

derepression of the fusion gene and of endogenous *Ubx*: β -galactosidase staining appears weak anteriorly and strong posteriorly, whereas antibody staining is even throughout. But the extension of the derepressed domain is the same in both cases and most probably corresponds to the addition of the normal *Ubx* and *abd-A* expression domains. We conclude that functional *abd-A* product determines the posterior limit of normal *Ubx* expression in the visceral mesoderm. Interestingly, neither the second nor the third midgut constriction can form properly in *abd-A*⁻ mutant embryos (Fig. 2*j-l*), suggesting that the formation of these constrictions depends on adjacent domains of differential homeotic gene activity in the visceral mesoderm.

The *Abdominal-B* (*Abd-B*) product functions to down-regulate *Ubx* expression in the posterior ectoderm⁸. In contrast, we find that an *Abd-B* null mutation¹⁴ (*Abd-B*^{M1}) does not affect *Ubx* expression in the visceral mesoderm, although the effect of this mutation is clearly apparent in ps13 of the ectoderm (Fig. 2*b*). We find unexpectedly that, in the absence of functional *abd-A* product, *Abd-B* can activate the fusion gene ectopically: β -galactosidase staining appears in the visceral mesoderm of the posterior midgut in *Ubx*⁻ *abd-A*⁻ double mutant embryos (Fig. 2*g*). This ectopic β -galactosidase staining is abolished in triple mutants (*Ubx*⁻ *abd-A*⁻ *Abd-B*⁻) and is therefore dependent on functional *Abd-B* product (Fig. 2*h*). The ectopic β -galactosidase staining domain probably corresponds to the *Abd-B* expression domain, implying that *abd-A* and *Abd-B* expression coincides in the posterior visceral mesoderm. It appears that *Abd-B* does not have any repressor function in this germ layer.

We have shown that, in the absence of functional *Ubx* prod-

uct, the *Ubx* gene cannot be expressed in ps7, whereas, in the absence of functional *abd-A* product, *Ubx* expression cannot be repressed posterior to ps7 in the visceral mesoderm (Fig. 3). The targets for *Ubx* autocatalysis and *abd-A* repression are evidently present on the *Ubx*/ β gal fusion gene, and it is possible that these regulatory mechanisms are mediated by direct DNA binding¹⁷ of the *Ubx* and *abd-A* homeoproteins to *Ubx* promoter sequences. It appears that in the visceral mesoderm autocatalysis and exclusion^{2,3} are important for the establishment and/or the maintenance of adjacent domains of homeotic gene expression. Whether these mechanisms also act in the ectoderm where expression domains of different homeotic genes partly overlap¹ is unclear. Indication for autocatalysis in the ectoderm has been obtained for *fushi tarazu* expression¹⁸, although in this case there is no evidence for exclusion by the adjacent gene *even-skipped*¹⁹.

It is puzzling that only the posteriorly adjacent gene *abd-A*, but not the anteriorly adjacent gene *Antp*, excludes *Ubx* expression in the visceral mesoderm. It is possible that the anterior limit of the *Ubx* expression domain in this germ layer is determined by an additional regulatory protein that provides a positional value with respect to the antero-posterior axis. This hypothetical regulator may be present at low concentration anteriorly and at high concentration posteriorly and allow *Ubx* expression only above a certain threshold concentration. The posterior limit of *Ubx* expression could be determined by the exclusion function of the *abd-A* gene.

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Erratum

A new superfamily of replicative proteins

T C Hodgman
Nature **333**, 22-23 (1988).

IN this piece of Scientific Correspondence, an unrevised version of the figure was used in error. The correct version is reproduced on the right.

Motif	I	II	III	IV	V	VI	Source ref.
AlMV	821 VDCVAGCGKTTMIK	55 RLIFDFECLQH	15 VIGFGDTQIIPF	22 IWRSPADA	66 IFTTHE-AQCK-TFDNYVFCR	13 NGLVALSRH (1)	
BW	687 VDCVAGCGKTTAIK	54 RLIVDEAGLLH	15 VLAFGDSEIISF	22 KTYRCPQV	78 IKTVHE-AQGI-SVDNVTIWR	13 YCLVALTRH (1)	
CMV	709 VDCVAGCGKTTAIK	54 RLIVDEVLLH	15 ALCFGDSEIISF	22 TFRSPQV	79 IKTVHE-SQGI-SEHDVTIWR	13 YCLVALTRH (1)	
TMV	829 VDCVPGCGKTRFII	57 RLFIDGGLMLH	15 AVYVGDITQIIPY	24 TILRCPADV	62 VHTVHE-VQGE-TYSDVSLVR	14 NGLVALSRH (1)	
TMV	829 VDCVPGCGKTRFII	57 RLFIDGGLMLH	15 AVYVGDITQIIPY	24 TILRCPADV	62 VHTVHE-VQGE-TYSDVSLVR	14 NGLVALSRH (17)	
TRV	901 VDCVPGCGKSTMIV	56 VLFDFEALMAH	15 CICQGDQMOISF	24 ETRYSPADV	64 VSTVHE-SQGE-TFKDVTIWR	13 YLVALSRH (1)	
SFV	183 VFGVPGSGKSAIIK	50 LLYVDEAFACH	16 VILCGDPRKQCF	21 ISRRCTRPV	58 VMTAAA-SQGL-TRKGVYAVR	14 BNVNLTTRT (1)	
SV	183 VFGVPGSGKSAIIK	50 LLYVDEAFACH	16 VILCGDPRKQCF	21 ISRRCTRPV	58 VMTAAA-SQGL-TRKGVYAVR	14 BNVNLTTRT (1)	
IBV	1209 VQGPVSGKSHFAI	54 LLLVDEVSMIT	15 VYVGDPAQLPA	30 KCYRCPKEI	82 VQTVDS-SQGS-EYDVIYFCV	11 RFNVALTRA (18)	
BNYV1	893 VGGPCTGKSFILR	48 IIFVDEFTAYD	11 IYLVGDEQOTGI	25 MFRNPVHD	72 KTVRA-ROGS-TYDNNVLPV	12 LNLVALSRH (19)	
BNYV2	121 VLGAPGVGKSTIIR	49 TMLVDEIVRVI	11 VICFGDPAQGLN	18 ASRRFGKAT	67 SILYSD-AHQG-TYDVTIIL	13 VRVALTRA (19)	
BSW2	267 ISQVPGSGKSTIIR	41 LLLIIDEYTLAE	11 VLLVGDVAQKRA	18 TTYRLIGET	62 CALAI1-VQGR-EFDSVTLFL	12 LRLVALSRH (20)	
uvrD	26 VLAGAGSGKTRVLV	17 MAVTE-TNKRAAEMHRI	140 NILVDEFQNTN	16 VMLVGDODOSIY	26 QNYRSTSMI	267 LMTLHS-AQGL-EFPQVIVG	23 LAYVGTVA (21)
rep	19 VLAGAGSGKTRVIT	17 AAVTF-TNKRAEMKERV	141 YLLVDEYQOTN	16 PTVVGDODOSIY	26 QNYRSGRT	271 LMTLHA-SQGL-EFVYVYHWG	22 LAYVGTVA (21)
recB	20 TEASAGTGGKTTFA	25 LAVTF-TEAAIAELRRI	303 VAMIDEFQTD	18 LLLIGDFQGIY	24 TWRSAQW	286 IYVTHL-SQGL-EYELWJWF	44 LLLVALTRH (4)
recD	164 ISGGPCGKSTIWA	17 RLAAE-TCKAARLTESL	48 VLVVDEASMD	16 VIFLGRDQLAS	24 QLSRLTGH	198 AMTVHR-SQGS-EFDHALLI	11 LVTAVTRA (22)
EBV	49 ITGTAGAGKSTSVS	7 CVITGTTVVAQNLISAIL	88 VLVVDEAGTLS	26 IVCVGSPTQIDA	44 NNRKCTDVG	426 AMTAK-AQGL-SIKRVAICF	9 BUVVALSRH (23)
HCMV	117 VDTAGAGKSTSIQ	7 CVITGTTVVAQNLISAIL	100 VLVVDEAGLML	26 IVCVGSPTQIDA	44 NNRKCTDVG	513 AMTAK-SQGL-SLERVAICF	10 BUVVALSRH (23)
HSV	94 ITGNAGAGKSTCVQ	7 CVITGATRIAAONHYAKL	111 VLVVDEAGLLG	26 IVCVGSPTQIDAS	44 NNRKCTDVG	442 AMTAK-SQGL-SLERVAICF	8 SAYVAMSR (6)
VZV	87 ISGNAGAGKSTCIQ	7 CVITGATRIAAONHYAKL	110 VLVVDEAGLLG	26 IVCVGSPTQIDAS	44 NNRKCTDVG	447 AMTAK-SQGL-SLERVAICF	8 SAYVAMSR (24)
PIF	255 YTSAGTIGKSIILLR	7 VAVTASTGLAACNIGGTI	21 ALVVDEAGLSMLO	25 IIFCGDFQQLPP	29 KVFQRGDDV	219 MCTIHSAGKRRRLVRFKA	33 QAYVALSRA (5)
Residue	V G A G K S	V T A A N L	V D E	G D Q	R	T S G S E V	V A L S R
distribo.	I A P T	I A T E I	F	S		L A K S A	T I U T
	Y	A R V	F			W H T	G M
						N A R	S I