# **Expression of mRNAs of Multiple Growth Factors and Receptors by Neuronal Cell Lines: Detection with RT-PCR**

Asgar Zaheer,<sup>1</sup> Weixiong Zhong,<sup>1</sup> and Ramon Lim<sup>1,2</sup>

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Neurons and glia are capable of both secreting and responding to a large variety of growth factors. However, information on multiple expression of growth factors and their receptors was usually obtained from uncorrelated observations, using cells from various animals of origin, developmental stages, growth phases, culture ages and culture conditions. Because of its specificity and extreme sensitivity, reverse transcription-polymerase chain reaction (RT-PCR) is uniquely suitable to study a large panel of growth factors and their receptors from a limited cell sample, free of these intervening variables. In this paper we evaluate the expression of mRNA of a total of 35 growth factorrelated proteins by conducting RT-PCR on three neuronal cell lines: the PC12 rat pheochromocytoma line, the MAH rat sympathoadrenal progenitor line, and the N18 mouse neuroblastoma line. Three types of results are presented. The first confirms the existing knowledge such as the presence of Trk-A (NFG receptor) in PC12. The second consists of new information that expands and extends earlier observations, such as the presence of CNTF receptor complex in PC12, which explains our previous report that CNTF enhances the biological effects of NGF on these cells. The third consists of novel information that leads the way to further experimentation by the more conventional methods. These include the strong expression of Trk-B by MAH, predicting the biological responsiveness of MAH to BDNF and NT-4, and the expression of CNTF receptor in N18. Our results also suggest that CNTF is an autocrine factor for PC12 and MAH, since both lines express the growth factor as well as the receptor. Thus, RT-PCR is a valuable tool in growth factor research that can be used in complement to, and interactively with, other approaches such as bioassay, receptor binding, and immunochemical determination. It will be particularly useful for screening a large number of growth factors in minute areas of the brain in patients suffering from neurodegenerative diseases such as Parkinson's and Alzheimer's.

KEY WORDS: Reverse transcription-polymerase chain reaction; growth factors; neuronal cell line.

## **INTRODUCTION**

Neurons are known to respond to a variety of growth factors, some of which are specific for neurons while others can affect non-neuronal cells as well. Likewise, neurons can secrete growth factors that may exert autocrine function or stimulate other cell types. The combinatorial and permutative relationships of these fac-

Abbreviations: BDNF, brain-derived neurotrophic factor; CNTF, ciliary neurotrophic factor; EGF, epidermal growth factor; bFGF, basic fibroblast growth factor; GMF- $\beta$ , glia maturation factor  $\beta$ ; IGF-1, insulin-like growth factor 1: IGF-2, insulin-like growth factor 2; IL-1, interleukin 1; IL-6, interleukin 6; INS, insulin; LIF, leukemia inhibitory factor; NGF, nerve growth factor; NT-3, neurotrophin 3; NT-4, neurotrophin 4; PDGF, platelet-derived growth factor; RT-PCR, reverse transcription—polymerase chain reaction; SCF, stem cell factor; TGF- $\beta$ , transforming growth factor  $\beta$ . "R" following a growth factor designates its receptor.

<sup>&</sup>lt;sup>1</sup> Department of Neurology (Division of Neurochemistry and Neurobiology), The University of Iowa College of Medicine and Veterans Affairs Medical Center, Iowa City, IA 52242.

<sup>&</sup>lt;sup>2</sup> To whom to address reprint requests.

tors makes possible the fine tuning of the neural network that is important for the adaptive and integrative behaviors of the organism. Recent molecular cloning and DNA sequencing of numerous growth factors along with their receptors provide an opportunity for the detection of their mRNAs by means of reverse transcription-polymerase chain reaction (RT-PCR). Because of the extreme sensitivity of the method, a large number of growth factors can be simultaneously studied in a limited sample size, eliminating variations usually arising from multi-sample comparisons. In a previous paper (51), we reported the use of RT-PCR to study the expression of growth factors in cultured glial cells. In this paper we conducted a similar study on three neuronal cell lines: the PC12 rat pheochromocytoma line, the MAH rat sympathoadrenal line, and the N18 mouse neuroblastoma line.

#### **EXPERIMENTAL PROCEDURE**

Cell Culture. PC12 rat pheochromocytoma cell line, originated from Greene and Tischler (13), was obtained from American Type Culture Collection and cultured in uncoated plastic culture plates in RPMI 1640 supplemented with 10% heat-inactivated horse serum and 5% heat-inactivated fetal bovine serum. MAH is a v-myc-immortalized sympathoadrenal progenitor cell line (4). It was a gift of S. J. Birren and D. J. Anderson (California Inst. of Tech.) and was grown in poly-L-lysine-coated plastic culture plates in L15-CO<sub>2</sub> medium with 10% heat-inactivated fetal bovine serum, 5 $\mu$ M dexamethasone, and other supplements as described (4). N18 mouse neuroblastoma cell line was provided by M. Nirenberg and grown in uncoated plastic culture plates in RPMI 1640 supplemented with 10% heat-inactivated fetal bovine serum. All cells were grown at 37°C in 5% CO<sub>25</sub> 95% air, and saturated humidity to near confluence before harvested for RT-PCR analysis.

*RNA Isolation and RT-PCR*. Total RNA was extracted from cultured cells by the acid guanidinium thiocyanate-phenol-chloroform method (6) using the proprietary RNAzol B solution (Tel-Test, Inc.). The integrity of the extracted RNA was verified with agarose gel electrophoresis, using the 18S and 28S ribosomal RNA as indicators.

Reverse transcription was conducted in a reaction volume of 40  $\mu$ l containing 2  $\mu$ g of total RNA, 1  $\mu$ g random hexamer primers (pd [N]<sub>6</sub>, Pharmacia), 20 units RNasin (Pharmacia), and 8  $\mu$ l of a solution comprising 250 mM Tris-HCI, pH 8.3, 15 mM MgCI<sub>2</sub>, 375 mM KCI and 50 mM dithiothreitol. After heating for 5 min at 68°C, the reaction was initiated by addition of 20  $\mu$ l of dNTP mix (dATP, dCTP, dGTP and dTTP, 1 mM each) and 300 units of Maloney murine leukemia virus (MMLV) reverse transcriptase (Pharmacia). The reaction was allowed to proceed at 37°C for 90 min and finally terminated by boiling for 5 min.

Polymerase chain reaction was carried out essentially as previously described (52). The first strand cDNA (2  $\mu$ l) was added to the PCR mixture in a total volume of 50  $\mu$ l containing the following components: 10 mM Tris-HCI, pH 8.3, 50 mM KCI, 3 mM MgCl<sub>2</sub>, 250  $\mu$ M each dNTP, 10  $\mu$ M TMAC (tetramethylammonium chloride), 0.2  $\mu$ M each oligonucleotide primer (sense and antisense) and 2.5 units of Taq polymerase. PCR was carried out on a Perkin-Elmer Thermal Cycler. The initial template denaturation was conducted at 94°C for 4

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min and was followed by the following: primer annealing at 52°C for 1 min; primer extension at 72°C for 2 min; denaturation at 94°C for 1 min. At the end of the 42nd cycle, the reaction mixture was kept at 72°C for 3 min and then brought to room temperature. Fifteen  $\mu$ l of the PCR product was electrophoretically analyzed on a 2% agarose gel containing ethidium bromide. All RT-PCR experiments were routinely controlled by conducting PCR without first doing a reverse transcription reaction.

For uniformity of comparison, all PCR experiments (except for actin standard) were conducted for 42 cycles. For most growth factors and receptors this was within the range of exponential progression, as pre-determined from several preliminary trials. Since PCR is sensitive to variations in pH and magnesium concentration, for each primer set and template cDNA we also pre-determined and optimized these two variables using an Invitrogen "PCR optimizer kit". As a result, all PCR were conducted at pH 8.3 and 3 mM MgCl<sub>2</sub> except for the following: Trk-A, Trk-B, Trk-C, PDGF-A, PDGF-B and EGF-R at pH 9.5 and 2 mM MgCl<sub>2</sub>; PDGF-R $\alpha$ , PDGF-R $\beta$  and IGF-1-R at pH 9.0 and 2 mM MgCl<sub>2</sub>; IL-6 and IL-6-R at pH 8.5 and 1.5 mM MgCl<sub>2</sub>.

*PCR Primers*. Table I shows all the oligonucleotide primers used for the PCR reactions. Details of the choice of these primer pairs were discussed in our previous publication (51). In general, primers of approximately 20–30 nucleotides long having equal A/T and G/C contents were selected from different exons. All primer sequences were checked with the database in GenBank to avoid inadvertent homology with other proteins. Oligonucleotide primers were synthesized on an Applied Biosystems 394 DNA Synthesizer using standard phosphoramidite chemistry.

In all experiments, RT-PCR of actin was carried out concurrently (25 cycles) to control for sample loading. Primers were taken from rat and mouse  $\beta$ -actin according to Yamamori (48) as shown below, with a predicted product size of 285 bp:

#### Sense 5'-TCATGAAGTGTGACGTTGACATCCGTAAAG-3' Antisense 5'CCTAGAAGCATTTGCGGTGCACGATGGAGG-3'

Sequencing of PCR Products. To verify authenticity of the PCR products, we sequenced all the amplified materials of expected molecular size. To this end the DNA bands of interest were excised from the agarose gel after electrophoresis and purified by the Geneclean procedure (B10-101, La Jolla, CA). The purified DNA was directly sequenced using Taq DNA polymerase in a cycling protocol with fluorescent dideoxynucleotide terminators (PRISM Ready Reaction Dye Deoxy Terminator Cycle Sequencing Kit, Applied Biosystems Division, Perkin Elmer, Foster City, CA). Reaction products were analyzed on an Applied Biosystems 373A DNA Sequencer. For authenticity check, published sequences were obtained from the GENBANK database (NCBI) using the MacDNASIS (Hitachi, San Bruno, CA) or Entrez (NCBI, Bethesda, MD). Comparisons of sequences of PCR products to published DNA sequences were performed using the Sequence Navigator program (Applied Biosystems).

### **RESULTS AND DISCUSSION**

In this study cultured neuronal cells at near-confluent density were harvested and the total RNA extracted for RT-PCR for the detection of mRNAs of various growth factors and their receptors. The following three cell types were investigated: PC12 rat pheochromocytoma cell line, MAH rat sympathoadrenal line, and N18

Growth Factor (or receptor)	wth FactorPrimer sequencereceptor)(5'-3')		Reference	
NGF	GTT TTG GCC AGT GGT CGT GCA G			
	CCG CTT GCT CCT GTG AGT CCT G (h)	498	32	
BDNF	ATG ACC ATC CTT TTC CTT ACT ATG GT	<b>5</b> .11		
NT 3	GAA AAT TAC CAG AGC ACC CT	/41	35	
N1-5	TGA CTC TTA TGC TCT GCA TA (r)	269	22	
Trk A	CTG GGC GGA GTG CCT GAA	209		
	GGC TGC CGG CTC CAG GAA (h)	523	25	
Trk B	AAT GAA ACA AGC CAC ACA CAG GGC			
<b>T</b> 1 (1	TGG AGT GTT ACT CCC ATT GGA GAT (r,m)	750	19	
Trk C	AGC AAT GGG AAT GCC AGC ATC AAC	1002	21	
n75	GAG CCG TGC AAG CCG TGC ACC	1002	21	
p/5	CTC AGG CTC CTG GGT GCT GGG (h,r)	438	33	
CNTF	TGG CTA GCA AGG AAG ATT CGT			
	ACG AAG GTC ATG GAT GGA CCT (h,r)	468	26	
CNTF-R	CAT GGC CTG GAA CTG GGC CAC AGT	(20	10	
T TE	GAA AAC GGC CTG CAT CTA AGG	638	10	
LIII	GCC ATT GAG CTG TGC CAG TTG (b)	240	45	
LIF-R	GTC TGT GAG GGA AGC AGT GC	2.0		
	TCT AGG AGA GTC TGG AGA CAC (h,m)	478	11	
IL-6	TGC TGG TGA CAA CCA CGG CC			
нор	GTA CTC CAG AAG ACC AGA GG (h)	308	45	
IL-0-K	CIC AGU AAT GIT GIT IGT GAG CGA TAT CTG AGC TCA AAC CGT (b)	304	36	
9m130	CCT CAC ACT CCT CCA AGG CAC	554	50	
SP120	CTG GAT TCA TGC TGA CTG CAG (h)	473	15	
PDGF-A	CCT GCC CAT TCG GAG GAA GAG			
	TTG GCC ACC TTG ACG CTG CG (h)	225	3	
PDGF-B	GAA GGA GCC TGG GTT CCC TG	217	2	
PDGF-Ra	CAC CTG AGT GAG ATT GTG GAG	217	3	
1001-100	AGA GTC TAT GCC GAT GTC GTC (h.m)	408	8	
PDGF-Rβ	TGA CCA CCC AGC CAT CCT TC			
	GAG GAG GTG TTG ACT TCA TTC (h,m) 228		8	
bFGF	GCC TTC CCG CCC GGC CAC TTC AAG G			
LECE D	GCA CAC ACT CCT TTG ATA GAC ACA A (h)	CAC ACT CCT TTG ATA GAC ACA A (h) 179		
UFUF-K	GCC AGC AGT CCC GCA TCA TCA T (b)	661	44	
EGF	ACA GCC CTG AAG TGG ATA GAG	001		
	GGG CTT CAG CAT GCT GCC TTG (h,m)	592	2	
EGF-R	AGG TCT TGA AGG CTC TCC AAC			
TOP 0	GTC TTT GTG TTC CCG GAC ATA (h)	526	41	
TGF-β	GAA GCC ATC CGT GGC CAG AT	461	5	
TGF-B-R	AAG TAC AGA TCA GGG ACC AGG	401	5	
ioi pic	GAG CAG GTC GTA TGT CAA CTA (r)	578	43	
GMF-β	CCG CTG ACG GCC GGA AGG			
	TTA TGT CTG GAT CCA GTA TGG TCA GGT (h,r)	512	50	
SCF	GCC TTT CCT TAT GAA GAA GA	576	24	
SCF-R	IGC AAC AGG GGG IAA CAT AAA IGG (n,r,m) CGT TGA CTA TCA GTT CAG CGA G	5/5	24	
5C1-K	CTA GGA ATG TGT AAG TGC CTC C (h)	360	49	
IL-1	CAG TTC TGC CAT TGA CCA TCT	200		
	CCG ATG AGT AGG CAT ACA TGT (r)	466	30	
IL-1-R	GAG GGA CAG TTT GGA TAC AAG		~-	
ICE 1	TGC CGG CAG TTT CTC CTT AGT (m)	452	37	
ICT-1	CCT GTA GTT CTT GTT TCC TGC (b)	377	31	
IGF-1-R	ATG GAG GAG AAG CCG ATG TGT	511	57	
	GTT CTC CAG CTC TGA AGC AAT (h)	572	40	
IGF-2	AAG TCG ATG CTG GTG CTT CTC			

Table I. PCR Primer Sequences for Growth Factors and Their Receptors

Growth Factor (or receptor)	Primer sequence (5'-3')	Predicted product size (bp)	Reference
	TTC CGA TTG CTG GCC ATC TCT (h)	520	34
IGF-2-R	CAT GGG AAG CTG TTG ATA CCA		
	CTC GTA GTG TGT CTA TGT CTC (h)	502	28
INS	ATG GCC CTG TGG ATG CGC		
	GTT GCA GTA GTT CTC CAG (h,r)	330	9
INS-R	AGG TTG CAT GAG CTG GAG AA		
	GAA CAG TTG CCC AGG CAC TC (h,r)	595	12

Table I. Continued

First primers are sense strands; second primers are antisense strands. Species of origin for primer sequences are indicated in parentheses following each primer pair (h = human, r = rat, m = mouse, p = porcine).

mouse neuroblastoma line. Fig. 1 is a composite photograph of the RT-PCR products of all the growth factors and receptors included in this study, as visualized on agarose gels after electrophoresis. The scores of band intensity of the products are summarized in Table II.

Among the neurotrophin family (20), our results show that PC12 is rich in Trk-A and p75, the high- and low-affinity receptors of NGF (25), in agreement with the well-known fact that PC12 is very responsive to NGF (13). On the other hand, MAH is rich in Trk-B, predicting its responsiveness to BDNF and NT-4, although we are not aware of any literature report to this effect. The lack of response of MAH to NGF in unprimed cultures as observed by Birren and Anderson (4) may be explained by the low level of Trk-A in these cells. None of the neuronal lines express any trace of neurotrophins, suggesting that the neurotrophins are not autocrine factors for these neurons under investigation.

Among the neuropoietic cytokine family (20,31) which includes CNTF, LIF, IL-6 and oncostatin M, we found that both CNTF and its receptor complex are expressed by PC12 and MAH. The CNTF receptor complex comprises CNTF-R, LIF-R, and gpl30 (38). Thus, our data not only provide a molecular basis for the observations that PC12 (52) and MAH (17) are responsive to CNTF, but also suggest that CNTF could be an autocrine growth factor for both cell lines. On the other hand, we observed that N18 expresses high levels of LIF-R and gpl30, the two components of the LIF receptor complex (38), predicting its responsiveness to LIF. However, LIF is probably not an autocrine factor for N18 because the cell line does not express LIF. None of the three neuronal lines express IL-6 or IL-6 receptor.

Like the glial cultures, all the three neuronal lines express high levels of PDGF-A but not its receptor. MAH expresses bFGF-R, in agreement with a previous report that MAH responds to bFGF (4). However, our failure to detect bFGF-R in PC12 is at variance with some reports that PC12 is responsive to bFGF (39,42). This probably resulted from divergence in cell passage between laboratories since we also failed to detect a neurite-extension effect of bFGF on our PC12 line (results not shown). For the same reason, our RT-PCR did not detect the presence of EGF-R in our PC12 line, nor were we able to observe a mitogenic effect on these cells (14). Nevertheless, a technical problem cannot be ruled out for these negative results.

Fig. 1 and Table II also show that PC12 and N18, but not MAH, strongly express TGF-β while none express the receptor. On the other hand, all the three lines express GMF-β at a significant level, suggesting neuronglia interaction. The lack of a GMF-B-R cDNA precluded our determination of the expression of the receptor. MAH expresses SCF-R, the receptor for a growth factor (SCF) known to stimulate the proliferation and maturation of hematopoietic stem cells (47). This finding is in line with the reports that SCF-R is present both adult and embryonic nervous system in (16,18,23,27,29). However, the function of SCF on neurons has not been clearly defined. All the three lines express insulin receptor, a finding consistent with the known survival effect of insulin on neuronal cells. In general, neurons express a more limited and selective number of growth factors and/or receptors compared to glia.

To our knowledge, the current work is the most comprehensive exploration of the use of RT-PCR for the study of growth factors in neuronal cells. We have attained three distinct goals. Firstly, we have demonstrated the reliability of RT-PCR for detecting growth factors and their receptors by confirming the existing knowledge on neurons, such as the presence of neurotrophin receptors. Secondly, we have obtained new information that can expand and extend what was previously known about neurons. For example, we have for the first time presented evidence on the presence of CNTF receptor

### **Expression of Growth Factors by Neurons**



Fig. 1. Composite photograph showing RT-PCR products from m-RNAs of various growth factors and receptors in PC12, MAH and N18 neuronal cell lines. Equivalent amounts of total RNA were used as starting material, and RT-PCR was carried out according to the procedure described in METHODS. The products were electrophoresed in 2% agarose gel stained with ethidium bromide and photographed under ultraviolet light. Each small photograph contains a size ladder (first lane) and samples from PC12 (second lane), MAH (third lane) and N18 (fourth lane). The size standards are (top to bottom): 1353 bp, 1078 bp, 872 bp, 603 pb, 310 bp. Growth factors or receptors to be studied are indicated above each photograph. All experiments were repeated several times on different batches of cultured cells, and the results presented are those that are reproducible in at least three cultures. A weak, false positive band (wrong size product) is seen in MAH for Trk-C.

complex in PC12, a finding that explains our earlier report that CNTF enhances the biological effects of NGF on PC12 (52). Thirdly, we have obtained novel information that can lead the way to further experiments using the more conventional methods such as bioassay, receptor binding, and immunochemical determination. This is exemplified by the expression of Trk-B in MAH, suggesting that this cell line is responsive to BDNF and NT-4.

Lastly, one should understand the inherent strength and limitations of RT-PCR. The enormous amplification

Growth Factor	PC12	MAH	N18
(or receptor)			
NGF		-	
BDNF		-	
NT-3	-	_	_
Trk-A	++++	+	<u>+</u>
Trk-B	+	+++	—
Trk-C	—		—
p75	++	-	_
CNTF	++++	++	
CNTF-R	+ + + +	++++	+
LIF		-	
LIF-R	+	+	+++
IL-6			
IL-6-R	-		-
gp130	++++	+++	++
PDGF-A	+++	++	+++
PDGF-B		-	_
PDGF-Ra	-	-	
PDGF-RB		-	
bFGF	-		_
bFGF-R		++	
EGF	±	++	+
EGF-R			-
TFG-β	+ + +	<u>+</u>	++++
TFG-β-R		-	
GMF-β	+++	+ + + +	+++
SCF	±	±	
SCF-R		++	
IL-1	-	-	-
IL-1-R		-	-
IGF-1	_	-	-
IGF-1-R		-	
IGF-2	<b>±</b>	±	-
IGF-2-R	-	_	
INS	-	_	-
INS-R	++	++	++

Results in Fig. 1 were scored as follows: (-) absent, (+) low abundance, (++) moderate abundance, (+++) high abundance, (++++) very high abundance. Products with at least one "+" in any cell type were sequenced. When more than one cell type showed positive results, the sequence was obtained from the most positive one. All such products yielded definitive sequences with at least 95% indentity matched to the respective published sequences.

power of PCR makes it feasible to analyze well over 50 different proteins simultaneously from a few thousand cells or a few milligrams of wet tissue. When applied in a clinical setting, one can easily screen all the known growth factors and their receptors from very discrete areas of the human brain. False positive reactions can be ruled out by proper controls (such as omitting the RT step) and by sequencing the PCR products. However, one should be aware of the fact that, although it can usually be assumed that the synthesis of a protein follows the expression of its mRNA, there are rare instances where this is not so. On the other hand, a negative reaction could mean either the absence of the mRNA or the presence of a technical problem. Thus, a

Table II. Relative Band Intensity of RT-PCR Products

final conclusion on protein expression (rather than mRNA expression) should await immunologic confirmation such as western blot. But since it is much easier to synthesize multiple PCR primers than to produce a large number of specific antibodies, the discretional use of RT-PCR for the study of mRNA is a logical first step for the simultaneous screening of the genetic expression of multiple growth factors (and their receptors) from a very limited sample size. The promise of this approach in pathologic studies of the brain as in Parkinson's or Alzheimer's disease and brain tumors is obvious from the current study.

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