Molecular Cloning, Expression, and Mapping of the High Affinity Actin-capping Domain of Chicken Cardiac Tensin

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Abstract. Tensin, an actin filament capping protein first purified from chicken gizzard, is localized to various types of adherens junctions in muscle and nonmuscle cells. In this paper, we describe the isolation and sequencing of tensin cDNA from a chicken cardiac library. The 6.3-kb chicken cardiac tensin cDNA encodes an open reading frame of 1,792 amino acids. Mammalian cells transfected with the chicken tensin cDNA expressed a polypeptide of ~200 kD recognizable by antibodies to chicken gizzard tensin. The expressed protein was incorporated into focal adhesions and other actin-containing structures in the transfected cells. To map the domain associated with tensin's high affinity, barbed-end F-actin–capping activity, bacterially expressed recombinant fusion proteins containing various segments of tensin were prepared and assayed for activity. The results of these experiments show that the high affinity capping domain (kD = 1-3 nM) lies within amino acid residues R1037-V1169. Additional studies on a shorter construct, S1061-H1145, showed that these 85 residues were sufficient for producing complete inhibition of actin polymerization and depolymerization. While this active domain is located within that of the "insertin" sequence (Weigt, C., A. Gaertner, A. Wegner, H. Korte, and H. E. Meyer. 1992. *J. Mol. Biol.* 227:593–595), our data showing complete inhibition of polymerization and shift in critical concentration are consistent with a simple barbed-end capping mechanism rather than the "insertin model." Our results also differ from those of a recent report (Lo, S. H., P. A. Janmey, J. H. Hartwig, and L. B. Chen. 1994. *J. Cell Biol.* 125:1067–1075), which concluded that their recombinant tensin has an "insertin-like" inhibitory effect on barbed-end actin polymerization, and that this activity is attributed to residues T936–R1037 (residues 888-989 in their numbering system). In our study, a fusion construct (N790-K1060) encompassing T936-R1037 had no significant effect on actin polymerization and depolymerization, even at high concentrations.

ADHESION plaques (also referred to as focal adhesions), which are found at locations of cell–substrate contacts in various types of cells, are of great interest to cell biologists because of their roles in actin–membrane association, cell–substrate adhesion, and signal transduction (Burridge et al., 1988; Geiger, 1989; Luna and Hitt, 1992). One of the proteins found in these structures is tensin, a protein originally identified in chicken gizzard extracts (Wilkins and Lin, 1986; Wilkins, J. A., M. A. Risinger and S. Lin. 1987. *J. Cell Biol.* 105:130 [Abstr.]) and shown to interact with high affinity with the barbed ends of actin filaments in vitro (for brief reviews of early work on this protein, see Lin et al., 1989, and Lin, 1993). In addition to adhesion plaques, antibodies to tensin have also been shown to label other types of adherens junctions (Bockholt et al., 1992). These properties of tensin suggest that the protein plays a general role in maintaining tension (hence its name) in actin filaments by connecting them to other cellular structures (Lin et al., 1989; Lin, 1993).

The polyclonal antibody preparation to gizzard tensin used in the original localization studies (Lin et al., 1989) was also used to isolate a partial tensin cDNA clone from a chicken embryo fibroblast cDNA library (Davis et al., 1991). Sequence analysis of the clone indicated that fibroblast tensin contains an "src homology 2" (SH2)[1] domain (Davis et al., 1991), a functional motif found in many proteins involved in signal transduction (Koch et al., 1991; Shen et al., 1991; Pawson and Gish, 1992). In this paper, we describe the isolation and sequencing of 6.3 kb of cDNA encoding a functional tensin from a chicken cardiac cDNA library, the expression of the tensin cDNA in mammalian cells and in bacteria, and the identification of a short sequence containing high affinity F-actin capping activity.

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1. *Abbreviations used in this paper*: AH1 and AH2, actin homology domains-1 and -2, respectively; CEF, chicken embryo fibroblast; ORF, open reading frame; SH2, src homology 2.

Materials and Methods

Cell Culture

Human 293 embryonic kidney cells (Gorman et al., 1990), kindly provided by Dr. Jeremy Nathans (Department of Molecular Biology and Genetics, Johns Hopkins School of Medicine), were cultured in a 1:1 mixture of DME and Ham's F12 medium supplemented with 10% fetal calf serum. NIH 3T3 mouse fibroblasts were cultured in DME supplemented with 10% calf serum. Chicken embryo fibroblasts (CEFs) were grown as described by Vogt (1969). Cells were grown on glass coverslips for immunofluorescence studies.

Antibody Preparations

Affinity-purified polyclonal antibodies, designated as T(D), raised in a rabbit to a preparation enriched in chicken gizzard 165-kD tensin was used in the screening of the cDNA library. A mouse mAb, TL-1, was also prepared by using chicken gizzard tensin as antigen. This antibody is chicken specific, and it does not cross-react with anything in human or mouse cells. A preparation of polyclonal antibodies to actin homology domain-1 (anti-AH1), was raised in a New Zealand rabbit against a synthetic peptide (Peptide Synthesis Facility, Biology Department, Johns Hopkins University) containing the deduced amino acid sequence of M49-T78 of tensin, a region with 50% sequence identity to amino acid residues 221-249 of actin (see Results and Discussion for details). The anti-AH1 antibody preparation for immunoblotting was purified by affinity chromatography on a column of tensin fusion protein G52-S887 linked to Sepharose CL-4B. For localization of vinculin, mAb vin 11.5 (Sigma Chemical Co., St. Louis, MO) was used. FITC-conjugated sheep anti-mouse IgG was from Cappel Laboratories (West Chester, PA). Biotinylated donkey anti-rabbit IgG and streptavidin Texas red were from Amersham Corp. (Arlington Heights, IL). FITC-phalloidin was from Molecular Probes, Inc. (Eugene, OR).

cDNA Cloning and Sequencing

A cDNA library made in the lambda ZAP II vector (Stratagene, La Jolla, CA) from the mRNA of a single adult chicken heart was a gift from Dr. Douglas M. Fambrough (Department of Biology, Johns Hopkins University). The library was first screened with antitensin antibody preparation, T(D), using the picoBlue immunostaining kit (Stratagene) according to the manufacturer's instructions. Additional clones were isolated by screening with a ^{32}P-labeled short restriction fragment or combination of two restriction fragments as probes according to Benton and Davis (1977). Probes were labeled by the use of hexamer primers and Klenow enzyme (Feinberg and Vogelstein, 1983). DNA sequencing was performed with the dideoxy method of Sanger et al. (1977) using the Sequenase DNA sequencing kit from U.S. Biochemical Corp. (Cleveland, OH). cDNA clones and subcloned restriction fragments in pBluescript were sequenced from both ends. To facilitate sequencing, unidirectional nested deletions were made using the ExoIII/Mung Bean nuclease from Stratagene according to the method of Henikoff (1984). In addition to the M13 reverse and M13 (−20) sequencing primers, oligonucleotide primers (synthesized by the Oligonucleotide Synthesis Service, Johns Hopkins University) were used for the determination of tensin DNA sequence. Both double-stranded and single-stranded templates were used. The entire length of cDNA has been sequenced at least twice.

Northern Blots

Total RNA from various chicken tissues and cultured CEF was obtained by extracting in RNAxol according to the manufacturer's directions (Biotecx B Laboratories, Friendswood, TX). 30 μg of each RNA sample was separated by electrophoresis in formaldehyde-agarose gels in MOPS buffer (Lehrach et al., 1977) and transferred to an Immobilon-N membrane (Millipore Corp., Bedford, MA). Hybridization probes used for Northern blotting were labeled with ^{32}P by using the random primed DNA labeling kit (Boehringer Mannheim Biochemicals, Indianapolis, IN).

Eukaryotic Expression Constructs

Two eukaryotic tensin expression constructs were prepared with the pCIS vector (Gorman et al., 1990; kindly provided by Dr. Gorman, Genetech, South San Francisco, CA). The 3′ SphI-XhoI of JC43 was replaced by the 3′ SphI-XhoI fragment of JC42 to obtain JC97. The cDNA insert of JC97 was then released by double digestion with XbaI and XhoI, ligated with the XbaI- and XhoI-digested pCIS vector to yield JC101, which contains the full-length cDNA except nucleotides 1-154. The 5′ XbaI-BsmI region of JC97 was replaced with that of JC91 to yield JC98. The full-length cDNA was released from JC98 by digestion with XbaI-XhoI, and it was ligated into XbaI- and XhoI-digested pCIS to obtain JC100.

Expression of Cardiac Tensin in Mammalian Cells

Transient transfection of mammalian cells was performed essentially as described by Gorman et al., (1990). Briefly, cells were seeded on culture plates or glass coverslips and cultured overnight. 3 h before transfection, the growth medium was changed. The cells were cotransfected with 5 μg of tensin expression plasmid and 0.5 μg of pRSVT^s, using a calcium phosphate method, followed by a 15% glycerol shock step 3 h after transfection. The human 293 cells were shocked for 15 s, and the mouse 3T3 cells were shocked for 90 s. Transfected cells were incubated for 18 h before they were used for immunofluorescence studies.

Tensin Fusion Constructs

All fusion constructs encoding tensin deletion derivatives were cloned into pMAL (New England Biolabs, Beverly, MA) or pGEX (Pharmacia Fine Chemicals, Piscataway, NJ). In addition to pMAL-c2 and pMAL-cRI, a modified vector, pMAL-cRI*, prepared by ligating EcoRI-digested, Klenow-polished pMAL-cRI, was used to generate in-frame fusion of certain constructs.

The fusion constructs are prepared as follows: The BglII- HindIII fragment from JC42 was ligated into BamHI- and HindIII-digested pMAL-cRI* to produce the NH_2-terminal-truncated construct JC111 (I311-R1792). The BamHI-SalI fragment from JC43 was ligated into BamHI- and SalI-digested pMAL-cRI* to produce JC112 (G52-S887). KpnI digestion of JC111 produces JC131, which encodes the COOH-terminal fragment, V1191-R1792. The SacI-KpnI region from Tn3.2 was inserted into SacI- and KpnI-digested pMAL-cRI to produce JC130 (S1061-P1192). A 2.4-kb ApaI-MscI fragment obtained by limited digestion of ApaI-linearized JC130 with MscI was ligated into ApaI- and XmnI-digested pMAL-c2 producing JC137, the 109-amino acid construct (S1061-V1169) that was used in detailed studies on capping activity. The 2.45-kb NcoI-SacI fragment obtained by limited digestion of NcoI-linearized JC111 with SacI was inserted into NcoI- and SacI-digested JC137, producing JC140, the long construct (I311-V1169) used in detailed capping studies (see Fig. 8). The 2.26-kb ApaI-MscI fragment from JC130 was ligated into ApaI- and XmnI-digested pMAL-c2, producing JC138 (S1061-L11124). JC124, encoding S1061-R1792, was generated by inserting the SacI-HindIII fragment of JC97 into SacI- and HindIII-digested pMAL-cRI vector. JC125, encoding S1061-T1642, was generated by inserting the SacI-SalI fragment of JC97 into a SacI- and SalI-digested pMAL-cRI vector. JC126, encoding S1061-Y1521, was generated by inserting the SacI-SalI fragment of Tn3.2 into a SacI- and SalI-digested pMAL-cRI vector. JC128, encoding S1061-G1289, was made by deleting the NgoMI-XmaI region of JC125 and then ligating the compatible cohesive ends. JC142, encoding P1086-V1169, was prepared by inserting BglII-HindIII-digested cDNA fragment generated using the PCR product with oligonucleotides (aacgacggccggtgccaagc and gaagatctcctggagggaggcc) as primers and JC137 as template into BamHI- and HindIII-digested pMAL-c2. JC146, encoding R1037-V1169, was prepared by replacing the ApaI-XmaI region of JC140 with the ApaI-XmaI fragment of JC112. JC150, encoding R1037-E1149^P1162-V1169, is a deletion derivative of JC146 designed to remove the 12-amino acid residues absent in both the CEF tensin (accession No. M74165) and gizzard insertin (Weigt et al., 1992). It was prepared by PCR-amplified JC146 using malE primer and oligonucleotide sequence gctctagactgactcaacatagctcctgggctctccactg-ggtgcagcagg as primers, and the product was digested with KpnI and XbaI and inserted into the KpnI-XbaI region of JC140. Sequence encoding S1061-H1145 (JC151) was PCR amplified from JC150 with oligonucleotides tgtctagaattcagctcaccggag-cccggt and gctctagatcagtgcagcaggatgtcagctgg, and was digested with EcoRI and XbaI, and ligated with EcoRI-XbaI digested pMAL-cRI. The 2.2-kb EcoRI fragment from Tn3.2 encoding N790-Y1521 was cloned into EcoRI-digested pGEX-3X and designated as Tn2.2. The EcoRI-EcL136II fragment of Tn2.2 was cloned into EcoRI-digested pGEX-3X,producing a construct that encodes N790-K1060. Sequences of all of the DNA constructs prepared by PCR amplification, as well as the construct encoding N790-K1060, have been confirmed by direct sequencing.

Immunoprecipitation and Immunoblotting

CEFs were grown on 100-mm plates, and the lysate was made by extraction with RIPA buffer (Davis et al., 1991). The 293 cells, also grown on 100-mm plates, were extracted with buffer containing 10 mM phosphate, pH 7.2, 0.25% Tween 20, 0.1 M NaCl, 10 mM dithiothreitol, 10 mM of EDTA and EGTA, 1 μM leupeptin, 20 μM E-64, and 1 μM pepstatin A. After clarification, the NaCl concentration in 293 cell lysate was brought up to 0.5 M. Tensin in CEF and tensin expressed in transiently transfected human 293 cells were immunoprecipitated from cell lysates with mAb TL-1 conjugated to Sepharose CL-4B beads. Immunoprecipitated proteins were separated by SDS-PAGE (10% gel), transferred to Immobilon-P (Millipore Corp.), and probed with anti-AH1 antibody.

Immunofluorescence Staining

Cells were fixed and stained 18 h after transfection. Concentration of antibodies used were: TL-1, 1:500 dilution of ascites fluid; anti-AH1, 1:200 dilution of antiserum; IgG from T(D), 5 μg/ml; and vin 11.5, 1:200 dilution of ascites fluid. FITC-conjugated anti-mouse and biotinylated donkey anti-rabbit were used at 20 μg/ml. Samples stained with biotinylated antibodies were washed in phosphate-buffered saline and further incubated with Texas red-streptavidin at 20 μg/ml. For actin staining, FITC-phalloidin was added along with the Texas red-streptavidin. Fluorescence microscopy was performed on an IM35 microscope (Carl Zeiss, Inc., Thornwood, NY) equipped with 40× and 100× objectives. Photographs were taken with TMAX 400 film (ASA 800-1600) (Eastman Kodak Co., Rochester, NY).

Preparation of Tensin Fusion Proteins

MBP-tensin fusion proteins and GST-tensin fusion proteins were prepared and purified according to suppliers' instructions (New England Biolabs and Pharmacia, respectively). A protease inhibitor mixture (1 μM leupeptin, 0.3 μM aprotinin, 1 μM pepstatin, 20 μM E-64, and 0.1 μM pefabloc SC) was included in all buffers used during purification. Protein concentrations were determined with the method of Bradford (1976), with the following exception. The concentration of fusion protein I311-V1169 was estimated from the intensity of stained bands on immunoblots probed with mAb TL-1. In the case of fusion proteins R1037-E1149^P1162-V1169 and S1061-H1145, proteins eluted from affinity columns were further purified by ammonium sulfate precipitation and gel filtration chromatography (Superdex-70; Pharmacia LKB Biotechnology, Uppsala, Sweden, in 20 mM Tris-HCl, pH 8, 0.1 M KCl, 1 mM EGTA, 1 mM EDTA, 10 mM dithiothreitol, 1 μM leupeptin, 0.3 μM aprotinin, 1 μM pepstatin, 20 μM E-64, 0.1 μM pefabloc SC, and 0.2 mM PMSF) to remove the major degradative fragments. Quantitation of the final products was based on UV absorbance at 280 nm, using extinction coefficients of $6.856 \times 10^4\ M^{-1}\cdot cm^{-1}$ for R1037-E1149^P1162-V1169 and $6.6 \times 10^4\ M^{-1}\cdot cm^{-1}$ for S1061-H1145, as calculated from the amino acid sequence of the fusion proteins according to the method of Gill and Von Hippel (1989).

Actin Polymerization Assays

Actin was isolated from chicken breast muscle using established methods (Spudich and Watt, 1971), followed by chromatography on a Sephacryl S-200 column in buffer A. Labeling of the actin with pyrene was carried out as described (Kouyama and Mihashi, 1981). Samples of labeled or unlabeled G-actin were flash frozen in liquid nitrogen after column purification and stored at −80°. The frozen actin samples were quickly defrosted and spun at 100,000 *g* for 30 min immediately before use (Young et al., 1990).

In the actin polymerization assays, the concentration of G-actin (10% pyrene-labeled) was 0.5 or 2.0 μM in buffer A. F-actin, used as nuclei in the assays, was prepared by polymerizing 20–30 μM G-actin in buffer A containing 0.1 M KCl, 2 mM $MgCl_2$ (buffer F) for 30 min at room temperature or overnight at 4°C, and then diluting to 3 μM with buffer F and equilibrating for 2 h at room temperature before use. 1 min before the addition of F-actin nuclei, a 20× concentrated salt mixture was added to the G-actin to bring the salt concentration to 100 mM KCl, 2 mM $MgCl_2$ and 1 mM EGTA. Aliquots of F-actin were first mixed in a vortex mixer for 30 s, and then mixed with tensin fusion protein or an equivalent amount of buffer before adding to the G-actin to start polymerization. The initial rate of polymerization was measured by following the increase of fluorescence of the pyrene label at room temperature using a fluorescence spectrophotometer (650-10S; Perkin-Elmer Corp., Norwalk, CT).

In the actin depolymerization assay, 20–30 μM of G-actin (20% pyrene-labeled) was polymerized and further diluted to 3 μM and equilibrated as above. Samples of this pyrene-labeled F-actin were mixed in a vortex mixer for 30 s, and then mixed with tensin fusion protein for 10 s before adding to buffer F to initiate depolymerization.

To estimate the critical monomer concentration in the presence of tensin fusion proteins, 2 μM G- or F-actin was mixed with various concentrations of protein in buffer F. The amounts of G- and F-actins were calculated from pyrene fluorescence measured after 24 h.

Amino Acid Sequence Analysis

The amino acid composition, molecular weight, isoelectric point (pI), and the properties of tensin were analyzed with the use of the MacVector software package. For nucleotide and amino acid sequence searches and comparisons, the software program GENmenu was run on a VAX 8530 computer at The Johns Hopkins Medical School.

Results

Isolation and Sequencing of Chicken Cardiac Tensin cDNA

A LambdaZap II chicken cDNA library made from mRNA from a single adult chicken heart was initially screened with an affinity-purified polyclonal antibody preparation, T(D), raised to chicken gizzard 165-kD tensin. A single clone, Tn3.2, was isolated and shown to contain a 3.2-kb cDNA insert that produced a fusion protein recognizable by both T(D) and an mAb to chicken gizzard tensin (TL-1). Eight more clones were isolated from the same library with the use of three nucleotide probes derived from Tn3.2 (Fig. 1).

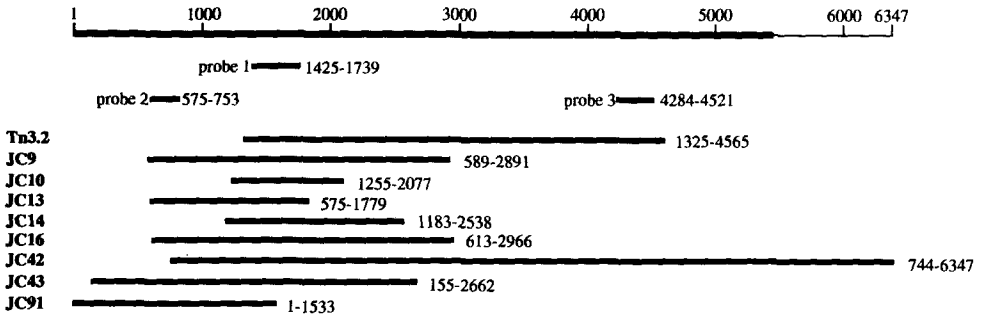


Figure 1. Tensin cDNA clones isolated from a chicken cardiac lambda ZapII library. A schematic diagram of tensin cDNA (nucleotides 1–6347) is shown at the top of the figure. The thick line marks the area of the open reading frame of tensin. Nucleotide 1 is the first nucleotide from the 5′ end of clone JC91, which is the clone that extends furthest at the 5′ end. Clone Tn3.2 was the first and only clone isolated with the use of affinity-purified polyclonal anti tensin T(D). ^{32}P-labeled 5′ ApaI-ApaI fragment of Tn3.2 (probe 1) was used to isolate clones JC9, JC10, JC13, JC14, and JC16 from the same cDNA library. A mixture of ^{32}P-labeled 5′ EcoRI-HaeII fragment of JC13 (probe 2) and 3′ HinfI-HinfI fragment of Tn3.2 (probe 3) were used for the isolation of clones JC42, JC43, and JC91. Alignment of the sequences of these overlapping clones resulted in the 6,347-nucleotide tensin cDNA as shown at the top of the figure.

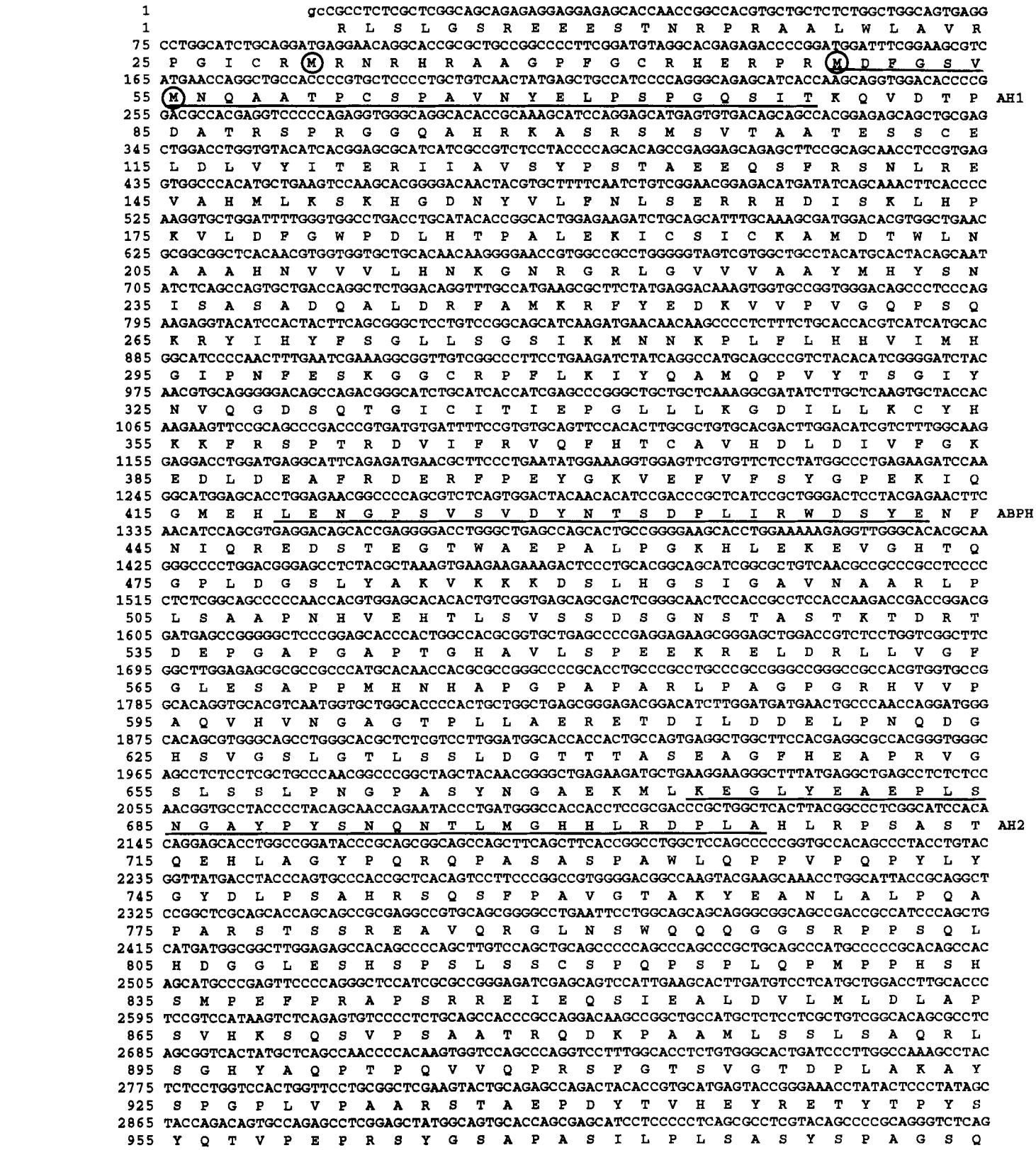


Figure 2. cDNA and deduced amino acid sequences of chicken cardiac tensin. The nucleotide (1–6347) and deduced amino acid sequences of the open reading frame (1,792 amino acid residues) of chicken cardiac cDNA are shown. The coding sequence is indicated by uppercase letters and the 5′ and 3′ noncoding sequences represented by lowercase letters. Actin homology domains (*AH1* and *AH2*), actin-binding protein homology domain (*ABPH*), as well as the *src* homology domain (*SH2*), are underlined. The area in which the high affinity actin filament capping domain is located (*cap*) is highlighted by dark shading.

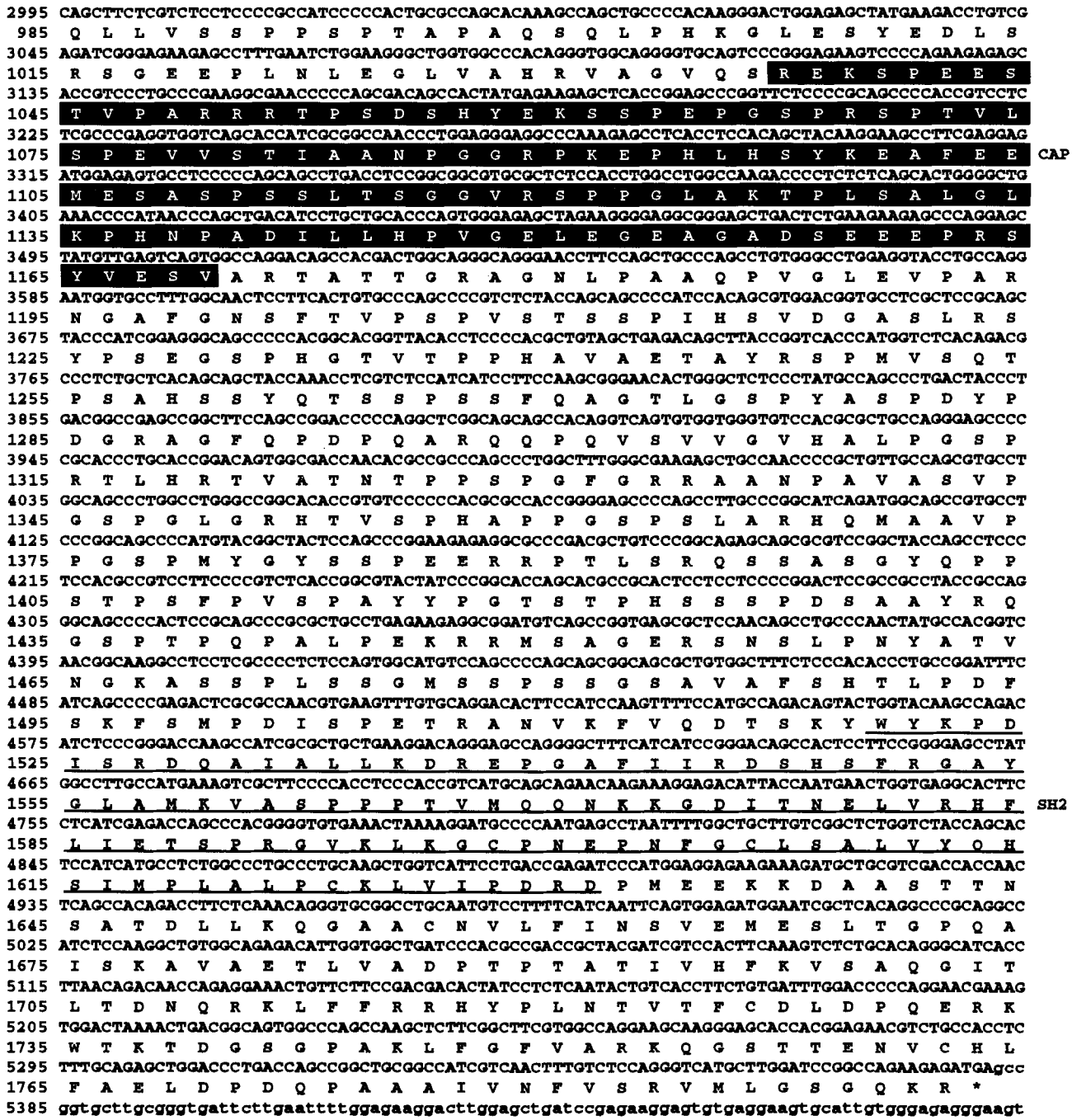


Figure 2.

Alignment of the sequences of the nine overlapping clones resulted in a composite tensin cDNA sequence of 6,347 nucleotides (Fig. 2). This sequence contains a single open reading frame (ORF) of 5,379 nucleotides, starting from nucleotide 3 and ending with the termination codon at nucleotide 5,381. Because cardiac tensin had not yet been isolated, and attempts to determine the NH_2-terminal of purified gizzard 215-kD tensin did not yield any useful information (presumably because of a blocked NH_2 terminus), the NH_2-terminal amino acid of cardiac tensin cannot be assigned at this time. To establish a point of reference, the arginine at the very beginning of the ORF is tentatively designated as amino acid residue 1 for cardiac tensin. The complete sequence of chicken cardiac tensin has been deposited in GenBank (accession No. L06662).

Examination of the amino acid composition deduced from tensin cDNA sequence indicated higher contents of proline (10.7%) and serine (11.9%) as compared to those of average vertebrate proteins (Doolittle, 1986). These high values are consistent with the results of amino acid composition analysis performed on 215- and 165-kD tensin isolated from chicken gizzard (Butler, J. A., and S. Lin, unpublished results). These two amino acids are unevenly distributed in the cardiac tensin sequence. Short stretches of high concentrations of proline or serine (20–30% of each) are found between amino acid residues 800 and 1,500. Of the 17 cysteine residues in the tensin sequence, all but one (C819) are distributed near the NH_2 or the COOH terminus of the molecule. The significance of these observations is not clear at this time.

The calculated overall pI of the entire ORF of cardiac tensin sequence was 7.94, whereas that of the sequence starting from M55 is 7.22. Analysis of pI by small sections (50 amino acids) of tensin sequence showed that the molecule can be divided into three domains on the basis of acidity. Both the NH_2-terminal and COOH-terminal portions of the molecule are highly basic (pI > 9), while the middle portion of the molecule (from amino acid residues 350–1,300) is highly acidic (pI of ~5). 41% of the amino acids in tensin are nonpolar, which falls in the range normal for nonmembrane proteins.

Unlike other large proteins such as dystrophin and spectrin, the amino acid sequence of tensin does not appear to be composed of repeated domains, except for four short stretches between residues 1,305 and 1,383 (Fig. 3).

Size and Distribution of Tensin mRNA in Chicken Tissues

Previous studies involving immunoblotting and immunofluorescence staining indicated that tensin is present at relatively high levels in fibroblasts, gizzard, intestine, and heart, and at lower levels in skeletal muscles, brain, and liver (Risinger, M. A., and S. Lin, unpublished results). For comparison at a different level, Northern blot analyses were performed on total RNA from various chicken cells and tissues, using a 3.2-kb probe corresponding to the cDNA insert of Tn3.2. As shown in Fig. 4, the probe hybridized to a 10-kb RNA species in samples from gizzard, heart, and CEF. In addition, an 8-kb RNA species was detected in the gizzard sample. All other tissues tested showed only a faint 10-kb band, suggesting lower levels of expression of tensin in these tissues. It is interesting that in all cases, the size of tensin RNA was much

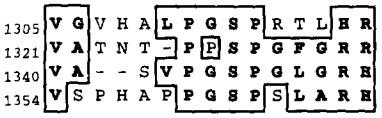


Figure 3. Repeated motifs in tensin sequence. The numbers at the left indicate the numbering of the first amino acid residues of each repeat in the tensin sequence. Homologous residues are outlined by the boxes.

larger than needed to encode a protein of 215 kD. Since the total length of cardiac tensin cDNA we have isolated so far is 6.3 kb, much of the noncoding sequences have apparently not been obtained.

Expression of Chicken Cardiac Tensin in Transiently Transfected Mammalian Cells

The 5,379 nucleotides of the ORF of chicken cardiac tensin cDNA can encode a polypeptide with a calculated molecular weight of 193,000. This value is somewhat less than the molecular weight of 215,000 estimated from the electrophoretic mobility of tensin from various tissues on SDS-polyacrylamide gels (Butler, J. A., and S. Lin, unpublished results).

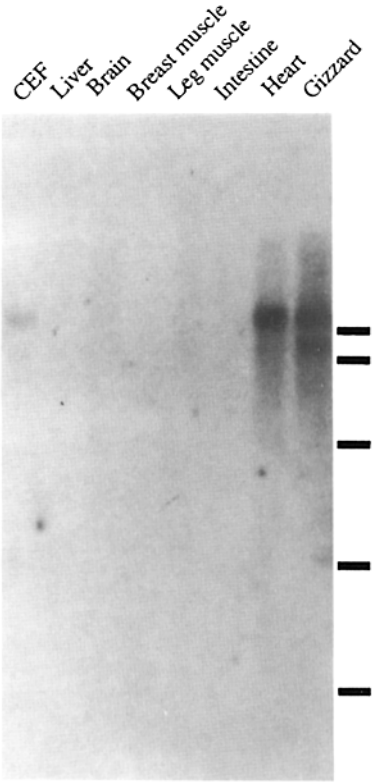


Figure 4. Detection of tensin transcripts in chicken tissues. On the Northern blot, samples of total RNA (30 μg) from chicken embryo fibroblasts (*CEF*) and chicken tissues as indicated were hybridized with a ^{32}P-labeled tensin probe (clone Tn3.2). The blot was washed under high stringency conditions and autoradiographed. The gizzard sample shows two bands of ~10 and 8 kb, while the heart and CEF samples show only the 10-kb band. Molecular sizes were estimated according to the migration of RNA ladder size markers, shown on the right (from top to bottom: 9.50, 7.50, 4.40, 2.40, and 1.35 kb).

For a more direct comparison of the size of the polypeptide encoded by the cardiac tensin cDNA with that of CEF tensin, human embryonic kidney cells (293 cells) were transfected with tensin cDNA. Protein expressed in the transiently transfected cells and in CEFs (serving as a control) was immunoprecipitated with mAb TL-1 and analyzed by SDS-PAGE followed by immunoblotting with polyclonal antibodies raised to a synthetic peptide with the deduced sequence of the AH1 domain (see Discussion for detailed description) of cardiac tensin. The immunoblots show that reactive polypeptides with similar electrophoretic mobility as CEF tensin (M_r ~215,000) were present in the 293 cell lysates prepared from both a full-length and a truncated (initiated from M55) tensin constructs, but not in the null-transfected 293 cell lysate (Fig. 5). This result shows that the coding region of the cardiac tensin cDNA we have obtained is probably complete, and that the AH1 region encoded by the nucleotide sequence near the beginning of the ORF was translated.

To test for biological activity of the cardiac tensin expressed in the human 293 kidney cells, immunolocalization experiments were performed. Over a background of nonspecific nuclear staining, filamentous structures in transfected 293 cells were brightly stained by the chicken-specific antitensin mAb TL-1 (an example is shown in Fig. 6 *a*). Furthermore, under conditions where the nontransfected cells showed only low levels of F-actin staining, the filamentous structures stained by TL-1 in transfected 293 cells were also brightly stained by phalloidin (compare Fig. 6, *a* vs *b*), suggesting that the expressed tensin promotes the formation of these actin filament bundles. Similarly, anti-AH1 antibodies also stained the structures stained by TL-1 in the expressed chicken tensin in the cells (Fig. 6, *c* and *d*).

Because human 293 kidney cells do not have well-defined focal adhesions, structures that have been shown in fibroblasts to be enriched in tensin (Lin et al., 1989; Lin, 1993) we extended the immunolocalization study on expressed cardiac tensin to mouse 3T3 fibroblasts. As shown in Fig. 7, *a* and *b*, while all cells in the field showed typical phalloidin-stained actin stress fibers, only the transfected cell in the center showed intense staining at the ends of stress fibers with mAb TL-1. Colocalization of tensin and vinculin in another double immunofluorescence staining experiment confirmed that the expressed chicken cardiac tensin was incorporated into the focal adhesions of the transfected cells (Fig. 7, *c* and *d*). These results indicate that certain functional domain(s) in tensin required for this type of cellular distribution is conserved across the different species and cell types studied here.

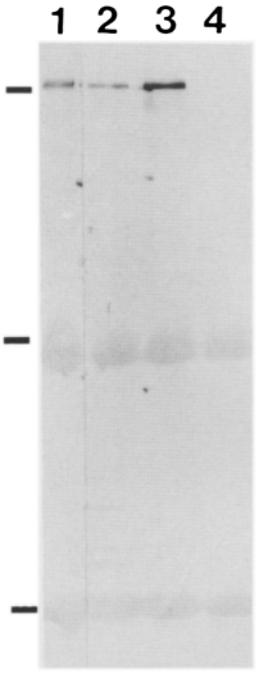


Figure 5. Determination of molecular weight of the cardiac tensin expressed in cells transfected with tensin eukaryotic expression constructs. Two constructs were made: one contains the entire tensin sequence and the other has a 154-nucleotide deletion at the 5′ end. The 3′ SphI-XhoI region of JC43 was replaced by the 3′ SphI-XhoI region of JC42. The cDNA insert of the resulting construct, JC97, was ligated into XbaI-XhoI–digested eukaryotic expression vector pCIS, and it was designated JC101. JC101 does not contain nucleotides 1–154, and it is initiated from M55, which is the third in-frame methionine. The full-length construct, JC100, was prepared by replacing the 5′ XbaI-BsmI region of JC97 with that of JC91, and ligating into XbaI-XhoI–digested pCIS. Human 293 cells were transiently transfected with the two expression constructs as described in Materials and Methods. Lane *1*, CEF; lane *2*, JC100-transfected 293 cells; lane *3*, JC101-transfected 293 cells; lane *4*, null-transfected 293 cells. Relative molecular mass markers are (from top to bottom) 200, 55, and 22 kd.

Studies on the High Affinity F-Actin Capping Domain in Tensin

Tensin isolated from chicken gizzard has previously been shown to have high affinity actin capping activity, reflecting a dissociation constant (K_d) for the barbed end of F-actin in the nanomolar range (Butler, J. A., and S. Lin, unpublished results). To locate the tensin domain responsible for this activity, a large number of fusion proteins from constructs containing different regions of tensin sequence were produced in bacteria and assayed for ability to inhibit barbed-end polymerization of pyrene-labeled actin (Fig. 8 *A*). In this survey part of the study, the fusion proteins scored "+" were able to reduce the initial rate of actin polymerization at the barbed end by >95% as compared to the control, while those scored "–" inhibited polymerization by <5%. As indicated in Fig. 8 *A*, fusion proteins containing the NH_2-terminal half of tensin up to residue K1060, which included regions of homology to actin and actin-binding protein sequences (see Discussion for details), had no significant activity. In contrast, all fusion proteins containing the COOH-terminal half (I311-R1792 and S1061-R1792) or the middle portion of tensin (I311-V1169 and N790-Y1521) were effective in inhibiting actin polymerization. Experiments on fusion proteins with further deletions showed that the high affinity actin capping domain definitely lies within the region of R1037-V1169. Furthermore, those from shorter constructs including S1061-V1169 and S1061-H1145 were also capable of complete inhibition of actin polymerization and depolymerization (see also Fig. 10 for additional data on the latter construct). In contrast, the region immediately adjacent to the NH_2-terminal side of the actin capping domain, N790-K1060, did not exhibit any significant activity (see also Fig. 10). Coomassie blue–stained gels of some of the fusion protein preparations purified by affinity chromatography or a combination of affinity and gel filtration chromatography were shown in Fig. 8, *B* and *C*. Most of the fusion proteins appeared to be proteolytically degraded, notably S1061-H1145, the shortest active fusion protein, while the inactive N790-K1060 appeared to be intact (Fig. 8 *C*).

Two of the fusion proteins from constructs that inhibited actin polymerization in the above experiments were studied in greater detail (Fig. 9). The first is from a long construct (I311-V1169), which also covers a region (L419-M443) homologous to the actin-binding domain found in a number of actin cross-linking proteins (see Fig. 2 and Discussion for details). The other fusion protein is from a short construct

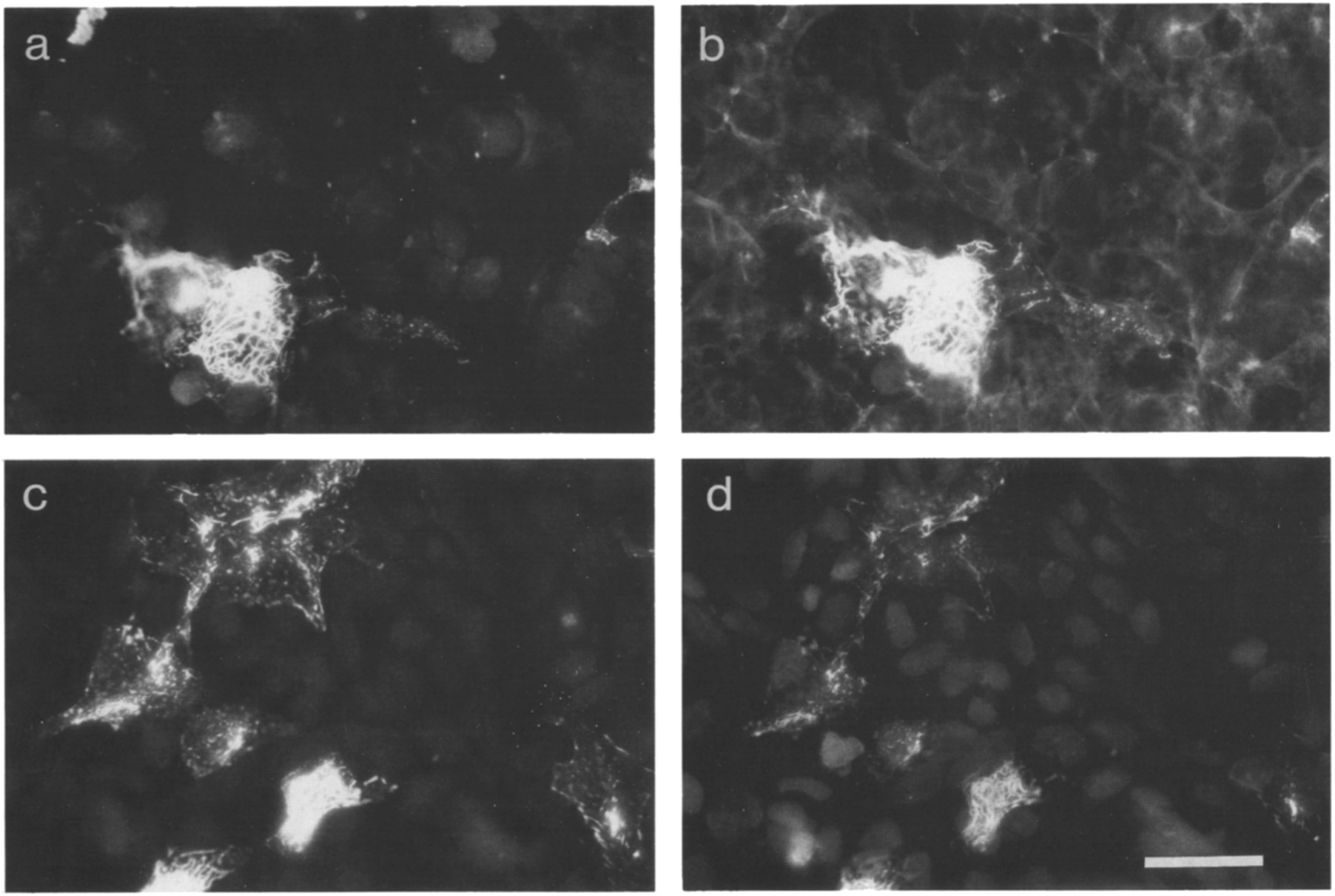


Figure 6. Immunolocalization of chicken tensin in transiently transfected human 293 cells. Cells transiently transfected with JC101 were double stained with mAb TL-1 for chicken tensin (*a* and *c*) and phalloidin for F-actin (*b*), or with anti-AH1 (*d*). In some cells, the expressed chicken tensin is localized to what appears to be adhesion plaques at the terminals of actin stress fibers (*c*), while in other cells, the expressed chicken tensin is colocalized with F-actin containing structures distinct from stress fibers (*a*). Bar, 150 μm.

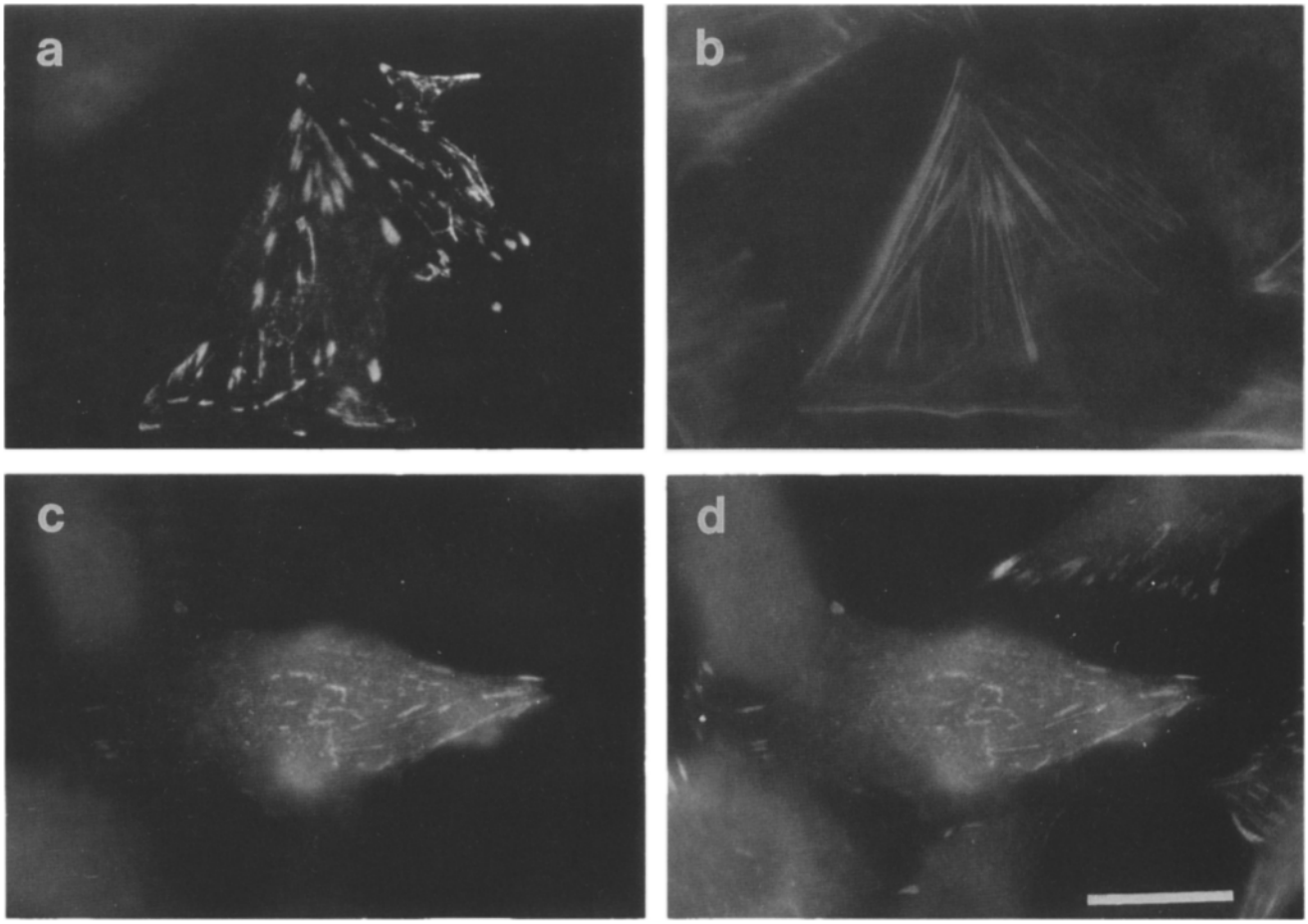


Figure 7. Colocalization of tensin with vinculin in transiently transfected mouse 3T3 cells. Cells transiently transfected with JC101 were double stained with TL-1 for the expressed chicken tensin (*a*) and phalloidin for F-actin (*b*), or they were double stained with polyclonal antibodies to tensin T(D) (*c*), and antivinculin (*d*). The micrographs showed that both polyclonal antibodies to tensin and mAb to vinculin-stained adhesion plaques in the transfected cells. Bar, 20 μm.

(R1037-E1149^P1162-V1169), which lacks the 12-amino acid stretch absent in the insertin sequence previously reported by Weigt et al. (1992) (see Discussion for details). In both cases, nanomolar concentrations of the proteins effectively inhibited actin polymerization under conditions where monomer addition was limited to the barbed end (at 0.5 μM G-actin); inhibition was essentially complete at the higher concentrations of fusion proteins used (Fig. 9, *A* and *D*). Analysis of the kinetic data from these polymerization experiments gave K_d's of ~1 and 3 nM for the long and short fusion proteins, respectively. Similarly, nanomolar concentrations of the two fusion proteins inhibited depolymerization of actin (Fig. 9, *B* and *E*). Furthermore, both proteins were capable of shifting the critical actin concentration from 0.1 μM to 0.5–0.6 μM (Fig. 9, *C* and *F*). All of these results are quite comparable to the K_d of 2–5 nM obtained with tensin isolated from chicken gizzard (Butler, J. A., and S. Lin, unpublished results), and with another actin capping protein isolated from chicken skeletal muscle (Casella et al., 1986).

After the completion of the above experiments and while this manuscript was in preparation, Lo et al. (1994*a*) reported the identification of T936-R1037 (888-989 in their numbering system) as the domain responsible for tensin's ability to inhibit actin polymerization. This apparent discrepancy between their conclusion and ours prompted us to carry out a side-by-side comparison of fusion proteins from three of our constructs: R1037-E1149^P1162-V1169, which had high affinity actin capping activity in the previous experiments (Fig. 9); a shorter construct, S1061-H1145; and N790-K1060, which encompasses the region of interest (T936-R1037) described by Lo et al. (1994*a*). In this set of experiments, activities were measured both by following polymerization of G-actin at concentrations below (0.5 μM) and above (2 μM) the critical concentration at the pointed end (0.8 μM under the salt conditions used in these experiments), as well as by following depolymerization of actin. As shown in Fig. 10 *A*, at 0.5 μM G-actin, R1037-E1149^P1162-V1169 and S1061-H1145 completely inhibited actin polymerization, whereas N790-K1060 did not have any appreciable effect. Similar results were obtained with the three fusion proteins in polymerization assays at 2 μM G-actin (Fig. 10 *B*). The residual level of actin polymerization observed in the presence of the two active fusion proteins under these conditions was presumably from monomer addition at the pointed ends of filaments. The lack of significant inhibitory effect by

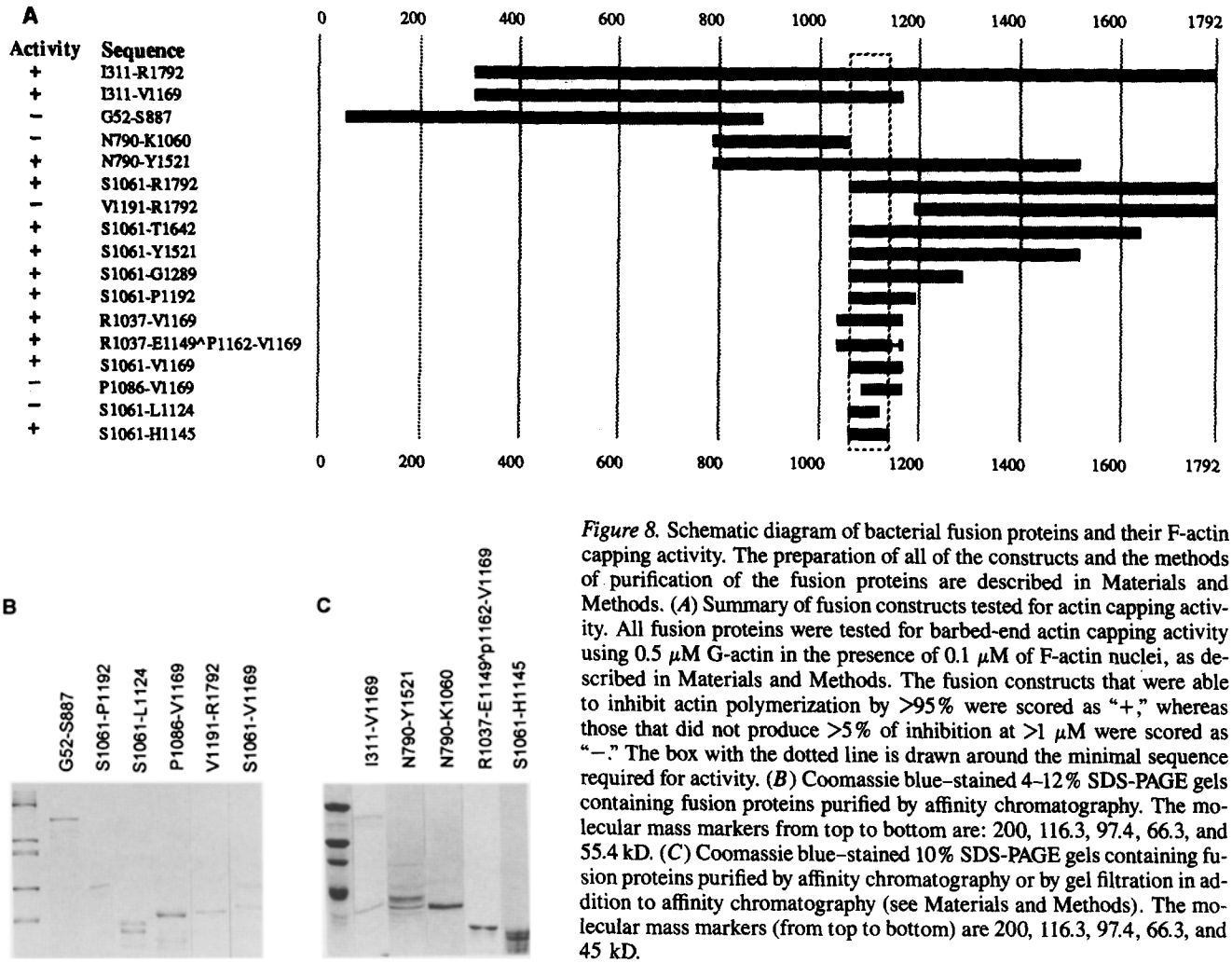


Figure 8. Schematic diagram of bacterial fusion proteins and their F-actin capping activity. The preparation of all of the constructs and the methods of purification of the fusion proteins are described in Materials and Methods. (*A*) Summary of fusion constructs tested for actin capping activity. All fusion proteins were tested for barbed-end actin capping activity using 0.5 μM G-actin in the presence of 0.1 μM of F-actin nuclei, as described in Materials and Methods. The fusion constructs that were able to inhibit actin polymerization by >95% were scored as "+," whereas those that did not produce >5% of inhibition at >1 μM were scored as "−." The box with the dotted line is drawn around the minimal sequence required for activity. (*B*) Coomassie blue-stained 4–12% SDS-PAGE gels containing fusion proteins purified by affinity chromatography. The molecular mass markers from top to bottom are: 200, 116.3, 97.4, 66.3, and 55.4 kD. (*C*) Coomassie blue-stained 10% SDS-PAGE gels containing fusion proteins purified by affinity chromatography or by gel filtration in addition to affinity chromatography (see Materials and Methods). The molecular mass markers (from top to bottom) are 200, 116.3, 97.4, 66.3, and 45 kD.

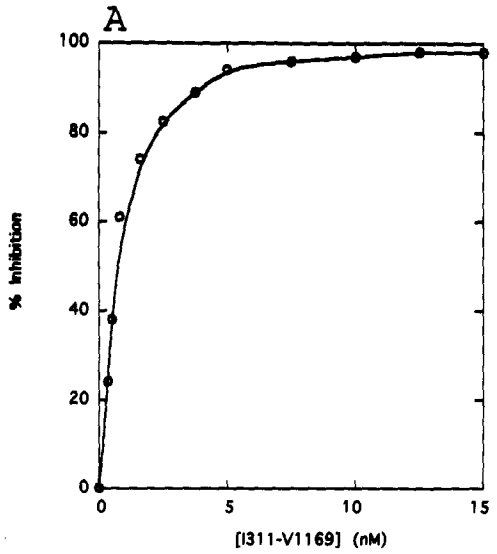
N790-K1060 was again demonstrated in an experiment in which R1037-E1149^P1162-V1169 and S1061-H1145 effectively blocked depolymerization of actin (Fig. 10 *C*). In conclusion, the high affinity actin capping domain of tensin is clearly within amino acid residues R1037-V1169 and not T936-R1037. Furthermore, although the presence of degradative products in S1061-H1145 (Fig. 8 *C*) precluded an accurate comparison of its specific activity with that of R1037-E1149^P1162-V1169, these experiments further narrow down the location of the essential sequence for capping activity to the 85 amino acid residues in tensin.

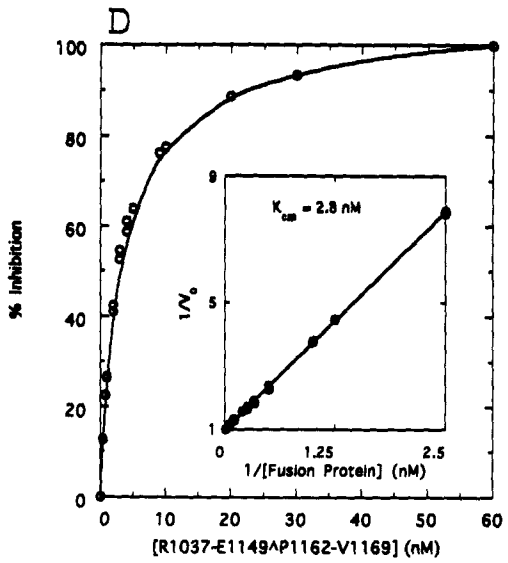
Discussion

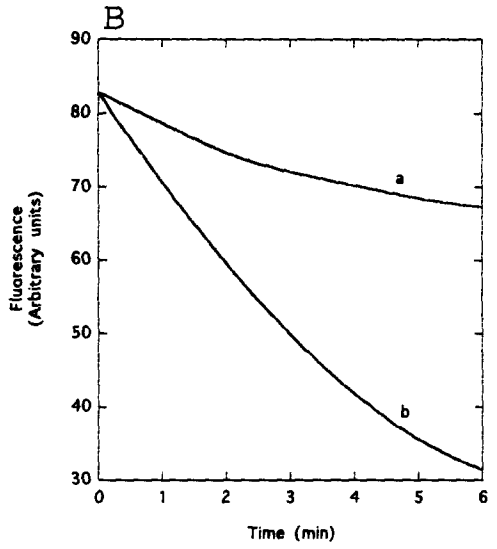
Several lines of evidence strongly support the authenticity of the cardiac tensin cDNA described here. First, the amino acid composition deduced from the cDNA is in good agreement with that of the 215-kD tensin purified from chicken gizzard (Butler, J. A., and S. Lin, unpublished results). Second, the cDNA was able to initiate translation of a polypeptide (M55-R1792) with similar electrophoretic mobility as that of CEF tensin on SDS-PAGE. Third, M55-R1792 and CEF tensin both reacted with polyclonal and monoclonal antibodies to gizzard tensin, as well as antibodies to the AH1 region (M49-T78) of the deduced sequence of cardiac tensin. Fourth, M55-R1792 was colocalized with vinculin to adhesion plaques of 3T3 cells. Finally, tensin fusion proteins exhibit all of the high affinity actin capping characteristics of purified gizzard tensin.

We do not yet know whether the total length of tensin cDNA we have isolated covers the complete sequence of the cardiac tensin molecule because the NH_2 terminus of the

Figure 9. Effects of tensin fusion proteins on actin polymerization and depolymerization. Conditions used for assays are described in Materials and Methods. For the polymerization assays, 0.5 μM of G-actin was used. (*A*) Inhibition of the rate of barbed-end actin polymerization in the presence of I311-V1169 at the indicated concentrations, expressed as the percent of inhibition as compared to the control sample where no tensin fusion protein was added. (*B*) Depolymerization of F-actin in the presence (*a*) or absence (*b*) of 10 nM of I311-V1169. (*C*) Effect of I311-V1169 on the critical monomer concentration of actin. (*D*) Inhibition of the initial rate of polymerization in the presence of R1037- E1149^P1162-V1169 at the indicated concentrations. Insert shows the graphical determination of dissociation constant for the interaction of the protein with the barbed ends of F-actin. (*E*) Depolymerization of F-actin in the presence of 100 nM (*a*), 10 nM (*b*), or absence (*c*) of R1037-E1149^P1162-V1169. (*F*) Effect of R1037-E1149^P1162-V1169 on the critical monomer concentration of actin.


A
% Inhibition
[I311-V1169] (nM)


D
% Inhibition
K_{as} = 2.8 nM
1/V_o
1/[Fusion Protein] (nM)
[R1037-E1149^P1162-V1169] (nM)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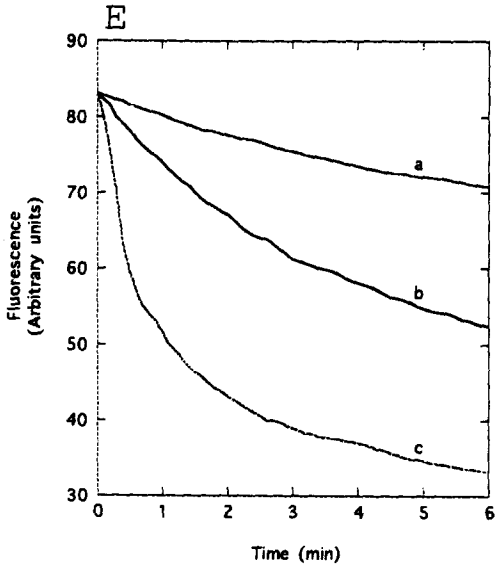
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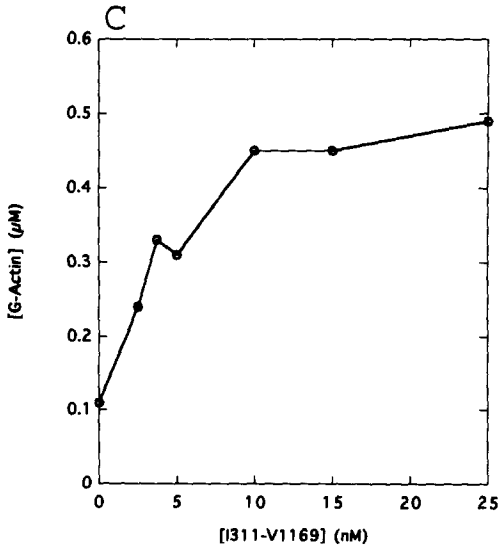
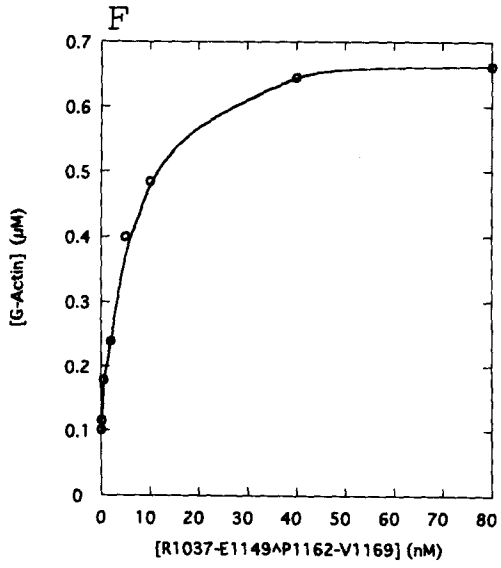

C
[G-Actin] (μM)
[I311-V1169] (nM)


F
[G-Actin] (μM)
[R1037-E1149^P1162-V1169] (nM)

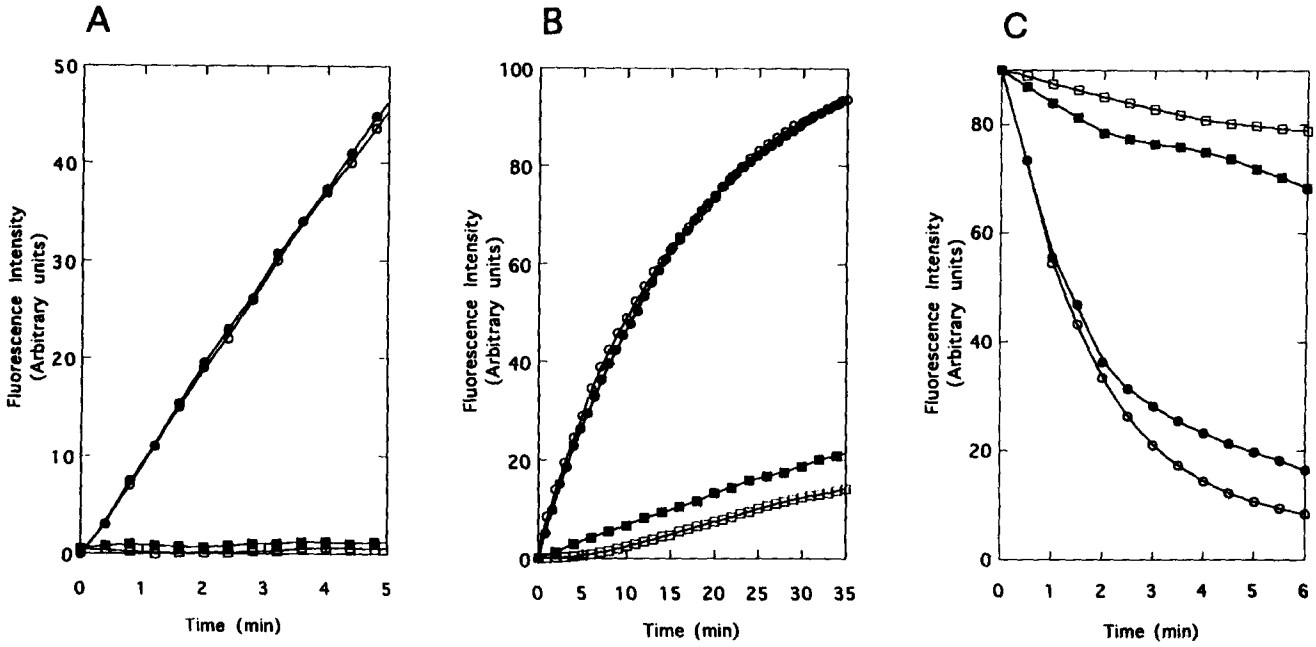


Figure 10. Direct comparison of the effects of three tensin fusion proteins on actin polymerization and depolymerization. The samples contained N790-K1060 (*filled circles*), R1037-E1149^P1162-V1169 (*open square*), S1061-H1145 (*filled square*), and the control (*open circle*). (*A*) Actin polymerization was measured at 0.5 μM of G-actin in the absence or presence of 0.5 μM N790-K1060, 90 nM R1037-E1149^P1162-V1169, or 1.8 μM S1061-H1145. (*B*) Actin polymerization was measured at 2 μM of G-actin in the absence or presence of 2.5 μM N790-K1060, 0.2 μM R1037-E1149^P1162-V1169, or 2.5 μM S1061-H1145. (*C*) Actin depolymerization in the absence or presence of the same concentrations of fusion proteins as in (*B*). Note that in these experiments, the concentrations given for S1060-H1145 are overestimates caused by the presence of substantial amounts of degradative products (see Fig. 8 *C*).

protein is unknown. However, the electrophoretic mobility of the immunoreactive polypeptide expressed in transfected cells indicates that the coding region of tensin cDNA should be close to full length. Since the size of chicken cardiac mRNA on Northern blots (10 kb) is larger than the 6.3 kb of tensin cDNA obtained in the present study, much of the noncoding sequence has clearly not been obtained. Recently, a 4.8-kb cDNA clone with sequences that overlap chicken cardiac tensin from nucleotides 4,550 to 6,347 was isolated from a chicken chondrocyte library (Van de Werken et al., 1993). The extraordinarily long 3′ noncoding sequence (4 kb) would make the total length of tensin mRNA ~10 kb.

The sequence of chicken cardiac tensin (GenBank accession No. L06662) has been compared to all other entries deposited in GenBank and in a report published after our sequencing work has been completed (Lo et al., 1994*b*). In general, our sequence is in good agreement with all other available tensin sequences, except for some minor discrepancies that might be artifacts of cDNA synthesis. However, two significant sequence variations were also detected. The more notable one is a stretch of 12 amino acids (L1150-E1161) in cardiac tensin that is not found in the CEF tensin (M74165) or gizzard insertin (Weigt et al., 1992; see below for details), a presumptive degradation product of tensin. This short segment in the cardiac tensin sequence is unlikely to be a cloning artifact because it was present in two independent cDNA clones (Tn3.2 and JC42), and it is present in the latest entry for chicken cardiac tensin from another laboratory (M96625; Lo et al., 1994*b*). The other notable variation is that the other tensin sequences (M96625 and M74165) lack the first 35 amino acids, including the first methionine, M30, in our ORF. This variation led Lo et al. (1994*b*) to designate M49 as the NH_2-terminal of their sequence. According to Kozak (1989), the requirement for a strong initiation site is having either A or G at position −3, and less importantly, G at position +4. M49 has G at the +4 position but C at the −3 position, making it less likely an initiation site. In contrast, both M30 and M55 have A or G at position −3 and A at position +4, making them more likely to be initiation sites. A 5′-deleted construct, in which the coding sequence for M30 and M49 was missing, expressed a polypeptide recognized by tensin antibodies in transfected 293 cells, suggesting that M55 can serve as an initiation site.

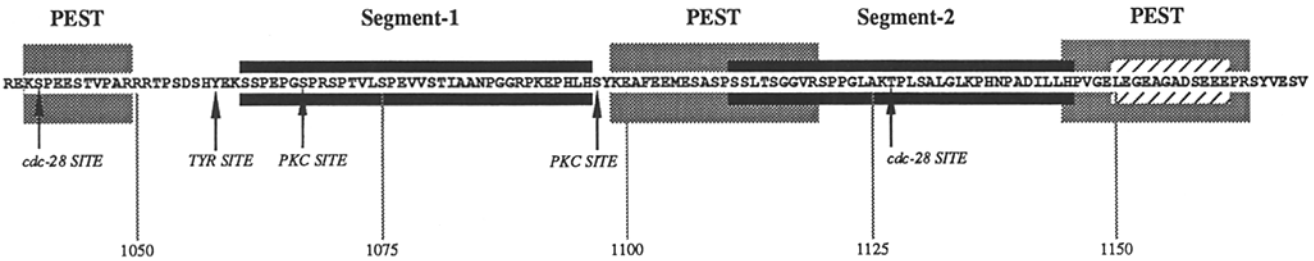
A most significant advance stemming from the molecular cloning work is our finding that a short sequence of ~120 amino acids (R1037-E1149^P1162-V1169) can produce all of the typical effects of a high affinity F-actin capping protein—complete inhibition of barbed-end polymerization with a K_d in the nanomolar range, inhibition of depolymerization, and shifting of critical monomer concentration. To our knowledge, this is the first time a single, short domain with comparable F-actin-capping activity as the native protein has ever been identified. Furthermore, experiments with the fusion protein containing S1061-H1145 showed that the sequence essential for capping activity can be reduced to 85 residues, although the presence of degradative products precluded an accurate comparison of its specific activity with that of fusion proteins with longer sequences.

Wegner and co-workers (Ruhnau et al., 1989) described a polypeptide designated as "insertin," with properties similar to a group of proteolytic fragments of gizzard tensin (HA1 peptides) previously reported by our laboratory (Wil-

kins and Lin, 1986). To explain why their preparation inhibited barbed-end actin elongation at a maximal level of 80%, they proposed a model in which insertin binds to one of the actin subunits at the end of a filament, inhibiting monomer addition to this subunit while allowing monomer insertion between this protein and the other actin subunit. The amino acid sequence of insertin has since been determined (Weigt et al., 1992). It is almost identical to the amino acid sequence of the CEF tensin sequence in the GenBank (accession No. M74165), and it is also missing the 12-amino acid stretch present in the region containing the high affinity capping domain of our cardiac tensin sequence. To test whether the absence of these 12 amino acids causes a change in mechanism from capping to "inserting," we made a construct (R1037-E1149^P1162-V1169) that lacks these residues. As stated above, we found that the fusion protein from this construct has all of the properties of a typical actin filament capping factor, completely inhibiting barbed end elongation and shifting critical concentration at substoichiometric concentrations. Our data, therefore, do not support the insertin model. It is possible that previous experiments on insertin were affected by such limiting factors as the extreme instability of the samples used (Ruhnau et al., 1989).

In the recent study of Lo et al. (1994*a*), fusion proteins from two short constructs (p27 and p11) containing sequences within the "insertin" sequence of Weigt et al. (1992) were prepared, and their effects on actin polymerization were studied. They concluded that the retardation of actin polymerization at the barbed-end, or "insertin," activity of tensin was associated with residues T936-R1037 (888-989 in their numbering system). In direct contrast to their conclusion, we found that a fusion protein (N790-K1060) that encompasses that particular region of the tensin molecule has no significant inhibitory activity on actin polymerization or depolymerization, even at high concentrations, while all fusion proteins containing the region S1061-H1145 had high levels of activity (Figs. 8–10). Since Lo et al. (1994*a*) showed only a single time course demonstrating partial retardation of polymerization rate by their fusion protein containing T936-R1037, their result probably reflects some effect unrelated to the high affinity actin capping activity described in this paper. Moreover, their study did not include any fusion protein that would allow them to test whether the sequence of R1037-V1169 has any effect on actin polymerization. It is also important to note that in their study, even the full-length recombinant tensin apparently had a K_d for interaction with the barbed ends of F-actin about an order of magnitude higher than the K_d's of 1 and 3 nM we obtained for I311-V1169 and R1037-E1149^P1162-V1169, respectively. Their model of tensin–actin interaction involving an "insertin-like" mechanism for explaining their results (incomplete inhibition of polymerization and no shift in critical monomer concentration) with their tensin preparations is also contradicted by the data presented in this paper.

Sequence analysis of the deduced amino acid sequence of the high affinity capping domain of cardiac tensin revealed a number of interesting features (Fig. 11). First, there is a tandem repeat (12 identical and 4 homologous residues out of 36) spanning S1061 to H1096 and S1111 to H1145. While the significance of this repeat remains to be determined, one possibility is that each of the repeat segments could bind one of the two actin subunits at the barbed end of an actin filament, thereby inhibiting monomer association and dissociation in a manner similar to that proposed for gelsolin (McLaughlin et al., 1993). Second, the overall cardiac tensin sequence is unusual in having nine PEST regions (Table I), conditional signals for rapid intracellular proteolysis found in many proteins involved in signal transduction (Rechsteiner, 1990). Of these nine regions, three are in the vicinity of the capping domain: one near the beginning, another at the middle between the repeats, and a third at the end of the capping domain. The third region, with 50% acidic residues, is of particular interest because it has the highest score of all of PEST regions in tensin, and it covers the 12 residues missing in CEF tensin and gizzard insertin. Third, within or close to the capping domain are several con-

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Tensin----1061 SSPEPGSPRSPTVLSPEVVSTIAANPGGRPKEPHLH 1169
               ||   |  |||  |    :| ::  |   | :  ||
Tensin----1111 SSLTSGGVRSPPGLAKTPLSALGLKP-HNPADILLH 1145
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Figure 11. Structural features and sequence homology in the vicinity of the tensin F-actin capping domain. Indicated in the diagram are the PEST regions (*dotted bars*), as well as the 12 residues missing in CEF tensin and gizzard insertin (*striped bars*). Also indicated are annotation of some of the amino acid residues (1,050, 1,075, etc.) and consensus phosphorylation sites for cdc-28 (*KSP* and *KTP*; Langan, 1978), tyrosine kinase (*RtpsDshY*; Cooper et al., 1984), and protein kinase C (*SpR* and *HSyK*; Kishimoto et al., 1985). The lower half of the figure shows sequence alignment of the repeated sequence in the tensin capping domain. Identical residues in the repeated sequence are connected by bars and conservative substitutions are connected by double dots. A Gap (−) was inserted for best alignment.

Table I. PEST Sequences of Cardiac Tensin

Residues	PEST sequence	PEST score
448-464	REDSTEGTWAEPALPGK	6.9
533-546	RTDEPGAPGAPTGH	5.0
610-625	RETDILDDELPNQDGH	5.6
947-962	RETYTPYSYQTVPEPR	4.9
1039-1049	KSPEESTVPAR	7.0
1099-1119	KEAFEEMESASPSSLTSGGVR	3.3
1145-1163	HPVGELEGEAGADSEEEPR	12.2
1258-1287	HSSYQTSSPSSFQAGTLGSPYASPDYPDGR	5.4
1433-1446	RQGSPTPQPALPEK	1.4

PEST sequences are identified by using the PEST-FIND computer program developed by Rogers, and PEST scores are calculated as described (Rogers et al., 1986). To qualify as a PEST sequence, the PEST score value has to be −5.0, and a PEST score >0 indicates a strong PEST region.

sensus phosphorylation sites, including two for cell cycle-dependent kinase (cdc-28), two for protein kinase C, and one for tyrosine kinase. These sites may be relevant to the reports that the dynamic assembly of the actin cytoskeleton at junctional complexes are associated with the cell cycle and the activities of protein kinase C and tyrosine kinase (Luna and Hitt, 1992). Finally, within the capping domain are sequences that show some similarity to those found in a number of proteins that interact with actin (villin, gelsolin, dystrophin, radixin, CapZ, yeast capping protein, and 25-kD inhibitor of actin polymerization) (Vandekerchhove and Vancompernolle, 1992). It will be interesting to see whether future research will show that all of these homologous regions represent motifs involved in binding to actin.

In addition to the ones within the capping domain, cardiac tensin also contains sequences in other parts of the molecule that are homologous with those found in other cytoskeletal proteins. The first is a SH2 domain (Fig. 2, *W1520-P1628*), which is identical to the one previously found in the sequence of chicken embryo fibroblast tensin (Davis et al., 1991). The second domain (M49-T78), designated here as "actin homology 1" (Fig. 2, *AH1*), shows ~50% identity to the amino acid residues 221-249 in the sequence of actin. This region of actin is located at the "pointed end" of the molecule (Holmes et al., 1990). Evidence supporting the involvement of this region in actin polymerization came from a study showing that a mutant actin produced by point mutation changing the glycine 245 to aspartic acid polymerized poorly (Taniguchi et al., 1988). This glycine residue is conserved in the AH1 domain of the tensin sequence. A third domain (L673-H707), designated as "actin homology 2" (AH2 in Fig. 2), shows significant homology to residues 291-321 of the actin sequence. Residues G302, T303, M305, and Y306 in this region of actin apparently participate in the binding of ADP and ATP (Holmes et al., 1990). Moreover, recent studies with cytochalasin B-resistant mutant KB cells showed that A295 and V139, located at the "barbed end" of the actin molecule, are involved in cytochalasin binding (Ohmori et al., 1992). All of the above-mentioned amino acid residues in actin are conserved in the AH2 domain of tensin. A fourth domain (L419-N443), designated as "actin-binding protein homology" (Fig. 2, ABPH), showed similarity to the actin-binding domain found in a class of dimeric actin filament cross-linking proteins, which includes spectrin, dystrophin, α-actinin, ABP120, as well as fimbrin, plastin, and ABP-280 (Bresnick et al., 1990, 1991). The recent report of Lo et al. (1994*a*) shows that fusion proteins containing this region of tensin has F-actin-binding activity in a cosedimentation assay. These observations are consistent with our finding that proteolytic fragments of chicken gizzard tensin promotes formation of actin filament bundles in in vitro (Wilkins and Lin, 1986) and that transfection of mammaliam cells with cardiac tensin cDNA causes an increase in such structures (Fig. 6).

In conclusion, the results reported here provide a basis for the understanding of how tensin binds with high affinity to the barbed ends of actin filaments. By acting as a direct link between filament ends and other cellular components, tensin could play an important role in force transmission at various types of cell-substrate and cell-cell junctions. These findings, together with previous findings that tensin has an SH2 domain and undergoes phosphorylation during changes of physiological states (Davis et al., 1991; Bockholt and Burridge, 1993), suggest that the protein plays an important role both in the association of actin filaments with other cellular structures and in signal transduction.

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