Osteoblasts Synthesize and Respond to Transforming Growth Factor-Type β (TGF-β) In Vitro

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Abstract. Transforming growth factor-type β (TGF-β) has been identified as a constituent of bone matrix (Seyedin, S. M., A. Y. Thompson, H. Bentz, D. M. Rosen, J. M. McPherson, A. Conti, N. R. Siegel, G. R. Gallupi, and K. A. Piez, 1986, *J. Biol. Chem.* 261:5693–5695). We used both developing bone and bone-forming cells in vitro to demonstrate the cellular origin of this peptide. TGF-β mRNA was detected by Northern analysis in both developing bone tissue and fetal bovine bone–forming cells using human cDNA probes. TGF-β was shown to be synthesized and secreted by metabolically labeled bone cell cultures by immunoprecipitation from the medium. Further, TGF-β activity was demonstrated in conditioned media from these cultures by competitive radioreceptor and growth promotion assays. Fetal bovine bone cells (FBBC) were found to have relatively few TGF-β receptors (5,800/cell) with an extremely low K_d of 2.2 pM (high binding affinity). In contrast to its inhibitory effects on the growth of many cell types including osteosarcoma cell lines, TGF-β stimulated the growth of subconfluent cultures of FBBC; it had little effect on the production of collagen by these cells. We conclude that bone-forming cells are a source for the TGF-β that is found in bone, and that these cells may be modulated by this factor in an autocrine fashion.

Transforming growth factor-type β (TGF-β),[1] discovered and named for its ability to phenotypically transform nonneoplastic fibroblasts in vitro (30), is emerging as the prototype for a family of multifunctional regulatory peptides (38). Many cells, both nonneoplastic and neoplastic, synthesize TGF-β and most of these cells have receptors for the peptide. The diverse effects of TGF-β on cell function have been further illuminated by the recent finding that TGF-β is similar, if not identical, to cartilage-inducing factor-A (36), a protein isolated from demineralized bone that induces the formation of cartilage proteoglycan and type II collagen from undifferentiated mesenchymal cells in vitro (35). Although platelets are the most concentrated source of TGF-β in the body (2), the high yield of TGF-β from bone (14) (~100-fold greater than from soft tissues such as placenta [10] and kidney [32]) suggests that bone has the greatest total amount of TGF-β. Since the level of serum-derived proteins in bone is high (e.g., α2 HS-glycoprotein, which is synthesized in the liver, can account for >2% of the total bone matrix [40]), the origin of TGF-β found in bone is not entirely clear, and some of it may simply be absorbed to the tissue from serum. Although recent studies of the production of growth factors by fetal rat calvaria have demonstrated secretion of TGF-β into bone organ culture medium (5), this developing tissue contains both mineralized and nonmineralized regions, with cells in nonmineralized regions exhibiting distinctly fibroblastic characteristics (i.e., production of types I and III collagen). Consequently, the cellular origin of TGF-β in this organ culture system also is unclear. In the present study, both developing bone tissue and bone cell cultures known to exhibit the osteoblastic phenotype were examined at molecular, biosynthetic, and functional levels.

1. *Abbreviations used in this paper*: FBBC, fetal bovine bone cells; TGF-β, transforming growth factor-type β; NRK, normal rat kidney fibroblasts.

Materials and Methods

Cell Culture

Primary cultures of FBBC were prepared as previously described (13) by incubating collagenase-treated subperiosteal bone fragments in low Ca^{++} nutrient medium until the cultures were confluent. Cells were then passaged by trypsin-EDTA, and plated at varying densities for the experiments described below. Cells were maintained in medium with normal levels of Ca^{++} for 48–72 h before the beginning of each experiment. Rat osteosarcoma cell lines, ROS 17/2 (22) and UMR 106 (26), were also used for comparison with the nontransformed FBBC.

Analysis of TGF-β mRNA

Various developing tissues dissected from fetal rats (day 19) and calves (3–5 mo of gestation), as well as from the Swarm rat chondrosarcoma were used for RNA extraction as previously described (6). RNA was also isolated from two rat osteosarcoma cell lines (ROS 17/2 and UMR 106), primary cultures of FBBC (42), cell cultures derived from bovine skin, tendon, articular cartilage, and smooth muscle, and from human lymphocytes (as a positive control). Northern analysis was performed using 1.2% agarose formaldehyde gels followed by transfer of RNA onto nitrocellulose (21). Either a nick-translated insert (1,060-bp Eco RI fragment) of a human TGF-β cDNA probe (7), kindly provided by Dr. Rik Derynck (Genentech, South San Francisco, CA) or a single stranded (219 bp) subclone of that probe was radiolabeled and hybridized (Fig. 1 *a*). The nitrocellulose blots were washed under standard stringent hybridization conditions (21).

Biosynthesis of TGF-β by FBBC

First passage FBBC were plated at a density of 20,000 cells/cm^2 and allowed to recover for 48–72 h. The cells were then incubated with 300 μCi of [^{35}S]cysteine for 20 h in DME containing 2% dialyzed calf serum and 10% of the usual concentration of methionine and cysteine. After incubation, the medium was saved, the cells were washed several times with PBS, and subsequently extracted with acid-ethanol. The extracts were sonicated, centrifuged to remove insoluble debris, and the resulting supernatants were used for immunoprecipitation. Aliquots of media and acid-ethanol extracts, containing 5×10^6 TCA-precipitable counts, were lyophilized and resuspended in 400 μl of immunoprecipitation buffer (50 mM Tris-HCl, pH 7.5, 0.15 M NaCl, 1% Triton X-100, 1% sodium deoxycholate, 0.1% SDS, 1 mM EDTA, 0.005% methiolate) and boiled for 4 min. The samples were precipitated three times with normal rabbit serum (20 μl) and washed *Staphylococcus aureus* (Immunoprecipitin from Bethesda Research Laboratories, Gaithersburg, MD) (20 μl of pelleted *S. aureus* resuspended in 100 μl of immunoprecipitation buffer). An IgG fraction of rabbit anti-human TGF-β (34), prepared by 50% ammonium sulfate precipitation, was added to the supernatant from the third preprecipitation, and the samples incubated overnight at 4°C. In some cases, the antibody was incubated overnight at 4°C with human platelet TGF-β before being added to the metabolically labeled sample in order to determine the specificity of the immunoprecipitation. The immunoreactive TGF-β was recovered by incubation with 100 μl equivalent *S. aureus* for 45 min at room temperature. After centrifugation the pellet was washed three times with immunoprecipitation buffer. The washed pellet was boiled for 4 min in a buffer containing 2% SDS and the supernatant obtained after centrifugation was subjected to electrophoresis on a 10% polyacrylamide gel according to Laemmli (17). In some cases, samples were boiled in the presence of 5% 2-mercaptoethanol and subjected to electrophoresis on 12.5% polyacrylamide gels. The gels were fixed, enhanced with 2,5 diphenyloxazole dissolved in DMSO, dried, and exposed to Kodak XAR-5 X-ray film at −70°C (4).

Secretion of TGF-β by FBBC

Cells were plated at varying densities and allowed to recover for 48 h. In addition, wells containing no cells were set up and incubated identically for the generation of control (no cell) medium to account for the possible release of serum during the subsequent incubations. The cells were then washed once with serum-free medium, and incubated in serum-free DME containing 50 μg/ml ascorbic acid, glutamine, and penicillin/streptomycin. After 48 h, the medium was removed and the cell number determined. The conditioned media samples (either tested directly or after acid activation [18, 19]) were assayed for TGF-β activity both by a competitive radioreceptor assay (simultaneous addition of competitor and radiolabeled TGF-β) using A549 cells (11) and by a bioassay that measures the ability of the peptide to induce normal rat kidney fibroblasts (NRK) colony formation in soft agar in the presence of epidermal growth factor (31). Human platelet TGF-β (2) was used as a standard in these assays. In both assays, the original concen-

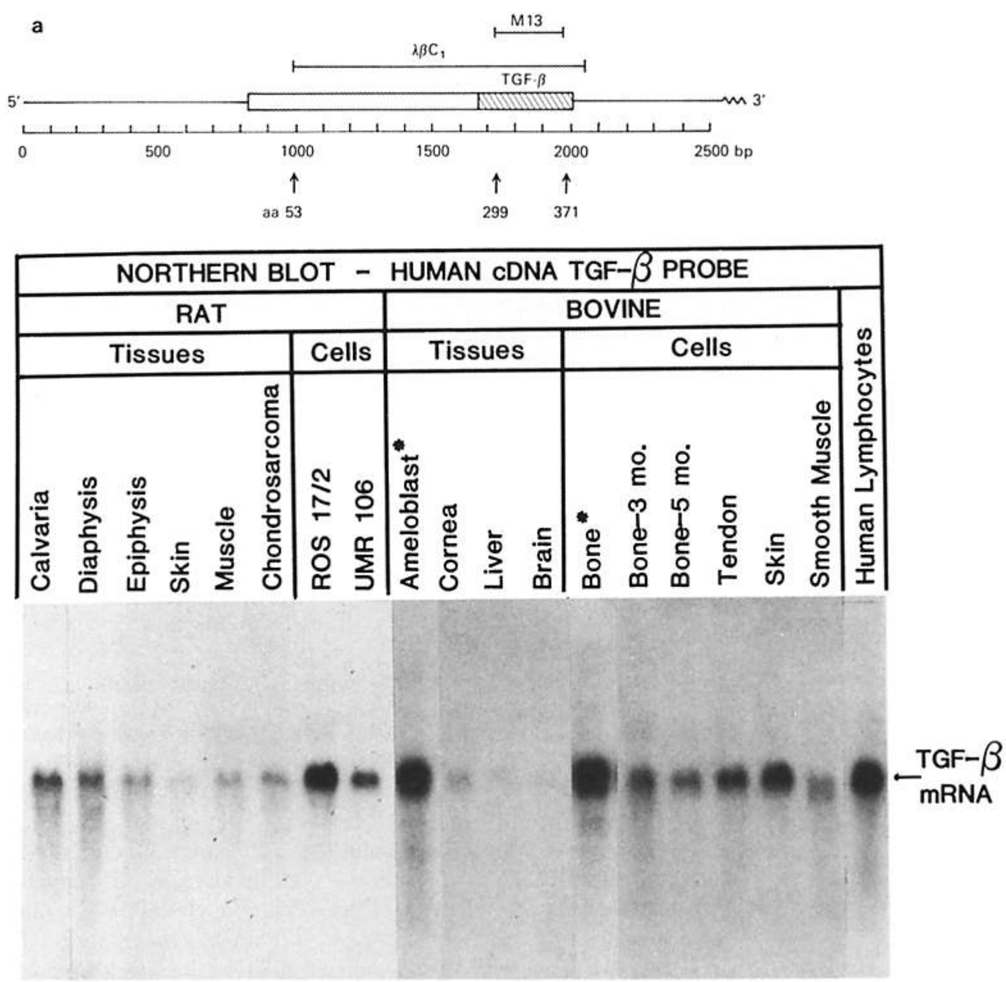

Figure 1. Northern blot analysis of TGF-β mRNA from rat and bovine tissues and cultured cells. (*a*) A human TGF-β cDNA was radiolabeled by hybridization of synthetic oligonucleotides complementary to the 3′ end of the cDNA followed by polymer extension using ^{32}P-nucleotides and DNA polymerase, or by electroelution of insert cDNA followed by nick translation with α-^{32}P-dCTP. Both probes contained the sequence encoding for the expressed amino acid sequence of TGF-β. The λβC$_1$ probe extends from nucleotide 996 to nucleotide 2,041 (amino acid 53 to beyond the end of the TGF-β molecule). The M13 probe begins at nucleotide 1,736 and ends at nucleotide 1,955 (aa 229–371). (*b*) RNA was isolated from fetal rat tissues (calvarial, ephiphyseal, and diaphyseal bone, skin, and muscle), the Swarm rat chondrosarcoma, and from bovine tissues (ameloblastic layer of developing teeth, cornea, liver, and brain). RNA from cultures of two rat osteoblastic cell lines (ROS 17/2, UMR 106), primary FBBC taken from fetuses of 3 and 5 mo, and fetal bovine tendon, skin, and smooth muscle cells were also analyzed. 15 μg of total RNA or 3.5 μg of poly A$^+$ RNA (*asterisk*) were subjected to electrophoresis in 1.2% agarose gels and transferred to nitrocellulose as described (21). Blots were hybridized with either the λβC$_1$ probe (rat tissues and cells) or the M13 probe (bovine tissues and cells). The blots were washed free of unbound probe (1.5 mM sodium citrate, 15 mM sodium chloride, 0.1% SDS at 55°C) and exposed to X-ray film for 72 h.

tration was calculated by comparison of a five or six point dilution (1:2) curve of the FBBC-conditioned medium with a standard curve as shown in Fig. 3 *A*.

Scatchard Analysis of TGF-β Binding

Cultures of FBBC as well as ROS 17/2 and UMR 106 rat osteosarcoma cell lines were plated at ∼70–95% confluency. After 24 h for recovery, cells were preincubated in serum-free medium for 2 h at 37°C to eliminate endogeneously bound ligand, and used for the determination of receptor number/cell and the dissociation constant (K_d) by Scatchard analysis using ^{125}I-labeled human platelet TGF-β as previously described (11).

Biological Effects of TGF-β

FBBC were plated at various densities and allowed to recover for 24 h in DME containing 10% FBS, at which time the plating efficiency was determined. The cells were washed once with serum-free medium, and subsequently treated with purified human platelet TGF-β (0–40 pM/ml) in DME containing 2% FBS. The effects of TGF-β on the growth of cells were assessed after 48 h (FBBC) or after 144 h (ROS 17/2 and UMR 106) by releasing 100% of the cells (as determined by microscopic evaluation) with trypsin-EDTA, and direct cell count using a Coulter counter.

The percentage of collagen synthesized by the cells in the absence and presence of TGF-β (10 and 50 ng/ml) after 18 h of treatment was determined by labeling the cells with [^{3}H]proline (20 μCi/ml) for 3 h as described (34) and analyzing both the medium and cell layer using the collagenase digestion method of Peterkofsky (28).

Results

Distribution of TGF-β mRNA in Tissues and Cultured Cells

The relative distribution of TGF-β mRNA in developing rat and bovine tissues, and in a variety of cell cultures was investigated by Northern analysis of extracted RNA using human TGF-β cDNA probes (Fig. 1 *a*). In fetal rat tissues, substantial amounts of hybridization were detected to a message of 2.4 kb in bone (calvarial, diaphyseal, and ephiphyseal bone), muscle, and in the rat Swarm chondrosarcoma. However, rat skin tissue contained relatively low levels. The rat osteosarcoma–derived cell lines, ROS 17/2 and UMR 106, also contained TGF-β message, the former of which contained the highest levels of all the rat samples analyzed (Fig. 1 *b*). In the fetal bovine tissues screened in this study, only the ameloblast layer of the developing tooth, an epithelium whose expression is crucial in enamel formation, showed a high degree of hybridization, while relatively low levels were found in cornea, and virtually none in liver and brain. Since extraction of mRNA from even fetal bovine bone is inefficient, mRNA was prepared from cultures of bone-forming cells and compared with cultures of cells derived from other tissues such as tendon, skin, and smooth muscle. Interestingly, all of the bovine cell cultures showed substantial levels of TGF-β message, and in contrast to the rat tissue, bovine skin fibroblasts contained relatively more TGF-β mRNA than the other cultures. In some, but not all experiments, the migration of TGF-β mRNA of smooth muscle cells was slightly faster than that of authentic TGF-β mRNA derived from human lymphocytes (Fig. 1 *b*).

Expression of TGF-β

Immunoprecipitation of [^{35}S]cysteine-labeled media from FBBC with a polyclonal antibody to TGF-β revealed a polypeptide of M_r 25,000 that was converted to a polypeptide of M_r 12,500 after reduction of disulfide bonds, identical to

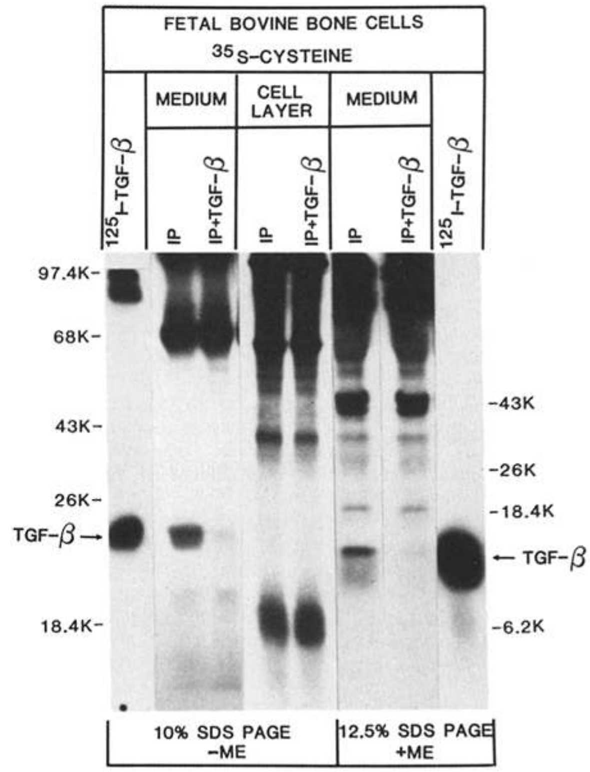

Figure 2. Immunoprecipitation of FBBC extracts and media. Cells were labeled for 20 h with [^{35}S]cysteine and media or acid-ethanol cell extracts were immunoprecipitated with either anti-TGF-β (IP), or with antibody preincubated with unlabeled TGF-β (IP+TGF-β). Nonreduced samples (−ME) were subjected to electrophoresis on 10% polyacrylamide gels while reduced samples (+ME) were subjected to electrophoresis on 12.5% polyacrylamide gels. In each case, ^{125}I-labeled human platelet TGF-β, along with standard molecular weight markers (the migration of which are indicated on the far left and far right of the figure) were subjected to electrophoresis on the same gels for comparison.

the behavior of ^{125}I-labeled human platelet TGF-β (Fig. 2). The immunoprecipitation of these polypeptides was blocked by the pretreatment of the antibody with pure, unlabeled TGF-β. Interestingly, relatively little TGF-β was identified in the cell layer fractions, suggesting that the peptide is secreted from, but not bound in the cell layer at the density used in this experiment, or in the absence of mineralization. A long radiolabeling time (20 h) was used in this experiment to assure that sufficient radiolabeled TGF-β accumulated in the medium to be detected by immunoprecipitation. The experimental design reduced the probability that a significant amount of TGF-β would be detected in the cell layer. However, studies with Ha-*ras*–transfected NIH-3T3 cells radiolabeled under a variety of conditions indicate that TGF-β is rapidly secreted from the cells making the intracellular TGF-β content below the detection limit (Flanders, K. C., unpublished results). Further, [^{35}S]cysteine-labeled TGF-β could only be precipitated from the medium (that was not acid activated) after boiling the sample, while ^{125}I-labeled human platelet TGF-β (which was previously acid activated) can be precipitated without boiling. This observation indicates that boiling either unmasks epitopes recognized by the antibody, or is equivalent to acid activation in the conversion of latent

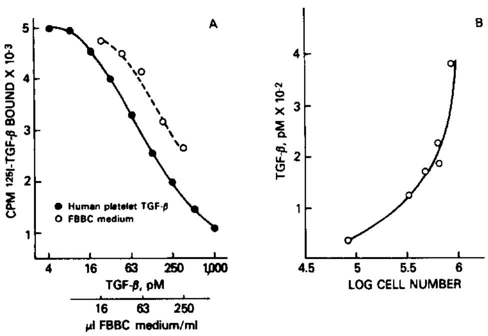

Figure 3. Secretion of biologically active TGF-β by FBBC. (*A*) Medium conditioned by 1.8×10^5 FBBC was acidified to pH 2, neutralized, and assayed in a competitive radioreceptor binding assay using A549 cells and human platelet TGF-β as a standard (11). (*B*) The concentration of TGF-β in 48-h medium conditioned by FBBC cells at varying densities was determined in the binding assay and plotted versus the log of the cell number. Monolayer confluency was reached at a log cell number of 5.7. Control (no cell) medium and unconditioned medium had no assayable TGF-β. Data represents the average of duplicate determinations for one of two representative experiments.

TGF-β to the active form (Flanders, K. C., unpublished results).

The biological activity of the TGF-β in the conditioned medium of FBBC was assayed both by competitive radioreceptor binding (Fig. 3) and by stimulation of NRK cell colony formation in soft agar in the presence of epidermal growth factor (not shown). The concentration of TGF-β present in the acid-activated conditioned medium of cultures ranging in density from 900 to 61,000 cells/cm² was determined in a competitive radioreceptor assay using A549 cells and a human platelet TGF-β standard (Fig. 3 *A*). The amount of TGF-β in the medium increased with increasing cell number, although the rate of secretion remained constant at ~14 fmol/10^6 cells/h; the concentration of TGF-β in the 48-h medium conditions by 0.84×10^6 cells was ~380 ± 80 pM compared with 35 ± 5 pM for 0.08×10^6 cells (Fig. 3 *B*). These results were verified by an assay using the FBBC-conditioned medium to induce NRK cell colony formation in soft agar (data not shown), thus ruling out any possibility of artifactual interference by a putative binding protein in the radioreceptor assay. Acid activation of FBBC-conditioned medium was necessary to determine the total amount of the TGF-β, confirming the latent nature of TGF-β secreted by FBBC. However, up to 25% of the TGF-β secreted was active without acid activation in this assay (data not shown), suggesting that latent TGF-β may serve as a more stable pool that is activated by the cells as needed.

Characterization of TGF-β Receptor Binding

The binding of ^{125}I-labeled human platelet TGF-β to receptors on FBBC was compared with that on the rat osteosarcoma cell lines (ROS 17/2 and UMR 106) by Scatchard analysis (Fig. 4). All three cell types had relatively few receptors per cell ($2,200 \pm 550$ for ROS, $7,100 \pm 3,300$ for UMR, and $5,600 \pm 160$ for FBBC) with very low K_d values of 3.0 ± 0.4, 7.8 ± 1.9, and 2.0 ± 0.2 pM, respectively. Analysis of the binding of TGF-β to the FBBC, but not the cloned osteosarcoma cell lines, suggested the existence of a second class of receptors of a higher abundance (10,000/cell) and relatively higher K_d of 12 pM.

Modulation of Osteoblast Activity in TGF-β

The addition of low levels (<40 pM) of human platelet TGF-β to FBBC plated at varying densities stimulated cell growth (Fig. 5 *A*). Two days after addition, 24–40 pM TGF-β caused a twofold increase in the number of cells plated at low density (10,000 cells/cm²). Interestingly, at both sparse and high cell densities, TGF-β had little mitogenic effect. The growth of both ROS 17/2 (Fig. 5 *B*) and UMR 106 (not shown) osteosarcoma cells at all densities studied was inhibited by TGF-β at the same concentrations that stimulated growth of first passage FBBC cells. Again, the inhibitory effect was less pronounced when the cells were plated at higher densities.

Since TGF-β has been shown to significantly increase synthesis of collagen and fibronectin by fibroblastic cells, its ability to modulate synthesis of matrix proteins by FBBC was also examined. TGF-β (10 and 50 ng/ml) had an overall stimulatory effect (1.5-fold) on protein synthesis in FBBC.

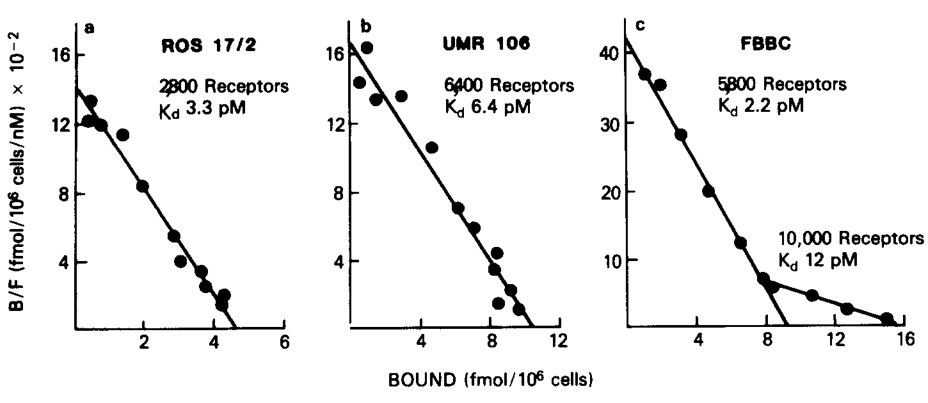

Figure 4. Scatchard analysis of TGF-β binding to ROS 17/2 (*a*), UMR 106 (*b*), and FBBC (*c*). Cells were plated at ~75–90% confluency in 35-mm dishes, washed, and incubated at 37°C for 2 h in serum-free medium to remove all bound ligands, and then incubated with increasing concentrations of ^{125}I-labeled human platelet TGF-β for 2 h at room temperature. Total cell-associated radioactivity and free TGF-β concentration were determined as previously described (11); data were corrected for nonspecific binding in the presence of 10 nM TGF-β. The data shown are from a representative determination; the experiments were repeated three additional times for each cell type with similar results.

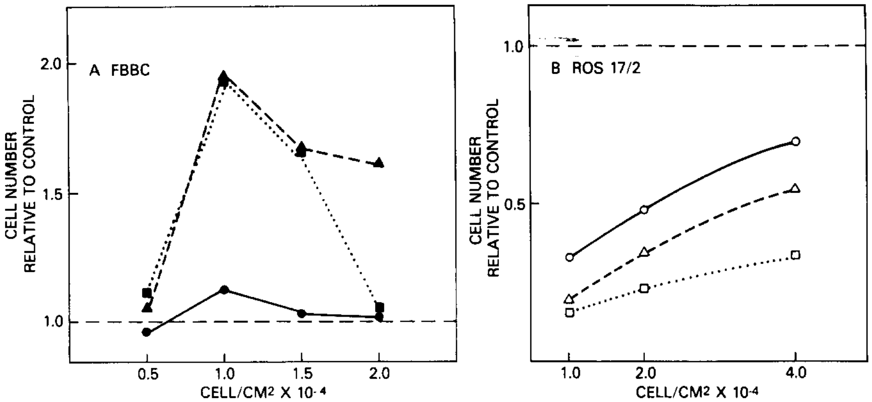

Figure 5. Effects of TGF-β on growth of FBBC (*solid symbols*) and ROS 17/2 (*open symbols*). FBBC were plated at four different densities and allowed to recover in DME containing 10% FCS. After 24 h, the cells were washed once with serum-free DME, and subsequently treated for 48 h with DME containing 2% FCS with 12 (●, ○), 24 (▲, △), or 40 pM (■, □) purified human platelet TGF-β. Cell number was determined by direct cell count of trypsin-EDTA released cells. ROS 17/2 cells were treated in a similar fashion except that after plating at similar densities, the cells were washed after 6 h of recovery and treated for 144 h with the same levels of TGF-β in DME containing 2% plasma-derived serum. The data shown are from one of two similar experiments. Each point is the mean of three different samples, and the cell counts from each sample were all within 10% of the mean. Of the cells plated at 1.0×10^4 cells/cm^2, FBBC were mitogenically stimulated ($28 \pm 1 \times 10^3$ cells in control wells and $54 \pm 5 \times 10^3$ cells in wells treated with 24 pM of TGF-β), whereas ROS cells were inhibited ($51 \pm 2 \times 10^3$ cells in control wells and $21 \pm 1 \times 10^3$ cells in wells treated with 12 pM TGF-β).

However, there was no effect on the percentage of bacterial collagenase-sensitive protein secreted by the cells, which was found to be 50% in control, and 45 and 47% in cultures treated with 10 and 50 ng/ml, respectively. Analysis of the cell layers fractions were similar. In contrast, TGF-β increased relative collagen secretion in ROS 17/2 cells from 1.4 (control) to 3.8% (50 ng/ml TGF-β treatment). While this is a threefold increase, it should be noted that the overall percentage of collagen secreted by these cells was substantially less than that of FBBC (1.4 as compared with 50%).

Discussion

The recently established identity of TGF-β and cartilage-inducing factor A (36) and the recently reported immunolocalization of TGF-β to bone (8), indicates that bone is perhaps the most abundant source of TGF-β in the body (14, 35), with a concentration ∼100-fold greater than that in soft tissues such as placenta (10) or kidney (32). We show here that one of the sources of TGF-β in bone is the bone-forming cells themselves. These cells were found to (*a*) transcribe TGF-β mRNA; (*b*) synthesize and secrete this peptide; (*c*) bear high affinity cell surface receptors, and (*d*) be mitogenically stimulated by TGF-β. The amount of TGF-β secreted by the confluent FBBC is ∼sixfold higher than from virally transformed cells and between 10- and 20-fold higher than from nontransformed cells (1). Although the TGF-β secreted by FBBC in vitro is predominantly in a latent form that must be activated before it can be recognized by antibodies or can bind to its receptor, up to 25% is in the active form. The implications of this for a potential autocrine action of TGF-β on FBBC are not presently understood.

The dissociation constants (K_d) for binding of TGF-β to receptors on either FBBC or the rat osteosarcoma cell lines, ROS 17/2 and UMR 106, are very low (2–6 pM), indicating the presence of very high affinity-binding sites on these cells. Scatchard analyses of the binding of TGF-β to 33 different cell lines has shown that cells of mesenchymal origin have 7,000–80,000 receptors/cell with dissociation constants ranging from 13 to 60 pM (41a); these osteoblastic cells are thus distinguished by their low receptor number and high binding affinity. A second, more abundant, class of receptors with a relatively lower affinity was also identified (Fig. 4 *c*). These receptors are not of the very low affinity class (K_d of 4 nm) previously described (11), but are similar to those found in bovine skin fibroblasts derived from fetuses of the same gestational age (Roberts, A. B., and P. Gehron Robey, unpublished results). Thus, they may be indicative of either the presence of undifferentiated osteoblasts or fibroblasts present in small numbers in the culture. Alternatively, this second class of receptors may account for the binding of TGF-β to a receptor for a closely related molecule, cartilage-inducing factor-B (35) with a relatively lower affinity for TGF-β.

In this system, TGF-β appears to promote the growth of the same cells that produce it. Moreover, the finding that ∼25% of the secreted TGF-β is in an active form suggests that it might potentially function as an autocrine growth factor for these cells. However, it is possible that the mitogenic effect of TGF-β may be the consequence of the induction of other growth factors by the cells as has been shown in the AKR-2B cell line (37, 20). The stimulation of the anchorage-dependent growth of FBBC by TGF-β is in striking contrast, however, to its inhibition of anchorage-dependent growth of the two osteosarcoma cell lines studied here, as well as that of many other cell types including a clonal murine calvaria-derived cell line, MC3T3E1 (25), fibroblasts (33, 41), epithelial cells (23, 33), myoblasts (9), hepatocytes (15, 24), and endothelial cells (3); before this, only primary human mesothelial cells have been reported to be stimulated to grow in monolayer culture by TGF-β (12). The density-dependent effects of TGF-β on stimulation of growth of FBBC are analogous to those seen on inhibition of growth of either fibroblasts (32) or the osteosarcoma cells (Fig. 5 *B*) by this peptide (i.e., the growth of subconfluent cultures of ROS 17/2 cells or of NRK fibroblasts is inhibited by TGF-β, but the effect is diminished as the cells approach confluency).

The different biological response patterns to TGF-β of the two rat osteosarcoma cell lines compared with FBBC emphasize that the osteosarcoma cell lines may not exhibit all of the characteristics of the osteoblastic phenotype as had been previously suggested, based on their response to parathyroid hormone (22, 27). Thus, identical concentrations of TGF-β inhibit the growth of the osteosarcoma cell lines and stimulate the growth of FBBC. Moreover, ROS 17/2 cells but not FBBC, respond to TGF-β with a selective increase in collagen synthesis compared with that of noncollagenous proteins. Significant differences were found, however, in the protein synthetic pattern of these two cell types (collagen secretion relative to total secreted proteins was 1.4 and 50% for ROS 17/2 and FBBC, respectively). Also in contrast to FBBC, fibroblastic cells are stimulated to increase collagen synthesis by TGF-β (16, 34). These data taken together suggest that TGF-β may serve as a mitogen for FBBC to expand this population of cells rather than to induce them to elaborate more matrix (i.e., become more differentiated). Expansion of this population of cells would also result in the elaboration of more TGF-β which could, in turn, act on other target cells. However, it should be noted that the effect of TGF-β on collagen production by FBBC cells may be density dependent, and further studies are needed to determine the effect of TGF-β on protein synthesis in superconfluent FBBC when matrix production and mineralization are initiated.

The abundance of TGF-β in bone (14, 35), the high affinity receptor binding, and the stimulation of the growth of FBBC, taken together with the finding that TGF-β can induce secretion of collagen and cartilage proteoglycans in mesenchymal cells (16, 34, 35) suggest a unique role for TGF-β in the growth and remodeling processes of hard tissues. Moreover, the findings that TGF-β stimulates bone resorption (39) and is itself released by organ cultures of developing bone exposed to parathyroid hormone (29) suggest that TGF-β may be involved in the "coupling" of bone resorption and bone formation to maintain normal rates of bone turnover (29). Further studies may clarify its role in bone metabolism in normal and diseased states.

The authors thank Lalage Wakefield for helpful suggestions on the Scatchard analysis of TGF-β binding, Rik Derynck for providing the $\lambda\beta C_1$ human TGF-β cDNA probe, and Camille I. Ramis, Kathleen M. Conn, and Deborah M. Naglak for their expert technical assistance.

Received for publication 17 December 1986, and in revised form 17 March 1987.

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