

# An Invertebrate Calcium-binding Protein of the Calbindin Subfamily: Protein Structure, Genomic Organization, and Expression Pattern of the Calbindin-32 Gene of *Drosophila*

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**Antisera against vertebrate calcium-binding proteins cross-react with *Drosophila* nervous and muscle tissue. We have used an antiserum against carp parvalbumin to isolate from a *Drosophila* head cDNA library immunopositive expression clones. Tissue *in situ* hybridization identified a clone that labeled specific neurons and muscles similar to the parvalbumin-like immunohistochemical staining pattern. Five independent cDNAs derive from an mRNA whose open reading frame codes for a 310 amino acid polypeptide. Sequence analysis identifies six EF-hand calcium-binding domains and reveals 42% and 37% homology to chicken calretinin and calbindin D-28k, respectively. Since the positions of 9 out of 10 introns within the ORF are conserved from the *Drosophila* gene to both vertebrate genes, we conclude that we have identified the first invertebrate member of the calbindin subfamily of calcium-binding protein genes of the EF-hand homolog family. The calbindin-32 gene (*cbn*) maps to 53E on the second chromosome. It is expressed through most of ontogenesis with a selective distribution in the nervous system and in a few small adult thoracic muscles. The cloning of a *Drosophila* homolog to vertebrate neuronal Ca<sup>2+</sup>-binding proteins opens new routes to study the so far largely elusive function of these brain molecules.**

**[Key words: calbindin D-28k, calretinin, parvalbumin, *Drosophila*, EF-hand, evolution]**

In excitable cells, calcium (Ca<sup>2+</sup>) plays multiple roles as charge carrier and second messenger (reviewed in Miller, 1988; Kennedy, 1989). A wide variety of interacting systems of channels, transporters, sequestering organelles, and binding proteins are responsible for the control of intracellular Ca<sup>2+</sup> levels (Blaustein, 1988; Heizmann and Hunziker, 1990; Pietrobon et al., 1990).

Most intracellular Ca<sup>2+</sup>-binding proteins (CBPs) known today belong to one of two groups, the annexin protein family or the EF-hand homolog family (Heizmann, 1991; Heizmann and Hunziker, 1991). The latter family at present consists of some 220 proteins that recently have been grouped into 29 subfamilies on the basis of structural features and mutational distances (Persechini et al., 1989; Kretsinger et al., 1991; Nakayama et al., 1992). While most proteins of this family contain four EF-hand domains, a single subfamily with six domains is formed by calbindin D-28k and calretinin. Information on tissue distribution of both these proteins has recently been reviewed (Parmentier, 1990; Rogers, 1991). Little is known, however, of their physiological function. They are found at high concentrations in a wide variety of central and peripheral neurons. Their distribution in various species displays certain conserved but also surprisingly variable features (Pasteels et al., 1990; Rogers, 1991).

First hints on the expression of a homolog to vertebrate CBPs in the brain and in muscles of *Drosophila* came from immunohistochemical cross-reactions of antisera against chicken or rat calbindin D-28k and carp-II and rat parvalbumin, all staining an apparently common set of neurons but various different muscles (Buchner et al., 1988; Störckuhl et al., 1988). Using the anti-carp-parvalbumin antiserum, we isolated a cDNA coding for a protein fragment with homology to EF-hand CBPs (Reifegerste et al., 1991). Here we describe the inferred primary structure of the complete protein, which we propose to name calbindin-32 (CBN). The chromosomal localization and intron-exon structure of the corresponding gene (*cbn*) and the distribution of both the transcript and the gene product by *in situ* hybridization and immunohistochemistry using antisera against fusion protein are presented.

## Materials and Methods

### *cDNA- and genomic-library screening*

Using a polyclonal antiserum against carp II parvalbumin, we screened 200,000 plaque-forming units of a *Drosophila* (wild-type Berlin K) head λgt11 cDNA expression library as described by Young and Davis (1985). A 900 base pair (bp) cDNA clone was isolated (cDNA 5 of Fig. 1a). The 200 bp EcoRI fragment at the 5' end of the isolated cDNA was used as randomly primed probe (Feinberg and Vogelstein, 1983; Amersham protocol) for hybridization screening of the same cDNA library. Four additional cDNAs (cDNAs 1–4 of Fig. 1a) were obtained.

cDNA 5 was also used as randomly primed probe for screening a λ-EMBL4 and a λ-GEM11 genomic library (Benton and Davis, 1977) of wild-type Oregon R flies (libraries kindly provided by W. L. Pak, J. Yoon, and K. Kaiser). The cloned genomic region was extended resulting

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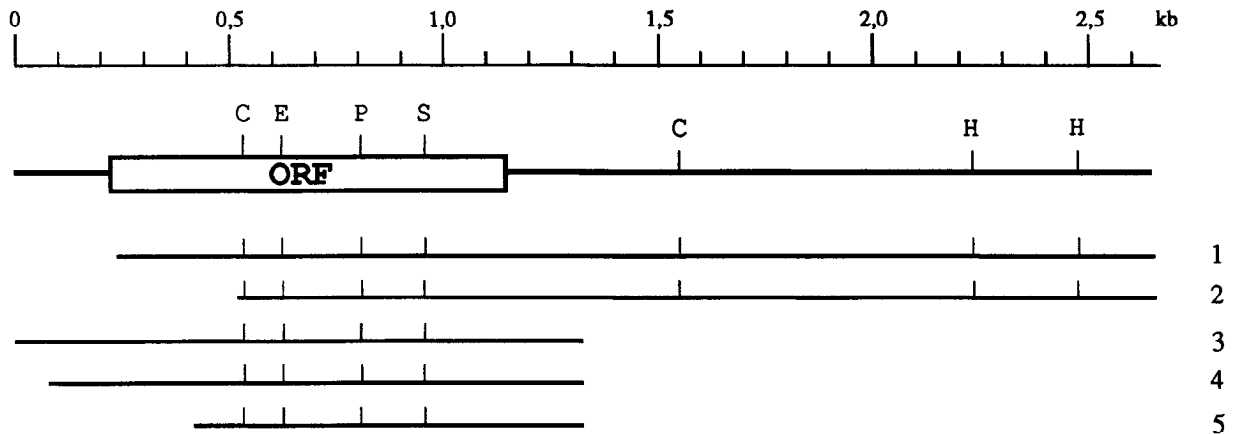
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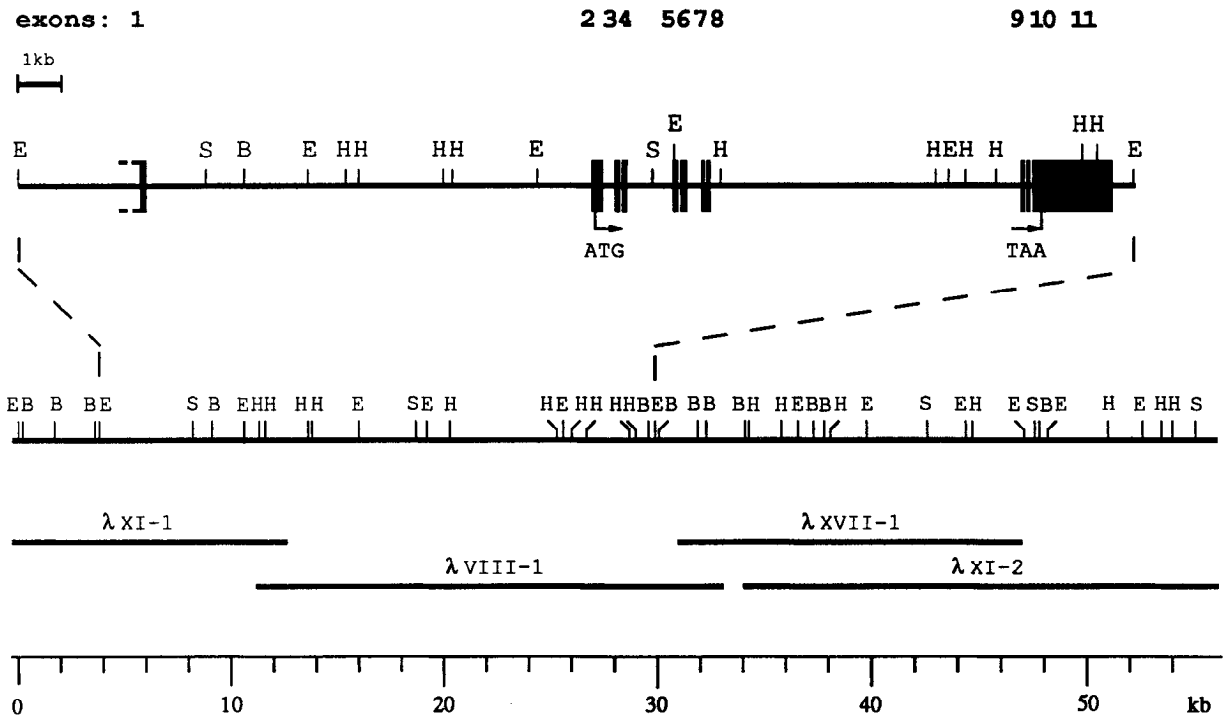
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**a**



**b**



**Figure 1.** cDNAs, intron–exon structure, and genomic map of the *cbn* gene. *a*, Restriction maps of the cloned cDNAs of the *cbn* gene. Presumably all cDNAs derive from the same mRNA. Sequence analysis suggests internal priming as the likely cause for the 3' ends of cDNAs 3–5. The complete ORF of the mRNA has been sequenced from cDNAs 1 and 4 and has been verified genomically. C, ClaI; E, EcoRI; H, HindIII; P, PstI; S, SstI. *b*, Restriction map of genomic region coding for the *cbn* transcript. Intron sizes range from 57 bp to 10.5 kb. Solid boxes, exons; length of nonsequenced introns inferred from restriction map and/or PCR analysis; the size of first exon (dashed) has not yet been determined; small arrows, start and stop codons of open reading frame. B, BamHI; E, EcoRI; H, HindIII; S, Sall. Several HindIII sites in the leftmost 12 kb of the walk have not yet been mapped. Bars below the genomic restriction map indicate the corresponding  $\lambda$ -phage clones spanning the entire genomic region.

in 14 overlapping phage clones that span a region of nearly 60 kilobases (kb).

**Subcloning and sequencing of cDNA and genomic fragments**

Phage DNA was isolated (Sambrook et al., 1989) and EcoRI fragments were inserted into pBluescript KS vectors (Stratagene). Templates were sequenced by the chain termination method of Sanger et al. (1977) using modified T7-polymerase (Tabor and Richardson, 1987). Genomic regions were sequenced directly with synthetic oligonucleotide primers, whereas cDNAs were subjected to deletions by exonuclease III/SI (Henikoff,

1987). Both strands of exonic DNA were sequenced and compared; for introns, in general only one strand was sequenced.

**Preparation of fusion protein and antisera**

Fusion proteins were produced utilizing the glutathione S-transferase (GST) expression vector system in *Escherichia coli* DH5 $\alpha$  cells. The 700 bp EcoRI fragment of cDNA 5 was cloned in frame to the GST of the pGEX-1 $\lambda$ T vector. This vector had been produced by deleting a single base pair from the pGEX-2T vector (Smith and Johnson, 1988) in the following reaction sequence:





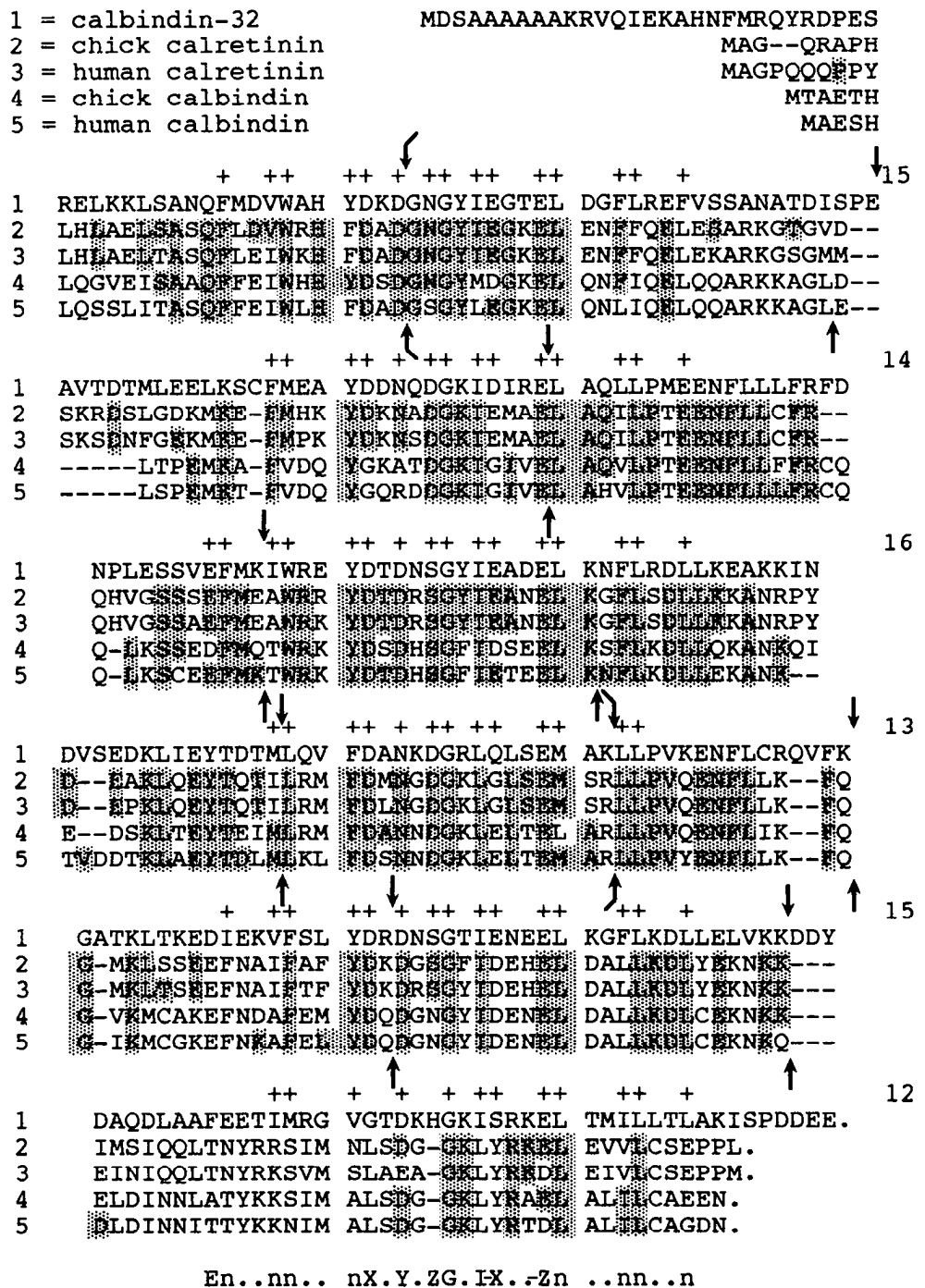


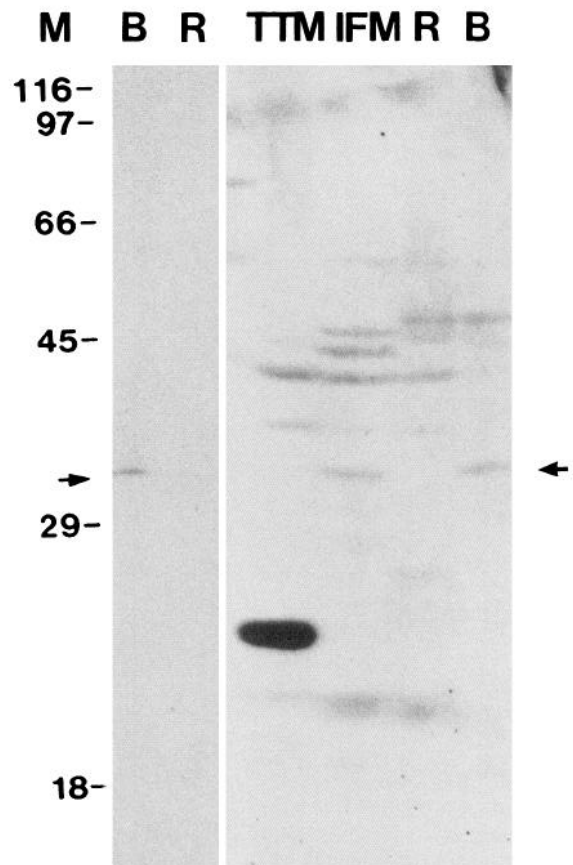
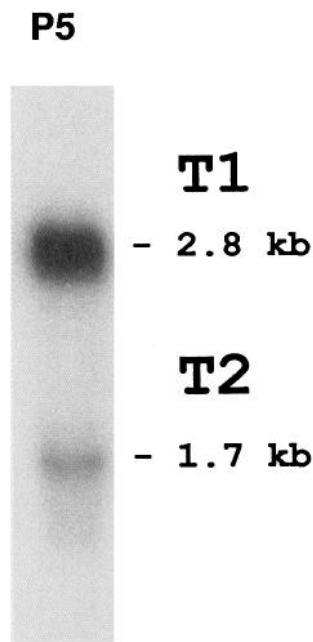
Figure 3. Primary structure of CBN of *Drosophila*. Comparison of amino acid sequences of CBN with calretinin and calbindin D-28k from chicken and human reveals high homology (shaded letters) for the Ca<sup>2+</sup>-binding domains (consensus sequence for EF-hand, bottom line; conformity indicated by +). Significant homology is also found outside EF-hand domains. Arrows above line 1, intron positions of *cbn* gene; arrows below line 5, common intron positions of the four vertebrate genes; straight arrows, introns between codons; bent arrows, introns within codon one bp from arrow position in the direction of bend. Bottom line, Canonical EF-hand consensus sequence. The EF-hand domain consists of 29 amino acids that form an  $\alpha$ -helix, calcium-binding loop,  $\alpha$ -helix conformation. The first  $\alpha$ -helix begins frequently with E, glutamic acid; G, glycine, is a highly conserved amino acid in the center of the calcium-binding loop; n stands for one of the hydrophobic residues Val, Ile, Leu, Met, Phe, Tyr, or Trp located at the inner part of the  $\alpha$ -helices. Calcium is coordinated by side-chain oxygen atoms of amino acids Asp, Asn, Ser, Thr, Glu, or Gln at positions X, Y, Z, -X, -Z, and by a peptide carbonyl oxygen atom of the (arbitrary) amino acid following G (glycine). Ile, Leu, or Val are important amino acids to occupy position I. They are involved in stabilizing the calcium-binding loop through apolar interaction with the hydrophobic core of the protein and in stabilizing paired EF-hand domains (after Kretsinger et al., 1991).

diographic *in situ* hybridization signal reminiscent of the antibody staining. By using this cDNA as a probe, four further cDNAs were isolated (Fig. 1a). Restriction mapping and analysis of hybridization to a genomic walk of 56 kb (Fig. 1b) indicates that all cDNAs derive from the same transcript. Sequence analysis of the cDNAs revealed that they code for a single large open reading frame (ORF). The cDNA sequences were verified by sequencing genomic DNA (exons in Fig. 2, capital letters).

**Inferred protein and gene structure.** A search of the genetic data bases for similarities with the ORF detected significant homologies to various EF-hand CBPs. Scores were highest for chicken calretinin (42%) and calbindin D-28k (37%). As shown

in Figure 3, the amino acid identity is up to 76% in the helix-loop-helix calcium-binding domains but remains significant in several regions outside these domains. All six Ca<sup>2+</sup>-binding domains conform to the EF-homology criterion, as they show 12 or more matches with the canonical EF-hand domain (Kretsinger, 1975; Kretsinger et al., 1991; for more detailed information about the consensus sequence, see Fig. 3 caption). However, this criterion does not guarantee Ca<sup>2+</sup> binding. Domain VI of CBN, in particular, is lacking two Ca<sup>2+</sup>-coordinating residues at positions X and Z. In vertebrate calbindin D-28k, this domain does not bind Ca<sup>2+</sup>. However, the two gaps in domains II and VI of calbindin D-28k are not found in CBN.

Speculating that along with the protein's amino acid sequence



**Figure 4.** Northern blot analysis of *cbn* transcripts. Electrophoretically separated polyA<sup>+</sup> mRNAs of late pupal stages (P5) were blotted to nylon membranes and probed with <sup>32</sup>P-labeled cDNA 1. The autoradiograph shows two transcripts with different levels of transcriptional activity, a prominent band at 2.8 kb (T1) and a weak band at 1.7 kb (T2).

the intron–exon structure of the gene might be conserved between *Drosophila* and vertebrates, we used exonic sequences close to the vertebrate exon–intron boundaries as primers to sequence cloned genomic DNA. Apart from introns 1, 4, and 8, which are of approximately 10.5, 1.1, and 7.5 kb length, respectively, the entire region containing translated exons was sequenced in this fashion from genomic DNA and compared to the cDNAs. A 15 bp deletion in the cDNAs, underlined in Figure 2, and a few mostly inconsequential base substitutions may represent polymorphisms or errors of reverse transcription during cDNA synthesis. Of the 10 introns in the translated genomic region of the vertebrate genes (lower arrows in Fig. 3) (Wilson et al., 1988), 7 positions are identical in *Drosophila* to the base, 2 are found in corresponding positions in nonconserved regions of the ORF, while one vertebrate intron is missing in the fly (upper arrows in Fig. 3). The intron–exon boundaries largely conform to the consensus sequences (Shapiro and Senapathy, 1987).

*In situ* hybridizations on polytene chromosomes localized the *cbn* gene to region 53E on the right arm of chromosome 2 (data not shown).

**Expression analysis of the *cbn* gene.** Northern blot analysis revealed two transcripts of about 2.8 kb (T1) and 1.7 kb (T2) in the late pupal stage (P5) (Fig. 4). The same signals were obtained for adults of two unrelated mutants (not shown). Tissue distribution of *cbn* transcript and CBN protein was investigated by *in situ* hybridization and immunohistochemistry, respectively. For *in situ* localization of *cbn* mRNA shown here (see Fig. 8a), digoxigenin-labeled cRNA/cDNA was used, followed by antibody detection. To obtain antisera directed against CBN, we expressed *cbn* cDNA in *E. coli* as GST fusion protein and injected six mice (see Materials and Methods). As antiserum 1 showed the highest titer, it was used for Western analysis of brain homogenates (Fig. 5) and immunohistochemical localiza-

**Figure 5.** Western blot (left two lanes) and <sup>45</sup>Ca<sup>2+</sup> blot. Immunoblots of electrophoretically separated homogenates of brain (B) and head-without-brain (R) stained with anti-CBN serum display a single, brain-specific protein band at  $M_r = 32$  kDa (left arrow). Several components of homogenates of TTM and indirect flight muscle (IFM), as well as brain and head-without-brain, bind <sup>45</sup>Ca<sup>2+</sup> as revealed autoradiographically in lanes 3–6. A single band at  $M_r = 32$  kDa (right arrow) is found in brain but not in residual head tissue. The 32 kDa signal detected in the indirect flight muscle lane (IFM) could derive from CBN protein from direct flight muscles (hg 1 and hg 2), which may have contaminated the indirect flight muscles preparation. The strong signal in TTM near  $M_r = 21$  kDa presumably corresponds to the CBP described previously (Tanaka et al., 1988). M, molecular weight marker.

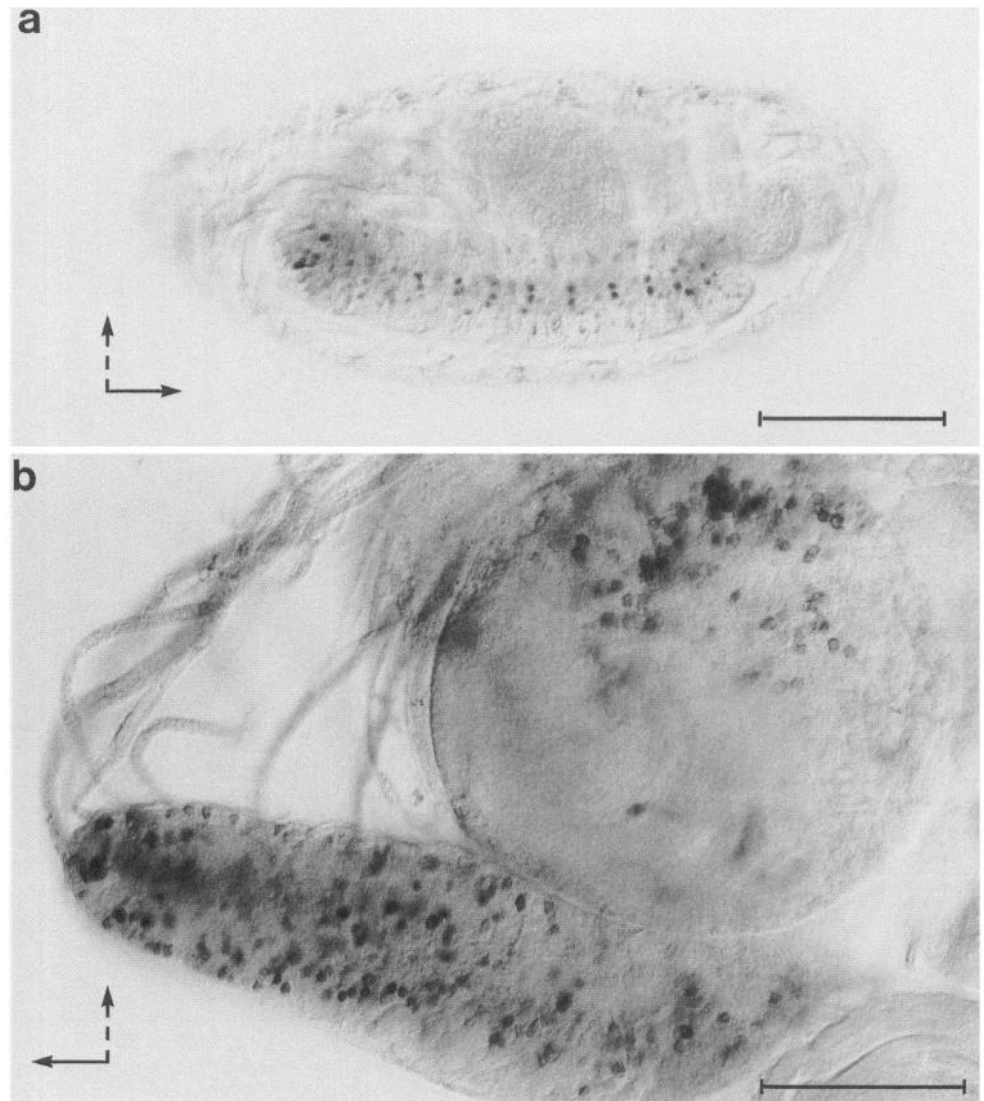
tion of CBN in embryos, larvae, and adult flies. Several arguments support the assumption that the staining patterns indeed reflect the tissue distribution of CBN (see Discussion).

In the late embryo (~16 hr), segmental pairs of cells along the midline express the gene and other cells of the nervous system, including a string of peripheral cells, follow soon, as demonstrated both by *in situ* hybridization (not shown) and immunohistochemistry (Fig. 6a).

Both techniques have also been used to demonstrate in third instar larvae the selective expression in perikarya of the two hemispheres and the ventral cord (Fig. 6b). Cells are stained throughout the thoracic and abdominal ganglia. In the hemispheres the labeled cells are restricted to the proximal part, whereas the lateral hemispheres consisting of the developing optic lobes appear free of staining with the exception of a few cells near the lateral surface.

Figure 7 gives an overview of CBN distribution demonstrating that it is mainly, but not exclusively, found in the nervous system. *In situ* hybridization verifies that the *cbn* gene is ex-





**Figure 6.** CBN distribution in 16 hr embryo (*a*) and third instar larva (*b*). Immunohistochemistry identifies CBN in a subgroup of neurons of the CNS and PNS at all stages after about 12 hr developmental time. CBN specificity of the staining may be assumed since whole-mount *in situ* hybridization experiments with digoxigenin-labeled cDNA or cRNA of the *cbn* gene mark very similar structures. The *broken* and *solid arrows* indicate ventral-dorsal and anterior-posterior body axes, respectively. Scale bars, 100  $\mu$ m.

pressed in a large number of neurons of the brain (Fig. 8*a*) and the thoracic ganglion as well as in two small muscles of the thorax (data not shown). Immunohistochemistry (Figs. 8*b*; 9*a,b*) illustrates the corresponding protein distribution at improved resolution (compare Fig. 8*a,b*) and demonstrates that only a subset of neurons express the *cbn* gene. In these cells the CBN protein is localized both in perikarya and in processes. In the visual system (Fig. 8*b*), tentative identification of certain CBN-positive columnar cells is possible by comparison with data from an extensive Golgi analysis of *Drosophila* visual system interneurons (Fischbach and Dittrich, 1989; Bausenwein et al., 1992). While the photoreceptors clearly are devoid of CBN, the layer of stained perikarya in the outer lamina cellular rind indicates that one of the three distal lamina monopolar cells L1, L2, or L3 expresses CBN. Interestingly, the dendritic arborizations of these cells in the lamina are not stained, suggesting that in the neuropil CBN may be found mainly in presynaptic terminals that branch in specific layers of the medulla. The selective staining of medulla layer M2, where lamina monopolar cells L2 terminate, suggests this cell as the best candidate for CBN expression in the lamina. This interpretation is compatible with the absence of staining of lamina monopolar cells in the mutant

“Vacuolar medulla” (Vam) (Coombe and Heisenberg, 1986), which shows a specific degeneration of L1 and L2 neurons within a few hours after hatching of the adult fly. In the medulla rind a large fraction of the columnar neurons apparently express CBN, perhaps at varying levels. In the lobula complex the most striking feature is the distinct absence of staining in the lobula plate cellular rind and neuropil (except for large tangential neurons), contrasting the prominent staining of a group of laterally adjacent perikarya (arrows in Fig. 8*a,b*) which, as judged by the labeled internal lobula neuropil layer (arrowheads), may include T2 and/or T3 cells. CBN is also found in the antennal system. Figure 8*c* shows a few distinctly stained cell bodies; the antennal lobes display a patchy staining pattern (Fig. 8*e*), suggesting that some glomeruli may contain no or very little CBN. In the central brain (Fig. 8*d,f*) the *cbn* gene is widely expressed, but again distinct cell groups and their processes are conspicuously devoid of staining. Regions with low levels of CBN include the calices, peduncle, and lobes of the mushroom bodies, the anterior part of the ellipsoid body, the noduli, and cells of the pars intercerebralis.

In the thorax staining is highly selective as well. While CBN is widely (but not ubiquitously) distributed in the thoraco-ab-

dominal ganglia (Figs. 7; 9*b,d*) and is found in cells and axons within the halteres (Fig. 9*c*), it is expressed in only a small number of muscles. The muscular network surrounding the ventriculus is stained in a central region but not throughout its length (Fig. 9*d*). The two most strongly stained muscles (Fig. 9*a*) have been tentatively identified as the hg1 and hg2 direct flight muscles (Heide, 1971; B. Bausenwein, personal communication). To our knowledge, this is the first identification of a CBP of the calbindin subfamily in muscle cells. Interestingly, the original anti-carp II-parvalbumin serum also stains these muscles, but in addition binds to the TTM (Störtkuhl et al., 1988), which never labels with CBN antisera. This muscle is known to contain large amounts of a CBP of  $M_r = 21$  kDa (Tanaka et al., 1988), a finding also demonstrated in a control lane of Figure 5 (see below).

## Discussion

We have cloned a *Drosophila* gene homologous to the two known members of the calbindin subfamily of vertebrate CBPs. The presence of two signals in Northern blots suggests the alternative use of different polyadenylation signals located in the 3' non-translated region of cDNA 1 or differential splicing, although only one type of cDNA has been found so far. Sequence comparison of the cDNAs with genomic clones identifies 11 exons and verifies the cDNA sequence. A single large ORF codes for the inferred protein described here. Four arguments support the presumed specificity of the immunohistochemical stainings in Figures 5–9. (1) In Western blots the anti-CBN antiserum recognizes the cDNA-encoded peptide (not shown) and a single, brain-specific protein of electrophoretic mobility equivalent to  $M_r$  32 kDa (Fig. 5, lanes 1, 2). This value approximately corresponds to the calculated molecular weight of the predicted protein (35 kDa). (2) At the same  $M_r$  value, a CBP is detected in  $^{45}\text{Ca}^{2+}$  blots of brains but not of residual head tissue (Fig. 5, lanes 5, 6). The 32 kDa signal seen in the indirect flight muscle lane (Fig. 5, IFM, lane 4) may represent contaminating material from direct flight muscles (hg1 and hg2) incompletely removed during the preparation of indirect flight muscles from freeze-dried thoraces. The presence of a different CBP of similar molecular weight of course cannot be excluded. (3) All six antisera stain essentially the same structures [antisera against pure GST carrier cross-react with a few cells at a characteristic position between medulla and central brain, which may be hidden among the CBN-positive cells in preparations stained with antisera 2 and 3 (not shown)]. (4) At all stages of development we find a close correspondence between tissue *in situ* hybridization and immunohistochemical data.

We would like to discuss the identification and cloning in *Drosophila* of a new member of the calbindin subfamily of EF-hand CBP under two aspects, function and evolution.

At the molecular level the known function of calbindin D-28k and calretinin is their cytosolic  $\text{Ca}^{2+}$  buffering. However, the high conservation within the vertebrate radiation of the two proteins contrasting their divergence from other EF-hand CBPs suggests specific unknown additional properties (Rogers, 1991). Recent *in vitro* experiments in fact imply a role in stimulating a membrane  $\text{Ca}^{2+}$ -ATPase and a 3',5'-cyclic nucleotide phosphodiesterase for calbindin D-28k (Reisner et al., 1992) and in modulation of brain protein phosphorylation for calretinin (Yamaguchi et al., 1991).

For the cellular function of calbindin D-28k and calretinin in

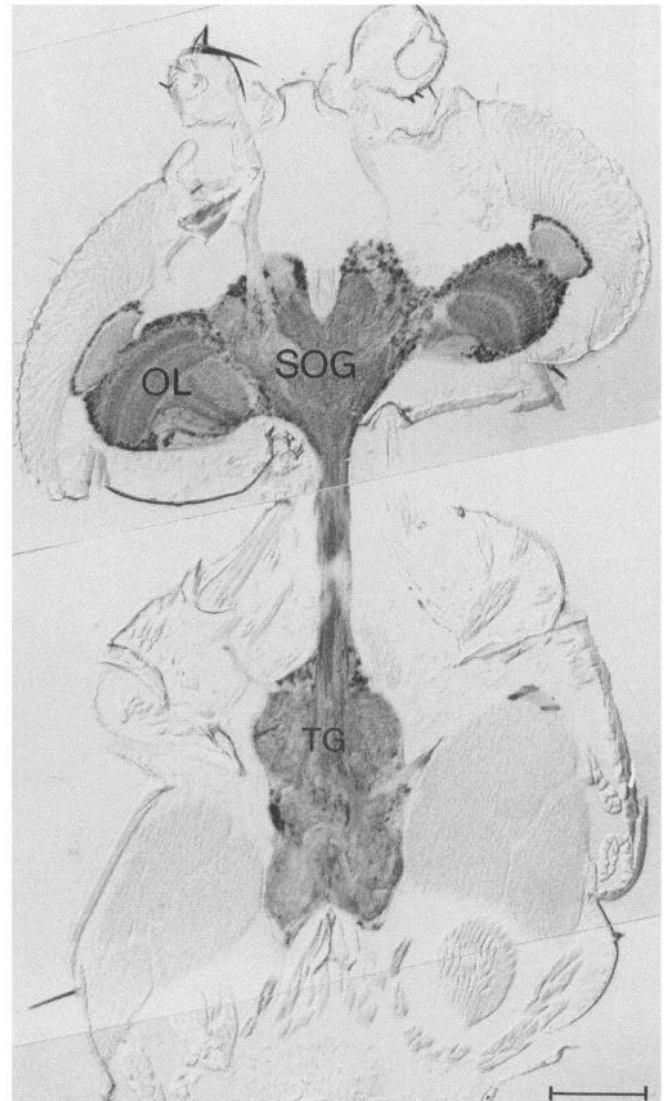
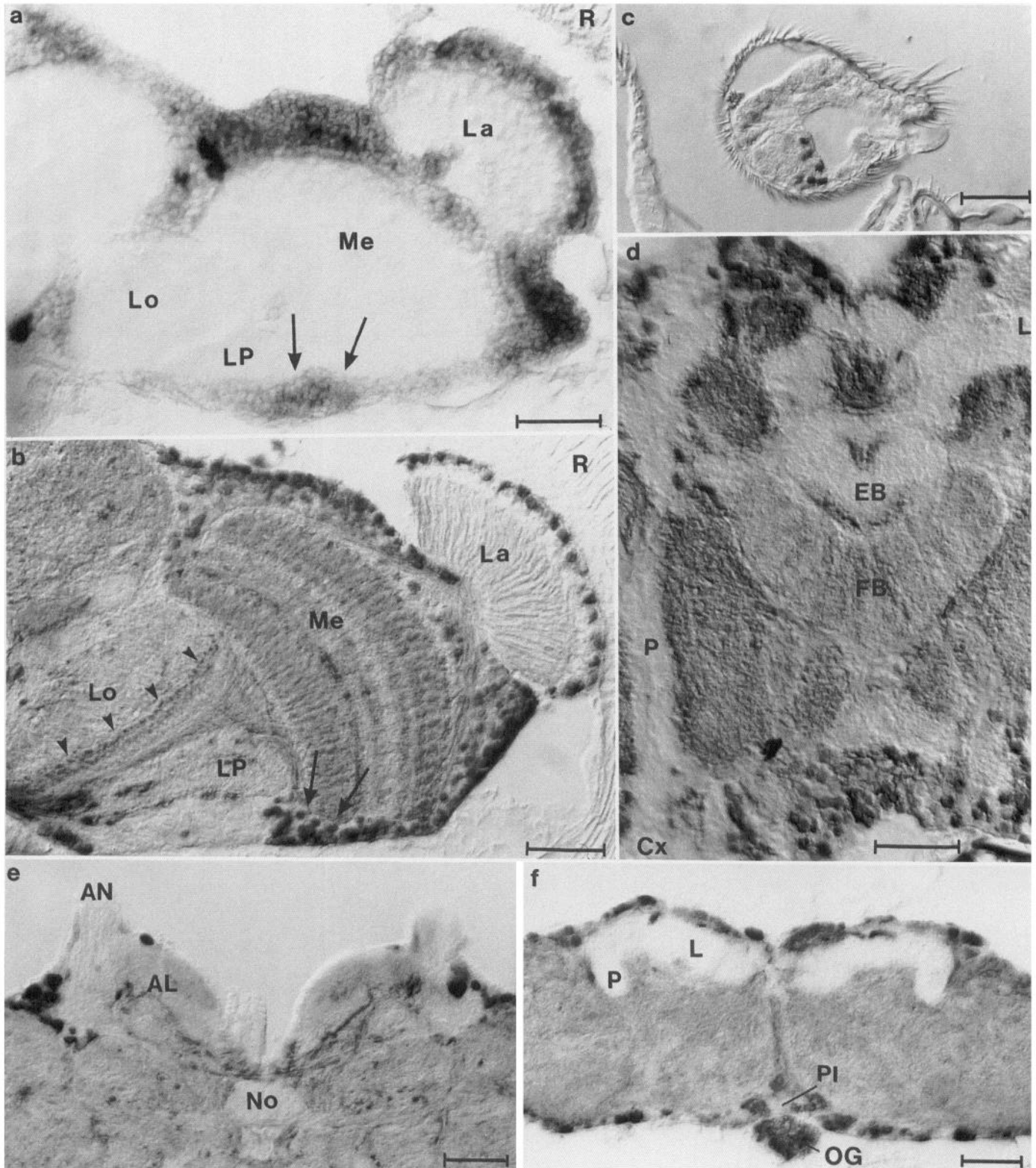


Figure 7. Overview of CBN distribution in a horizontal section through the imago at the level of the cervical connective. OL, optic lobes; SOG, suboesophageal ganglion; TG, thoracic ganglion. Scale bar, 100  $\mu\text{m}$ .

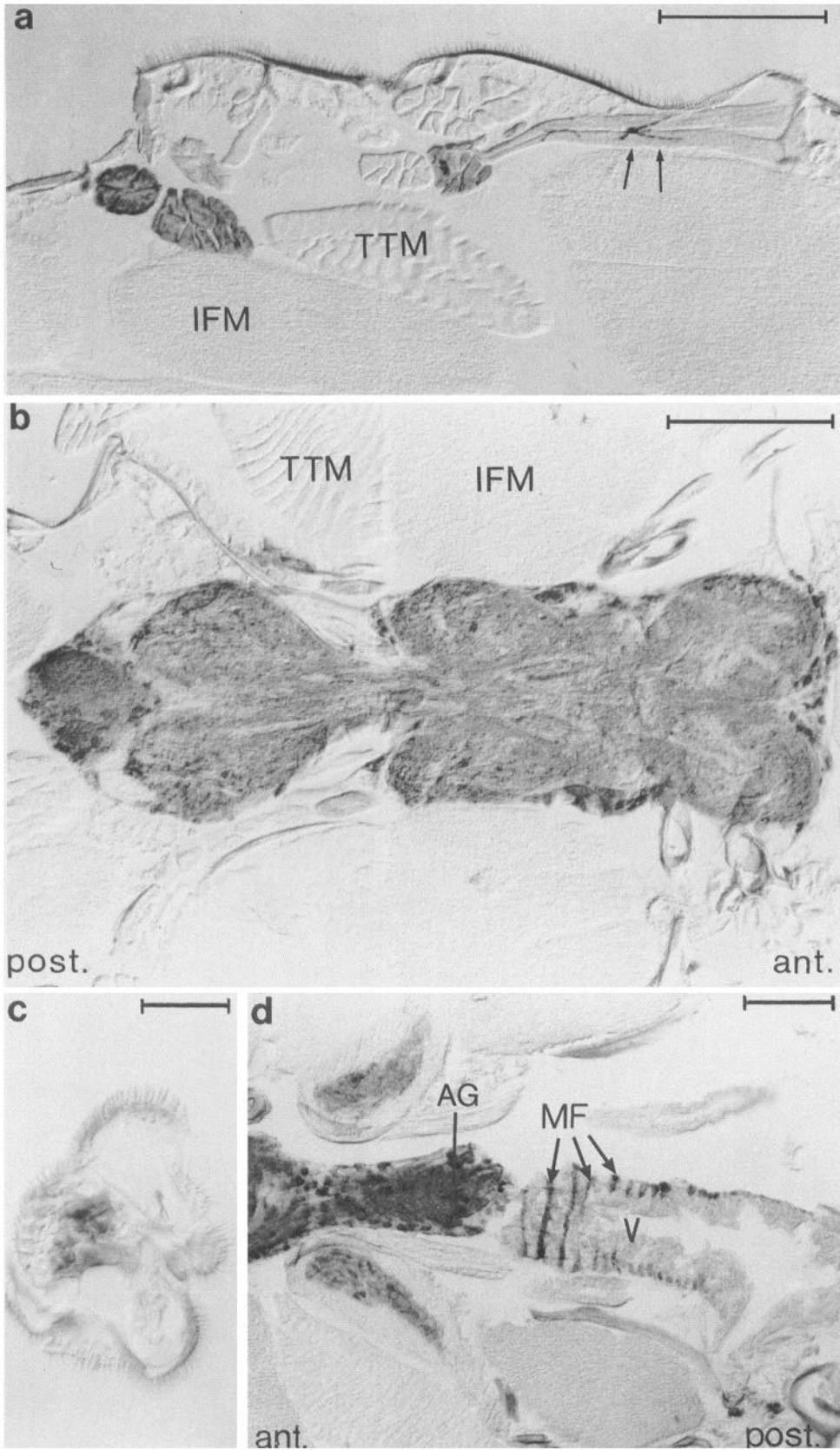
the nervous system, only vague hypotheses have been proposed on the basis of their rather selective distribution. On the other hand, calbindin D-28k is found also in renal and intestinal epithelia of many higher vertebrates where its synthesis is induced by 1,25-dihydroxy-vitamin  $\text{D}_3$  (Hunziker et al., 1983; Hunziker, 1986; Parmentier et al., 1987). In these tissues calbindin D-28k presumably mediates the vitamin D-dependent facilitation of transcellular transport of  $\text{Ca}^{2+}$  from the absorbing apical zone of the epithelial cells to the ATP-dependent  $\text{Ca}^{2+}$  pump at the basolateral membrane.

In the nervous system the  $\text{Ca}^{2+}$  buffering capacity of calbindin D-28k and calretinin has been speculatively associated with diverse functions such as neuronal development (Ellis et al., 1991) or maturation (Braun et al., 1991),  $\text{Ca}^{2+}$  current modulation (Jande et al., 1981), protection against hypoxic or excitotoxic damage (Baimbridge and Kao, 1988), or modulation of second messenger signalling (reviewed by Rogers, 1991). The two proteins are expressed in mostly separate cell populations, although examples of double-immunopositive cells have been





**Figure 8.** CBN expression in adult head. *a*, *In situ* hybridization using a digoxigenin-labeled *cbn* probe on frozen head section (optic lobe). *Arrows*, perikarya of presumed T2 and/or T3 interneurons. *b–f*, Immunohistochemical anti-CBN staining. *b*, optic lobes. *Arrows* and *arrowheads*, perikarya and terminals, respectively, of T2 and/or T3 interneurons. *c*, stained cells in the antenna. *d–f*, Immunostaining in the antennal lobes (*e*) and central brain (*d, f*) reveals differential distribution of CBN both in neuropil and in perikarya. Note the low level of staining in mushroom body calyces (*Cx*), peduncle (*P*), and lobes (*L*), as well as in the frontal part of the ellipsoid body (*EB*) and the noduli (*No*). In the antennal lobes (*e*) the patchy staining may outline individual glomeruli. Strong staining is found in many perikarya and in the ocellar ganglion (*OG*). *AN*, antennal nerve; *AL*, antennal lobes; *FB*, fan-shaped body of central complex; *La*, lamina; *Lo*, lobula; *LP*, lobula plate; *Me*, medulla; *PI*, pars intercerebralis; *R*, retina. Scale bars, 25  $\mu$ m.



**Figure 9.** CBN in thorax. *a*, Immunostaining of two small direct flight muscles (presumably hg1 and hg2) (Heide, 1971; Bausenwein, personal communication). A few other small muscles show weak staining. Note the staining of synaptic boutons on a small muscle sectioned tangentially (arrows). TTM and indirect flight muscle (IFM) never stain. *b*, CBN immunostaining of thoracic ganglion showing numerous CBN-positive cell bodies and structured neuropil. *c*, Stained cells in haltere. *d*, Slightly oblique section through dorsal cellular rind of abdominal ganglion (AG) and the ventriculus (V). The stained structures on the ventricular surface presumably are muscle fibers (MF). The inner portion of a pair of muscles located in the vicinity of the stained abdominal ganglion displays staining of unidentified structures. *ant.*, anterior; *post.*, posterior. Scale bars: *a* and *b*, 100 μm; *c* and *d*, 25 μm.

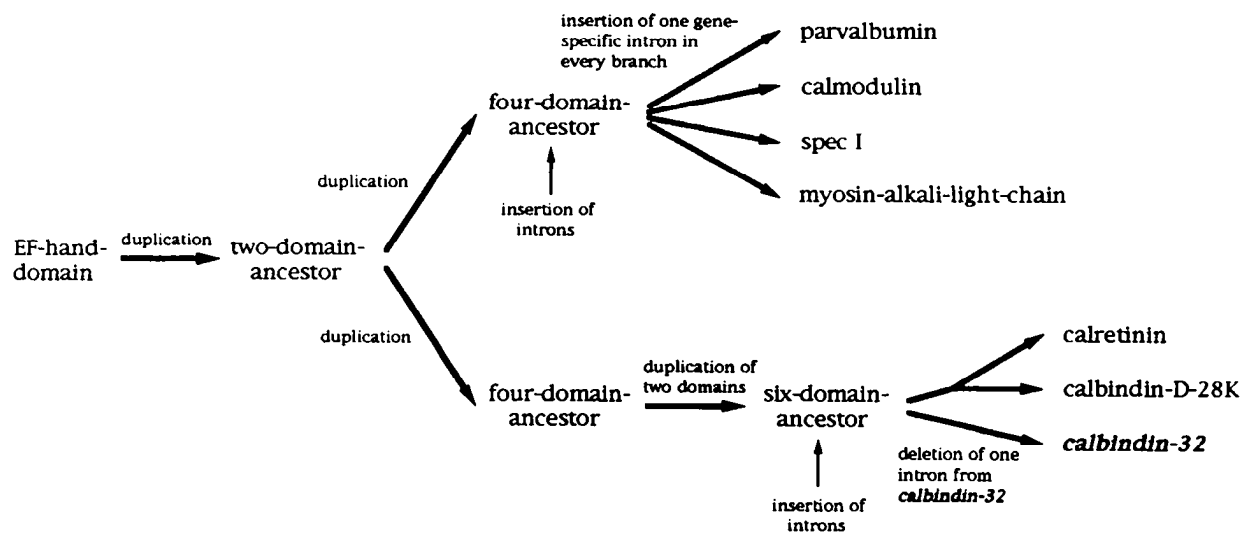


Figure 10. Possible evolutionary tree of calbindin subfamily. Modified after Wilson et al. (1988).

described (Rogers, 1989). In contrast to parvalbumin-expressing neurons and muscles, no common properties of calbindin D-28k- or calretinin-immunopositive cells have as yet been found, although there seems to exist a certain degree of complementarity both in the distribution and in functional aspects of parvalbumin- and calbindin D-28k-containing neurons (Braun et al., 1991; Ohm et al., 1991).

As is true for many brain molecules, a link between calbindin D-28k and Alzheimer's disease has been proposed on the basis of reduced numbers of calbindin D-28k-immunoreactive cortical neurons in postmortem brains of morbus Alzheimer patients (Ichimiya et al., 1988). Also, some forms of epilepsy may relate to calbindin D-28k expression (Sonnenberg et al., 1991). Abnormal levels or distribution of calbindin D-28k are associated with ischemia, Parkinson's disease, and Down syndrome (reviewed in Heizmann and Braun, 1992).

Evolutionary traits of a gene are reflected by sequence homologies and intron-exon structures. The fact that amino acid identity between CBN and calbindin D-28k/calretinin (37%/42%) lies in a range similar to the identity between calbindin D-28k and calretinin (57%) is compatible with the assumption of a gene duplication early in the vertebrate radiation. Of course, a more ancient duplication is also possible, as we cannot at present exclude the existence of other six-EF-hand-domain protein genes in *Drosophila*. On the other hand, the generation of the six  $\text{Ca}^{2+}$ -binding domains, presumably by exon duplication, surely dates back to before the phylogenetic separation of vertebrates and insects, considering the conserved exon-intron structure of *cbn*. Introns 3, 8, and 10 are situated between domains and may have aided in the presumed domain duplication. Since six out of seven introns within the  $\text{Ca}^{2+}$ -binding domains are conserved to the base from *Drosophila* to vertebrates but are found at different positions in each domain, intron insertion may have occurred subsequent to the formation of the six-EF-hand subfamily but before the separation of chordates and arthropods. Figure 10 supplements a phylogenetic tree proposed by Wilson et al. (1988).

The cloning in *Drosophila* of a new member of the calbindin subfamily that is selectively expressed in few muscles and numerous neurons not only sheds new light on the evolution of

the corresponding genes but also opens intriguing perspectives for the investigation of the function of this family of cytosolic CBPs in the nervous system. A powerful approach to the function of a *Drosophila* protein is the search for, or induction of, mutations in the corresponding gene. *Drosophila* data bases reveal no presently known mutations or chromosomal aberrations in region 53E where *cbn* is localized, although two protein kinase C genes have been shown to lie in 53E4-7 (Rosenthal et al., 1987; Schaeffer et al., 1989). Four P-strains with P hybridization signals in the 53E region are presently being tested for transposon insertion in the *cbn* walk. Independent of the outcome of these experiments, it has recently become possible to produce small deficiencies in the cloned *Drosophila* genes by several variants of "gene targeting" techniques (Ballinger and Benzer, 1989; Kaiser and Goodwin, 1990; Hamilton et al., 1991; Walter, 1992), such that mutations of the *cbn* gene may soon be available. The present work constitutes the basis for the mutant approach to brain CBP function.

In addition, in *Drosophila* it is possible by germ-line transformation to express a gene arbitrarily in defined sets of identified cells for which specific promoters have been cloned, for example, photoreceptors, or cholinergic, GABAergic, dopaminergic, serotonergic, or various peptidergic interneurons (cf. Buchner, 1991), and the functional consequences can be studied by electrophysiology, metabolic mapping, and behavioral analysis.

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