

# Alterations in the Level of Phosphotyrosine Signal Transduction Constituents in Human Parotid Tumors (43969)

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**Abstract.** Human parotid tumors were evaluated for the activation of the phosphotyrosine signaling pathway by Western blot, enzyme activity assay, and reverse transcriptase-polymerase chain reaction. Warthin's tumor and mucoepidermoid carcinomas had the greatest level of tyrosine phosphorylated proteins identified in plasma membrane fractions. These tumors, along with pleomorphic adenocarcinoma, showed high levels of membrane expression of the tyrosine kinase receptor, *c-erbB-2*, and phosphatidylinositol-3-kinase. Expression of the epidermal growth factor receptor was confined to normal tissue. The level of mRNA for *c-erbB* was elevated only in mucoepidermoid carcinomas. Messenger RNA levels for *ras* were unchanged from control levels in all tumors, while the level of *src* mRNA was higher in the tumor samples than the normal parotid tissue. The activities of several signal transduction kinases, including protein kinase A and C were elevated in tumor tissue (7.7- to 18.9- and 0.4- to 3.7-fold higher, respectively), relative to surrounding normal tissue. While the level of glandular amylase was reduced (22%–0% of normal levels) in the tumor tissue, epidermal growth factor (EGF) and transforming growth factor- $\alpha$  (TGF $\alpha$ ) content was dramatically higher in the neoplastic tissue (10- to 170-fold and 4.6- to 6.0-fold, respectively). These results suggest that with the presence of elevated levels of EGF, TGF $\alpha$ , and the oncoprotein receptor *c-erbB-2* in the membrane of parotid tumors, cell proliferation and activation of the phosphotyrosine signal transduction pathway may involve autocrine stimulation through the expression of high levels of growth factor and receptor in the same tissue.

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Protein phosphorylation patterns generated in response to extracellular stimuli have been shown to be involved in regulating a diverse array of cellular phenotypic and biochemical responses. Prominent among these is the role postulated for the tyro-

sine kinases in coordinating normal and neoplastic cell growth and function (1, 2). The initiation of signal transduction typically takes place through the binding of ligand (growth factor) to its cell surface receptor. This interaction results in the activation of receptor intrinsic tyrosine kinase activity (3, 4). Intracellular perpetuation of the signal involves the tyrosine phosphorylation cascade and activation of a series of proteins which become membrane associated in a complex with the receptor through the presence of SH-2 (*src* homology) domains in the primary structure (5). One of these proteins, phospholipase C $\gamma$ , causes the hydrolysis of phosphatidylinositol-4,5-bisphosphate to generate the second messenger molecules, inositol-1,4,5-trisphosphate (IP<sub>3</sub>) and diacylglycerol (DAG) (6,

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7). This results in the release of intracellular  $\text{Ca}^{2+}$  and the activation of protein kinase C (PKC). The activation of *ser/thr* kinases such as PKC subsequently phosphorylate the tyrosine kinase receptor leading to the downregulation of receptor intrinsic tyrosine kinase activity (7). In exocrine tissues, the activation of not only PKC and increased intracellular  $\text{Ca}^{2+}$  but also the activation of protein kinase A (PKA) are involved in the regulation of glandular secretory function (8). The activation of PKA typically results from increases in intracellular cAMP subsequent to the stimulation of the  $\beta$ -adrenergic receptor (9). However, for a number of tissues, including the rat parotid glands, activation of PKA in response to epidermal growth factor (EGF) treatment results from an  $\beta$ -adrenergic receptor independent mechanism through signal transduction pathway crosstalk (10–12).

The oncoprotein receptor *c-erbB-2*, is the transformation-associated homolog of the EGF receptor (EGF-R). The overexpression of this protein and its accompanying tyrosine kinase activity has been observed in breast cell carcinoma, colorectal carcinomas, and carcinomas of the salivary glands, as well as other malignancies (13–15). Other kinases of membrane phosphatidylinositol metabolism, such as the phosphatidylinositol-3-kinase (PI3-kinase) are also activated by the EGF-R (16). These kinase products have as yet undefined roles in second messenger signaling.

In the present investigation, we report on the presence of elevated levels of the *c-erbB-2* receptor in various neoplastic tissues from the parotid gland along with the activation of or increased RNA levels for components of the phosphotyrosine signaling pathway. In addition, we evaluated the presence of several secretory proteins produced by the parotid gland: amylase, which is synthesized by the acinar cells (17), and EGF and transforming growth factor- $\alpha$  (TGF $\alpha$ ), both products of the duct cells (18, 19).

## Materials and Methods

**Reagents.** Antibodies to the human EGF-R, *c-erbB-2*, PI3-kinase, and phosphotyrosine were purchased from Upstate Biotechnology Inc. (Lake Placid, NY). [ $^{125}\text{I}$ ]Labeled protein-A and [ $^{32}\text{P}$ - $\gamma$ ]-ATP were obtained from Amersham (Arlington Heights, IL). Pep-Tag, a nonradioactive assay kit for measuring protein kinase A, was purchased from Promega Co. (Madison, WI). The reagent for assaying protein kinase C activity was obtained from Gibco (Grand Island, NY). All other reagents were of ultrapure quality and purchased from commercial sources.

**Surgical Specimens.** Parotid tumor samples were obtained from biopsy material, flash frozen in liquid nitrogen, along with surrounding normal tissue where possible. Biopsy material was identified in ac-

cordance with World Health Organization specifications and obtained through the Tissue Procurement Bank of the University of Florida Cancer Research Center with approval from the University of Florida Institutional Review Board for use of human tissue samples and the E.N.T. Clinic of the University of Bergen, Bergen, Norway. Confirmation of biopsy diagnosis of parotid gland normal tissue surrounding tumor tissue (eight cases), pleomorphic adenoma (PMA) (four cases), mucoepidermoid carcinomas (MEC) (six cases), Warthin's tumor (WT) (three cases), and carcinoma in pleomorphic adenoma (CaPMA) (three cases), as well as necrotic tissue (1 case) were performed by the Pathology Service of Shands Hospital, University of Florida, Gainesville, FL.

**Preparation of Total Membrane and Cytosolic Fractions.** Frozen parotid tissue samples from biopsy were homogenized on ice in 5 ml of 10 mM Tris pH 7.4 containing 1.0  $\mu\text{M}$  leupeptin, 4  $\mu\text{g/ml}$  phenylmethylsulfonyl fluoride, 1 mM Na-orthovanadate, and 10  $\mu\text{M}$  Na-pyrophosphate by Dounce homogenization. The total membrane pellet was collected by centrifugation of the gland lysate at 100,000g for 1 hr at 4°C. The membrane fraction was resuspended in 1.0 ml of the above Tris buffer. Protein concentration was subsequently determined by the method of Bradford using bovine serum albumin (BSA) as a standard (20).

**Measurement of Amylase Activity in Cell Lysates.** The level of cellular amylase activity was measured following the activity assay described by Bernfeld (21) using starch as the substrate. The incubation solution consisted of 0.4 g of soluble starch in 60 mM Tris HCl containing 0.15 M NaCl and 3 mM  $\text{CaCl}_2$ . The stop solution contained 0.0045%  $\text{I}_2$ , 0.045% KI, and 0.03 N HCl. After terminating the reactions (at 5 and 10 min), absorbance was measured at 620 nm. The enzyme activity was expressed as the mean micrograms of starch hydrolyzed per minute per microgram of cytoplasmic lysate  $\pm$  SEM.

**Western Blot Analysis of Proteins.** Separation of gland lysate proteins was achieved by electrophoresis on a 10% SDS-polyacrylamide gel using the Tris-glycine system of Pugsley and Schnaitman (22), followed by transfer to nitrocellulose at 17 V overnight (23). Phosphotyrosine containing proteins, PI-3 kinase, *c-erbB-2* and EGF-R were detected by reaction of the nitrocellulose with a 1:500 dilution of the antibody into Tris buffered saline containing the blocking components 3% BSA and 3% nonfat dry milk. Proteins were detected by incubation with either [ $^{125}\text{I}$ ] protein-A followed by autoradiography at  $-80^\circ\text{C}$  with Kodak XAR-5 film or using a goat anti-rabbit polyclonal second antibody conjugated to alkaline phosphatase and color development using standard techniques.

**Protein Kinase C Assay.** The protein kinase C activity in the cytosolic and plasma membrane fractions was measured following the protocol developed by Gibco/BRL and described elsewhere (24). In brief, reaction mixtures (50  $\mu$ l) contained 20  $\mu$ l of 20 mM Tris, pH 7.5, 10 mM  $\beta$ -mercaptoethanol, 0.2 M NaCl, 5  $\mu$ l enzyme (tumor or normal tissue samples), and water. The reactions were initiated by the addition of [ $\gamma$ <sup>32</sup>P]-ATP (specific activity: 3000 Ci/mmol) and the substrate peptide followed by incubation for a total of 5 min at 30°C.

**Determination of Protein Kinase A Activity.** Cyclic AMP-dependent PKA activity in parotid gland biopsy lysates was measured by using the Pep-Tag nonradioactive detection system as described previously by Hu *et al.* (25). The brightly colored fluorescent peptide substrate, upon phosphorylation by PKA in the tissue sample, alters the charge and subsequent mobility, which allows distinguishing the phosphorylated from the nonphosphorylated version of the substrate when separated by agarose gel electrophoresis. The fluorescence associated with the phosphorylated band was measured in a spectrofluorimeter (Perkin-Elmer, Norwalk, CT) with excitation at 570 nm and emission at 593 nm.

**Radioimmunoassay of EGF and TGF $\alpha$  Levels.** EGF and transforming growth factor- $\alpha$  (TGF $\alpha$ ) levels in the cytosolic fraction of parotid gland biopsy tissue were measured using a radioimmunoassay (RIA) specific for the growth factor (19, 26). Briefly, 200  $\mu$ l of gland lysate were incubated with 25  $\mu$ l of a 1:50 dilution of a rabbit polyclonal antibody to human recombinant EGF (rhEGF) or rhTGF $\alpha$  in phosphate-buffered saline (PBS) containing 0.1% BSA for 1 hr at 37°C. [<sup>125</sup>I]Labeled EGF (60,000 cpm) in 25  $\mu$ l were added and incubated for an additional hour at 37°C. Immune complexes were subsequently precipitated by the addition of 50  $\mu$ l human immunoglobulin G (20

mg/ml) and 3.5 ml 15% polyethylene glycol (mol wt: 6000) in PBS, followed by centrifugation at 7000g for 20 min at 4°C in a Sorvall RC 5B (Norwalk, CT). Radioactivity in the pellet was quantified by a Beckman gamma counter model 3008. Concentrations of EGF or TGF $\alpha$  were calculated by averaging the amounts of growth factor interpolated from the linear regression curve of the EGF or TGF $\alpha$  standard and expressed as nanograms per milligram of protein. All values for growth factor concentrations were the result of two determinations assayed in duplicate. Student's *t* test was used for statistical analysis of data. Concentrations were expressed as the mean nanograms per milligram of gland protein  $\pm$  SEM.

**RNA Extraction and Reverse Transcriptase-Polymerase Chain Reaction.** Frozen specimens were homogenized on ice in a guanidinium thiocyanate lysis buffer by Dounce homogenization and total RNA was purified by phenol-chloroform extraction and sodium acetate/isopropanol precipitation (19).

Five hundred nanograms of RNA were used for each 20- $\mu$ l reverse transcriptase-polymerase chain reaction (RT-PCR) reaction, following instructions provided with the Perkin-Elmer GeneAmp kit with a modification in which 5  $\mu$ l of cDNA were used for each 50- $\mu$ l PCR reaction. Each PCR reaction contained primer pairs for one of the oncogene products and a primer pair for  $\beta$ -actin gene, with the latter serving as the single copy control gene. The oligonucleotide sequences of the primer sets are as shown in Table I. Reverse transcription reaction of total RNA was carried out using 1  $\mu$ g of RNA along with random hexamer primers at 42°C for 20 min to obtain first strand cDNA synthesis. Reverse transcriptase and RNasin were inactivated by heating to 99°C for 5 min followed by incubation at 5°C for 5 min. With the addition of the appropriate specific upstream and downstream primers for proto-oncogene and  $\beta$ -actin coding sequences,

**Table I.** Oligonucleotides Used for RT-PCR Amplification

<i>c-erbB-2</i>	Upstream	5'AACCTGGAACCTCACCTACCTG3'
	Downstream	5'CAGGCTCTGACAATCCTCAGA3'
<i>src</i>	Upstream	5'TACCAAACCTCAGCCTCATGCC3'
	Downstream	5'GTGGCGTCGTTCTTAATGCAC3'
<i>ras</i>	Upstream	5'CTCATGAGCTATGCCAACGA3'
	Downstream	5'TTTGGGGTCATCTCGGAGATC3'
$\beta$ -Actin <sup>a</sup>	Upstream	5'TCTACAATGAGCTGCGTGTGG3'
	Downstream	5'CTTCATGAGGTAGTCCGTCAG3'
$\beta$ -Actin <sup>b</sup>	Upstream	5'GTGGGCCGCTCTAGGCACCA3'
	Downstream	5'GGTGCCAAATCTTCTCCATAT3'

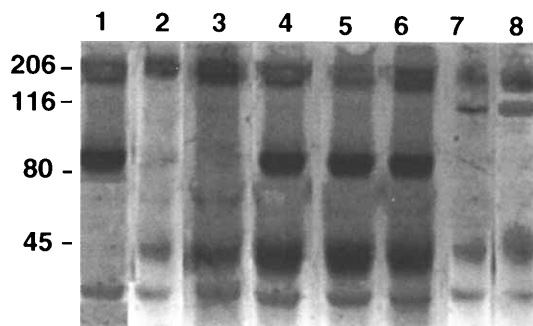
*Note.* These primers generated *c-erbB-2*, *src*, and *ras* amplification products of 471, 465, and 315, respectively.  $\beta$ -Actin primers produced amplification products of <sup>a</sup>305 and <sup>b</sup>246bp. Confirmation of the individual RT-PCR products of each oncogene amplification was obtained by restriction endonuclease digestion with *PvuII* and *TaqI* for *c-erbB-2*, with *KpnI* and *TaqI* for *ras* and with *PstI* and *TaqI* for *src* bands.

amplification was initiated with the addition of *Taq* polymerase after a 4-min initial melt at 94°C. This was followed by 40 cycles at 94°C for 1 min, 58°C for 2 min, and 72°C for 3 min. The amplification products from control and tumor tissue using the primer sets presented in Table I were generated in the linear range of *Taq* polymerase activity for amplicons in the size range of 300–500 bp (data not included). Confirmation of amplification of the correct cDNA was obtained by specific restriction endonuclease digestion as determined through Genbank sequences (27). Densitometric analysis of band density from RT-PCR products separated on 1.5% agarose gels stained with ethidium bromide was obtained using an HP flatbed scanner, Scanjet IICx, coupled to a computer equipped with NIH image and Adobe analysis software.

**Statistical Analysis.** The statistical significance of variance among means was determined by a single factor analysis of variance followed by a multiple comparisons test using SAS computer programs.  $P < 0.05$  was considered significant. All enzyme assays were performed within the linear range of each enzyme activity as determined for control and tumor tissues prior to the determination of the results presented here (data not shown).

## Results

In order to assess the involvement of the tyrosine kinase second messenger signaling pathway in the uncontrolled growth of tumor cells of the parotid gland, Western blot analysis of total membrane preparations was performed using an antibody directed against tyrosine-phosphorylated proteins. As shown in Figure 1, a large number of proteins were identified by the an-



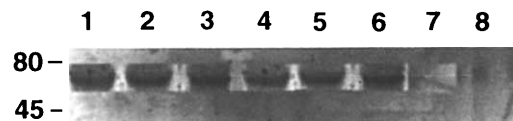
**Figure 1.** Western blot profile of phosphotyrosine containing proteins from human parotid tumor tissue and normal tissue. An equal quantity of protein (40 µg) isolated in total membrane fractions were separated on a 10% SDS–polyacrylamide gel prior to transfer to nitrocellulose. The proteins were visualized with color development reagents following incubation with an alkaline phosphatase-conjugated goat anti-rabbit second antibody. Prestained molecular weight standards are: 206,000 Daltons, myosin; 116,000 Daltons, β-galactosidase; 80,000 Daltons, bovine serum albumin; 45,000 Daltons, ovalbumin. Lane 1, pleomorphic adenocarcinoma (PMA); Lane 2 and 3, Warthin's tumor (WT); Lane 4, 5, and 6, mucoepidermoid carcinoma (MEC); Lane 7 and 8, normal parotid tissue (N).

tibody in the WT and MEC. By contrast, tissue material removed from the surrounding gland and identified as normal based upon its histology shows very few proteins as being tyrosine phosphorylated. The tissue associated with CaPMA demonstrated a pattern of protein staining different from normal and MEC and Warthin's tumors.

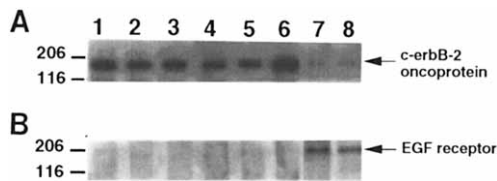
The specific identification of the PI3-kinase, a signal transduction molecule known to be activated by tyrosine phosphorylation in association with the membrane, was performed using an antibody monospecific for the protein (28). The PI3-kinase was only identified in the membrane samples from the neoplastic tissue and not in the control normal tissue (Fig. 2).

Since it has previously been reported that parotid tumors possess elevated levels of *c-erbB-2* receptors by immunohistochemistry (15), we analyzed membrane preparations for the presence of *c-erbB* in our parotid tumor samples and normal tissue. The results presented in Figure 3A indicate that all tissue material had this isoform of the receptor present. However, only in the tumor tissue was high level of expression observed relative to the normal parotid tissue (confirmed by densitometer analysis). On the other hand, specific analysis for the presence of the normal human EGF-R revealed it to be detectable only in the normal tissue (Fig. 3B).

To investigate potential changes in *c-erbB-2* mRNA which would correspond to the alterations in membrane receptor profiles, RT-PCR was performed on isolated total cellular RNA. Primers for β-actin expression were included so as to semiquantitate the relative levels of transcripts for *c-erb*, *src*, and *ras* proto-oncogenes following densitometer analysis. The *c-erb* primer set will hybridize to cDNA from both the normal EGF-R as well as sequences for *c-erbB-2*, since the region chosen for amplification contains common internal coding regions. The typical profile of RT-PCR amplicons is presented in Figure 4, B–D. The profile of expected restriction endonuclease fragments predicted by digestion of the specific amplicons for *c-erb*, *src*, and *ras* is presented in Figure 4A. Digestion of *src* (predicted size: 465 bp; Fig. 4A, Lane 10) with *Pst*I and *Taq*I endonucleases gave fragments of 375, and 90, and 267, and 198 bp, respectively; *c-erbB-2* (predicted size: 471 bp; Fig. 4A, Lane 10) digested with *Pvu*II and *Taq*I gave products of 360 and 111, and 252 and 299 bp, respectively; *ras* (predicted size: 315 bp;



**Figure 2.** Identification of phosphatidylinositol-3-kinase in association with the plasma membrane of human parotid tumors or normal tissue. Visualization of the protein and order of tumor material was as in Figure 1.



**Figure 3.** Autoradiographic visualization of the oncoprotein receptor *c-erbB-2* (A) and the EGF-R (B) in membrane preparations of human parotid tumors and normal tissue. Following incubation of the nitrocellulose filters with a primary rabbit polyclonal antibody to the *c-erbB-2* or EGF-R, the filters were washed and incubated with [<sup>125</sup>I]protein-A followed by autoradiography at -80°C for 48-72 hr using Kodak X-AR5 film. Lanes representing tumor or normal tissue are as indicated in Figure 1.

Fig. 4A, Lane 4) digested with *KpnI* and *TaqI* gave restriction products of 238 and 77, and 262 and 53 bp, respectively. In the digestion of *src* amplicons with *PstI*, there is residual uncut product at 465 bp while the expected larger fragment of 375 bp is clearly visible. The smaller fragment of 90 bp was present but did not photograph due to its weak intensity under ultraviolet detection. As summarized in Table II, only MEC tumors had an elevated ratio of >1 for *c-erbB-2* (Fig. 4B) relative to normal tissue ( $F = 2.99 > F_{0.05(4,17)} 2.96$ ,  $P < 0.05$ ) and other types of tumor tissue. For the level of *src* mRNA (Fig. 4D), again all MEC tumors, WT, PMA, and CaPMA had ratios to  $\beta$ -actin >1 and  $F = 3.12 > F_{0.05(4,17)} 2.96$ ,  $P < 0.05$ . There was, however, no difference between benign and carcinoma in pleomorphic adenomas. The *ras*/ $\beta$ -actin ratio of the band intensities (Fig. 4C) from the RT-PCR reactions of the various tumors and normal tissue had no significant statistical differences ( $F = 2.04 < F_{0.05(4,17)} 2.96$ ,  $P > 0.095$ ) (Fig. 4 and Table II).

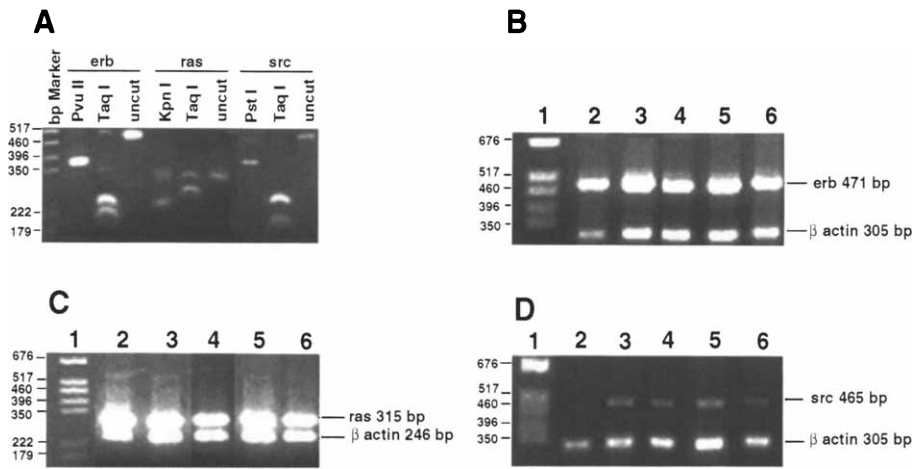
Two soluble, cytoplasmic kinases, PKA and PKC, have been identified as participants in the control of cell growth by downregulating the activity of the Raf-1-MAP kinase pathway (29) and the tyrosine kinase activity of the EGF-R (7) respectively. Along with intracellular free  $Ca^{2+}$ , these kinases are also involved in the secretory response of the salivary gland following sympathetic agonist stimulation (8). Elevated kinase activity for PKC was found in MEC, PMA, and WT as shown in Figure 5 ( $F = 3.57 > F_{0.05(4,14)} 3.11$ ,  $P < 0.05$ ). The activity in the WT was 3.7-fold higher and PMAs 2.7-fold higher than the normal tissue, while the MEC level was only increased by 0.4-fold. For the PKA enzyme, all three parotid tumor groups had higher kinase activity. The increase in MEC was to 18.9-fold; WT, 7.7-fold, PMA, 8.57-fold; and CaPMA, 9.1-fold greater than the normal control parotid tissue (Fig. 6) ( $F = 2.80 > F_{(0.10(4,14))} 2.39$ ,  $P < 0.10$ ).

Finally, the level of the three secretory proteins of the parotid gland: amylase (17), synthesized by the acinar cells, and EGF (18) and TGF $\alpha$  (19), both synthesized by the ductal cells, was evaluated by enzyme assay (20) or radioimmunoassay. The highest

level of amylase activity was recorded in the normal tissue, consistent with reports from other laboratories (30). Dramatic reductions in amylase activity were observed in the tumor tissues ( $F = 10.9048 > F_{0.10(4,14)} 5.04$ ,  $P < 0.01$ ), while there is no significant difference in amylase activity between PMA, WT, CaPMA, and MEC through the *F-Q* test (Fig. 7). The level of amylase in the MECs was approximately 22% of the control tissue, while in PMAs and CaPMAs, as well as WTs, it was almost zero. EGF and TGF $\alpha$  associated with the parotid tumor tissue was substantially elevated relative to control tissue ( $F = 3.59$ ,  $16.35$ ,  $> F_{0.05(4,14)} 3.11$ ;  $0.01(4,14) 5.04$ ,  $P < 0.05$ ,  $0.01$ , respectively). The EGF concentrations were 170-, 60-, 25-, and 10-fold higher for the PMA, WT, MEC, and CaPMA tumor groups, respectively (Fig. 8A). For TGF $\alpha$ , the concentrations of growth factor were 4.6-, 4.7-, and 6.0-fold higher for the PMAs, WTs, and MECs, respectively (Fig. 8B). The EGF concentrations in PMA were much higher than other tumors according to *F-Q* test.

## Discussion

The presence of oncoproteins in replacement of the normal cellular homolog in many transformed cells is a hallmark of cancer (3, 4). Previous studies have, in fact, identified the presence of mutant forms of *H-ras* and the oncoprotein form of the EGF-R, *c-erbB-2*, in tumors of the parotid gland (15, 31). Both of these proteins are also integral components of the tyrosine kinase second messenger signaling pathway (4) that transduces normal cell responses leading to DNA synthesis and cell division via tyrosine phosphorylation of the intracellular protein components (1-4). The identification of higher levels of tyrosine phosphoprotein profiles as well as the membrane association of *c-erbB-2* and PI3-kinase suggests that this holds true for different parotid gland tumors. However, increased mRNA levels were observed consistently only for *src* expression in all tumors examined and *c-erbB* in MEC tumors when compared with normal tissue. The fact that we could not demonstrate a correlation between mRNA levels and protein expression such as for the *erbB* receptor, suggests there are differences in the tumor tissue in regards to post-translational regulatory mechanisms. The most significant and consistent finding of this study was the observation of dramatically elevated levels of EGF present in parotid tumors. This provides a potential mechanism for the self-regulation (autocrine stimulation) of growth based upon the higher concentration of both the ligand (EGF) and its receptor (*c-erbB-2*) in the same proximity for the cells from the neoplastic tissue. Transforming growth factor- $\alpha$  is a member of EGF-like growth factor family which binds to the 170-kDa EGF-R nec-

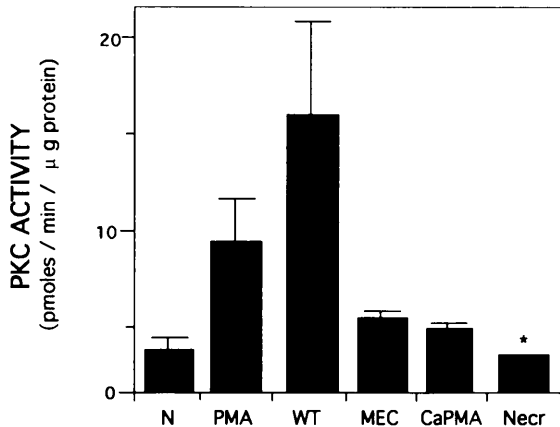


**Figure 4.** RT-PCR amplification of proto-oncogene products for *erbB*, *ras*, and *src* from human parotid tumors. Total RNA was isolated from parotid gland lysates. Ethidium bromide stained products of amplification: Lane 1, pGEM (Promega; Madison, WI) DNA molecular weight markers; Lane 2 and 4, normal parotid tissue; Lane 3, MEC tumor; Lane 6, PMA. (A) The product generated from normal tissue isolated from the agarose gel and digested with the indicated restriction endonuclease to indicate proper amplification of the predicted cDNA product. Amplification products and restriction endonuclease digestion fragment size for *PvuII*, *TaqI*, and uncut PCR amplicons: (B) PCR amplification products generated with  $\beta$ -actin and *erbB* primers; (C) PCR amplification products generated with  $\beta$ -actin and *ras* primers; (D) PCR amplification products generated with  $\beta$ -actin and *src* primers.

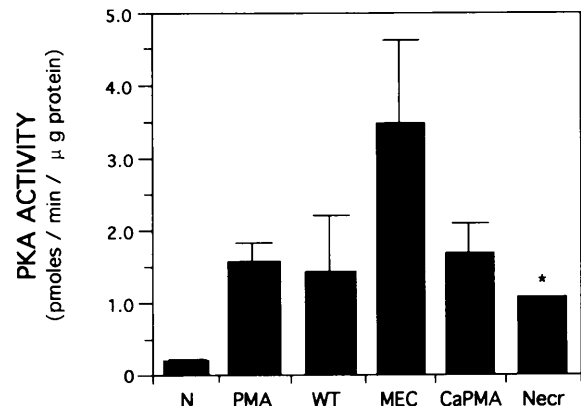
**Table II.** The Average Oncogene/ $\beta$ -Actin mRNA Ratio of Electrophoretic Band Intensity Following RT-PCR

	N	PMA	WT	MEC	CaPMA
<i>c-erbB</i>	0.92 $\pm$ 0.13	0.76 $\pm$ 0.25	1.12 $\pm$ 0.24	1.83 $\pm$ 0.21	0.88 $\pm$ 0.09
<i>ras</i>	0.94 $\pm$ 0.18	0.99 $\pm$ 0.21	0.78 $\pm$ 0.27	1.21 $\pm$ 0.28	1.03 $\pm$ 0.25
<i>src</i>	0.14 $\pm$ 0.02	3.11 $\pm$ 1.52	2.57 $\pm$ 0.39	5.2 $\pm$ 1.78	2.45 $\pm$ 0.45

*Note.* All values are presented in arbitrary intensity units determined by densitometric analysis expressed as mean  $\pm$  SEM;  $n = 8$  normal tissues;  $n = 4$  PMA;  $n = 3$  WT;  $n = 3$  MEC; and  $n = 6$  CaPMA. N, normal tissues.



**Figure 5.** Histogram of protein kinase C activity in human parotid gland lysates. All values are expressed as the mean micrograms of phosphate transferred to substrate per microgram of gland protein  $\pm$  SEM for multiple samples performed in duplicate as indicated in the methods section. N, normal parotid tissue; PMA, pleomorphic adenoma; WT, Warthin's tumor; MEC, mucoepidermoid carcinomas; CaPMA, carcinoma in pleomorphic adenoma; Necr, necrotic tissue. \*Single sample.

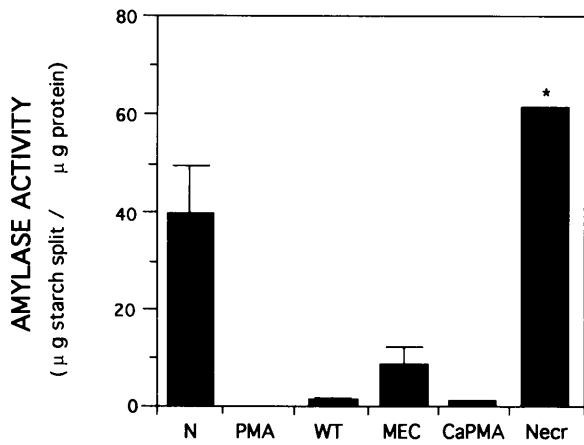


**Figure 6.** Histogram of protein kinase A activity in human parotid gland lysates. All values are expressed as the mean micrograms of phosphate transferred to substrate per microgram of gland protein  $\pm$  SEM for multiple samples performed in duplicate as indicated in the methods section. Abbreviations for tumor and normal tissue are as listed in Figure 5. \*Single sample.

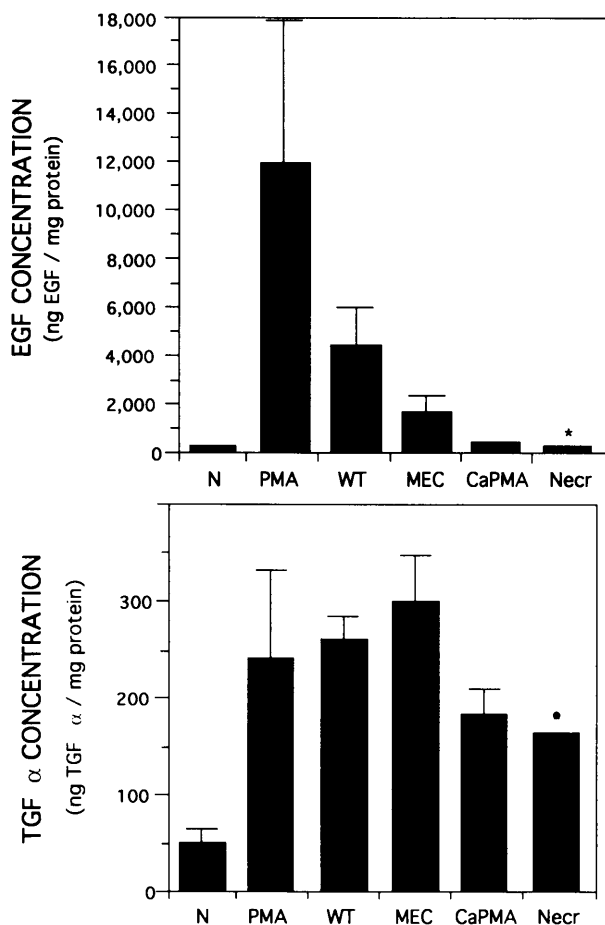
essary for activation of receptor tyrosine kinase activity (32, 33).

While PKA and PKC are normal components of the cAMP signal transduction involved in protein secretion by exocrine tissue, these kinases have also

been shown to be activated in numerous transformed tissue (7, 34). Studies on PKC activity, elevated by the growth factor GM-CSF, prostaglandin E<sub>2</sub>, or genetic manipulation, have shown transformed cells to undergo an increase in their metastatic properties concomitant with increases in PKA levels (35, 36). However, in this study, benign tumors also showed the



**Figure 7.** Histogram of parotid gland amylase activity. Values are expressed as the mean micrograms of starch split per microgram of gland protein  $\pm$  SEM for multiple samples assayed in duplicate. Parotid tissue identification is as in Figure 5. \*Single sample.



**Figure 8.** Histogram of human parotid gland EGF (A) and TGF $\alpha$  (B) levels in soluble lysates. All values represent the mean nanogram of growth factor per milligram of gland protein  $\pm$  SEM for multiple samples performed in duplicate. Parotid tissue identification is as in Figure 5. \*Single sample.

higher levels of PKA activity, even though they have no metastatic property (14, 15). This elevated PKA activity in exocrine gland may be more related to the need of PKA for secretory function rather than in-

volvement in cell growth. Both benign and metastatic parotid cancers appear to have activated components of a number of signal transduction pathways. From this data it is not clear what is the genetic change responsible for differentiating whether a specific type of salivary gland tumor is aggressive or benign. The activation of PKA and PKC may, therefore, be the result of signal transduction pathway crosstalk. It is not known what role the continuous activation of these signaling pathways have on the normal function of the gland and its ability to secrete saliva.

The loss of the ability of parotid gland tumors to synthesize and secrete amylase has been previously reported (30). The loss of amylase activity in the gland appears to be a general characteristic of neoplastic transformation and is thought to result from the loss of differentiated function (30). On the other hand, certain tumors other than salivary gland have been shown to gain the ability to synthesize amylase. The extent of the loss of amylase activity in the salivary gland appears to depend on the type of tumor, with MECs maintaining the greatest ability to continue enzyme production. With the high level of PKA, which is also necessary for active secretion, one possible explanation is that MECs are able to retain differentiated secretory function and thus amylase synthesis by virtue of its release from the cell. How this affects the synthesis of other proteins, specifically synthesis by the salivary glands (such as the histatins or proline-rich protein), is not known at this time.

In conclusion, we have presented evidence for the activation of several unique signal transduction pathways in parotid gland tumors. However, due to the limited number of samples available for evaluation, we are unable to draw concrete conclusions regarding what role these activated protein components of the different signal transduction pathways have in regards to defining the histological characteristics of these different tumor types. Most notable among the observations on these tumors was the consistent upregulation of the phosphotyrosine signaling pathway which may be activated as a consequence of *c-erbB-2* receptor expression and the presence of high levels of the receptor specific ligand EGF and TGF $\alpha$  which may stimulate parotid tumor growth by autocrine type mechanisms.

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