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SPIERER-ROYER, Anne, et al.

Abstract
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Anne Spierer, Carole Seum, Marion Delattre and Pierre Spierer*
Department of Zoology and Animal Biology, University of Geneva, 30 quai Ernest-Ansermet, CH-1211 Geneva 4, Switzerland
*Author for correspondence (e-mail: pierre.spierer@zoo.unige.ch)

Summary
Loss of Su(var)3-7 or HP1 suppresses the genomic silencing of position-effect variegation, whereas over-expression enhances it. In addition, loss of Su(var)3-7 results in preferential male lethality. In polytene chromosomes deprived of Su(var)3-7, we observe a specific bloating of the male X chromosome, leading to shortening of the chromosome and to blurring of its banding pattern. In addition, the chromocenter, where heterochromatin from all polytene chromosomes fuses, appears decondensed. The same chromosomal phenotypes are observed as a result of loss of HP1. Mutations of Su(var)3-7 or of Su(var)2-5, the gene encoding HP1, also cause developmental defects, including a spectacular increase in size of the prothoracic gland and its polytene chromosomes. Thus, although structurally very different, the two proteins cooperate closely in chromosome organization and development. Finally, bloating of the male X chromosome in the Su(var)3-7 mutant depends on the presence of a functional dosage compensation complex on this chromosome. This observation reveals a new and intriguing genetic interaction between epigenetic silencing and compensation of dose.

Key words: Dosage compensation, Drosophila, HP1, Mitotic chromosome, Polytenes, Su(var)3-7

Introduction
Euchromatic genes placed near or within heterochromatin by chromosomal rearrangements often become epigenetically silenced in some cells and not in others, a phenomenon called position-effect variegation (PEV). By contrast, heterochromatic genes can become silenced in euchromatin (reviewed by Weiler and Wakimoto, 1995). Because of the importance of epigenetics in gene regulation, studying the different partners involved in establishing large silent chromatin domains in PEV has become an extremely useful tool. Among these components, the proteins HP1, Su(var)3-9 and Su(var)3-7 are mainly associated with pericentric heterochromatin and play a key role (Wallrath, 1998; Li et al., 2002; Schotta et al., 2003). The genes coding for these three proteins are haplo-suppressor, triplo-enhancer of PEV. HP1 and Su(var)3-9 have a central function in heterochromatin establishment and maintenance (Bannister et al., 2001), and in gene regulation (Nielsen et al., 2001; Hwang et al., 2001; Greil et al., 2003). The mode of action of HP1 and of the histone methyltransferase Su(var)3-9 has been demonstrated in part: Su(var)3-9 methylates lysine 9 of histone H3 (H3-MeK9), thus creating a binding site for HP1 (Rea et al., 2000; Bannister et al., 2001; Lachner et al., 2001). The cooperative action of Su(var)3-9 and HP1 is instrumental in forming silent heterochromatin (reviewed by Grewal and Rice, 2004).

Su(var)3-7 function is still poorly understood. It encodes a large protein associated with pericentric heterochromatin, telomeres and a few euchromatic sites on interphase polytene chromosomes. Seven widely spaced zinc fingers stand out in the sequence of the N-terminal half (Reuter et al., 1990; Cléard et al., 1995; Cléard et al., 1997). In vitro, the zinc finger region of Su(var)3-7 has affinity for DNA, and preferentially for some satellite sequences (Cléard and Spierer, 2001). There is also evidence for direct binding of Su(var)3-7 with DNA in vivo (Perrini et al., 2004). The N-terminal half of Su(var)3-7 interacts nonspecifically in vivo with heterochromatin and euchromatin, whereas the C-terminal half promotes interaction with itself, and with pericentric heterochromatin (Jaquet et al., 2002). Su(var)3-7 also interacts genetically and physically with HP1 (Cléard et al., 1997; Delattre et al., 2000) and with Su(var)3-9, as determined in yeast by the two-hybrid assay (Schotta et al., 2002) and in vivo (Delattre et al., 2004). To decipher the function of Su(var)3-7, we have generated mutants by homologous recombination (Seum et al., 2002), and have undertaken a detailed examination of their phenotype. Su(var)3-7 was shown to be essential, the maternal contribution being sufficient for viability. Interestingly, males are more sensitive than females to the lack of Su(var)3-7 (Seum et al., 2002). The cause of this lethality is unknown.

Here, we report the building of a new mutant of Su(var)3-7 by homologous recombination, and describe the phenotypes of mutations on polytene chromosome morphology and on the organism, which we find similar to phenotypes resulting from mutational loss of HP1. The male X chromosome is more sensitive to these effects, leading us to unravel an interaction...
between the modifier of PEV Su(var)3-7 and the dosage compensation machinery. We conclude that the importance of the roles and partnership of Su(var)3-7 and HP1 extend beyond genomic silencing in the maintenance of chromosome integrity and function, including the male X-specific chromosome-wide mechanism of dosage compensation.

Materials and Methods

Genetic crosses

CROSSES AND CULTURE were at 25°C on standard media. Homozygous

Materials and Methods

mechanism of dosage compensation. We conclude that the importance of the modifier of PEV Su(var)3-7 and the dosage compensation machinery. We conclude that the importance of the roles and partnership of Su(var)3-7 and HP1 extend beyond genomic silencing in the maintenance of chromosome integrity and function, including the male X-specific chromosome-wide mechanism of dosage compensation.

Cloning of the donor

The 5' noncoding region of Su(var)3-7 was amplified using oligos 5'-CTAACGGCGGAAAACCATGTTAGA3' (forward) and 5'-GTCC

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ACCCCGCATCGGGTACCTGTCCTC-3' (reverse) on genomic DNA of wild-type adult flies. The 2.6 kb PCR product was digested with

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HindIII and cloned into pH7-30 (Seifert et al., 1986) (=pH7-30HK5*). The 3' noncoding region of Su(var)3-7 was amplified as two fragments using primers: 5'-GGCCGAGCTGAGCTTCATACGGGAC-3' (forward) and 5'-CGGGCAGCTGAGCTTCATACGGGAC-3' (reverse) for the most 5' part (1.95 kb) and primers 5'-GTCCGATCTGAGCTTCATACGGGAC-3' (forward) and 5'-ATCCGATCTGAGCTTCATACGGGAC-3' (reverse) for the third portion (2.05 kb). Both PCR fragments were digested with SacI/HindIII and inserted into pGemT easy (Promega). Two oligos containing the I-SceI recognition site and flanked with incomplete HindIII sites were generated (5'-AGCTGCTAGGATAACAGGTAA-3' and 5'-AGCTGCTAGGATAACAGGTAA-3') and annealed and inserted into the HindIII site of this vector (pGemI S I-SceI S3). This construct was then digested with SacI and the 4 kb fragment containing the whole 3' untranslated region was cloned into pH7-30HK5* (partial SacI). The 5' and 3' noncoding regions of Su(var)3-7 were finally joined into pTV2 (Rong and Golic, 2001) as an 8 kb NotI fragment, the 3' part facing the I-Cre site [pTV2ΔSu(var)].

Targeting screen

We followed a procedure described previously (Rong and Golic, 2001). The pTV2ΔSu(var) plasmid was injected into a w1118 strain and four donors on the second or X chromosomes were used for the recombination [rapid scheme (Rong and Golic, 2001)]. We carried out about 10 crosses, implicating 20 homozygous female donors andyw; 70FLP (site-specific recombine), 70 I-SceI, Sco/CyO males. Two heat shocks were done on first- and second-instar larvae for one hour at 37°C. We then made 267 crosses, each time using four mosaic females carrying the 70FLP, 70 I-SceI chromosome with yw homozygous males expressing 70FLP constitutively. Screening was by selecting non-mosaic w+ flies on the third chromosome. Homologous recombinants were obtained containing the deletion and a wild-type copy of the Su(var)3-7 gene separated by the w½ marker (Fig. 7C).

Reduction

The reduction step was performed to eliminate the Su(var)3-7 sequence (Cléard et al., 1997) and the w½ marker. The targeted allele used for the reduction was not intact. We chose a homologous recombinant bearing a 1033 bp deletion in CG8449 (R2a, characterized with primers 1 and 2 and sequenced with primer 3 in order to increase the number of recombination events in the 5' region of Su(var)3-7; Fig. 7D,F, R2a/T[2;3]apXa males were crossed with 70-Cre 1A, SbI/TM6 females (Bloomingston stock 6937). Heat shocks were made on first-instar larvae for one hour at 37°C and Sb variegated males were balanced with w1118; CyO; TM3/T[2;3]apXa females. w+/TM3 flies were crossed with each other and homozygotes for the deletion were analyzed by PCR using primers 4 and 5 but also crossed together to confirm the recessive lethal maternal effect of the mutation. Different couples of primers were used to confirm the deletion: we tested the absence of FRT (FLP recognition target) and Su(var)3-7 using primers in FRT and all along the Su(var)3-7 gene, and comparing homozygotes to heterozygote single flies. Finally, the deletion was amplified using primers 4 and 5 and sequenced with primer 5 (Fig. 7F).

Staining and immunostaining of polytene chromosomes

Larvae were dissected, and salivary glands transferred and squashed in 45% acetic acid. Slides were dehydrated for at least 20 minutes in 100% ethanol and air-dried. A drop of staining solution (1% orcein

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in a 1:1 mix of 60% acetic acid and lactic acid) was deposited on a coverslip and applied on the polytene chromosomes. Excess of staining solution was removed, and the coverslip sealed with nail polish. Procedures for immunostaining were as described previously (Platero et al., 1995). Briefly, salivary glands were dissected in Cohen’s buffer; fixed for 2 minutes in 2% formaldehyde, 2% Triton X-100, and then squashed in 2% formaldehyde, 45% acetic acid. Primary antibodies were used at the following dilutions: 1:10 for anti-Su(var)3-7 antibody (Cléard et al., 1997), 1:400 for anti-HPI antibody (a gift of L. Wallrath, University of Iowa, Iowa City, IA), and 1:200 for anti-MSL2 antibody (a gift of M. Kuroda, Harvard Medical School, Boston, MA) and for anti-H4AcK16 antibody (a gift of B. Turner, University of Birmingham, UK).

**Immunostaining of neuroblasts mitotic chromosomes**

Immunostaining of mitotic chromosomes was carried out according to the procedure of Roxane Blattes and Emmanuel Käs (personal communication). Larval brains were incubated for 15 minutes in 0.5% sodium citrate, then in HEN buffer [5 mM MgCl2, 0.1% Triton X-100, 1× HEN (10 mM Hepes pH 7.4, 1 mM EDTA, 0.1 M NaCl)] for 2 hours. Brains were fixed in 2% paraformaldehyde in HEN buffer for 10 minutes and in 2% paraformaldehyde/45% acetic acid for 8 minutes after squashing. Rehydration was for 45 minutes in blocking solution (PMT-5% dried milk: 1× PBS, 0.1% Triton X-100, 1 mM MgCl2, 5% dried milk). PMT-5% was removed and squashes were incubated with the primary antibodies overnight at 4°C in PMT with 0.5% dried milk (PMT-0.5%). After washing in PMT-0.5%, squashes were incubated with the secondary antibodies for 90 minutes in PMT-0.5%. Squashes were washed in PT (PMT without dried milk), stained with DAPI and mounted. Primary antibodies were used at the same dilutions as for polytene.

**Results**

**Su(var)3-7 mutants**

We have previously generated three Su(var)3-7 mutants by homologous recombination: Su(var)3-714, Su(var)3-71A and Su(var)3-79 (Seum et al., 2002). Although the mutants still contain Su(var)3-7 sequences, one of them, Su(var)3-71A, behaves genetically as a null mutation. This latter allele produces significant amounts of a chimeric protein made of Su(var)3-7 and Yellow (Seum et al., 2002). As we could not exclude an effect of this aberrant product, we report here the generation by homologous recombination of a new mutant, Su(var)3-7R2a8. The strategy allowed us to delete precisely all the protein-coding sequence published by Cléard et al. (Cléard et al., 1995). Targeted mutagenesis in Drosophila is still far from trivial, and we recount in detail the design and construction of the mutant in the Materials and Methods section. In short, we used the ‘ends-in’ technology (Rong and Golic, 2001) and selected regions of homology 5’ and 3’ of the coding sequence to generate a null allele after homologous recombination (Xie and Golic, 2004). Unfortunately, a very recent correction of the Su(var)3-7 gene sequence by the Berkeley Drosophila Genome Project has added a translation start in the Su(var)3-7 transcript upstream of the one previously considered. This adds 81 amino acids to the previously reported 1169 amino acids, resulting in a new size of 1250 amino acids. These 81 amino acids out of 1250 do not contain nuclear localization signals, nor any known sequence motif, and were absent from transgene constructs rescuing the function (Jaquet et al., 2002). It is thus extremely unlikely that the fragment potentially produced by this mutant has any biological activity.

The new allele Su(var)3-7R2a8 is a recessive maternal-effect lethal mutant. Progeny of homozygous mutant flies stops developing during the second larval stage. A zygotic wild-type dose rescues the maternal effect, but only half of the expected male progeny is recovered. This underlines the particular sensitivity of males to loss of Su(var)3-7. However, the maternal product alone allows about 90% viability of zygotic male and female null mutant progeny in equal proportion. These phenotypes are similar to those we observed with Su(var)3-714 (Seum et al., 2002).

In summary, we have four Su(var)3-7 alleles: Su(var)3-7R2a8, Su(var)3-714, Su(var)3-71A and Su(var)3-79. Su(var)3-79 is the weakest and the only homozygous viable allele. Su(var)3-7R2a8 and Su(var)3-714 have very similar phenotypes and behave genetically as null mutations.

The male X polytene chromosome and the chromocenter are affected by loss of either Su(var)3-7 or HP1

As Su(var)3-7 and HP1 are chromosome-associated proteins, we examined polytene chromosomes from salivary glands of mutant third-instar larvae. In order to reduce both maternal and zygotic doses of Su(var)3-7, we tested several homozygous and trans-heterozygous combinations of Su(var)3-7 mutants allowing viability of third-instar larvae. One phenotype in particular is striking: the morphology of the X chromosome of affected male larvae is dramatically modified by severe loss of Su(var)3-7 (Fig. 1). The male X chromosome becomes shorter and bloated. The banding pattern is blurred and the whole

Fig. 1. Bloated X phenotype of salivary gland polytene chromosomes from Su(var)3-7 or Su(var)2-5 mutant males. (A) Su(var)3-71A homozygote mutant. (B) Su(var)3-79/Su(var)3-714 mutant. (C) Su(var)2-505/Su(var)2-505 mutant. (D) Wild-type control male. Chromosomes are stained with orcein. X indicates the X chromosome.
heterochromatin in polytene chromosomes affects the compensation complex (DCC) (Lyman et al., 1997). In polytene chromosomes of Su(var)2-5 mutants, we found the same bloating of the male X chromosome as in Su(var)3-7 mutants (Fig. 1).

A second phenotype seen in males and in females of all mutants concerns the morphology of the chromocenter. This region, where pericentric heterochromatin from all chromosomes coalesces, has a modified aspect in Su(var)3-7 and Su(var)2-5 mutants. It becomes larger than in wild type, and the chromosomes arms are not held together as tightly, but instead are attached by a loose net of thin fibers and aggregates of granules, occasionally forming small outgrowths (Fig. 2).

We conclude that severe loss of Su(var)3-7 or HP1 causes the same phenotypes on polytene chromosomes, suggesting strong similarity or cooperation in their chromatin-condensing function.

Su(var)3-7 requires HP1 for heterochromatin binding on interphase chromosomes

Immunostaining of polytene chromosomes has shown that Su(var)3-7 and HP1 colocalize on polytene chromosomes at the chromocenter, some telomeres and at several euchromatic sites (Cléard et al., 1997; Delattre et al., 2000). As mutations in Su(var)3-7 and Su(var)2-5 share common phenotypes, we wondered whether the loss of one protein influences the localization of the other. To answer this question, we examined the distribution of HP1 on polytene chromosomes of Su(var)3-7 mutants. HP1 immunostaining is not perturbed on polytene chromosomes of Su(var)3-7/Su(var)3-7[4] larvae (Fig. 3) nor on Su(var)3-7/Su(var)3-7[4] and Su(var)3-7/7 homozygous mutant polytene (not shown). The distribution of H3-diMe-K9, another marker of heterochromatin (Jacobs et al., 2001) that colocalizes in wild-type heterochromatin with HP1 and also with Su(var)3-7 (Delattre et al., 2004), is also not affected (not shown).

We investigated then whether, conversely, Su(var)3-7 binding to polytene chromosomes was modified in a trans-heterozygous null mutant of Su(var)2-5, namely after loss of the heterochromatin HP1 [as Su(var)2-5[4]/Su(var)2-5[3]]. Indeed, Su(var)3-7 loses its specific association with heterochromatin of polytene chromosomes and is found on euchromatin (Fig. 3). In addition, Fig. 3 illustrates, as a control, the situation in the Su(var)2-5/+ heterozygous mutant, where one dose of HP1 suffices to keep Su(var)3-7 in heterochromatin. These experiments demonstrate that Su(var)3-7 relies on HP1 to associate specifically with pericentric heterochromatin on interphase polytene chromosomes. However, we still wondered how the loss of proteins mainly associated with heterochromatin in polytene chromosomes affects the morphology of a whole chromosome. We therefore examined mitotic chromosomes.

Su(var)3-7 and HP1 do not overlap on mitotic chromosomes

We stained mitotic chromosomes from wild-type larval neuroblasts with antibodies against Su(var)3-7. Surprisingly, the pattern of Su(var)3-7 is different from the characteristic chromocentric staining of interphase polytene chromosomes. Fig. 4 shows an association of Su(var)3-7 throughout euchromatic chromosome arms, although with discontinuities.
Within the limit of the method, the Su(var)3-7 protein was neither detected on the fourth chromosome, nor on heterochromatin of the third, second and X chromosomes. The Y chromosome is partially stained (Fig. 4B). By contrast, using the same fixation conditions, HP1 is seen on heterochromatin of all mitotic chromosomes including the fourth and the Y chromosome (Fig. 4C). Anti-H3-diMe-K9, another heterochromatin marker, shows the same staining pattern as HP1 (not shown). Thus, in contrast to polytene chromosomes, Su(var)3-7 and HP1 form an almost complementary pattern on larval brain mitotic chromosomes. HP1 staining appears unchanged in Su(var)3-7 mutant brain neuroblasts (as illustrated for the Su(var)3-7/Su(var)3-7 mutant (arrow) with heterozygote control Su(var)2-5/05/CyO on the same slide (dotted arrow). (D,E) Detection of HP1 protein on Su(var)3-7/Su(var)3-7 mutant.

Severe loss of either Su(var)3-7 or HP1 causes similar developmental defects

In our search for causes and consequences of chromosome defects in mutants, we wondered whether loss of Su(var)3-7 and HP1 results in developmental abnormalities. Indeed, we detected several interesting and unexpected phenotypes shared by larvae affected by a severe decrease in amounts of Su(var)3-7 or HP1. The most spectacular and penetrant phenotype concerns the ring gland. The ring gland is a composite endocrine organ containing the cells of the prothoracic gland (source of the moultin hormone ecdysone), the corpus allatum (source of the juvenile hormone) and the corpus cardiacum (source of peptide hormones). In wild-type larvae, the ring gland represents a small flat ring anterior to the brain hemispheres. Su(var)3-7 and Su(var)2-5 mutant larvae exhibit an extreme enlargement of their ring gland owing to an increase in size of the ecdysone-secreting prothoracic gland cells (Fig. 5A,B). These cells exhibit highly endoreplicated polytene chromosomes (Fig. 5D). In wild-type larvae, polytene chromosomes of prothoracic gland cells can reach a degree of polyteny of 256C, whereas salivary gland chromosomes reach 1024C or even 2048C (Hochtrasser and Sedat, 1987). Here, we show that Su(var)3-7 and Su(var)2-5 mutant larvae exhibit prothoracic gland cell nuclei that have polytene chromosomes similar in size to those of the salivary gland. As salivary glands and their polytene chromosomes are not larger in mutants than in wild type, we conclude that reduced levels of Su(var)3-7 or HP1 affect endoreplication specifically in certain polytene tissues. Other phenotypes are observed in both mutants. The gastric ceca are abnormal. Gastric ceca consist of four appendages growing out of the proventriculus (the larva stomach), at the junction between the foregut and the midgut. In larvae of Su(var)3-7 and Su(var)2-5 mutants, the ceca are shorter and wider, and pairs of appendages are often fused (Fig. 5F). Moreover, the proventriculus and the anterior midgut are swollen in mutants (Fig. 5F). These parallel phenotypes provide additional evidence of a functional link between Su(var)3-7 and HP1, with an impact on development.

The chromosome phenotype of Su(var)3-7 mutants is suppressed by mutation of dosage compensation

We have been puzzled by two unexpected observations of Su(var)3-7 mutant phenotypes. First, the greater sensitivity of males to lack of Su(var)3-7 (Seum et al., 2002) (M.D., unpublished observations), and second the bloated male X chromosome, a phenotype shared by mutants of Su(var)2-5. What could explain the specific sensitivity of the male X chromosome to low doses of Su(var)3-7 or HP1? A specific feature of the male X chromosome in Drosophila is dosage compensation, a mechanism by which the single male X chromosome is hyperactivated in order to reach the transcription level of the two female X chromosomes. This
activation is driven by a complex of at least five main proteins (MSL1, MSL2, MSL3, MLE and MOF) and two noncoding RNAs (roX-1 and roX-2) that assemble specifically on the male X chromosome (for reviews, see Akhtar, 2003; Kelley, 2004). Hyperactivation results from acetylation of lysine 16 of histone H4, leading to an increase in transcription of X-linked genes (Smith et al., 2001).

We first tested by immunostaining whether the absence of Su(var)3-7 prevents the DCC from forming on the male X chromosome. The DCC is present, as the bloated male X of Su(var)3-7 mutants is entirely stained by antibodies against MSL2 or histone H4 acetylated on lysine 16 (Fig. 6A,B). To examine the possible link between Su(var)3-7 and dosage compensation further, we looked at polytene chromosomes of flies mutant in mle, a gene coding for the RNA helicase component of the DCC (Kuroda et al., 1991; Lee et al., 1997). Mutants of this gene do not compensate for dose and die at the third-instar larval stage, allowing examination of polytene chromosomes (Kuroda et al., 1991). When we combined the mle1 null mutation (Rastelli and Kuroda, 1998) and the Su(var)3-714 mutation, both as homozygotes, the bloated X phenotype expected from the loss of Su(var)3-7 was rescued. The male X has an mle1/mle1 configuration (Fig. 6). To ascertain that the effect was due to mutation of mle, we repeated this experiment with the mle9 allele, a mutation produced with another mutagen in another genetic background (Kernan et al., 1991). We obtained the same result (not shown). These experiments suggest that the presence of the DCC is necessary for the bloated X phenotype in Su(var)3-7 mutant larvae. The fact that the loss of a component of dosage compensation counteracts the loss of Su(var)3-7 implies that the mle and Su(var)3-7 genes interact, and reveals a possible participation of Su(var)3-7 in the chromatin structure of the male X chromosome.

Discussion
Polytene chromosome phenotypes of Su(var)3-7 and HP1 mutants
Polytene chromosomes are affected similarly by severe loss of Su(var)3-7 or HP1. In both cases, the main mutant phenotype is a bloated X in males, and an expanded chromocenter in males and females. Why is chromosome morphology modified when HP1 or Su(var)3-7 amounts are strongly reduced? We see several possible explanations. First, Su(var)3-7 and HP1 are both required for stability of chromatin association, and reduction of dose could lead to dissociation. As discussed below, Umbetova and Zhimulev proposed this mechanism for similar phenotypes in other conditions (Umbetova and Zhimulev, 1987). This hypothesis could be tested by determining whether a phenomenon based on chromatin association, such as transvection, is affected in Su(var)3-7 or HP1 mutants. A second possibility is that Su(var)3-7 and HP1 are required for compaction of intercalary heterochromatin on euchromatic arms. The loss of this compaction, similar to what we have seen at the chromocenter, could lead to bloating and disruption of the banding pattern. If indeed Su(var)3-7 and HP1 are instrumental in chromosome compaction, then one could expect that excess amounts of the proteins lead in turn to an excess of compaction. This is actually the case for Su(var)3-7, as increasing amounts of Su(var)3-7 first affect the male X chromosome, which becomes strongly compacted (Delattre et al., 2004). Furthermore, we have shown that targeting HP1 to an ectopic site promotes chromosomal loops linking this ectopic site with sites of intercalary heterochromatin (Seum et al., 2001). The question remains of the particular sensitivity of the male X chromosome to loss and excess of Su(var)3-7 and to loss of HP1.

That the male X chromosome is affected first and most severely could result from association of this chromosome with
the DCC. Chromatin relaxation triggered by the DCC in the male X would render it more sensitive to variations of the amount of chromatin-associated proteins. Indeed, male X bloating and shortening has been observed in several conditions, and has been named the ‘pompon’ phenotype by Pavan and described as resulting from specific environmental aggressions or mutations (see Zhimulev, 1996). More recently, although less spectacularly, male X bloating was described as resulting from the loss of several chromatin-modifying factors such as Jil-1 (Wang et al., 2001) or the Nurf complex (Deuring et al., 2000; Badenhorst et al., 2002). The various environmental and genetic conditions in which bloating of the male X occurs underline the peculiar sensitivity of the phenotype, and could explain the differences of phenotype intensity we see using different X chromosomes.

Finally, the X-chromosome-specific phenotype might result from a direct interaction between the DCC and silencing factors. In this paper, we demonstrate indeed a genetic interaction between an essential gene of the dosage compensation machinery, mle, and Su(var)3-7. However, we have not detected, in the wild type, preferential association of Su(var)3-7 with the polytene male X chromosome using either a polyclonal antibody raised against Su(var)3-7 sequences, or a monoclonal antibody raised against the tag of HA-Su(var)3-7. However, we clearly see preferential association with the male X when Su(var)3-7 is over-expressed from a transgene (Delattre et al., 2004). We cannot at this point distinguish between two possibilities: either Su(var)3-7 modulates the transcription level of the X chromosome by counteracting the DCC relaxing effect, or it protects the X-linked genes that do not need to be dosage compensated. We are currently exploring further the interaction of Su(var)3-7 and the DCC. The role of HP1 also remains to be explored. We and others have not seen preferential association of HP1 with the male X polytene chromosome. Nevertheless, when Su(var)3-7 is over-expressed, HP1 is found associated preferentially with the male X (Delattre et al., 2004).

The ‘null’ mutant described in this paper, in which only weak and variable bloating of the male X polytene chromosome occurs, leads us to reconsider the phenotypes of previously obtained mutants where some altered Su(var)3-7 is still produced. For example, an hypothesis would be that the truncated portions of Su(var)3-7 synthesized in Su(var)3-7 or Su(var)3-7 have the ability to titrate away a component stabilizing or participating in the DCC/X chromatin interaction. Nonetheless, other truncations of Su(var)3-7 expressed from a transgene do not cause bloating of the X chromosome (Y. Jaquet, personal communication). We do not know whether this last observation disfavors the titration...
Fig. 7. Targeted mutagenesis of Su(var)3-7. (A) The Su(var)3-7 locus and neighboring genes. (B) Donor construct using 2.6 kb of homology upstream of Su(var)3-7 (red) and 4 kb downstream (blue). (C) Combination of the donor transgenic lines with an I-SceI and FLP-producing strain leads to a double-strand break in the middle of the downstream region (blue) and can give rise to homologous recombination. (D) Use of homologous recombinant bearing a 1033 bp deletion 5′ of the I-SceI site displaces the equilibrium towards a reduction in the 5′ region of Su(var)3-7. (E,F) Crosses of recombinants with a strain expressing the I-CreI restriction enzyme lead to a double-strand break permitting many different reduction events. (F) Repair of the break in the 5′ region of Su(var)3-7 results in deletion of the gene. B, BamHI; H, HindIII; R, EcoRI; X, XbaI.
hypothesis, or whether the explanation resides in the different times, amounts and distributions resulting from expression of a transgene.

The second observation made on polytene chromosomes of Su(var)3-7 and Su(var)2-5 mutants is the decondensed aspect of the chromocenter, where pericentric heterochromatin from the different chromosomes coalesces. As heterochromatin is under-replicated in polytene chromosomes, a possible explanation is that heterochromatin, freed from the ‘condensing’ constraint of Su(var)3-7 or HP1 in mutants, reaches higher degrees of polyploidy and expands. The phenotype we describe for Su(var)3-7 and Su(var)2-5 mutants (large amount of granules and loose reticulum of fibers) is however very different from the phenotype seen in Suppressor of Underreplication mutants where blocks of heterochromatin are more replicated, become polytenized and acquire a banding pattern (Belyaeva et al., 1998). We rather believe that heterochromatin of Su(var)3-7 and Su(var)2-5 mutants adopts a less tightly packed conformation. Moreover, the loosened and expanded chromocenter phenotype makes sense as Su(var)3-7 and HP1 are both known to associate primarily with pericentric heterochromatin and to promote genomic silencing of PEV (Reuter et al., 1990; Cléard et al., 1997; James et al., 1989; Eissenberg et al., 1992). The silencing of PEV is relieved by loss of a dose of either factor, and it is therefore not surprising that the characteristic condensed state of heterochromatin is affected. This phenotype strongly suggests a direct role of Su(var)3-7 and HP1 in compacting heterochromatin.

We must also consider that the phenotypes described in this study could be indirect, and result from mis-regulation of Su(var)3-7 and HP1 target genes. Amounts of HP1 do affect expression of genes embedded in heterochromatin (Lu et al., 2000), but also seem to regulate euchromatinic genes (Hwang et al., 2001; Nielsen et al., 2001; Greil et al., 2003; Piacentini et al., 2003). Microarray experiments suggest that Su(var)3-7 also regulates euchromatic genes (Y. Jaquet, Functional dissection of Su(var)3-7, a heterochromatic protein from Drosophila melanogaster, PhD thesis, University of Geneva, 2004). There is therefore a significant body of data arguing for a role of Su(var)3-7 and HP1 on gene regulation not only in heterochromatinic context, but also in euchromatin.

Su(var)3-7 and HP1 do not overlap on mitotic chromosomes

We find Su(var)3-7 associated with diploid chromosomes undergoing mitosis in wild-type larval brains. Whereas Su(var)3-7 is associated with euchromatin arms, it is not detected on heterochromatin, except for partial staining of the Y chromosome. This is in contrast to HP1, which is primarily associated with heterochromatin. Detection of Su(var)3-7 on euchromatin is not unexpected. On polytenic chromosomes, several sites have indeed been detected on euchromatin for both Su(var)3-7 and HP1 (Delattre et al., 2000; Fantì et al., 2003; Piacentini et al., 2003). Moreover, in excess amounts of Su(var)3-7, association is seen all over the euchromatic arms (Delattre et al., 2000; Jaquet et al., 2002), suggesting general affinity of the protein for euchromatin. Finally, Su(var)3-7 expansion on polytenic chromosome euchromatic arms in a Su(var)2-5 mutant background further confirms its capacity to bind euchromatin. This might result from the affinity of Su(var)3-7 for DNA in vitro (Cléard and Spierer, 2001) and in vivo (Perrini et al., 2004). It is interesting to note that Su(var)3-9 localization in heterochromatin depends also on HP1 and that, in the absence of HP1, Su(var)3-9 also expands in euchromatin (Schotta et al., 2002).

We propose several possible explanations for the different pattern of Su(var)3-7, namely on heterochromatin of polytene chromosomes and euchromatin of mitotic chromosomes. First, on mitotic chromosomes, interaction between HP1 and Su(var)3-7 could be prevented by a competitor recruited by HP1 such as, for example, the cohesin complex that is highly enriched in heterochromatin regions during mitosis and not in interphase (Nonaka et al., 2002). Second, a specific modification of HP1 (Eissenberg et al., 1994; Huang et al., 1998) in mitotic chromosomes could abolish its interaction with Su(var)3-7. In this case, Su(var)3-7 would associate with other partners yet to be determined. The Su(var)3-7 pattern in the Su(var)2-5 mutant supports this model as we showed that it does not move away from mitotic euchromatic arms. Other chromatin-associated proteins, such as for example GAGA or PROD (Platero et al., 1998; Torok et al., 1997), are known to exhibit a cycling pattern, although in the opposite way, as these proteins are on heterochromatin during mitosis and on euchromatin on interphase chromosomes. Another hypothesis is that Su(var)3-7 has a specific affinity for condensed chromatin, and consequently is associated with condensed heterochromatin of polytenic chromosomes and with condensed euchromatinic arms of neuroblast mitotic chromosomes.

In conclusion, we have shown that Su(var)3-7 and HP1 participate in chromocenter and male X polytenic chromosome integrity. The similarity of the phenotypes seen in mutations of either one, the partial compensation of the loss of dose of one by an increase of dose of the other in PEV (Cléard et al., 1997), and the physical interaction seen in vitro and in vivo (Cléard et al., 1997; Delattre et al., 2000) all point to the same conclusion. These two structurally very different proteins cooperate closely in chromosome organization. We have also discovered an interaction between Su(var)3-7 and compensation of dose. This interaction between the genomic silencing of PEV dependent on Su(var)3-7 association, and hyperactivation dependent on association of the DCC, need to be unravelled.

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