Identification and Analysis of Discrete Functional Domains in the Pro Region of Pre-Pro-Transforming Growth Factor Beta 1

Xue Sha,* Li Yang,‡ and Larry E. Gentry*

*Department of Biochemistry and Molecular Biology, Medical College of Ohio, Toledo, Ohio 43699-0008; and ‡Department of Biochemistry, University of Illinois, Urbana-Champaign, Illinois 61801

Abstract. A series of site-specific insertion and deletion mutants was prepared in the pro domain of transforming growth factor $\beta 1$ (TGF$\beta 1$) encoded by simian TGF$\beta 1$ cDNA. These mutants were transiently expressed in COS-1 cells and the ability of each to be properly processed, folded correctly, and secreted was determined by immunoblot analysis of cells and culture supernatants. Insertions in regions corresponding to amino acid residues 50, 154, and 170 blocked secretion; culture supernatants from COS-1 cells showed no immunologically reactive proteins, whereas intact cells contained high levels of the mutant polypeptides. Insertions in the middle portion of the pro domain at residues 81, 85, and 144 affected disulfide maturation of the mature TGF$\beta 1$. An insertion at residue 110, on the other hand, appeared to destabilize the mature TGF$\beta 1$ polypeptide, resulting in degraded growth factor. Relatively small (10 amino acids) to large (125 amino acids) deletion mutations in the pro domain of TGF$\beta 1$, when expressed as the full-length pre-pro-TGF$\beta 1$, appeared to block secretion. By contrast, if the pro domain (designated $\beta 1$-latency-associated peptide [$\beta 1$-LAP]) was expressed independently, deletion mutants in the region 40–110 were readily secreted by the COS-1 cells, whereas deletions in residues 110–210 either destabilized the structure of the protein or blocked its intracellular transport. Cross-linking assays employing radioiodinated TGF$\beta 1$ and biological assays indicate that residues 50–85 of $\beta 1$-LAP are required for association with mature TGF$\beta 1$.

TRANSFORMING growth factor-beta-1 (TGF$\beta 1$)[1] is a potent regulator of cell growth and differentiation (Roberts and Sporn, 1988, 1990; Barnard et al., 1990). Following the initial purification and characterization of TGF$\beta 1$ as a homodimeric, 24-kD polypeptide (Assoian et al., 1983; Frolik et al., 1983; Roberts et al., 1983), several distinct but related TGFβ family members have been cloned and analyzed by cDNA sequencing (Derynck et al., 1985, 1988; deMartin et al., 1987; ten-Dijke et al., 1988; Hanks et al., 1988; Jakowlew et al., 1988*a,b*; Madisen et al., 1988), indicating that they share similar structural properties. These novel TGFβs are encoded as large precursors and each is processed from the carboxyl-terminus of its precursor by proteolytic cleavage. The mature TGFβs all show considerable sequence similarity (~80%) and contain nine cysteine residues which can be perfectly aligned in sequence. The pro domains of each precursor contain three aligned cysteine residues as well as several sites for N-linked glycosylation. Since the pro portions of each precursor show less sequence similarity (<50%), each form of the growth factor may be secreted and activated differently.

Studies on posttranslational modification and processing of the TGF$\beta 1$ precursor have been derived from sequence analysis of cDNA clones (Derynck et al., 1985, 1986; Sharples et al., 1987) and from the high-level expression of these proteins in CHO cells (Gentry et al., 1987, 1988, 1989); these studies have indicated that a signal sequence of 29 amino acids is removed from the amino-terminus between Gly-29/Leu-30 (Gentry et al., 1988). Glycosylation occurs at all three predicted N-linked sites within the pro region followed by phosphorylation at mannose residues of the attached oligosaccharides (Purchio et al., 1988; Brunner et al., 1988). At some stage during synthesis or transit, proteolytic cleavage at dibasic residues and disulfide bond formation occur and the mature growth factor is released (Gentry et al., 1988). The precise order of the processing, and the pathway of the intracellular routine of TGF$\beta 1$ precursor have not been characterized.

The independently expressed pro domain of TGF$\beta 1$, when cotransfected with the mature TGF$\beta 1$, aids in the folding of the growth factor within the cell resulting in a small percentage of secreted, mature TGF$\beta 1$ (Gray and Mason, 1990). Furthermore, the pro portion of TGF$\beta 1$ represents a functional binding protein for mature TGF$\beta 1$ (Gentry et al., 1987; Miyazomo et al., 1988; Wakefield et al., 1989; Gentry and Nash, 1990). The dimer of this pro domain, termed $\beta 1$-latency–associated peptide ($\beta 1$-LAP), appears to be important for its biological function (Brunner et al., 1989; Gentry and Nash, 1990). The resulting latent form may then be acti-

1. *Abbreviations used in this paper*: LAP, latency-associated peptide; TGF$\beta 1$, transforming growth factor $\beta 1$.

vated by extreme pH values, by heat, or by treatment with selected chaotropic agents or proteases (Lawrence et al., 1985; Pircher et al., 1986; Lyons et al., 1988, 1990; Gentry and Nash, 1990). These results suggest that the TGFβ1 pro domain serves an important role in disulfide folding of mature TGFβ1 and latent complex formation.

As an initial step towards understanding the mechanisms by which cells control TGFβ1 activities, we undertook a systematic dissection of the pro domain of TGFβ1 by site-specific insertion and deletion mutagenesis. Our approach was to place a unique 12-mer oligonucleotide at specific restriction sites in the pro domain of TGFβ1, resulting in the in-frame placement of four amino acids. Such insertions should disrupt the local protein structure and allow our assignment of functional regions. The mutant TGFβ1 molecules were transfected in COS-1 cells and the proteins were identified by immunoblotting and then analyzed for proteolytic processing, secretion, and disulfide maturation. We found by these approaches that the structural integrity of the pro region, when expressed as pre-pro-TGFβ1, is essential for secretory exit of mature and precursor forms of TGFβ1 from cells. Several insertions resulted in mutants of TGFβ1 precursors which were not secreted, while insertions at other sites resulted in high levels of disulfide-linked TGFβ1 aggregates, indicating that mature TGFβ1 was not properly folded at disulfide bonds. Independently expressed deletion mutants of β1-LAP reveal that the amino-terminal portion of the pro region is involved in noncovalent association of the mature TGFβ1 to form a latent complex.

Materials and Methods

Cell Culture Condition

COS-1 cells (ATCC CRL 1650), a simian fibroblast cell line transformed by an origin-defective mutant of SV40, and mink lung epithelial cells (ATCC CCL 64) were grown in DMEM supplemented with FBS (10% vol/vol), penicillin (100 U/ml), and streptomycin (100 μg/ml). These cells were passaged by treatment with 0.5% (wt/vol) trypsin (Gibco Laboratories, Grand Island, NY) at a 1:5 splitting ratio.

Mutagenesis

The basic strategy used to construct a series of in-phase linker insertion mutations in the pro region of TGFβ1 peptide was based on the method of Stone et al. (1984). The pUC19-TGFβ1 vector DNA was linearized at RsaI, AluI, or BstUI restriction sites in the pro domain of TGFβ1 by employing ethidium bromide to limit the restriction endonuclease cleavage reaction (Stone et al., 1984). The nonphosphorylated dodecanucleotide linkers 5'-d(GGAAGATCTTCC) were inserted into the linear DNA by linker tailing (Lathe et al., 1984), resulting in the insertion of only one oligonucleotide linker specifying a unique BglII recognition sequence. The insertion mutations resulted in the in-frame placement of four amino acids within the coding region of the precursor of TGFβ1. Out of a total of 13 restriction sites, we prepared 12 insertion mutants throughout the pro region of TGFβ1. The insertion mutants were designated In, followed by the position of the first codon containing nucleotide derived from the inserted oligomer. These insertion mutants and amino acid changes due to the insertions are shown in Fig. 1 and Table I. All plasmids carrying a single BglII linker in the coding region of the pro domain of TGFβ1 were sequenced (Sanger and Coulson, 1975) to confirm the position of the linker and the integrity of the TGFβ1 precursor mutants.

The insertion mutant cDNAs were placed into the expression vector pCDM8 (Seed, 1987). This vector contains an SV40 origin of replication which allows for high copy numbers of plasmid molecules in COS-1 cells. Furthermore, transcription of the mutant pre-pro-TGFβ1 cDNAs is controlled by the powerful CMV promoter, a promoter that functions quite well in monkey fibroblasts (Seed, 1987). The pUC19-TGFβ1 mutant DNA was digested with EcoRI and the overhang was filled in with Klenow DNA polymerase. This blunt end DNA was digested with HindIII and the 1.4-kb fragments were isolated from an agarose gel. The expression vector pCDM8 (Seed, 1987) was cut with NotI, filled in with Klenow DNA polymerase, and then digested with HindIII. The HindIII to EcoRI (blunt) fragment of pre-pro-TGFβ1 mutant was ligated into the pCDM8 vector.

The placement of unique restriction sites within the precursor of TGFβ1 cDNA allowed for the creation of in-frame deletion mutants by using pairs of insertion mutants. Pairs with BglII linkers inserted in the same reading frame were directly recombined by ligating the appropriate fragments isolated after digestion of plasmid with both BglII and HindIII. In-frame deletions between BglII sites that were not in the proper reading frame required either digestion with single strand-specific mung bean nuclease or were filled in with the Klenow DNA polymerase and ligated. In all cases, ligation of ends produced by BglII digestion and treatment with mung bean nuclease generates unique EcoRI sites which could be used for screening mini-preparation DNA samples. The recombinant plasmids bearing deletions at different sites were identified, mapped by restriction enzyme analysis, and/or sequenced. The deletion mutants expressing pre-pro-TGFβ1 were identified by Δ followed by the positions of the two insertion mutants used for their construction (see Table II).

To prepare deletion mutants which express the pro region independent of the mature TGFβ1, the plasmid pCDM8-Stop278 was utilized (Gentry and Nash, 1990). Each deletion mutant cDNA was excised from its respective pCDM8 expression vector with HindIII and BstXI and used to replace the wild-type sequence of the pro domain of TGFβ1 in the plasmid vector pCDM8-Stop278. These deletion mutants expressing the pro domain independently were named as β1-LAP deletion mutants, and designated L, followed by the same definition as previously described for the pre-pro-TGFβ1 deletion mutants (see Table II).

Transient Expression

The pCDM8 constructs containing the mutant genes were transfected into COS-1 cells by a modified DEAE-dextran/chloroquine method (Seed and Aruffo, 1987). Each transfection was repeated at least three times. COS-1 cells were plated onto 10-cm plates and transfected at 30–60% confluence. After a brief incubation with DME containing 10% Nu-serum (Collaborative Research, Lexington, MA), 50 μg of DNA in a total volume of 5 ml (DME/Nu-serum) was added to each plate for 2.5 h. After further incubation of the cells for 48 h in DME supplemented with 10% FBS, the medium was changed to serum-free DME (5 ml/10-cm dish) and collected after 48 h. Each experiment included control plates containing cells transfected by pCDM8 and pCDM8-TGFβ1 or pCDM8-Stop278. The transfected cells were washed three times with cold PBS, scraped from the culture plate in cold PBS, and collected by low-speed centrifugation.

Immunoblot Analysis

Secreted and cellular forms of the precursor for TGFβ1 were analyzed by immunoblotting (Gentry et al., 1987). Serum-free conditioned medium was collected at the end of transfection. PMSF was added to the medium at a final concentration of 1 mM, which was then clarified by low-speed centrifugation. The medium was then dialyzed against 0.2 M acetic acid and 1-ml aliquots were lyophilized. Each lyophilized sample was resuspended in 20 μl of sample preparation buffer and fractionated on 7.5–17.5% gradient or 12% SDS-polyacrylamide gels (Laemmli, 1970). The cells were lysed with equal volume of 2× sample preparation buffer and heated at 95°C for 4 min before analysis. After electrophoresis, proteins were electrophoretically transferred to nitrocellulose and stained for immunoreactive mature and precursor forms of the TGFβ1 proteins as described previously (Gentry et al., 1987). The antisera used were directed against residues 225–236 of the pro portion of TGFβ1 or residues 369–381 of the mature growth factor (see Fig. 3). In some experiments, affinity-purified antipeptide antibodies were utilized for immunostaining.

Affinity-purified antipeptide antibodies were prepared using the procedure described by Smith and Fisher (1984). Briefly, concentrated culture supernatants from CHO cells expressing high levels of rTGFβ1 precursor (Gentry et al., 1987) were fractionated by SDS-polyacrylamide gels and transferred to nitrocellulose membranes. The protein bands corresponding to the mature and pro region of TGFβ1 were visualized after the membrane was stained with 0.5% ponceau S, excised, and incubated overnight with the antipeptide antiserum, respectively. The antibodies were eluted with 0.1 M glycine-HCl, 0.1 M NaCl (pH 2.5), and immediately neutralized with 1 M Tris-HCl, pH 8.0. Alkaline phosphatase–conjugated-Protein A or alkaline phosphatase–conjugated, affinity-purified goat anti-rabbit IgG (Cappel, West Chester, PA) was utilized for antigen detection.

Quantitation of Mature and Precursor Forms of TGFβ1

The levels of mature TGFβ1 monomers and the 44–56-kD precursor forms (Fig. 3 *C*, form *a* and *c*, respectively), as well as mature TGFβ1 dimers and the disulfide aggregates (Fig. 3 *B*, form *A* and *C*, respectively) in culture supernatants were measured by densitometer scanning of the immunoblots. The relative amounts of mature TGFβ1 monomers (Fig. 3 *C*) and dimers (Fig. 3 *B*) in the culture medium were expressed as a percentage of that observed from wild-type, pCDM8-TGFβ1 transfections (Table I). To measure effects on disulfide formation of mature TGFβ1 from pre-pro-TGFβ1 and the various mutants, the A and C values from nonreducing gels measured above (Fig. 3 *B*) were manipulated by the following formula, $[C/(A+C)] \times 100$, and will be referred to as disulfide folding percentage (see text) (see Table I).

Digestion with N-Glycanase

Conditioned culture medium (1 ml) was lyophilized and suspended in 10 mM ethylenediaminetetraacetic acid, 0.2% SDS, 0.1 M 2-mercaptoethanol, and 1% NP-40 (pH 7.5). Digestion was performed at 30°C overnight using 1.25 U N-glycanase (Genzyme, Boston, MA). After digestion, the samples were mixed with an equal volume of 2× SDS-gel buffer and analyzed on immunoblots.

Growth Inhibition Assay

Mink lung epithelial cells were utilized for growth inhibition assay of TGFβ1 and its mutant precursors. The assay was performed using a modified procedure combining a method described previously (Ikeda et al., 1987) and a colorimetric assay to assess cell proliferation (Mosmann, 1983). A colorless tetrazolium salt (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl) tetrazolium bromide (Sigma Chemical Co., St. Louis, MO) is converted to a colored product by the cells and the optical density at 590 nm is proportional to the number of living cells. Serum-free supernatants containing mature TGFβ1 or its precursor mutants were concentrated threefold by ultrafiltration (YM10 membrane, 10,000 molecular weight cutoff; Amicon Corp., Danvers, MA), heated for 5 min at 85°C, and diluted in complete medium. Samples were added to mink lung cells in 96-well microtiter dishes in triplicate. After incubation of the cells for 72 h at 37°C in a humidified 5% CO_2 atmosphere, the incubation media was removed, tetrazolium salt was added to each well (50 μl at 0.83 mg/ml in complete medium), and the cells were further incubated at 37°C for 0.5 h. Dimethyl sulfoxide (50 μl) was added to each well, the plates were shaken, and the amount of colored product was determined with a Dynatech MR 580 Microelisa reader at 590 nM. The use of standard amounts of mature TGFβ1 indicated that 3–4 pM inhibited cell growth by 50%.

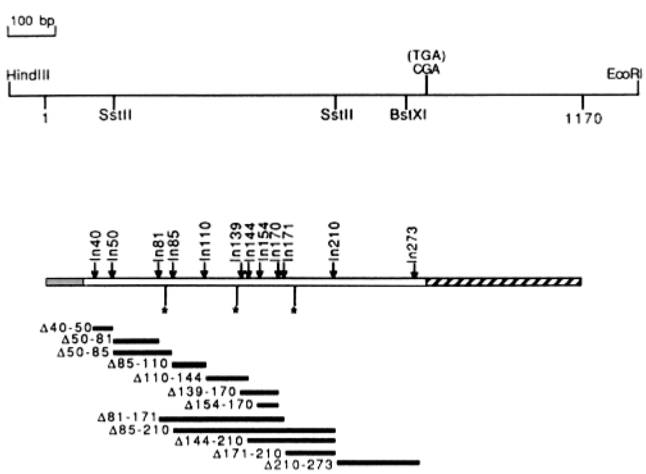

Figure 1. Insertion and deletion mutations in the pro region of TGFβ1 used in this study. The HindIII to EcoRI fragment of simian pre-pro-TGFβ1 was the substrate for insertion mutagenesis. For reference, the SstII restriction sites are noted. The open bar represents the coding region of the pro domain of TGFβ1. The dotted bar and the hatched bar indicate signal peptide and mature TGFβ1 coding region, respectively. Asterisks denote the N-linked glycosylation sites. The Arg codon (*CGA*) is replaced by a stop codon (*TGA*) for expression of β1-LAP independently. The restriction site BstXI used in construction of β1-LAP deletion mutants is shown in the above diagram. The position of each BglII linker is shown in the bottom diagram and is indicated by the arrows above the open bar. The solid bars located below the plane of the figure shows the deletion regions made. For reference, the distance for 100 bp is indicated in the above diagram.

Cross-Linking of β1-LAP and Its Mutants to Radioiodinated TGFβ1

Carrier-free, mature TGFβ1 was purchased from R & D systems (Minneapolis, MN) and labeled with $Na^{125}I$ (Amersham Corp., Arlington Heights, IL) by using chloramine-T as described previously (Ruff and Rizzino, 1986). The radioiodinated TGFβ1 was biologically active and had a specific activity of 55 μCi/μg. Cross-linking experiments were performed as described previously (Gentry and Nash, 1990). The amounts of pro region dimer of TGFβ1 in the supernatants from cells transfected by Stop278 and β1-LAP deletion mutants were determined by densitometer scanning the immunoblot (see Fig. 6 *A*). Control medium (2 μl) containing pCDM8 vector or Stop278, or an equivalent amount of medium containing β1-LAP mutant proteins was added to a total reaction volume of 20 μl, including 2 μl of radioiodinated TGFβ1 (170,000 dpm). After cross-linking and after SDS-PAGE, the protein bands were excised and the amount of iodinated cross-linking product was measured in a γ-counter. Nonspecific binding was determined using equivalent amounts of medium from cells transfected with pCDM8 and was <20%.

Results

Construction of a Series of In-frame Insertion and Deletion Mutations in the Pro Region of TGFβ1 Precursor Sequence

Our general approach was mutational dissection of the pro region of the TGFβ1 precursor to investigate the structural features that are important in posttranslational events such as proteolytic processing, disulfide bridge formation, protein secretion and latent complex formation. Linker insertional mutagenesis has been successfully used to study functional domains within the v-fps (Stone et al., 1984), glucocorticoid receptor (Giguere et al., 1986), c-myc (Stone et al., 1987), v-fms (Lyman et al., 1987), and HSV-1 (Hardwicke et al., 1989). This type of mutagenesis provides evenly distributed in-frame insertion of several amino acids throughout the protein coding region by introducing synthetic oligonucleotide linkers at specific restriction sites. The inserted amino acids should disrupt the local protein structure and allow for identification of functional domains of the proteins.

The sites of linker insertion in the pro region are shown in Fig. 1 and listed in Table I. Restriction sites that were used for mutant construction and the amino acid codons that were inserted are also shown here (Table I). Four different amino acid insertions were possible from the above restriction sites, depending on what mRNA reading frame the insertion occurred. Insertion of GRSS and EDLP were considered "true insertions" since they were placed between original amino acid residues, whereas insertion of WKIFH and REDLP changed one amino acid of the coding sequence of the TGFβ1 precursor.

A set of site-specific, in-frame deletion mutants which comprehensively covers the pro region coding sequence was

Table I. TGFβ1 Insertion Mutants

Insertion mutants	Restriction sites mutated	Codons inserted*	Secreted TGβ1 monomer (*% of* wild-type)‡	Secreted TGFβ1 dimer (*% of* wild-type)§	Biologically active TGFβ (*% of* wild-type)‖	Disulfide folding percentage¶
CDM8			2	7	8.0 ± 2.0	ND
CDM8-TGFβ1			100	100	100 ± 11.3	20
In40	AluI	E(GRSS)L	59	88	46.8 ± 3.5	30
In50	BstUI	R(EDLP)G	3	6	10.0 ± 2.9	ND
In81	RsaI	L(WKIFH)N Y	33	13	9.0 ± 1.8	5
In85	BstUI	R(EDLP)E	31	14	9.7 ± 2.0	6
In110	BstUI	R(EDLP)V	7	4	8.5 ± 2.3	ND
In144	RsaI	V(EDLP)P	38	15	10.3 ± 2.9	4
In154	AluI	E(GRSS)L	2	7	6.9 ± 2.0	ND
In170	AluI	E(GRSS)L	3	7	8.7 ± 1.5	ND
In171	RsaI	L(WKIFH)Q Y	13	23	25.4 ± 8.8	29
In210	BstUI	R(EDLP)G	31	32	29.8 ± 3.3	20
In273	AluI	Q(REDLP)S S	48	53	40.5 ± 8.4	23

* In parentheses are the inserted amino acids, whereas original codons are shown outside. Amino acids appearing below the plane are deleted due to insertional interruption.

‡ The immunoblot run under reducing conditions (shown in Fig. 3 *C*) was quantitated by densitometry as described in Materials and Methods. The amounts of 12-kD monomeric TGFβ1 (form c) in the supernatants are expressed as a percentage of wild-type TGFβ1 (CDM8-TGFβ1).

§ The amounts of mature TGFβ1 dimer were quantitated by densitometer scanning of the nonreducing immunoblot shown in Fig. 3 *B* (form C) and expressed as a percentage of wild-type TGFβ1 (CDM8-TGFβ1).

‖ The amounts of bioactive TGFβ secreted by COS-1 cell transfectants were determined as described in Materials and Methods. Wild-type TGFβ1 produced ~70 ng/ml active TGFβ. The results were expressed as a percentage of wild-type activity ± standard deviation (CDM8-TGFβ1). Results are based on six independent determinations.

¶ The immunoreactive disulfide complex (form A) and the mature TGFβ1 dimer (form C) shown in Fig. 3 *B* were quantitated by densitometry as described in Materials and Methods. The disulfide folding percentage shown is based on the following equation, $[C/(A+C)] \times 100$, using the results obtained from densitometer scanning. A disulfide folding percentage of 20 for wild-type, pre-pro-TGFβ1 is similar to results obtained from CHO cells expressing large amounts of rTGFβ1 and its precursors (unpublished observations). For more information see Results section.

also prepared (Table II); it covers the whole sequence of the pro region in blocks from 10 to 125 residues. Some of the deletions were designed to encompass one, two, or all three potential glycosylation signals in the pro region.

pCDM8 vectors containing insertion mutants in the precursor of TGFβ1 were transiently expressed in COS-1 cells. As controls, the pCDM8 vector itself without an insert and pCDM8 containing a wild-type, pre-pro-TGFβ1 cDNA (pCDM8-TGFβ1) were used as controls. After transfection, the cells and the serum-free supernatants from the transfected cells were analyzed by Western blot analysis using either mature TGFβ1 specific or pro region–specific antibodies (Gentry et al., 1987). Immunoblotting was necessary since these antibodies do not recognize the native protein and can not be used for immunoprecipitation analysis.

Effects of the Insertion Mutations in the Pro Region of TGFβ1 on Synthesis, Proteolytic Processing, Disulfide Maturation, and Secretion of Mature TGFβ1 Polypeptides

Fig. 2 shows an immunoblot of cells transfected by pre-pro-TGFβ1 and its insertion mutants. Proteins were electrophoresed under reducing conditions and the blot was incubated with serum against mature TGFβ1 followed by staining with alkaline phosphatase–conjugated Protein A. The pCDM8 control transfection showed no immunoreactive TGFβ1 precursors. In all other cases, however, the precursor of TGFβ1 and its insertion mutants were readily expressed in COS-1 cells and produced proteins possessing molecular masses of ~44 kD (Fig. 2). These results indicate that wild-type and insertion mutants of the TGFβ1 precursors were expressed by COS-1 cells and that steady-state levels of the intracellular mutant pre-pro-TGFβ1s were comparable to that of wild-type. The intracellular form of the TGFβ1 precursor probably represents the partially glycosylated pro-TGFβ1, as observed previously in CHO cells expressing high levels of rTGFβ1 precursor (Sha et al., 1989). Use of alkaline phosphatase–conjugated goat anti–rabbit IgG for staining resulted in greater sensitivity, and consistently showed the existence of mature TGFβ1 in the intact cells transfected with wild-type, pre-pro-TGFβ1 (see Fig. 4 *B*).

An immunoblot of serum-free media from each of the transfectants is shown in Fig. 3 *B*. Under nonreducing condition of electrophoresis, peptide-specific antiserum against mature TGFβ1 identified a 100–120-kD protein, and a 24-kD protein in medium from cells transfected with wild-type, pre-pro-TGFβ1 (pCDM8-TGFβ1). These immunoreactive forms comigrated with rTGFβ1 precursors produced by CHO cells, suggesting that the high molecular weight band probably represented a complex of the pro-TGFβ1 (form a), the pro region (form b) and the mature TGFβ1 (form c) linked by intersubunit disulfide bonds. The low molecular weight band corresponds to mature TGFβ1 dimer (Gentry et al., 1987, 1988). These forms were not present in the supernatants from cells transfected with pCDM8 vector. Mutants In50, In110, In154, and In170 showed no immunostainable levels of mature or larger molecular mass forms of TGFβ1

Table II. TGFβ1-LAP Deletion Mutants

TGFβ1 deletion mutants*	Position of amino acids deleted and inserted‡	Secreted TGFβ1§	β1-LAP deletion mutants‖	Secreted β1-Lap¶	Cross-linking (% of wild-type)**
CDM8-TGFβ1		(+)	Stop278	(+)	100
Δ40–50	E^{39}(GIP)G^{51}	(−)	L40–50	(+)	10
Δ50–81	R^{50}(EHF)N^{82}	(−)	L50–81	(+)	0
Δ50–85	R^{50}(EDLP)D^{86}	(−)	L50–85	(+)	0
Δ85–110	R^{110}(EDLP)V^{111}	(−)	L85–110	(+)	12
Δ110–144	R^{110}(EDLP)P^{145}	(−)	L110–144	(−)	
Δ139–170	E^{139}(GRSS)L^{170}	(−)			
Δ154–170	E^{154}(GRSS)L^{170}	(−)	L154–170	(−)	
Δ81–171	L^{80}(WKIFH)Q^{172}	(−)	L81–171	(−)	
Δ85–210	R^{85}(EDLP)G^{211}	(−)	L85–210	(±)	ND
Δ144–210	V^{144}(EDLP)G^{211}	(−)	L144–210	(−)	
Δ171–210	L^{170}(WKIDLP)G^{211}	(−)	L177–210	(−)	
Δ210–273	R^{210}(EDLP)S^{274}	(−)			

* TGFβ1 deletion mutant was expressed as pre-pro-TGFβ1 by transfected COS-1 cells, and designated as Δ, followed by the numbers of the paired insertion mutants used for its construction.

‡ In parentheses are the inserted amino acids derived from the mutant construction. The original codons and their positions after deletion are shown outside.

§ +, the immunoreactive TGFβ1 in the supernatant from cells expressing TGFβ1 deletion mutant was detected by immunoblot as shown in Fig. 4 *A*. −, not detected.

‖ β1-LAP deletion mutant was expressed as pro region of TGFβ1 independent of mature TGFβ1, and identified as L, followed by the designation described for TGFβ1 deletion mutants. Stop278 expresses wild-type β1-LAP.

¶ Detection of secreted β1-LAP deletion mutants as shown in Fig. 5 *A*. + and − indicate the same as described for §. ±, marginal secretion.

** The cross-linking of the pro region dimer of TGFβ1 in the supernatants from cells transfected by Stop278 or β1-LAP deletion mutants with radioiodinated TGFβ1 is described in Materials and Methods. After SDS-PAGE, the protein bands were excised and the amount of cross-linking was assessed by a γ counter (Fig. 6 *B*). The results are represented as a percentage of the wild-type. Nonspecific binding was <20%. ND, not determined.

precursors. All other insertional mutants produced lower levels of rTGFβ1 polypeptides. These mutants, except In210, migrated at similar positions to wild-type, TGFβ1 precursors on SDS-gels; however, In210 migrated as a larger molecular mass. Since we did restriction analysis as well as DNA sequencing, and did not find additional insertions beside the introduced linker sequence, the retarded mobility of the high molecular form of In210 may be due to differences in the disulfide folding pattern of this molecule. Note that for In210, pro-TGFβ1 and its pro domain migrate similar to other mutants on the reducing gels shown in Fig. 3 (*C* and *D*).

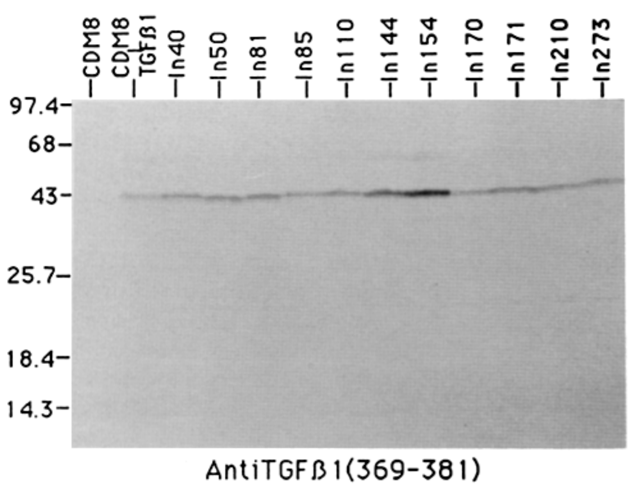

Figure 2. Immunoblot of intracellular forms of pre-pro-TGFβ1 insertion mutants from COS-1 cells. Transfected cells were collected and processed as described in Materials and Methods. Cells (10^6) from wild-type or mutants were used for the immunoblot. The immunoblot was performed under reducing conditions and stained with mature TGFβ1-specific antibodies (anti-TGFβ$1_{369-381}$; see Fig. 3). Alkaline phosphatase–conjugated protein A was used. Markers are located to the left of the figure.

Under reducing conditions of sample preparation (Fig. 3 *C*), the immunoblot probed with the same antibodies revealed the existence of two forms of recombinant TGFβ1 precursors in the supernatant from the wild-type transfectant, a 44–56-kD band representing uncleaved pro-TGFβ1 (form a), and a 12-kD band corresponding to mature TGFβ1 monomer (form c) (Gentry et al., 1987; 1988). Immunoreactive mature or precursor forms of TGFβ1 were not detected in the supernatants from cells transfected with insertion mutants In50, In154, and In170. In110 still made a small amount of mature monomer. The other mutants appeared to secrete lower levels of immunostained monomer than CDM8-TGFβ1 (Fig. 3 *C*, band c). To determine the degree of proteolytic processing, immunoblots (Fig. 3 *C*) were scanned by densitometry. The percentage of mature TGFβ1 (band c) relative to precursor (form a) generated by wild-type or its various insertion mutants was similar (∼40%). Therefore, the amount of mature 12-kD species is representative of the level of secreted TGFβ1; these values are listed in Table I using 100 for wild-type, mature TGFβ1.

The amount of mature, monomeric TGFβ1 (Fig. 3 *C*) detected by immunoblotting appeared greater than that of mature, dimeric TGFβ1 detected under nonreducing conditions, especially for mutants In81, In85, and In144 (Fig. 3 *B*). Such an inconsistency may be due to a greater percentage of mature, monomeric TGFβ1 forming disulfide cross-links through Cys-33 of their precursors (Fig. 3 *B*) (Gentry et al., 1988). To test this possibility, immunoblots showing the mature dimers (form C) and larger disulfide aggregates of TGFβ1 (form A) were scanned by densitometry (Fig. 3 *B*). After subtracting the appropriate background (i.e., pCDM8),

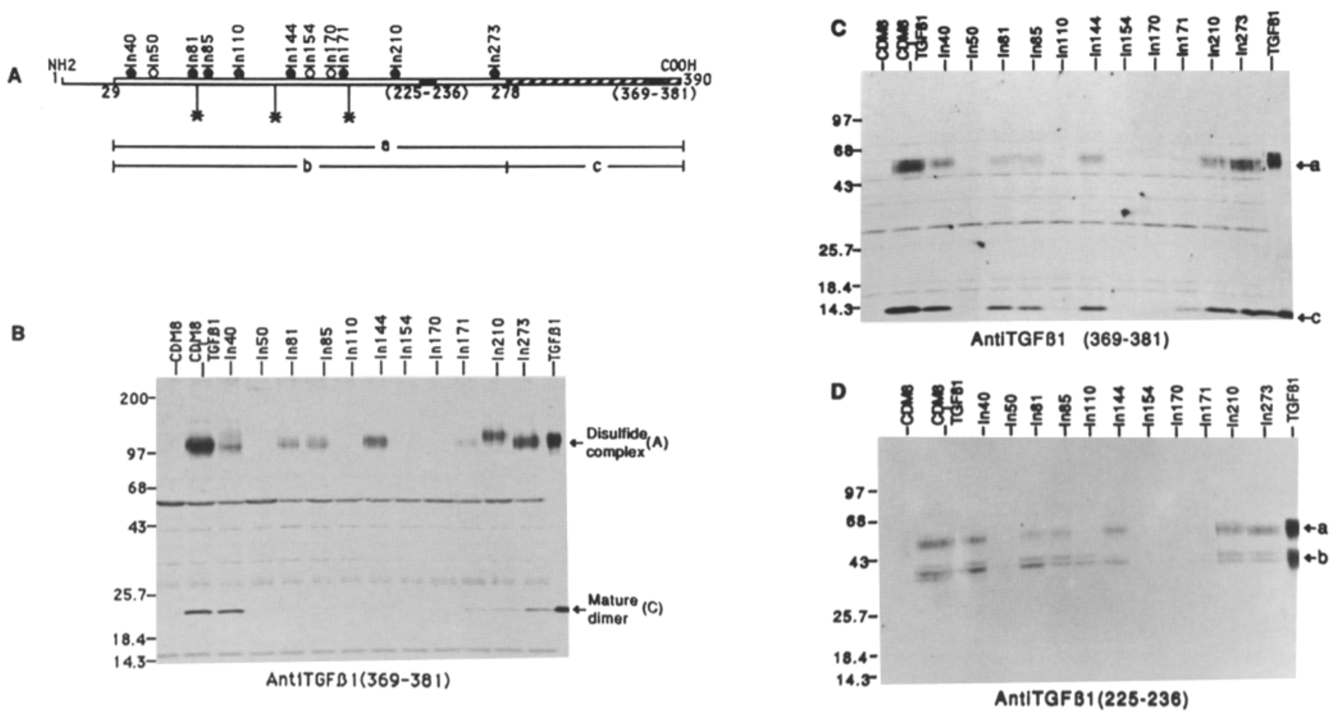

Figure 3. Immunoblots of culture supernatants from transfected COS-1 cells expressing pre-pro-TGFβ1 insertion mutants. Serum-free media from transfected COS-1 cells were collected and processed as described in Materials and Methods. Conditioned, concentrated medium from CHO cells (2 μl) which express high levels of rTGFβ1 precursor (Gentry et al., 1987) was used in these experiments as a standard; this is indicated above the immunoblots as TGFβ1. Molecular size standards in kilodaltons are shown on the left of each panel. Results are representative of three independent transfection experiments. (*A*) The diagram shown is a schematic representation of the structure of pre-pro-TGFβ1 polypeptide and the sites of insertion mutations. Pro-TGFβ1, the pro region of TGFβ1, and mature TGFβ1 are indicated by *a*, *b*, and *c*, respectively. The asterisks denote N-linked glycosylation signals. Positions of the insertion mutants are designated by overlying circles. The shaded circles indicate reduced amounts of TGFβ1 precursor in the supernatant, and the open circles represent no detectable amount of the precursors in the supernatant. (*B*) Medium from cells (1 ml) expressing the mutants was fractionated on a 12% SDS polyacrylamide gel under nonreducing condition and stained for immunoreactive TGFβ1 precursor using anti-TGF$\beta 1_{369-381}$. The identity of each mutant is located above each lane. The letter A represents the disulfide aggregates expressed by the transfected COS-1 cells, and C denotes the mature TGFβ1 dimer secreted. (*C*) Immunoblot of supernatants fractionated on 7.5–20% gradient SDS-polyacrylamide gels under reducing condition. Blots were probed with same antibodies as described above. (*D*) Immunoblot of supernatants fractionated on 7.5–20% gradient SDS-polyacrylamide gels. Blots were probed with anti-TGF$\beta 1_{225-236}$ antibodies.

the relative amount of mature, dimeric TGFβ1 was then calculated using the formula [C/(A + C)] $\times$ 100. This result is listed in Table I as disulfide folding percentage.

The arbitrary value of disulfide folding percentage refers to the relative amount of mature, dimeric TGFβ1 present in the culture medium. A value of 100% would mean that all of pre-pro-TGFβ1 is processed properly and that the mature growth factor contains no disulfide formation with Cys-33 of the pro domain. A value of 0%, on the other hand, would mean that mature TGFβ1 was linked to Cys-33 of the larger disulfide form. Wild-type, pre-pro-TGFβ1 transfectants produced mature TGFβ1, which represented ~20% of the total immunoreactive TGFβ1 (Fig. 3 *B*), a value in close agreement with results from CHO cells expressing large amounts of this growth factor (unpublished observations). Mutants In81, In85, and In144 produced lower amounts of dimer ranging from 4-6%. Mutants in the amino- and carboxyl-portion of the TGFβ1 pro domain (In40, In171, In210, and In273) had virtually no effect on this Disulfide Folding Percentage (Table I), displaying values ranging from 20–30%. These results indicate that regions surrounding residues 81, 85, and 144 of the TGFβ1 pro domain may play an important role in the disulfide modeling of mature TGFβ1.

The corresponding biological activities of wild-type, mature TGFβ1 and mutants were determined in a standard bioassay, using growth inhibition of mink lung epithelial cells (Table I). Wild-type, mature TGFβ1 (pCDM8-TGFβ1) produced ~70 ng/ml of TGFβ, a value similar to a previous report (Brunner et al., 1989). This value has been normalized to 100 for wild-type TGFβ (Table I). Mutants In50, In154, and In170, which do not show immunoreactive TGFβ1 monomers and dimers in their supernatants, had biological activities similar to that produced by pCDM8 vector alone. The amounts of biologically active TGFβ correlated well with the amount of mature TGFβ1 dimers detected by immunological methods (see above; Fig. 3 *B*; Table I).

Processed pro domains in the culture supernatants from various transfected COS-1 cells were demonstrated by immunoblot analysis with antibodies against the pro region of TGFβ1 (Fig. 3 *D*). Wild-type, precursor forms of TGFβ1 were apparent as two forms, both of which comigrated with the rTGFβ1 precursor. A 44–56-kD band represents the unprocessed pro-TGFβ1 (form a), and the 30–42-kD species indicates the pro region of TGFβ1 (form b). These results indicate that both wild-type and mutant TGFβ1 precursors expressed by transfected COS-1 cells were properly processed. Like the results shown in Fig. 3 (*B* and *C*), supernatants from cells transfected by mutants In50, In154, and In170 did not demonstrate any immunoreactive TGFβ1 precursors. The antibodies detected the existence of the pro domain and minute amounts of mature monomeric TGFβ1 in the tissue culture supernatant from In110-transfected cells (Fig. 3, *C* and *D*).

Deletion Mutations in the TGFβ1 Pro Region Abolished Secretion of Mature Growth Factor

To examine the role of the pro domain in secretion, a large deletion of the TGFβ1 precursor was made using the two naturally occurring SstII restriction sites (Fig. 1). The deletion removes 162 amino acid residues in the pro domain including all three glycosylation signals. When this deletion construct was expressed in COS-1 cells, no secreted product was detected. When cells were examined, an immunoreactive protein corresponding to the size of the modified protein was readily detected and was present at higher levels than normal pro-TGFβ1 (data not shown), suggesting that either glycosylation or the pro domain was important in secretion (Sha et al., 1989).

To examine the pro domain in more detail, deletion mutants of pre-pro-TGFβ1 were transfected into COS-1 cells and the secreted and cell-associated mutant proteins were detected by immunoblotting using affinity-purified antipeptide antiserum as shown in Fig. 4. The results are summarized in Table II. Immunoblots of supernatants probed with mature (Fig. 4 *A*) or pro region–specific antibodies (data not shown) from cells transfected with wild-type, pre-pro-TGFβ1 confirmed that TGFβ1 was expressed and secreted normally. However, when any of the deletion mutants were expressed in COS-1 cells, immunoblots of supernatants did not show any corresponding immunoreactive TGFβ1 precursor proteins (Fig. 4 *A*). These mutants of TGFβ1 were readily expressed in COS-1 cells, as demonstrated by immunoblotting of cell extracts (Fig. 4 *B*). Under reducing conditions, these affinity-purified antibodies against mature TGFβ1 identified the partially glycosylated TGFβ1 precursor (Sha et al., 1989) and the mature form of wild-type TGFβ1 (see pCDM8-TGFβ1 in the left two immunoblots), confirming that proteolytic processing of the TGFβ1 precursor occurred intracellularly. In cells transfected with the deletion mutants, mature forms were not detected, while all mutant precursor forms were expressed and appeared to accumulate to different extents. Previous work has demonstrated that proteolytic processing of rTGFβ1 precursor by CHO cells occurred in acidic intracellular organelles (Sha et al., 1989), where endoproteolytic cleavages at paired basic residues commonly occur within acidic, clathrin-coated vesicles (Orci et al., 1987). The results from our studies indicate that deletion mutations within the TGFβ1 pro domain might either affect routing of TGFβ1 precursor to the proper intracellular compartment for proteolytic processing, or alternatively affect protein stability.

The mutant precursor forms migrated at shifted molecular weights relative to wild-type, pre-pro-TGFβ1. Mutant proteins would probably not migrate according to size since carbohydrate addition would not be uniform; Δ50–85, Δ81–171, Δ85–210, Δ110–144, Δ144–210, and Δ171–210 contain deletions in N-linked carbohydrate addition sites.

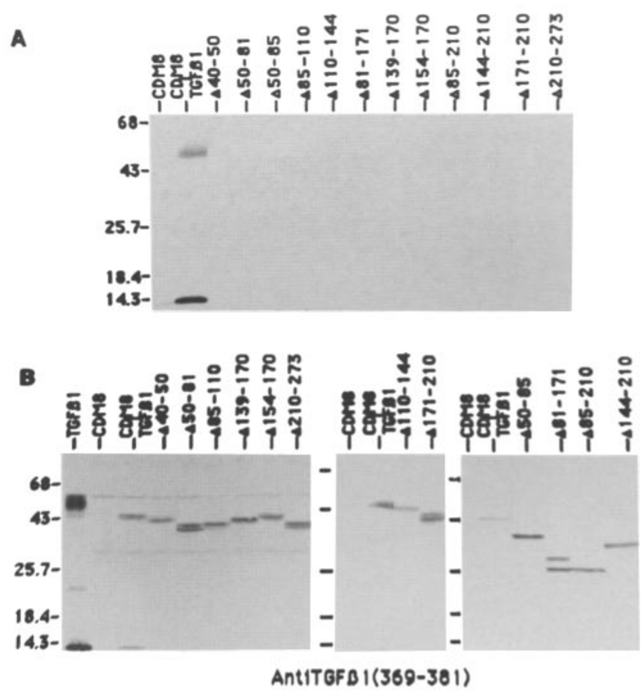

Figure 4. Determination of secreted and cell-associated precursor forms of TGFβ1 deletion mutants. (*A*) Immunoblot of supernatants from COS-1 cells transfected by deletion mutants of pre-pro-TGFβ1. The Δ in each case represents the pre-pro-TGFβ1 deletion mutant; numbers following the Δ represent insertion mutants used for its construction. Supernatant from the various transfectants were fractionated on 7.5–20% gradient SDS-polyacrylamide gels under reducing conditions. The secreted protein was probed with affinity-purified anti-TGFβ1$_{369-381}$ antibodies. The results have been repeated three times and appear to be consistent. Marker proteins are shown to the left. (*B*) Immunoblots of transfected cells expressing pre-pro-TGFβ1 deletion mutants. Cells were collected as described in Materials and Methods. For each mutant, 10^6 cells were analyzed by immunoblotting under reducing conditions. Affinity-purified anti-TGFβ1$_{369-381}$ antibodies were used for these immunoblots. Alkaline phosphatase–conjugated anti-rabbit IgG was used for the immunoblots in the left two panels. Alkaline phosphatase-conjugated Protein A was used for the right panel. Markers are shown to the left.

Expression of β1-LAP Deletion Mutants Independent of Mature TGFβ1

The pro region of TGFβ1, when expressed independent of the mature growth factor in recombinant systems, was able to fold properly and be secreted from the transfected cells (Gentry and Nash, 1990). The insertion and deletion studies indicated that disruption of the pro domain of pre-pro-TGFβ1 affected folding and secretion of mature TGFβ1. These results imply that information for protein conformation and/or secretory transit of pre-pro-TGFβ1 are probably stored in the pro domain, and that mature TGFβ1 must somehow associate with this domain using covalent and/or noncovalent bonds for proper folding and secretion from the cells.

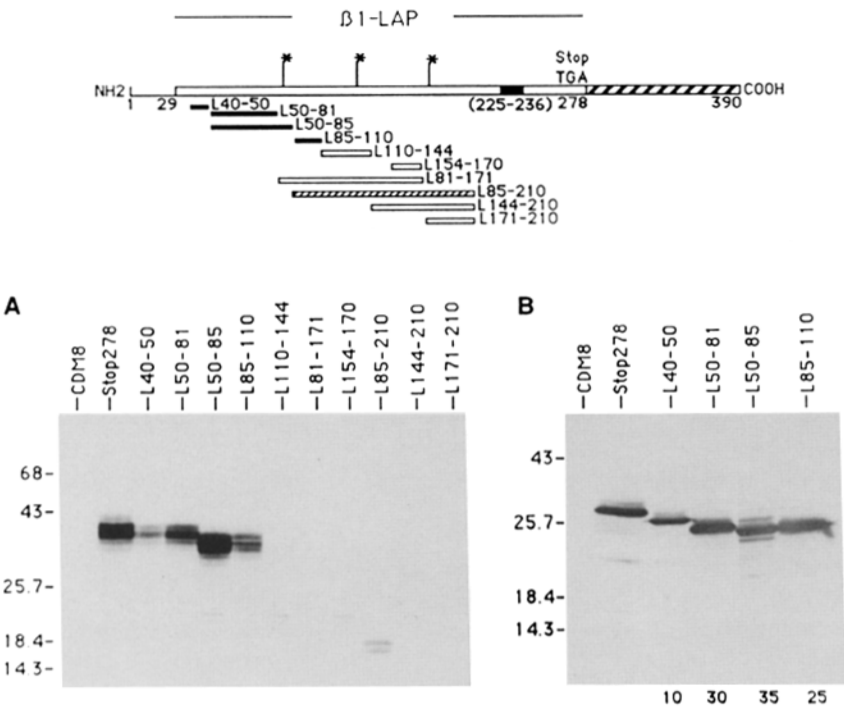

Figure 5. Identification of β1-LAP deletion mutants secreted from transfected COS-1 cells. A diagram showing the positions of β1-LAP deletion mutants is shown above. The schematic representing the structure of pre-pro-TGFβ1 polypeptide is the same as described for Fig. 3. The solid bars represent the immunoreactive β1-LAP mutants which were observed, open bars indicate no detectable mutant proteins in the supernatants, and the cross-hatched bar shows marginally detectable β1-LAP in the culture medium. L represents the deletion mutants for β1-LAP; numbers that follow are identical to those shown in Fig. 4. Supernatant from each transfection was fractionated on 7.5–20% SDS-polyacrylamide gels and probed with pro region-specific, affinity-purified antiserum (anti-TGF$\beta 1_{225-236}$) under reducing conditions (*A*). Immunoblot of N-glycanase-treated supernatants containing β1-LAP deletion proteins is shown in *B*. Digestion of the culture supernatants with N-glycanase was performed as described in Materials and Methods. Numbers shown below are the amino acids deleted for each mutant.

Deletion mutants were prepared in β1-LAP and placed into the same expression vector (Table II). The β1-LAP deletion mutants were transfected into COS-1 cells, and tested for their secreted pro region by immunoblotting with affinity-purified antiserum against the pro domain (Fig. 5). Under reducing conditions (Fig. 5 *A*), cells transfected with β1-LAP (Stop278) produced a 30–42-kD immunoreactive protein representing the wild-type, pro domain (Gentry and Nash, 1990). Interestingly, the pro regions in the supernatants from cells transfected with L40-50, L50-81, L50-85, and L85-110 were also detected, suggesting that deletions in the amino-terminal residues 40–110 of the pro region did not abolish secretion of β1-LAP. However, mutants containing deletions in residues 110–210 were not detected in the supernatants from COS-1 cells. In cells expressing these mutants, the levels of the mutant proteins were slightly higher than that produced by wild-type β1-LAP (data not shown), suggesting that these β1-LAP mutants may have protein secretion defects. Mutant L85-210 reproducibly showed a small amount of mutant protein secreted, while smaller deletion mutants covering the same region gave no detectable, secreted pro region.

To demonstrate the different molecular sizes of wild-type β1-LAP (Stop278) and its deletion mutants, the culture supernatants were treated with N-glycanase, and then further analyzed by immunoblotting (Fig. 5 *B*). Under reducing condition, digestion with N-glycanase caused wild-type β1-LAP (Stop278) to migrate as a sharp band of 26–28 kD, which corresponds to the calculated molecular size of unglycosylated pro peptide (Brunner et al., 1988; Sha et al., 1989). Similarly, the protein bands of β1-LAP deletion mutants were shifted and had gel mobilities corresponding to their sizes following deletion mutations.

Deletions in the Amino-terminal Portion of β1-LAP Severely Reduce Binding to Mature TGFβ1

Mutants that were able to secrete the β1-LAP pro regions were examined for their abilities to generate functional dimer forms by immunoblotting of culture supernatants under nonreducing conditions (Fig. 6 *A*). Consistent with a previous report (Gentry and Nash, 1990), β1-LAP (Stop278) produced a major protein band with a molecular mass around 80 kD, and a minor band of 40–42 kD. The two protein species represent the dimer and monomer forms of β1-LAP, respectively. The β1-LAP deletion mutants also appeared to form dimers.

Previous studies reported that the independently expressed β1-LAP could associate with biologically active, mature TGFβ1 to form a latent complex in vitro (Gentry and Nash, 1990). Removal of the amino-terminal sequence of the pro region by protease treatment resulted in dissociation of the latent complex (Lyons et al., 1990). We examined the association of the β1-LAP deletion mutants with radioiodinated mature TGFβ1 by cross-linking the two proteins (Gentry and Nash, 1990). Equivalent amounts of supernatants from cells transfected with Stop278 or L40-50, L50-81, L50-85, and L85-110 were incubated with radioiodinated TGFβ1 and subsequently treated with cross-linker (Fig. 6 *B*). The cross-linked proteins were fractionated by nonreducing SDS-PAGE followed by autoradiography (see Materials and Methods). Incorporation of radioiodinated TGFβ1 into wild-type and mutant β1-LAPs was then determined and expressed as percentage of the wild-type (Table II). When β1-LAP (Stop-278) supernatant without cross-linker was included as a control, only the 24-kD radioiodinated, mature TGFβ1 was detected. After addition of cross-linker, a large aggregate of

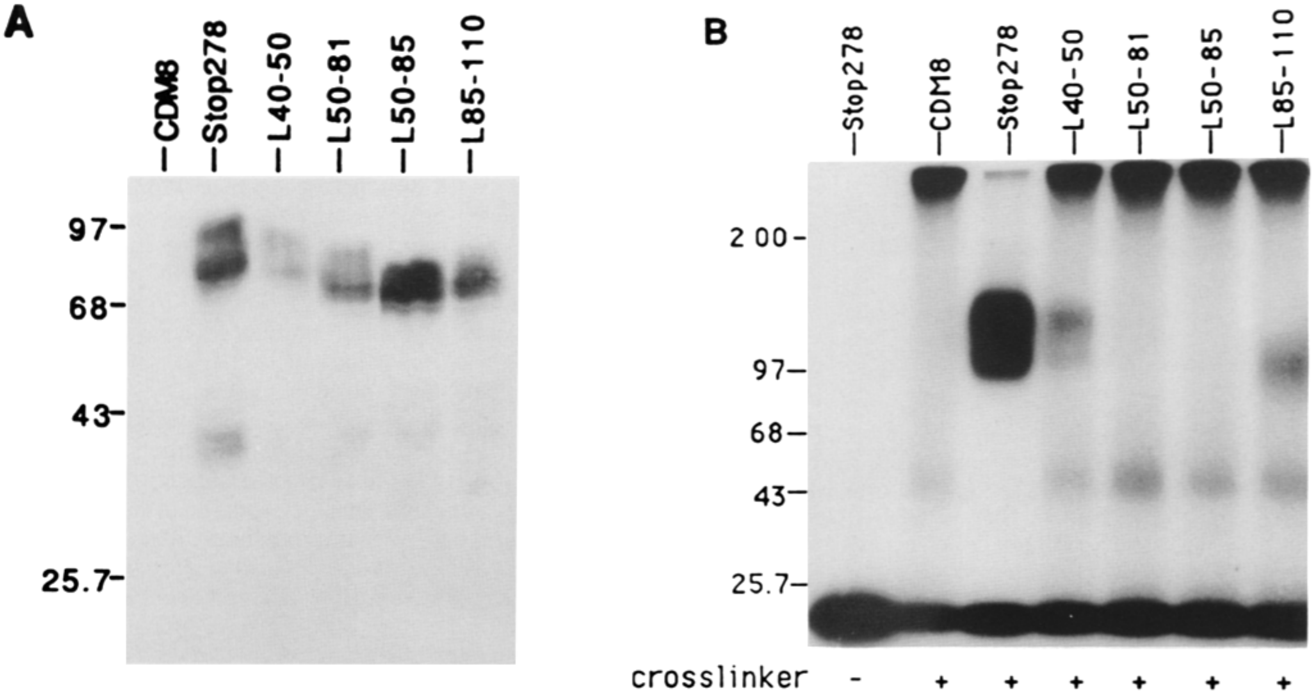

Figure 6. Detection of dimeric forms of β1-LAP deletion mutants and subsequent cross-linking with radioiodinated, mature TGFβ1. (*A*) Supernatants from the β1-LAP deletion mutants were analyzed by SDS-PAGE on a 12% SDS polyacrylamide gel under nonreducing conditions; immunoreactive protein was identified by affinity-purified anti-TGF$\beta1_{225-236}$. Markers are shown to the left. (*B*) Culture medium from the control transfectants or from cells expressing β1-LAP deletion mutants was first normalized and then incubated with radioiodinated, mature TGFβ1 and cross-linked with bis(sulfosuccinimidyl) suberate as described in Materials and Methods. Cross-linked TGFβ1 complexes were fractionated on 7.5% SDS-polyacrylamide gel followed by autoradiography. The + and − at the bottom of the figure indicate whether or not cross-linker was added. γ-Spectroscopy counts of each mutant are shown in Table II.

cross-linked TGFβ1 was observed at the top of the gel (>200 kD). A limited amount of cross-linked TGFβ1 complex was observed in the lane marked Stop278. This lane contains wild-type β1-LAP protein which efficiently binds to mature TGFβ1 and prevents excessive aggregation. Cross-linking β1-LAP (Stop278) generated a 100–110-kD species which represented 47% of the input TGFβ1 radioactivity. No such protein was detected in the pCDM8 medium. This 100–110-kD species represents the cross-linked complex containing one dimer of the pro domain (80 kD) and one mature TGFβ1 dimer (24 kD) (Gentry and Nash, 1990).

Deletion mutations in the amino-terminal part of the pro region affected formation of the cross-linked complex (Fig. 6 *B*). Mutant L40–50 and L85–110 reduced the amount of the cross-linked complex formed giving 10 and 12% of wild-type β1-LAP (Stop278), respectively. Mutants L50–81 and L50−85 did not form cross-linked complexes. The complex of L85–110 had a lower molecular size compared with wild-type β1-LAP (Stop278), probably from its 25 residue deletion. The mobility shift of L40–50 was not observed under these conditions due to its smaller deletion. A minor cross-linked species (45 kD) was observed in all mutants and pCDM8 supernatants.

β1-LAP (Stop278) and the four β1-LAP deletion mutants were also tested by bioassay for their abilities to regulate the growth inhibition activity of the mature TGFβ1. Consistent with a previous report (Gentry and Nash, 1990), β1-LAP (Stop278) medium inhibited the TGFβ1 bioactivity, whereas L40–50 and L85–110 had 2–4% the activity of Stop278, and L50–81 and L50–85 were not inhibitory (data not shown). These results indicate the importance of the amino-terminal region (residue 50–85) of β1-LAP in latent complex formation. Although this region contains the first glycosylation signal, one of the deletion mutants of β1-LAP (L50–85) that lacks this site was readily secreted, suggesting that this N-linked oligosaccharide addition site is not essential for secretory transport of β1-LAP. The carboxyl-terminal half of β1-LAP, on the other hand, appears to contain sequences that are essential for secretory exit of β1-LAP and pre-pro-TGFβ1.

Discussion

TGFβ1 possesses multiple functional properties that affect cell growth and differentiation (Robert and Sporn, 1990). TGFβ1 is synthesized as a precursor, which subsequently undergoes extensive posttranslational processing events for mature TGFβ1, which is secreted (Derynck et al., 1985; Gentry et al., 1988; Brunner et al., 1988). The secreted TGFβ1 exists as a biologically inactive or latent form that is not able to bind to its cell surface receptors (Lawrence et al., 1985). Latency results from the binding of mature growth factor to a dimer of its own pro region, termed β1-LAP (Gentry et al., 1987; Miyazono et al., 1988; Wakefield et al., 1988; Gentry and Nash, 1990). Since the presence of TGFβ1 receptors is universal (Wakefield et al., 1987), latent complex formation and its activation through an unknown

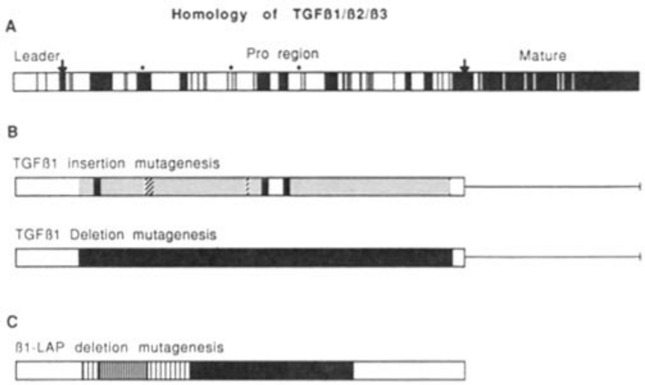

Figure 7. (*A*) Sequence homology of human TGFβ1, β2, and β3. The diagram represents the structure of pre-pro-TGFβ1. Glycosylational signals and sites of proteolytic processing are shown as asterisks and arrows, respectively. The blackened areas indicate the conserved amino acids between human TGFβ1, β2, and β3. (*B*) Schematic representation of functionally important regions in pre-pro-TGFβ1. The blackened areas indicate that mutations in these regions abolished detection of secreted TGFβ1 precursor. The shaded areas show that mutations in these regions reduced the levels of TGFβ1 precursor detected in the culture supernatants. Insertions in areas represented by diagonal lines resulted in misfolded pro and mature TGFβ1. (*C*) Schematic representation of β1-LAP and the various deletion mutants. The blackened areas are important for secretion of β1-LAP. The vertical lined areas represent regions important for binding mature TGFβ1 to form the latent complex. The closely packed vertical lines identify regions resulting in β1-LAP mutants which no longer bind mature TGFβ1. In each of the above diagrams, the position of the sequences has been aligned for direct comparison.

mechanism must be an important part of the control of TGFβ1 function. The pro domain also aids in proper folding of the mature growth factor intracellularly (Gray and Mason, 1990). Despite these known functional roles, very little is known about structure/function relationships of the pro region. Using mutants generated by linker insertion, we have demonstrated that the structural integrity of the pro region is required for export of mature TGFβ1. In addition, we have defined several regions in the pro domain that are important in the folding, stability, secretion, and latent complex formation of TGFβ1.

An illustration demonstrating the results from our experiments and how these results relate to the sequence homology of human TGFβ1, β2, or β3 is shown in Fig. 7. Linker insertion mutagenesis at three sites in the pro domain of simian TGFβ1 (amino acids 50, 154, and 170) abolished detection of all three forms of mutant TGFβ1 precursor in culture supernatants, whereas insertion in other regions resulted in diminished levels of the secreted precursor to TGFβ1 (Fig. 3). Deletion mutations have provided similar results. All deletion mutants, even the mutant lacking 10 amino acids, were not secreted (Fig. 4). This does not appear to be the result of decreased protein expression, since mutant proteins were expressed intracellularly at levels comparable to wild-type, pre-pro-TGFβ1 (Fig. 2). Previous work has indicated that the independently expressed mature TGFβ1 was not properly folded and/or secreted from transformed cells unless coexpressed with its pro domain (Gray and Mason, 1990). Together with our results, we speculate that either the primary sequence of the pro domain and/or its resultant conformation is essential in secretory export of mature TGFβ1.

Does the amino acid sequence of the inserted linker play a specific role in the degradation of the mutant TGFβ1 precursor? Table I lists the four different linker sequences which were placed into the precursor of TGFβ1. In40 and In273 resulted in the insertion of an Arg residue, an amino acid sensitive to hydrolysis by plasmin and many cellular proteases. In154 and In170 also contain insertions that result in the placement of specific Arg residues. Why then are In40 and In273 stable to this insertion and In154 and In170 unstable? Perhaps insertions at the ends of the molecule (In40 and In273) will not affect the biological activity of β1-LAP. Placement of this linker sequence toward the middle of the molecule (In154 and In170) somehow disrupts the normal functional properties of β1-LAP, either through the inclusion of a positive charge or through the addition of an amino acid that is recognized by cellular proteases. SDS-gel electrophoresis of these mutant TGFβ1 molecules did not reveal the presence of any degraded protein precursor either in the cell or in the culture medium (Figs. 2 and 3). Insertions after an Arg residue for In50 may have resulted in degraded protein by providing a hydrolyzable "kink" in the precursor polypeptide chain, resulting in degradation. However, this seems unlikely, since In85, In110, and In210 also contain insertions after Arg residues and produce mutants that were readily detected in the culture medium (Fig. 3). Moreover, In50 produced intracellular levels of precursor similar or greater to wild-type TGFβ1 with no detectable degradation products (Fig. 2). We have yet to test the effects of two different four amino acid insertions at the same position in the TGFβ1 precursor.

Independently expressed β1-LAPs lacking amino-terminal sequences 40–110 were readily secreted from cells and these mutants appeared to exist as dimeric structures. By contrast, β1-LAPs with mutations between residues 110 and 210 were apparently not secreted (Fig. 5). Cross-linking studies and bioassays indicated that the secreted β1-LAP deletion mutants interacted marginally with mature TGFβ1 (L40–50 and L85–110) or not at all (L50–81 and L50–85), suggesting an importance of these deleted sequences in latent complex formation (Fig. 6). These results indicate that amino acid residues 50–85 of β1-LAP are probably involved in maintaining the structure of the latent complex. Residues 40–50 and 85–110 may only be superficially involved in binding mature TGFβ1.

A similar suggestion has recently been made looking at the latent form of rTGFβ1 precursor after plasmin digestion. In those studies, activation of the latent complex occurred after removal of the amino-terminal portion of the pro domain after plasmin digestion; these results suggest that this region of β1-LAP is important for stabilizing the latent complex (Lyons et al., 1990). Analysis of the TGFβ1 precursor sequence indicates that residues 40–60 are the largest conserved continuous sequence of the pro domain in all three TGFβs, and appear to be rich in basic residues. It is likely that residues 40–60 may be involved in the binding of TGFβ1 through electrostatic interactions. This interaction could stabilize the entire protein complex, which is essential to form the latent complex. Residues 110–210 of β1-LAP may also be involved in the protein interaction; no such pro region mutants were secreted from COS-1 cells (Fig. 5). Based on these results, it appears that latent complex formation is required for proper secretory exit of the mature growth factor or its stability. In deletions that eliminate residues 40–110, the β1-LAPs were still folded into a transportable structure. However, when expressed as pre-pro-TGFβ1, these mutants were not detected as secreted forms. We presume that the mature growth factor was unable to associate with the mutant pro domain and resulted in an altered conformation that could affect the mature TGFβ1 stability or its export. Insertion mutant In50, which did not show secreted TGFβ1, might also fail to form the latent complex, resulting in a defect in protein secretion (Fig. 3).

The region corresponding to residues 110–210 of pre-pro-TGFβ1 appears to be essential in export of the mature growth factor (Figs. 4 and 5). Mutants In154 and In170 had secretion or stability defects when expressed both as pre-pro-TGFβ1 (Fig. 3) and β1-LAPs (data not shown). Regions containing amino acids 154 and 170 appear to lie in strictly conserved regions among the sequenced human TGFβs (Fig. 7). TGFβ1 precursor polypeptides could not be detected in COS-1 supernatants when the linker sequence GRSS was inserted in these regions. Presumably this region of the protein could form secondary structures which may be essential for proper folding of the pro domain and may be used for secretory exit.

One of the best known examples concerning domains involved in protein transport has come from studies of intracellular transport of vesicular stomatitis virus (VSV) G protein (Rose and Bergmann, 1983; Dams et al., 1987, 1988). Using in vitro mutagenesis of the VSV G cDNA, these researchers found that deletion of the carboxyl-domain, a domain lying in the cellular cytoplasm, had profound effects on secretion of the VSV G protein without altering the whole protein conformation, indicating that this domain must fulfill structural requirements for intracellular routing independent of other protein domains. In addition, assembly of the VSV G protein into a trimer was required for normal transport. Experiments to determine the cell-associated mutant TGFβ1 precursors by immunoblotting under nonreducing conditions showed that dimers of In50, In54, and In170, which were not secreted, were readily identified intracellularly along with wild-type, pre-pro-TGFβ1 (data not shown) indicating that formation of a dimer was not a prerequisite for transport of TGFβ1.

The pro domain of TGFβ1 may function analogously to the pro domain of somatostatin, a domain that is important for secretion of the mature somatostatin. This neuropeptide has a structure analogous to pre-pro-TGFβ1 consisting of a signal peptide followed by a pro peptide and the mature hormone (Hobart et al., 1980). The pre-pro sequence, when fused to α-globin mediated the cytoplasmic protein to be secreted in a regulatory pathway. In contrast, if α-globin was fused to a signal peptide alone, it was translocated to ER, but in the absence of the pro domain it was rapidly degraded, suggesting that the pro peptide protected nascent precursor from protease attack, probably by enhancing its folding and facilitating efficient export (Stoller and Shields, 1989). It is likely that mutation in the pro region of TGFβ1 resulted in misfolding of the newly synthesized precursor, which was recognized and degraded by intracellular enzymes. To confirm this, additional experiments using antibodies that immunoprecipitate wild-type and mutant TGFβ1 precursors to determine the kinetics of intracellular routing of these TGFβ1 forms will be necessary to provide important information about their eventual fate.

N-linked oligosaccharides are often crucial in promoting export of protein. However, this requirement for carbohydrate in transport of membrane or secretory proteins is not universal and is highly protein specific as well as cell specific (reviewed by Olden et al., 1982). Using glycosylational inhibitors, we have determined that glycosylation and its maturation state affected secretion of rTGFβ1 precursors from CHO cells (Sha et al., 1989). The effects of oligosaccharides on protein secretion most likely results from incorrect protein folding and protein instability as reported by many investigators (Grafl et al., 1987; Slieker et al., 1986; Dams et al., 1988). Initially, when we designed the deletion mutants, we hoped to see some correlation with carbohydrate sites and secretion. Deletion mutants lacking each of the three glycosylational signals in the pro portion of pre-pro-TGFβ1 were prepared to assess the role of the individual oligosaccharides on protein secretion (Fig. 1). However, all deletion mutants of pre-pro-TGFβ1 were not secreted (Fig. 4 *A*). Deletion mutant Δ81–171 which lacks the first and second glycosylational signals was partially degraded in the COS-1 cells (Fig. 4 *B*), indicating that these carbohydrates may be important for protein stability. The first carbohydrate moiety does not appear to play a role in the secretion of β1-LAP, since such mutants that delete this N-linked addition site were readily observed in the culture medium (Fig. 6). Selective removal of glycosylational sites without disrupting sequences on either side of this signal using site-directed mutagenesis are in progress and should allow for proper evaluation of the role of individual oligosaccharides in proper folding and secretion of mature TGFβ1 and β1-LAP.

Insertion mutations which reduced transport did not apparently affect proteolytic processing of mature TGFβ1, suggesting that the dibasic cleavage site before the aminoterminus of mature TGFβ1 is readily exposed on the protein even with altered folding. The intracellular forms of the deletion mutants which had defects in secretion were not processed properly. We suggest that the misfolded mutant proteins were probably not transferred to the Golgi apparatus where the proteolytic processing of protein precursors begins (Steiner et al., 1984). Dibasic cleavage sites releasing the mature portion of TGFβ1 are usually not accessible to protease attack in wild-type, pre-pro-TGFβ1. Insertion mutation in region 110 secreted the pro piece of TGFβ1 but very little mature TGFβ1. Antibodies against mature TGFβ1 detected the existence of mutant precursor intracellularly, suggesting that the pro domain affected proper folding of the mature TGFβ1. The misfolded mutant was probably degraded during secretion.

Unlike most tissue culture cells which secrete mature TGFβ1 and the pro form together as a latent complex, the transfected CHO and COS-1 cells were unable to completely process TGFβ1 precursor (pro-TGFβ1), and secreted all three forms of rTGFβ1. Furthermore, these transformed cells released a disulfide aggregate of rTGFβ1 precursor, where the pro domain is disulfide linked to mature TGFβ1 through Cys-33 and an unknown Cys residue in the mature region (Gentry et al., 1987, 1988; Brunner et al., 1989; Lyons et al., 1990). Latent TGFβ1 is secreted from tissue culture cells as a tri-peptide complex containing a cysteine-rich "binding protein", the pro domain of TGFβ1, and mature TGFβ1 (Miyazono et al., 1988; Wakefield et al., 1988; Kanazaki et al., 1990; Tsuji et al., 1990). Thus, it appears that secretion of this larger disulfide-linked form may represent an expression artifact. From our insertional mutation studies, we found that mutations in amino acid 81, 85, and 144 of the pro domain resulted in a large amount of disulfide aggregate, further indicating that the pro domain plays an important role in the proper folding of mature TGFβ1.

In summary, site-specific insertion and deletion mutagenesis of the pro domain of pre-pro-TGFβ1 indicate that the structural integrity of the pro region is required in secretory transport of TGFβ1 precursors. Additionally, our results highlight the amino-terminal region of the pro domain as being important for interaction with the mature TGFβ1 and indicated that this interaction must be maintained for latent complex formation and protein secretion. Finally, a comparison of the amino acid sequences of the pro domains from TGFβ1, β2, and β3 indicate that, even though these domains share <50% amino acid identity, functionally important regions identified by insertional mutagenesis are strictly conserved among them. The sequence homology in these regions presumably reflects their biological importance.

We gratefully acknowledge Dave Dignam, Manohar Ratnam, Melvyn Soloff, and James Trempe for critical review of the manuscript; other members of the Department for helpful comments; and Kay Waggoner for the typescript. We would like to thank Ron Manger for supplying the colorimetric protocol for measuring cell growth; Mary Harte and Grainne McMahon for helpful suggestions; and Danielle Miller for supplying radioiodinated TGFβ1. During the course of this work, use was made of the Harold and Helen McMaster recombinant DNA Laboratory.

This work was supported by a grant to L. E. Gentry from the National Institutes of Health, National Cancer Institute (CA48091). L. E. Gentry is the recipient of the American Cancer Society Junior Faculty Research Award.

Received for publication 12 February 1991 and in revised form 3 May 1991.

References

Assoian, R. K., A. Komoriya, C. A. Meyers, D. M. Miller, and M. B. Sporn. 1983. Transforming growth factor-β in human platelets. *J. Biol. Chem.* 258:7155–7160.

Barnard, J. A., R. M. Lyons, and H. L. Moses. 1990. The cell biology of transforming growth factor β. *Biochim. Biophys. Acta.* 1032:79–87.

Brunner, A. M., L. E. Gentry, J. A. Cooper, and A. F. Purchio. 1988. Recombinant type 1 transforming growth factor β precursor preduced in chinese hamster ovary cells is glycosylated and phosphorylated. *Mol. Cell. Biol.* 8:2229–2232.

Brunner, A. M., H. Marquardt, A. R. Malacko, M. N. Lioubin, and A. F. Purchio. 1989. Site-directed mutagenesis of cysteine residues in the pro region of the transforming growth factor β1 precursor. *J. Biol. Chem.* 264:13660–13664.

de Martin, R., B. Haendler, R. Hofer-Warbinek, H. Gaugitsch, M. Wrann, H. Schlusener, J. M. Seifert, S. Bodmer, A. Fontana, and E. Hofer. 1987. Complementary DNA for human glioblastoma-derived T cell suppressor factor, a novel member of the transforming growth factor-β gene family. *EMBO (Eur. Mol. Biol. Organ.) J.* 6:3673–3677.

Derynck, R., J. A. Jarrett, E. Y. Chen, D. H. Eaton, J. R. Bell, R. K. Assoian, A. B. Roberts, M. B. Sporn, and D. V. Goeddel. 1985. Human transforming growth factor-β complementary DNA sequence and expression in normal and transformed cells. *Nature (Lond.).* 316:701–705.

Derynck, R., J. A. Jarrett, E. Y. Chen, and D. V. Goeddel. 1986. The murine transforming growth factor-β precursor. *J. Biol. Chem.* 261:4377–4379.

Derynck, R., P. B. Lindquist, A. Lee, D. Wen, J. Tamm, J. L. Graycar, L. Rhee, A. J. Mason, D. A. Miller, R. J. Coffey, H. L. Moses, and E. Y. Chen. 1988. A new type of transforming growth factor-β, TGF-β3. *EMBO (Eur. Mol. Biol. Organ.) J.* 7:3737–3743.

Doms, R. W., D. S. Keller, A. Helenius, and W. E. Balch. 1987. Role of adenosine triphosphate in regulating the assembly and transport of vesicular stomatitis virus G protein trimers. *J. Cell Biol.* 105:1957–1969.

Doms, R. W., A. Ruusala, C. Machamer, J. Helenius, A. Helenius, and J. K. Rose. 1988. Differential effects of mutations in three domains on folding, quarternary structure, and intracellular transport of vesicular stomatitis virus G protein. *J. Cell Biol.* 107:89–99.

Frolik, C. A., L. L. Dart, C. A. Meyers, D. M. Smith, and M. B. Sporn. 1983. Purification and initial characterization of a type β transforming growth factor from human placenta. *Proc. Natl. Acad. Sci. USA.* 80:3676–3680.

Gentry, L. E., and B. W. Nash. 1990. The pro domain of pre-pro-transforming growth factor β1 when independently expressed is a functional binding protein for the mature growth factor. *Biochemistry.* 29:6851–6857.

Gentry, L. E., N. R. Webb, G. J. Lim, A. M. Brunner, J. E. Ranchalis, D. R. Twardzik, M. N. Lioubin, H. Marquardt, and A. F. Purchio. 1987. Type 1 transforming growth factor beta: amplified expression and secretion of mature and precursor polypeptides in chinese hamster ovary cells. *Mol. Cell Biol.* 7:4318–4327.

Gentry, L. E., M. N. Lioubin, A. F. Purchio, and H. Marquardt. 1988. Molecular events in the processing of recombinant type 1 pre-pro transforming growth factor beta to the mature golypeptide. *Mol. Cell. Biol.* 8:4162–4168.

Gentry, L. E., X. Sha, H. Marquardt, and A. F. Purchio. 1989. Expression and processing of recombinant pre-pro-transforming growth factor beta-1. *In* Growth Inhibitory and Cytotoxic Polypeptides. Moses, H. L., P. Lengyel, and C. D. Stiles, editors. Alan R. Liss, Inc., New York. 143–154.

Giguere, V., S. M. Hollenberg, M. G. Rosenfeld, and R. M. Evans. 1986. Functional domains of the human glucocorticoid receptor. *Cell.* 46:645–652.

Grafl, R., K. Lang, H. Vogl, and F. X. Schmid. 1987. The mechanism of folding of pancreatic ribonucleases is independent of the presence of covalently linked carbohydrate. *J. Biol. Chem.* 262:10624–10629.

Gray, A. M., and A. J. Mason. 1990. Requirement for activin A and transforming growth factor-β1 pro-region in homodimer assembly. *Science (Wash. DC).* 247:1328–1330.

Hanks, S. K., R. Armour, J. H. Baldwin, F. Maldonado, J. Spiess, and R. W. Holley. 1988. Amino acid sequence of the BSC-1 cell growth inhibitor (polyergin) deduced from the nucleotide sequence of the cDNA. *Proc. Natl. Acad. Sci. USA.* 85:79–83.

Hardwicke, M. A., P. J. Vaughan, R. E. Sekulovich, R. O'Conner, and R. M. Sandri-goldin. 1989. The regions important for the activator and repressor functions of herpes simplex virus type 1 α protein ICP27 map to the c-terminal half of the molecule. *J. Virol.* 63:4590–4602.

Hobart, P., R. Crawford, L. Shen, R. Pictet, and W. J. Rutter. 1980. Cloning and sequence analysis of cDNAs encoding two distinct somatostatin precursors found in the endocrine pancreas of Anglerfish. *Nature (Lond.).* 288: 137–141.

Ikeda, T., M. N. Lioubin, and H. Marquardt. 1987. Human transforming growth factor type β2; production by a prostatic adenocarcinoma cell line, purification, and initial characterization. *Biochemistry.* 26:2406–2410.

Jakowlew, S. B., P. J. Dillard, P. Kondaiah, M. B. Sporn, and A. B. Roberts. 1988*a*. Complementary deoxyribonucleic acid cloning of a novel transforming growth factor-beta messenger ribonucleic acid from chicken embryo chondrocytes. *Mol. Endocrinol.* 2:747–755.

Jakowlew, S. B., P. J. Dillard, M. B. Sporn, and A. B. Roberts. 1988*b*. Complementary deoxyribonucleic acid cloning of a messenger ribonucleic acid encoding transforming growth factor-beta 4 from chicken embryo chondrocytes. *Mol. Endocrinol.* 2:1186–1195.

Kanazaki, T., A. Olofsson, A. Moren, C. Wernstedt, U. Hellman, K. Miyazono, L. Claesson-Welsh, and C. H. Heldin. 1990. TGF-β1 binding protein: a component of the large latent complex of TGF-β1 with multiple repeat sequences. *Cell.* 61:1051–1061.

Laemmli, U. K. 1970. Cleavage of structural proteins during the assembly of the head of bacteriophage T4. *Nature (Lond.).* 227:680–685.

Lathe, R., M. P. Kieny, S. Skory, and J. P. Lecocq. 1984. Linker tailing: unphosphorylated linker oligonucleotides for joining DNA termini. *DNA.* 3: 173–181.

Lawrence, D. A., R. Pircher, and P. Jullien. 1985. Conversion of a high molecular weight latent β-TGF from chicken embryo fibroblasts into a low molecular weight active beta-TGF under acidic conditions. *Biochem. Biophys. Res. Commun.* 133:1026–1034.

Lyman, S. D., and L. R. Rohrschneider. 1987. Analysis of functional domains of the v-fms-encoded protein of Susan McDonough strain feline sarcoma virus by linker insertion mutagenesis. *Mol. Cell. Biol.* 7:3287–3296.

Lyons, R. M., J. Keski-Oja, and H. L. Moses. 1988. Proteolytic activation of latent transforming growth factor-β from fibroblast-conditioned medium. *J. Cell Biol.* 106:1659–1665.

Lyons, R. M., L. E. Gentry, A. F. Purchio, and H. L. Moses. 1990. Mechanism of activation of latent recombinant transforming growth factor β1 by plasmin. *J. Cell Biol.* 110:1361–1367.

Madisen, L., N. R. Webb, T. M. Rose, H. Marquardt, T. Ikeda, D. Twardzick, S. Seyedin, and A. F. Purchio. 1988. Transforming growth factor-β2: cDNA cloning and sequence analysis. *DNA.* 7:1–8.

Miyazono, K., U. Hellman, C. Wernstedt, and C. H. Heldin. 1988. Latent high molecular weight complex of transforming growth factor β1. *J. Biol. Chem.* 263:6407–6415.

Mosmann, T. 1983. Rapid colorimetric assay for cellular growth and survival: application to proliferation and cytotoxicity assays. *J. Immunol. Methods.* 65:55–63.

Olden, K., J. B. Parent, and S. L. White. 1982. Carbohydrate moieties of glycoproteins. A re-evaluation of their function. *Biochim. Biophys. Acta.* 650:209–232.

Orci, L., M. Ravazzola, M. Amherdt, A. Perrelet, S. K. Powell, D. L. Quinn, and H. H. Moore. 1987. The trans-most cisternae of the Golgi complex: a compartment for sorting of secretory and plasma membrane proteins. *Cell.* 51:1039–1051.

Pircher, R., P. Jullien, and D. A. Lawrence. 1986. β-Transforming growth factor is stored in human blood platelets as a latent high molecular weight complex. *Biochem. Biophys. Res. Commun.* 136:30–37.

Purchio, A. F., J. A. Cooper, A. M. Brunner, M. N. Lioubin, L. E. Gentry, K. S. Kovacina, R. A. Roth, and H. Marquardt. 1988. Identification of mannose 6-phosphate in two asparagine-linked sugar chains of recombinant transforming growth factor β1 precursor. *J. Biol. Chem.* 263:14211–14215.

Roberts, A. B., M. A. Anzano, C. A. Meyers, J. Wideman, R. Blacher, Y.-C. Pan, S. Stien, S. R. Lehrman, J. M. Smith, L. C. Lamb, and M. B. Sporn. 1983. Purification and properties of a type β transforming growth factor from bovine kidney. *Biochemistry.* 22:5692–5698.

Roberts, A. B., and M. B. Sporn. 1988. Transforming growth factor β. *Adv. Cancer Res.* 51:107–145.

Roberts, A. B., and M. B. Sporn. 1990. The transforming growth factor-betas. *In* Peptide Growth Factors and Their Receptors. Sporn M. B., and A. B. Roberts, editors. Spring-Verlag, Heidelberg. 95:418–483.

Rose, J. K., and J. E. Bergman. 1983. Altered cytoplasmic domains affect intracellular transport of the vesicular stomatitis virus glycoprotein. *Cell.* 34:513–524.

Ruff, E., and A. Rizzino. 1986. Preparation and binding of radioactively labeled porcine transforming growth factor type β. *Biochem. Biophys. Res. Commun.* 138:714–719.

Sanger, F., and A. R. Coulson. 1975. A rapid method for determining sequences in DNA by primed synthesis with DNA polymerase. *J. Mol. Biol.* 94:441–448.

Seed, B. 1987. An LFA-3 cDNA encodes a phospholipid-linked membrane protein homologous to its receptor CD2. *Nature (Lond.).* 329:840–842.

Seed, B., and A. Aruffo. 1987. Molecular cloning of the CD2 antigen, the T-cell erythrocyte receptor, by a rapid immunoselection procedure. *Proc. Natl. Acad. Sci. USA.* 84:3365–3369.

Sha, X., A. M. Brunner, A. F. Purchio, and L. E. Gentry. 1989. Transforming growth factor β1: importance of glycosylation and acidic proteases for processing and secretion. *Mol. Endocrinol.* 3:1090–1098.

Sharples, K., G. D. Plowman, T. M. Rose, D. R. Twardzik, and A. F. Purchio. 1987. Cloning and sequence analysis of simian transforming growth factor-β cDNA. *DNA.* 6:239–244.

Slieker, L. J., T. M. Martensen, and M. D. Lane. 1986. Synthesis of epidermal growth factor receptor in human A431 cells. Glycosylation-dependent aquisition of ligand binding activity occurs post-translationally in the endoplasmic reticulum. *J. Biol. Chem.* 261:15233–15241.

Smith, D. E., and P. A. Fisher. 1984. Identification, developmental regulation, and response to heat shock of two antigenically related forms of a major nuclear envelope protein in *Drosophila* embryos: application of an improved method for affinity purification of antibodies using polypeptides immobilized on nitrocellulose blots. *J. Cell Biol.* 99:20–28.

Steiner, D. F., K. Docherty, and R. Carroll. 1984. Golgi/granule processing of peptide hormone and neuropeptide precursors: a minireview. *J. Cell. Biochem.* 24:121–130.

Stoller, T. J., and D. Shields. 1989. The propeptide of preprosomatostatin mediates intracellular transport and secretion of α-globin from mammalian cells. *J. Cell Biol.* 108:1647–1655.

Stone, J. C., T. Atkinson, M. Smith, and T. Pawson. 1984. Identification of functional regions in the transforming protein of fujinami sarcoma virus by inphase insertion mutagenesis. *Cell.* 37:549–558.

Stone, J., T. de Lange, G. Ramsay, E. Jakobovits, J. M. Bishop, H. Varmus, and W. Lee. 1987. Definition of regions in human c-myc that are involved in transformation and nuclear localization. *Mol. Cell. Biol.* 7:1697–1709.

ten Dijke, P., P. Hanson, K. K. Iwata, C. Pieler, and J. G. Foulkes. 1988. Identification of another member of the transforming growth factor type beta gene family. *Proc. Natl. Acad. Sci. USA.* 85:4715–4719.

Tsuji, T., F. Okada, K. Yamaguchi, and T. Nakamura. 1990. Molecular cloning of the large subunit of transforming growth factor type beta masking protein and expression of the mRNA in various tissues. *Proc. Natl. Acad. Sci. USA.* 87:8835–8839.

Wakefield, L. M., D. M. Smith, T. Masui, C. C. Harris, and M. B. Sporn. 1987. Distribution and modulation of the cellular receptor for transforming growth factor-beta. *J. Cell Biol.* 105:965–975.

Wakefield, L. M., D. M. Smith, K. C. Flanders, and M. B. Sporn. 1988. Latent transforming growth factor-β from human platelets. A high molecular weight complex containing precursor sequences. *J. Biol. Chem.* 263:7646–7654.

Wakefield, L. M., D. M. Smith, S. Broz, M. Jackson, A. D. Levinson, and M. B. Sporn. 1989. Recombinant TGF-β1 is synthesized as a two-component latent complex that shares some structural features with the native platelet latent TGF-β1 complex. *Growth Factors.* 1:203–218.