth (ranging from one-eighth to a quarter) the number of abdominal histoblasts as controls, suggesting a lag of about two to three cell cycles. Double staining with DAPI and rhodamine-labeled phalloidin (an F-actin specific stain that highlights cell boundaries) showed that at these time points, each cell contained a single nucleus (not shown).

The spreading of histoblast cells to displace adjacent larval epidermal cells, and the subsequent flattening of the adult cells, also occurred more slowly in Dm myb mutants. The rate of abdominal development was returned to normal when a wild-type Dm myb transgene was reintroduced into myb^2/Df(1)sd^{72a} animals (Fig. 2H), demonstrating that the defects in abdominal development were specifically due to reductions in Dm myb function. There was no evidence of elevated apoptosis in Dm myb mutants, either by DAPI staining (pyknotic nuclei) or by TUNEL assay (not shown). Therefore, we conclude that the differences in developmental rates can largely be accounted for by differing rates of cell proliferation and spreading, rather than cell death.

In previous studies, the myb^1 allele displayed a stronger phenotype than myb^2 when the flies were raised at the same temperature (Katzen and Bishop, 1996; Katzen et al., 1998). This is not the case, however, in abdominal development. At 24°C, the rate of abdominal histoblast proliferation and spreading for myb^1 was somewhat faster than for myb^2 (Fig. 2I), and the mitotic defects were similar for both alleles. At 18°C, the rate of abdominal development appeared to be nearly normal in both myb^1 and myb^2 mutants (not shown). As the myb^1 allele is less healthy and more difficult to work with at 24°C than myb^2, we concentrated on the latter for these studies, although similar results were obtained with both mutants.

Delayed and abnormal mitoses occur in abdominal epidermal cells of Dm myb mutants

We used an antibody for a mitotic-specific phospho-epitope on histone H3 (PH3) (Hendzel et al., 1997) to identify mitotic abdominal histoblasts. To compare mutant and wild-type cells at the same time points during pupal development, abdominal epidermal samples were prepared from controls and Dm myb mutants at 24 hours APF. To compare mutant and wild type
Dm myb in mitosis and genomic stability

In order to study the effect of Dm myb mutants on cells at equivalent stages during later development, it was necessary to use different time points, as Dm myb mutants developed more slowly than wild type. Therefore, samples were prepared from wild-type controls at 30 hours APF (roughly equivalent to 42 hours APF in myb mutants; Fig. 2B,E), and from myb2 and myb2/Df(1)sd72a at multiple time points, ranging from 40 to 50 hours APF. In addition to proliferating more slowly, mutant myb cells continued to divide well beyond 41 hours APF, the time when wild type cells become postmitotic (Madhavan and Madhavan, 1980). Mitotic cells were detected through to at least 50 hours APF in both myb2 and myb2/Df(1)sd72a cells (Table 1). In spite of their slower proliferation, at 24 hours APF, the mitotic index of myb2 histoblasts was similar to that of wild-type cells (Table 1). Surprisingly, the mitotic index of myb2/Df(1)sd72a cells at 24 hours APF was higher than for myb2 or controls, and it remained higher throughout the experimental time course. The relatively high mitotic indices in myb2/Df(1)sd72a cells, which are proliferating so slowly, is indicative of delayed progress through mitosis.

We also analyzed the percentage of cells in S-phase, as judged by 5-bromo-2-deoxyuridine (BrdU) incorporation, and

![Fig. 3. Chromosome condensation is delayed in abdominal histoblasts that are mutant for Dm myb. Abdominal epidermal samples from females were doubly stained with DAPI to visualize nuclei (blue in merged panels) and with the PH3 antibody to identify mitotic cells (red in merged panels, but appearing as magenta because of superimposition on blue). Scale bars: in A, 0.01 mm for A-C; in E, 0.01 mm for D,E. (A,D) w/Df(1)sd72a controls at 36 hours APF; (B) myb2 at 36-42 hours APF; (C,E) myb2/Df(1)sd72a at 42-47 hours APF. Asterisks in (B,C) indicate examples of 'pre-prophase' cells. For comparison, examples of prophase (D) and 'pre-prophase' (E) cells are shown at higher magnification.]

Table 1. Mitotic index and distribution of mitotic stages in wild-type and and Dm myb mutants

<table>
<thead>
<tr>
<th>Hours APF</th>
<th>Total number of cells (number of abdomens)</th>
<th>Mitotic index (% of PH3 staining cells)</th>
<th>% of PH3 staining cells in specific mitotic stages</th>
<th>% of PH3 staining cells</th>
</tr>
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<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>Pre-prophase*</td>
<td>Prophase†</td>
</tr>
<tr>
<td>w/Df(1)sd72a</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>24 hours APF</td>
<td>491 (3)</td>
<td>2.7%±0.4</td>
<td>1.1%</td>
<td>10.8%</td>
</tr>
<tr>
<td>30 hours APF</td>
<td>900 (2)</td>
<td>3.2%±0.04</td>
<td>0.3%</td>
<td>18.7%</td>
</tr>
<tr>
<td>w: myb2/w: myb2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>24 hours APF</td>
<td>2523 (4)</td>
<td>3.5%±0.6</td>
<td>0%</td>
<td>19.1%</td>
</tr>
<tr>
<td>40-42 hours APF</td>
<td>6489 (4)</td>
<td>1.9%±0.5</td>
<td>13.6%</td>
<td>20.8%</td>
</tr>
<tr>
<td>44-46 hours APF</td>
<td>9468 (4)</td>
<td>2.3%±0.3</td>
<td>20.6%</td>
<td>14.0%</td>
</tr>
<tr>
<td>48-50 hours APF</td>
<td>11321 (4)</td>
<td>1.1%±0.1</td>
<td>31.1%</td>
<td>11.5%</td>
</tr>
<tr>
<td>w: myb2/Df(1)sd72a</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>24 hours APF</td>
<td>662 (5)</td>
<td>5.7%±0.7</td>
<td>7.9%</td>
<td>34.2%</td>
</tr>
<tr>
<td>40-42 hours APF</td>
<td>2501 (7)</td>
<td>4.2%±1.6</td>
<td>20.0%</td>
<td>24.8%</td>
</tr>
<tr>
<td>44-46 hours APF</td>
<td>4410 (7)</td>
<td>4.2%±1.4</td>
<td>41.9%</td>
<td>9.2%</td>
</tr>
<tr>
<td>48-50 hours APF</td>
<td>2753 (4)</td>
<td>3.8%±1.1</td>
<td>44.2%</td>
<td>11.6%</td>
</tr>
</tbody>
</table>

*‘Pre-prophase’ cells are defined here as cells that stain weakly and non-uniformly with PH3, and appear to be in interphase by DAPI staining. Similar staining patterns have been previously described (Hendzel et al., 1997).
†Excludes ‘pre-prophase’ cells.
§Standard error between samples.
found no significant difference in either the total percentage of cells in S-phase or in the percentage of cells in late S (at which point BrdU labeling is confined to chromocenters) (Lilly and Spradling, 1996) between wild type and mutant cells at 24 hours APF (not shown). As mutant myb histoblasts proliferate more slowly than wild type, this finding indicates that S-phase is also lengthened in the mutant cells. The percentage of cells in S-phase decreased in all genotypes at later timepoints, albeit more slowly in mutant cells, a result that is in accordance with their extended proliferation. No conclusions could be drawn about the effects of myb mutations on the gap phases as it was not possible in these samples to determine the percentage of cells in G1 or G2.

The distribution of cells between the various stages of mitosis was significantly different between myb mutants and controls (Table 1). Most notably, there was a higher percentage of mutant cells in the early stages of mitosis, before metaphase, and a corresponding decrease in the percentage of cells in metaphase and anaphase. The number of cells in telophase may be an underestimate as rapid dephosphorylation of histone H3 phosphorylation at the G2/M transition (Hendzel et al., 1997). In wild-type cells, this stage must progress rapidly, as it is rarely observed (1% or less of PH3 staining cells). In mutant cells, however, the frequency of pre-prophase cells increases as puation proceeds, reaching as high as 30% of all PH3 staining cells in myb2 and over 40% in myb2/Df(1)sd72a (Table 1). To determine whether the increase in the pre-prophase staining pattern might be characteristic of cells that continue to divide past the normal cessation of proliferation, we stained abdomens prepared from the Minute mutant, Rp531 (also known as M(3)95A) (Andersson et al., 1994; Lindsley and Zimm, 1992), with the PH3 antibody. Although mitotic cells were observed through 50 hours APF in this mutant, an increase in pre-prophase cells was not evident (not shown).

Therefore, we conclude that the progression of mutant Dm myb cells through the early stages of prophase is abnormally slow.

**Centrosome abnormalities in Dm myb mutant histoblasts**

The indications that mutant Dm myb abdominal histoblasts progress slowly through mitosis prompted us to examine mitotic cells for cytological defects. Centrosomes were detected using two polyclonal rabbit antibodies raised against

### Table 2. The percentage of abnormal mitoses in mutant myb abdominal histoblasts increased during development

<table>
<thead>
<tr>
<th>Hours APF</th>
<th>Metaphase</th>
<th>Anaphase/telophase</th>
<th>All mitotic cells (excluding those in prophase)</th>
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<tr>
<td></td>
<td>Number of cells examined</td>
<td>% abnormal†</td>
<td>Number of cells examined</td>
</tr>
<tr>
<td>w/Df(1)sd72a</td>
<td>27-42 hours</td>
<td>487</td>
<td>0%</td>
</tr>
<tr>
<td>w, myb2/w, myb2</td>
<td>27-32 hours</td>
<td>572</td>
<td>1%</td>
</tr>
<tr>
<td></td>
<td>36-40 hours</td>
<td>258</td>
<td>2%</td>
</tr>
<tr>
<td></td>
<td>42-45 hours</td>
<td>159</td>
<td>4%</td>
</tr>
<tr>
<td></td>
<td>47-50 hours</td>
<td>25</td>
<td>12%</td>
</tr>
<tr>
<td>w, myb2/Df(1)sd72a</td>
<td>27-32 hours</td>
<td>209</td>
<td>0.5%</td>
</tr>
<tr>
<td></td>
<td>36-40 hours</td>
<td>27</td>
<td>2%</td>
</tr>
<tr>
<td></td>
<td>42-45 hours</td>
<td>57</td>
<td>18%</td>
</tr>
<tr>
<td></td>
<td>47-50 hours</td>
<td>37</td>
<td>43%</td>
</tr>
</tbody>
</table>

† Mitoses were scored as abnormal if they displayed abnormalities in centrosome numbers, mitotic spindles (invariably reflecting aberrant numbers of chromosomes), and/or churosomosomal morphology. (see Fig. 4 and Fig. 7 for examples).

### Table 3. Most aberrant mitoses in Dm myb mutants contained abnormal numbers of centrosomes

<table>
<thead>
<tr>
<th>Genotype</th>
<th>% of abnormal mitoses that contained less or more than two centrosomes</th>
<th>% of cells with three centrosomes</th>
<th>% of cells with four centrosomes</th>
<th>Range of centrosome number per cell</th>
<th>Average number of centrosomes per cell</th>
</tr>
</thead>
<tbody>
<tr>
<td>w, myb2/w, myb2</td>
<td>91%</td>
<td>42%</td>
<td>42%</td>
<td>1-6</td>
<td>3.7</td>
</tr>
<tr>
<td>w, myb2/Df(1)sd72a</td>
<td>71%</td>
<td>38%</td>
<td>36%</td>
<td>1-8</td>
<td>3.8</td>
</tr>
</tbody>
</table>

*The balance of abnormal mitoses contained two centrosomes, but displayed abnormalities in chromosomal morphology.

†Out of the mitotic cells with more or less than two centrosomes.
Previously described centrosomal proteins, CP60 and CP190, both of which localize to the centrosome during mitosis and are otherwise nuclear (Kellogg and Alberts, 1992; Kellogg et al., 1995; Whitfield et al., 1988). Antibodies raised against two other centrosomal proteins, \( \gamma \)-tubulin and centrosomin (Heuer et al., 1995), produced similar results. A monoclonal rat antibody raised against \( \beta \)-tubulin was used to visualize the microtubule spindle.

Although histoblast proliferation was slower in \( Dm \) myb mutants throughout pupal development, mitotic defects were not detected in early divisions (up to 24 hours APF), but became increasingly commonplace later (Table 2). No defects were observed in greater than 99% of wild-type mitoses, whereas abnormalities occurred in as many as 22% of myb\(^2\) and 48% of myb\(^2\)/Df(1)sd\(^{72a}\) mitotic histoblasts. One defect, in which two centrosomes were present at, or near each pole during anaphase (Fig. 4A) w/Df(1)sd\(^{72a}\), 40 hours APF; whereas two centrosomes were frequently seen at each pole in \( Dm \) myb mutant homozygotes (B) myb\(^2\), 44 hours APF. (C-F) Additional representatives of mutant cells with abnormal numbers of centrosomes. (C) myb\(^2\)/Df(1)sd\(^{72a}\), 48 hours APF, five centrosomes; relatively normal anaphase with evidence of straggling DNA (arrow). (D) myb\(^2\)/Df(1)sd\(^{72a}\), 48 hours APF, three centrosomes; disrupted organization of spindles and chromosomes during metaphase. (E) myb\(^1\)/Df(1)sd\(^{72a}\), 67 hours APF at 18°C, four centrosomes; two metaphase plates. (F) myb\(^2\), 42 hours APF, one centrosome organizing a monopolar spindle.

The majority of mitotic abnormalities were associated with aberrant numbers of centrosomes, ranging from one to eight, with the most common numbers being three or four (Table 3; Fig. 4). Most, if not all of the supernumerary centrosomes nucleated mitotic spindles. When the additional centrosomes were located at, or near each pole, a bipolar spindle was still

![Diagram](image-url)
Fig. 6. Chromosomal dynamics are disturbed during mitosis in mutant Dm myb abdominal histoblasts. Abdominal epidermal samples from females were doubly stained with DAPI to visualize nuclei (blue in merged panels) and with antibodies against the kinetochore associated protein, Bub1 (red in merged panels). (A–C) Mutations in Dm myb disturbed kinetochore arrangement during metaphase. (A) w/Df(1)sd72a control, 24 hours APF. (B) myb2, 42 hours APF. (C) The presence of more than 16 Bub1 signals in this myb2/Df(1)sd72a cell (42 hours APF) is indicative of polyploidy and demonstrates that such cells continue to progress into mitosis. Scale bar: 0.01 mm.

formed allowing for chromosome separation (Fig. 4C). More commonly, extra centrosomes formed multipolar spindles, pulling chromosomes in multiple directions (Fig. 4D,E). When a large number of centrosomes were distributed throughout the cell, a proper spindle apparatus was not formed (not shown). Cells with single centrosomes organizing monopolar spindles were occasionally seen (Fig. 4F). Chromosomal abnormalities were common in mitotic cells with aberrant centrosome numbers (Fig. 4), but were also observed in mitotic cells containing two centrosomes (Table 3).

Two approaches were taken to determine whether mitotic defects are characteristic of cells that continue to divide past the normal cessation of proliferation. First, samples were prepared from two Minute mutants, RpS31 and Mf(3)65F3 (Andersson et al., 1994; Lindsley and Zimm, 1992), at 42 and 50 hours APF. Out of 61 mitotic cells examined, no abnormalities were found. However, Minute mutants may not provide an ideal control as these mutations lead to a generalized slowing of proliferation throughout development owing to decreased protein synthesis. Therefore, we used the GAL4/UAS binary system to induce ectopic expression of the Drosophila retinoblastoma-family protein (RBF), a negative regulator of cell cycle progression (Du and Dyson, 1999). We chose to use the hsp70-GAL4 driver to induce ectopic expression during pupal development. Although heat shock treatment will induce UAS-RBF expression in all cells, it should have a particularly strong effect on abdominal histoblasts during early pupation at a time when these cells divide rapidly (as opposed to imaginal disc cells which have completed most of their divisions before this stage). Ectopic expression of RBF significantly delayed abdominal development (Fig. 5A,B). For control abdomens (UAS-RBF alone), only five mitoses were detected in eight abdominal preparations (dorsal surface only; no mitoses were observed in ventral surface, but muscles make the analysis difficult at this stage). By contrast, 122 mitoses were found and examined in the dorsal surface of only three abdominal preparations from the experimental samples (43 more mitoses detected on the ventral surface). No abnormalities in centrosome number or spindle morphology were detected in these dividing cells (Fig. 5C,D). We conclude that delaying the cell cycle via RBF expression does not lead to centrosomal/spindle defects, demonstrating that the defects observed in the myb mutants are not merely a secondary event of delayed cell cycle progression.

Metaphase cells with lagging chromosomes were observed much more often in Dm myb mutants than in wild-type controls (see Fig. 4D). When we used an antibody against the mitotic checkpoint control protein Bub1, which localizes most strongly to the kinetochore of mitotic chromosomes that have not yet reached metaphase plate (Basu et al., 1999), we found that kinetochores were less uniformly arranged in mutant than wild-type cells, even when all chromosomes appeared to be lined up at the metaphase plate (Fig. 6A,B). In some mutant cells, we observed more than the 16 kinetochores that should be present in a mitotic Drosophila cell, indicating that these cells were polyploid and/or aneuploid, and that they were continuing to progress through the cell cycle (Fig. 6C). Another chromosomal defect was the presence of more than one metaphase plate in a single cell (Fig. 6E). During anaphase, straggling strands of DNA were frequently observed (Fig. 4C). However, there was no significant Bub1 staining in anaphase cells, regardless of DNA morphology (not shown), indicating that APC pathways were not grossly disturbed in Dm myb mutants.

Centrosome amplification causes unequal chromosome segregation, resulting in aneuploidy and polyploidy

How are the abnormal mitoses with extra centrosomes forming multipolar spindles in myb mutants resolved? Do they apoptose, become trapped in metaphase indefinitely, complete division and form multiple daughter cells with unbalanced chromosome segregation or return to an interphase state? A definitive answer is difficult as mitoses in abdominal histoblasts cannot be readily monitored in vivo. However, the first two possibilities appear to be rare, because neither elevated
levels of apoptosis nor ever increasing levels of metaphase chromosomes were observed. The lack of increased apoptosis was surprising given the severity of mitotic defects and evidence that vertebrate Myb genes can suppress apoptosis (Frampton et al., 1996; Taylor et al., 1996), thereby raising the possibility that apoptosis may be suppressed in abdominal epidermal cells.

When a probe representing a 359 bp repeat present in X-chromosome heterochromatin (Dernburg, 2000), was used for FISH on samples prepared from females, two signals were detected in each of two separating nuclei in w/Df(1)sd72a controls during anaphase. (B) By contrast, a different number of signals (1, 4 and 6) were evident in each of three separating nuclei in a mutant myb2 cell. (C-K) Abdominal epidermal samples from females at 30 hours APF for controls and at 44-46 hours APF for Dm myb mutants were stained with DAPI for DNA quantitation (blue in D-K) and rhodamine-labeled phalloidin (red in D-K), and optically sectioned by confocal microscopy under identical conditions. For each of three experiments, nuclear fluorescent intensities were measured. The average value of the G1 control nuclei was determined and used as the base value of 1X. Values of other nuclei were adjusted accordingly to calculate relative fluorescent intensities.

Fig. 7. Aneuploidy, polyploidy and variable nuclear morphology in mutant Dm myb abdominal epidermal cells. 
(A,B) Abdominal epidermal samples from female pupae hybridized with an X-chromosome probe (red), and stained with DAPI (blue) and PH3 antibodies (green). (A) Two signals were seen in each of two separating nuclei in w/Df(1)sd72a controls during anaphase. (B) By contrast, a different number of signals (1, 4 and 6) were evident in each of three separating nuclei in a mutant myb2 cell. (C-K) Abdominal epidermal samples from females at 30 hours APF for controls and at 44-46 hours APF for Dm myb mutants were stained with DAPI for DNA quantitation (blue in D-K) and rhodamine-labeled phalloidin (red in D-K), and optically sectioned by confocal microscopy under identical conditions. For each of three experiments, nuclear fluorescent intensities were measured. The average value of the G1 control nuclei was determined and used as the base value of 1X. Values of other nuclei were adjusted accordingly to calculate relative fluorescent intensities.

(C) Results of analyzing 121 control (w/Df(1)sd72a); 124 myb2, and 83 myb2/Df(1)sd72a nuclei are graphically represented. The range of values included in each category are indicated in parentheses as follows: ≤0.5X (≤0.6); 1X (0.7-1.5X); 2X (1.6-2.5X) and ≥3X (≥2.6). (D-K) Examples of control and mutant cells with relative DNA quantitation values as indicated. (D) Three control w/Df(1)sd72a G1 nuclei; (E) a control G2 nucleus is centered; (F) enlarged myb2 nucleus; (G) binucleate myb2 cell; (H) mis-shapen and enlarged myb2/Df(1)sd72a nucleus; (I) multilobed myb2/Df(1)sd72a nucleus; (J) a myb2/Df(1)sd72a nucleus with subdiploid DNA content (arrow); (K) a myb2/Df(1)sd72a cell containing a large nucleus and a micronucleus indicated by arrow. Scale bars: in A, 0.01 mm in A,B; in K, 0.01 mm in D-K.
result in polyploidy. Mutant cells with subdiploid nuclei or that contained a micronucleus in addition to a larger nucleus were also detected (Fig. 7J,K).

To assess relative DNA contents (Fig. 7C), we measured the relative fluorescent intensities of DAPI-stained nuclei from a series of confocal images (see Materials and Methods). DNA content was calculated on a per cell basis, regardless of nuclear morphology or the presence of more than one nucleus. As expected for proliferating cells, the DNA content of control cells varied over a twofold range, with only 1 of 121 nuclei falling slightly outside the one- to twofold range. By contrast, both the average and range of DNA contents were larger for mutant Dm myb cells than for wild type, with more than 20% of myb² and 25% of myb²/Df(1)sd²/a nuclei falling outside the one- to twofold range. These figures are likely to be an underestimate, as several of the larger mutant nuclei could not be measured because they were not entirely contained within the z-stack of optical sections. The mitotic defects observed in the mutant cells (see Fig. 4, Fig. 5, Fig. 7) indicate that some of the cells within the one- to twofold range were likely to be aneuploid. Variability was especially pronounced in myb²/Df(1)sd²/a cells, where small nuclei were occasionally seen that contained less than diploid levels of DNA (approximately half, Fig. 7I), while other nuclei had DNA contents that ranged as high as sevenfold more than the normal diploid levels in wild-type cells. Our results confirm that the abnormal mitoses occurring in Dm myb mutant histoblast cells give rise to unequal chromosome segregation and produce aneuploid and polyploid nuclei.

To investigate whether nuclear morphology abnormalities and polyploidy were already apparent by the time the first centrosomal defects were observed, control and mutant samples at 28-30 hours after puparium formation were prepared as described above. Greater than 100 control and 175 mutant cells (myb² and myb²/Df(1)sd²/a combined) were examined. No examples of cells with either two nuclei or a multinucleated nucleus were observed at this stage of development. The DNA content of more than 98% of control and mutant cells varied over the same twofold range as was previously observed for control cells at 30 hours APF. These data indicate that the observed centrosome abnormalities are unlikely to arise from failure to complete mitosis or cytokinesis as these defects do not precede the centrosome defects.

**DISCUSSION**

**Distinctions between wing and abdominal phenotypes in Dm myb mutants**

In previous analysis of the mutant Dm myb wing phenotype, we found that wing cells were arrested in G2 of their final cell cycle during pupal development, and that some of the arrested cells had entered endoreduplication, indicating that Dm myb is required for both promotion of the G2/M transition and suppression of endoreduplication (Katzen et al., 1998). While current studies of the abdominal phenotype also display defects in cellular proliferation, there are several distinctions in the specific defects observed, revealing that Dm myb function is required not only to enter mitosis, but to proceed through mitosis. Discrepancies cannot be rationalized by differences in mutations, as the same alleles were used for both studies.

Instead, new aspects of Dm myb function may be revealed in abdominal histoblasts because of the demands of their developmental program. Histoblasts proliferate more rapidly than wing cells (doubling times of less than 3 hours versus 10-12 hours for wing cells) (Madhavan and Madhavan, 1980), and the levels of Dm myb mRNA are lower in histoblasts than in wing discs (Katzen and Bishop, 1996). Comparison of developmental delays indicates that abdominal histoblasts are indeed more sensitive to reductions in Dm myb function. In Dm myb mutants, wing development only lagged behind wild type by about 1.5 hours (Katzen et al., 1998), whereas abdominal development lagged by 10 to 12 hours. It is also possible that additional mitotic functions for Dm myb are revealed in abdominal cells because regulation of the G2/M transition is not as restrictive as it is in wing cells.

Defects in esg and cdc2 mutants have been attributed to a failure to suppress endoreduplication in abdominal histoblasts during larval development when they are normally arrested in G2 (Hayashi, 1996; Hayashi et al., 1993). Although the abdominal phenotype in Dm myb mutants resembles those of esg and cdc2 (Hayashi et al., 1993; Stern et al., 1993), mutant Dm myb histoblast nests contain appropriate numbers of cells with no apparent abnormalities. This indicates that although Dm myb function appears to be required to suppress endoreduplication during an aberrant G2 arrest, it is not essential for keeping abdominal histoblasts in the normal extended G2 phase that persists throughout larval development.

In previous analyses of the mutant myb phenotype, the myb¹ allele inevitably produced a stronger phenotype than myb² at equivalent temperatures (Katzen and Bishop, 1996; Katzen et al., 1998). By contrast, the abdominal phenotype is as strong or stronger in myb² than in myb¹ at the same temperatures (see Fig. 1, Fig. 2), indicating that the relationship between the two temperature-sensitive alleles is more complex than previously thought. Although each mutation results in the change of an amino acid perfectly conserved between Myb and its vertebrate counterparts, different regions of the protein are affected: for myb², the DNA-binding domain; and for myb¹, a conserved domain (region IV) near the C terminus for which no specific biochemical activity has yet been ascribed (Katzen et al., 1998). The finding that the myb¹ phenotype is stronger than myb² in wing cells, but weaker in abdominal cells indicates that Myb activity is differentially regulated in these two tissues.

**Analysis of the abdominal phenotype in myb mutants expands our understanding of Dm myb function in mitosis**

Although several abnormalities are observed in Dm myb mutant abdominal histoblasts, the earliest developmental defects are likely to represent the primary cellular defect. Abdominal histoblast cells in Dm myb mutants appeared normal during larval development, a period during which they are arrested in G2, but their rate of proliferation after puparium formation was considerably slower than for wild-type cells. The sluggish proliferation did not correlate with a commensurate decrease in mitosis. For example, although histoblasts in myb²/Df(1)sd²/a animals lagged behind wild-type cells by two to three cell division cycles, the mitotic index in the mutants was considerably higher (5.7% versus 2.7% at 24 hours APF), indicating that at least part of the reduced rate of proliferation is due to cell cycle defects that are not mitotic in nature.
of proliferation in mutants can be attributed to abnormally slow progression through mitosis.

Examination of the mitotic cells revealed an enrichment of cells in the early stages of mitosis (pre-metaphase; see Table 1). Even at 24 hours APF, there is an increased ratio of prophase to metaphase cells, and as development proceeds, an increasing number of cells stall in pre-prophase. Whether the majority of pre-prophase cells ever proceed further into mitosis is unclear. It is also possible that some of the weakly staining PH3 cells were not in pre-prophase, but were instead undergoing chromosome decondensation after having failed to complete mitosis or cytokinesis. We believe these are likely to be in the minority for several reasons: an increased percentage of pre-prophase cells can be seen as early as 24 hours APF, before other mitotic or ploidy abnormalities are evident. Up until 30 hours APF, double staining with rhodamine-labeled phalloidin and DAPI revealed an absolute correspondence of one nucleus per cell. In addition, weakly staining PH3 cells did not have abnormally shaped nuclei, even at later developmental timepoints, as did most cells that failed to complete mitosis; instead, the morphology and PH3 staining of the pre-prophase nuclei closely resembled those shown by Hendzel et al. (Hendzel et al., 1997) and the occasional pre-prophase nuclei that we observed in wild-type cells. One further possibility, which cannot be ruled out at present, is that the regulation of histone H3 phosphorylation is somewhat abnormal in these cells, and therefore, the weak staining may not always reflect pre-prophase. Our scoring of mitotic cells did not distinguish between prometaphase and metaphase, but the Bub1 staining patterns suggest that in the mutants, the ‘metaphase’ population is likely to be enriched for prometaphase cells. Therefore, we conclude that Dm myb mutant histoblasts appear to suffer delays or partial blocks in chromatin condensation, in the process of kinetochore attachment to the mitotic spindle and in chromosome alignment on the metaphase plate.

The percentage of Dm myb mutant histoblasts with visible mitotic abnormalities increases dramatically as pupal development proceeds, implying that initial defects are compounded in subsequent divisions. These mitotic defects, which include aberrant numbers of centrosomes, grossly abnormal DNA morphology, aneuploidy and polyploidy, are characteristic of situations in which the coordination of centrosome and nuclear cycles has been disturbed. Failure to precisely coordinate centrosome doubling with the nuclear cell cycle produces mitotic cells with less than or greater than two centrosomes, a situation that generally results in the formation of abnormal spindles (Sluder and Hinchcliffe, 1999). Examples of such abnormalities, which inevitably lead to genomic instability, are represented among Dm myb mutant abdominal cells. Mitotic cells with only one centrosome forming a monopolar spindle are occasionally seen. These cells cannot divide and will inevitably produce polyploid cells. More commonly observed are mitotic cells with more than two centrosomes forming multipolar spindles. In such a situation, chromosomes will be randomly distributed into multiple daughter cells which will be aneuploid if cell division is successfully completed. Alternatively, if the mitotic cell fails to complete division and returns to an interphase state, the resulting cell would either be multinucleate or contain a single polyploid nucleus. Our results indicate that all of these possible outcomes occur in mutant Dm myb cells. Therefore, we believe that defects observed during later stages of abdominal epidermal development are the consequence of disturbing the coordination between centrosome reproduction and the nuclear cell cycle.

In a recent study that compared gene expression in actively proliferating fibroblasts isolated from people of different ages or from individuals with the premature aging disease progeria, Mybl2 expression was significantly downregulated in both progeria fibroblasts and in ‘normal’ fibroblasts isolated from old-aged (~90 years) people (Ly et al., 2000). A significant proportion of these ‘aged’ fibroblasts exhibited abnormalities, including multilobed nuclei and multiple nuclei within a cell. These nuclear defects are reminiscent of those observed in the abdominal epidermal cells of Dm myb mutants, suggesting the possibility that reduced levels of Mybl2 might lead to centrosomal abnormalities, which in turn cause aneuploidy and polyploidy.

Is the disturbance in centrosome regulation a primary defect of the mutation in Dm myb or a secondary consequence of the slow rate of proliferation and/or delays in early mitotic stages, which occur earlier in development? Our analysis indicates that the centrosome defect may be primary, as the first abnormalities in centrosome numbers precede the appearance of multilobed and binucleated cells, allowing us to exclude the possibility that a failure in mitosis or cytokinesis represents the primary defect. Once present, however, the extra centrosomes do lead to defective mitoses and failed cell divisions.

Many links have been established between the regulation of the cell division cycle and centrosome duplication. Artificial prolongation of mitosis leads to premature splitting and separation of centrosomes, while prolongation of S-phase allows multiple rounds of centrosome duplication to occur (Sluder and Hinchcliffe, 1999). The mildest centrosome defect in Dm myb mutants appears to be a premature separation of centriole pairs during late anaphase/early telophase, which could be the result of delayed progression through mitosis. Premature separation might explain why the percentage of centrosome abnormalities is always higher in anaphase/telophase cells than in metaphase cells (see Table 2). This early separation may therefore represent the first step in a breakdown of the coordination between nuclear and centrosome cell cycles.

Another indication that splitting and/or duplication of centrosomes is not occurring in a coordinated fashion is the frequent occurrence of odd numbers of centrosomes within the mutant cells. Four centrosomes in mutant cells could result from failure to complete the previous cell division, followed by re-entry into the cell cycle. A subsequent mitosis could then easily lead to an assortment of an odd number of centrosomes in each daughter cell (e.g. three in one and one in the other), but they should be duplicated during the subsequent cycle, thereby generating an even number by the following mitosis (six and two, respectively). Intriguingly, odd numbers of centrosomes are also a common feature in vertebrate cells that have suffered a mutation in a tumor suppressor gene such as p53, Brca1 or Brca2 (Fukasawa et al., 1996; Tutt et al., 1999; Xu et al., 1999).

Can Myb genes function as both oncogenes and tumor suppressor genes?

The normal function of many proto-oncogenes is to participate in signal transduction pathways that regulate cellular
proliferation. When proto-oncogenes suffer mutations that convert them to activated oncogenes, they promote uncontrolled cell growth. Specific aspects of the phenotypic defects observed in the Dm myb mutants, such as sluggish proliferation and stalling or arresting at the G2/M transition, match expectations for loss-of-function mutations in a proto-oncogene. Centrosome amplification and genomic instability, however, are frequently associated with loss-of-function mutations in tumor suppressor genes, not proto-oncogenes (Fukasawa et al., 1996; Tutt et al., 1999; Xu et al., 1999). As genomic instability is associated with oncogenic progression and aggressive tumors, the disturbance in the regulation of centrosome reproduction may be the primary mechanism by which tumorigenesis is promoted when some tumor suppressor genes are mutated (Sluder and Hinchcliffe, 1999; Tutt et al., 1999; Xu et al., 1999). Therefore, the Dm myb gene shares some properties with proto-oncogenes and others with tumor suppressor genes, raising the possibility that mutations which decrease the activity of one of the vertebrate Myb genes could contribute to genomic instability and subsequent oncogenesis or aging.

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Drosophila and vertebrate myb proteins share two conserved regions, one of which functions as a DNA-binding domain. EMBO J. 6, 3085.


