Specific Degenerate Codons Enhanced Selective Expression of Human Parathyroid Hormone in *Escherichia coli**

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Specific degenerate codons in the amino-terminal region of a synthetic human parathyroid hormone (PTH) gene exerted dramatic effects on both products and yield of expression of this 84-amino acid polypeptide in *Escherichia coli*. With adenine-rich degenerate codons constituting the PTH-(1-5) region, intact PTH has been expressed as the only PTH product at 6.5 mg/ liter. In contrast, with guanine-rich degenerate codons, the predominent product was analogue PTH-(8-84). Use of cytosine- or thymine-rich degenerate codons generated only a small amount of immunoreactive product (0.2 mg/l).

With the amino terminal region reconstituted with adenine-rich degenerate codons, the mid and carboxyl regions of the synthetic gene were also reconstructed to imitate the *E. coli*-favored codon degeneracy. Expression yielded the intact PTH at 20 mg/liter. Gel electrophoresis and Western blots, with antibodies specific to the amino or carboxyl terminus of PTH, indicated only a single PTH-related polypeptide, with the same mobility as a synthetic intact PTH sample. Amino acid sequencing, composition analysis, mass spectrometry, and the adenylate cyclase bioassays confirmed the purified product as the processed intact PTH.

Human parathyroid hormone, a polypeptide of 84-amino acid residues (Hendy *et al.*, 1981), is a major regulator of serum calcium. Synthetic fragments have demonstrated characteristic effects in bone metabolism (Reeve *et al.*, 1980) that may potentially be useful in the treatment of some bone disorders. Various attempts to produce the intact polypeptide via expression of the prepro-PTH¹ cDNA have been reported. However, the prepro-PTH sequence was unable to facilitate secretion and processing of PTH in yeast (Born *et al.*; 1987a) and *Escherichia coli* (Born *et al.*, 1987b). Substitution with a bacterial leader sequence yielded a secreted immunoreactive mixture (1 mg/liter) of intact PTH and fragments (Hogset *et al.*, 1990). Direct expression of the PTH cDNA (minus the prepro sequence) intracellularly generated immunoreactive PTH at 0.2 mg/liter in *E. coli* (Breyel *et al.*, 1984). It was postulated that the low yield was due to instability of both PTH and its mRNA (Morelle *et al.*, 1988).

In our laboratory, a synthetic PTH gene was assembled and directly expressed in *E. coli* to yield immunoreactive PTH at 0.2 mg/liter (Rabbani *et al.*, 1988). Analysis of this mixture revealed fragment PTH-(8-84), fMet-PTH and intact PTH. Recently the synthetic gene has been redesigned with specific degenerate codons, resulting in dramatically improved efficiency of expression (20 mg/liter) and selective production of intact PTH or fragment PTH-(8-84). Intact PTH was isolated, characterized, and assayed for bioactivity.

DISCUSSION²

An efficient expression system for human PTH has been developed, through (i) the usage of adenine-rich degenerate codons in the amino-terminal domain, (ii) adaptation of the "*E. coli*-like" codon degeneracy in the mid/carboxyl-terminal domains, and (iii) selection of an appropriate expression host. The choice of degenerate codons or the specific nucleotide composition of the amino-terminal coding sequence exerts a strong influence in both the efficiency of expression and the expressed product (or analogue).

Other studies have previously demonstrated that expression of some genes can be improved by elimination (or weakening) of secondary structure of mRNA (Hall et al., 1982). In the PTH mRNA of our plasmids pPTH-CC and pPTH-TT (Table 1), indeed hairpin structure can potentially be formed between the A,G-rich ribosome-binding site and the aminoterminal region with respective ΔG values of -7.0 and -9.6kcal (Tinoco et al., 1973), to interrupt the translation process. The A-rich degenerate codons in the PTH-(1-5) region of plasmid pPTH-AA (Table 1), might have weakened such secondary structure ($\Delta G = -3.2$ kcal) and consequently improved PTH expression. However, such mechanism is inadequate to explain the poor expression by plasmid pPTH-84c (Table 1), which has an identically weakened secondary structure in the PTH mRNA ($\Delta G = -3.4$ kcal). The efficient PTH production by the plasmids pPTH-AA and pPTH-AA-Eco (Tables 1 and 2) also contradicts earlier conclusions that tandem repeats of rare degenerate codons (Varenne and Lazdunski, 1986) and their proximity to the initiation codon would dramatically reduce the maximal level of protein synthesis (Chen and Inouye, 1990). Clustered at the PTH aminoterminal region of both plasmids, the five codons TCA-1, GTA-2, TCA-3, ATA-5, and TTA-7 are rare degenerate codons in E. coli (Chen et al., 1982).

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¹ The abbreviations used are: PTH, human parathyroid hormone; PAGE, polyacrylamide gel electrophoresis; SDS, sodium dodecyl sulfate; HPLC, high performance liquid chromatography; TFA, trifluoroacetic acid; IPTG, isopropyl-D-thiogalactoside; RIA, radioimmunoassay.

² Portions of this paper (including "Experimental Procedures," "Results," Figs. 1-7, Tables 1-3) are presented in miniprint at the end of this paper. Miniprint is easily read with the aid of a standard magnifying glass. Full size photocopies are included in the microfilm edition of the Journal that is available from Waverly Press.

Comparison of the plasmids pPTH-AA, pPTH-CompB, pPTH-AA-Eco, pPTH-CompE-Eco, pPTH-GG, and pPTH-GG-Eco with the other plasmids much less efficient in PTH expression (Tables 1 and 2), indicates that the efficiency of PTH expression instead might be determined by the nucleotide (adenine, and likely to a small extent, guanine) composition of the amino-terminal coding sequence.

Selection of degenerate codons in PTH gene design also influenced the products of expression. Though designed to produce intact PTH, plasmids pPTH-GG and pPTH-GG-Eco selectively generated the short fragment PTH-(8-84), with the intact PTH only as a minor product. Although this short analogue could conceivably be derived from intact PTH through (unknown) specific proteolysis, the mere difference of four silent point mutations between plasmids pPTH-GG-Eco and pPTH-AA-Eco supported a previously proposed hypothesis of internal initiation of translation (Born et al., 1987b). In plasmid pPTH-GG-Eco, the codons 3, 4, and 5, TCG-GAG-ATA can potentially constitute a strong ribosomebinding site (underlined) to initiate a competing translation from ATG-8 to yield PTH-(8-84). In another plasmid pPTH-84c, with a potentially weaker ribosome-binding site (TCT-GAG-ATC) in the same region, a 2:1 mixture of PTH and PTH-(8-84) was produced (Rabbani et al., 1988). This hypothesis is also consistent with the exclusive production of intact PTH by both plasmids pPTH-AA and pPTH-AA-Eco, which possess no similar internal ribosome-binding site. However, the precise mechanism remains to be confirmed.

As for the production of the intact PTH, the residue SerI adjacent to fMet, has a small radius of gyration essential for the efficient removal of fMet residue from the nascent polypeptide (Sherman et al., 1985).

The present approach of direct expression of a synthetic gene has successfully yielded biologically active, intact PTH. The extraction and purification procedures would efficiently generate adequate amounts for future studies.

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Supplementary Material To Specific Degenerate Codons Enhanced Selective Expression of Human Parathyroid Hormone in *Escherichia coli*.

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EXPERIMENTAL PROCEDURES

Materials. E. coli strains JMIO3 (A(lac pro), thi, str A, sup E, gend A, sbc s, had R, Fra D16, pro AB, lac 19, Z M15), HB101 (F, had S20 (1², M³), rec Al3, ara-14, pro A2, lac Y1, gal K2, rps L20 (SB⁷), xy1-5, mtl-1, sup E44, X⁻), Y1091 (Alsc UL69, pro A^{*}, Alon, ara D139, str A, sup F [trp C22:171 016] (Clontech Lab, Palo Alto, CA) were used as the transformation and expression hosts. Synthetic oligonucleotides were prepared with an Applied Biosystem DMA Synthesizer, Model 308B. Plasmid pUCS and enzymes were purchased from Bethesda Research Laboratories. Plasmid pTM-84 has previously been prepared via insertion of a synthetic PfW gene between the EcoRI and HIAI III sites of plasmid pUCS (Sung et al., 1986a). The two-site Allegro Intact PTH RIA kit was from Michols Institute Diagnostics (San Juan Capistrano, A). Syntheman PTH-(1-84) was from Bachen Corp., Torrance, CA.

http://www.from/Bachem Corp., Torrance, CA.
Construction of Expression Plasmids. Plasmids pPTH-AA, PpTH-GG, pPTH-CC,
pPTH-TT, pPTH-CompB, pPTH-WA, pPTH-WA and pPTH-HA (Table 1) were all prepared
in the same manner. Construction of plasmid pPTH-HA. (Table 1) were maintered
(Figure 1), Oligonucleotides Coth EcotA, Pett-linearized plasmid pPTH-HA
expression of the same manner. Construction of plasmid pPTH-HA. After transformation of E.
coil JM1001, 144 of the transformants were identified to possess plasmid pPTH-HA
h by DNA hybridization and nucleotide sequencing.
The protocol for the construction of plasmid pPTH-HA.FEco was identical to
phosphorylated oligonucleotides P104, P105, P106, P201, P202, P203 and
P204a with the Patt/HindIIT-linearized plasmid pPTH-HA. (Figure 2).
Plasmid pPTH-(29-84)-Eco was prepared via ligation of the pM=HAA-Eco, with plasmid pUC-cut at the ease sites. Substitution of the sami and pPTH-HA-Eco (Table 2).
Plasmid pPTH-HA-Eco (Table 2).
Plasmi

Expression in R. coll. One liter of 2VT + 1% CA medium (15g Bacto-tryptone, 10g Bacto-yeast extract, 10g NaCl, and 10g Casamino acid in 1 liter; informatining ampicillin (100 mg/1) was innoculated with a 10 ml overnight growth of S. coll Y1091 or HB101 transformants and incubated at 37°C with shaking. Cells were harvested by centrifygation after 9 h. For S. coll 3M103 transformants, IPTG (final concentration 0.7 mM) was added after 1.5 h of initial growth. For obtaining a whole cell lysate, cells from 5 ml culture were sonicated in 1.25 ml of 1% SOS.

Extraction Procedure. Cells were sonicated (1 min, pulsed) at 4° C in a mixture (1 ml/g) of 1 M HCl containing 1% (v/v) NaCl, and 1% (v/v) TFA (Rabbani et al., 1988) and centrifuged. The cell debris was reextracted. The extracts were pooled.

NPLC. The extract was adjusted to pH 3.8 with NaOH, diluted with water (4:1), and applied to a HL 10/10 Mono S column (Pharmacia). The column was eluted with a gradient of 0-2 M NaCl in 50 mM formic acid (pH 3.8) and fractions were evaluated by RLA. Immunoreactive fractions were pooled and applied to a 1 x 25 cm Clg silica (10 μ m) column (Vydkc) (Rabbani et al., 1988). It was then eluted with a 1 k min gradient 0 0.1% TPA/actonitrile in 0.1% TPA/water. Immunoreactive fractions containing mainly intact PTH were combined and lyceholized. lyopholized

Antibodies Specific to Amino and Carboxyl Termini. PTH-(69-84) amide was synthesized on methybenzhydrylamine resin, using tBoc chemistry (Stewart and Young, 1984). PTH-(1-17) was constructed on a branched lysine core as described (Posnett et al., 1988). The core was constructed on a phenylacetamidomethyl resin, with a g-alanyl spacer, and using bis-tBoc-Lys. Rabbit antibodies were developed directly to the PTH-(1-17)-Lys complex and to PTM-(69-84) coupled to keyhole Limpet hemocyanin. The antibodies were affinity purified by passage through a column of PTM-(1-17) coupled to AffiGel 15 or PTH-(69-84) coupled to AffiGel 10.

Immunoblots. Western blots (Towbin et al.,1979) were saturated with 10% fetal calf serum, then reacted with either rabbit anti-PTH-(1-17) or anti-PTH-(69-84) antibodies. Final development was with anti-rabbit IgG conjugated to alkaline phosphatase.

Amine Acid Sequencing. PTH samples (500 pmole) on polyvinylidene difluoride membrane were analysed via gas-phase sequencing as described (Mataudaira, 1987). PTH sample was also digested with endoproteinase Asp-M (Boehringer Mannheim). The resulting peptides, separated by MFLC on Clg Silica using a 1 /min gradient of acetonitrils in 0.1 % TFA/water, were sequenced as above. a 14

Amino Acid Composition Abalysis. Amino acid composition analyses of protein and of purified peptides were performed with a Durrum D-500 Analyser. Samples (100 Mg) were hydrolyzed in vacuo at 110°C in 6 N HCI for 24, 48 and 72 h and the data extrapolated to 0 h to correct for hydrolytic losses. Tryptophan was determined following hydrolysis in 4 N methane sulphonic acid containing 0.2 3 -(2-aminoethyl)indole at 110°C for 20 h in vacuo (Simpson et al., 1976). The combined cystime and cystem content was determined after oxidation to cysteic acid (Hirs, 1976) and hydrolysis in 6 N HCI at 110°C for 24 h.

Nass Spectrometry. IonSpray mass spectra of the purified recombinant PTH-(1-84) was obtained by the API III LC/MS System with an ionspray interface (SCIEX, Mississauga, OMT).

Bioassays. Adenyiate cyclase assays of recombinant PTH-(1-84) were perform in vitro in cloned rat exteosarcoma cells (URR 106) as described previously (Rabbani et al., 1988). The standards used were synthetic hPTH-(1-84) and hPTM-(1-34).

RESULTS

Effect of different maine-terminal nucleotide sequences on the expression of PTM. A series of synthetic PTM genes were designed to possess maximum numbers of adenine(A). cytosine(C), guanine(G), or thymine(T) in the first five codons at the amino-terminus, as permitted by codon degeneracy, without mutating the polyopetide sequence. Precurser plasmid pPTM-84, possessing a synthetic PTM gene constituted with yeast-favored codons (Sung et al., 1986a), was linearized at the ZecORI and PETI mites for the deletion of its PTM-(1-28) region. Oligonucleotides constituting the new PTM-(1-28) nucleotide sequence were ligated with the PETI end of the plasmid (Figure 1). Through an intramolecular recombination, the crossover linker of the oligonucleotides recombined with the lac ribosome-hinding site upstream for the circularization of the plasmid (Sung et al., 1986b). The reconstructed PTM gene was under the

direct control of the lac promotor. In this way, plasmids pPTH-AA, pPTH-CC, pPTH-GG, and pPTH-TT, enriched with a specific nucleotide (λ , C, G, and T, respective(γ) in their PTH-(1-5) regions, were constructed. The efficiencies of expression of the E. coli JH103 transformants possessing these plasmids, upon induction by IPTG, were compared (Table 1).

Table 1. Expression of PTH genes possessing different amino-terminal nucleotide sequences in E. coli strain JM103.

PTH gene -containing plasmids	PTH ^a mg∕l	N-tei l Ser	rmina 2 Val	al co J Ser	odine 4 Glu	g seq 5 Ile	uences ^b
DPTH-AA	3.9	TCA	GTA	TCA	GÀA	ATA	
pPTH-wAC	3.4						
pPTH-wxAd	3.5						
pPTH-CC	0,15 ^e	С	с	C		С	
pPTH-GG	10 ^r	G	G	G	G		
pPTH-TT	0.25 ^e	т	т	т		т	
pPTH-CompB	1.1	AGT	т	AGT		т	
pPTH-hA	0.3 ^e	т	G	AGT			
pPTH-84c ^g	0.19 ⁿ	c	т	т	G	С	

а

Estimated by the Allegro RIA. Nucleotide sequence encoding the PTH-(1-5) region of pPTH-AA is presented. For other plasmids, only nucleotides different from pPTH-AA are presented in this Table. Codon differences in other regions are stated individually. GTA-21 and TTA-24. AAA-13, 26, 27, TTA-15, 24, TCA-17 and GTA-21. Nature of the immunoreactive PTH not determined. Mixture of PTH-(1-84) and PTH-(8-84). See Fig. 4. Previously synthesized (Rabbani et al., 1988). Mixture of PTH and PTH-(8-84) in ratio of 2:1.

Radioimmunoassay indicated that the transformant JN103:pPTH-AA produced PTK at 3.9 mg/l culture, a 20-fold increase as compared to 0.2 mg/l by the previously constructed vector pPTM-84c (Rabbani et al.,1988) (Table 1). Transformants with plasmid pPTH-CC or pPTH-TT gave only low yields of 0.2 mg/l. Incidentally, the degenerate codons for the PTH-{l-5} region of the plasmid pPTH-TT are generally considered as "5. coll-favored" (Chen et al., 1982). Substitution of the Ser-1 and 3 codons TCT with the other adenine-containing serine codon ACT yielded plasmid pPTH-CompB, and the PTH production was increased by 4-fold (Table 1). Unexpectedly, transformant with plasmid pPTH-CG produced immunoreactive PTH at an even higher yield (10 mg/l, Table 1), which was later identified as a mixture of PTH-(8-84) and PTH-(1-84) with the short analogue as the major Component.

component. For a comparative study, plasmid pPTN-hA was designed with its codons in the PTH-(1-5) region identical to those in the human cDNA (Mendy et al., 1981). Expression of this plasmid generated immunoreactive PTH, uncharacterized, at a yield of 0.3 mg/l (Table 1), comparable to the efficiency of plasmids inserted with the human PTH CDNA (Breyel et al.,

efficiency of plasmids inserted with the numeric in series of the PTH-(1-5) region 1984). Since the utilization of A-rich degenerate codons at the PTH-(1-5) region of plasmid pPTH-AA had dramatically improved the expression, two plasmids pPTH-WA and pPTH-WA were constructed with more A-rich degenerate codons further downstream. However, both plasmids could not generate more PTH than pPTH-AA during expression (Table 1).

further downstream. However, both plasmids could not generate codons pPTH-AA during expression (Table 1). Effect of E. coli-favored codon degeneracy in the mid and carboxyl-terminal regions on expression of PTM. Plasmid pPTH-AA was linearized at the PstI and Bindl11 sites for the removal of its PTH-(29-84) sequence. This region was then reconstituted, with degenerate codons used in a frequency supposed to be favored by E. coli (figure 2)(Chen et al.,1982). The new transformant JH03:pPTH-AA-Eco demonstrated a moderate increase in the efficiency of expression (7 mg/l). The new plasmid pPTH-AA-Eco was recovered to transform other bacture to 2) mg/l (Table 2). The new transformant and the yield to 2) mg/l (Table 2), lowge the 1. 1942. The new transformant provide the yield to 2) mg/l (Table 2), lowge the 1. 1944. Worelle et al., 1946 require induction by IFG. The expressed product was ventually identified as intact PTH (described below). A prolonged growth period (16 h) significantly reduced the yield of PTM. Preliminary adenylate cyclase bioasay indicated strong bioactivity in a SDS whole cell lysate of this ion transformant (Y1091:pUCB) failed to stimulate the formation of cAMP. Expression of PTH by plasmid pTH-AA was also improved (6.5 mg/l) with the use of this bacterial host. All subsequent expression studies were conducted in strain Y1091. For further studies of the effect of this "E. coli-like" TH-(29-84) coding sequence on expression, the new insert was recovered through linearization at the FstI and Hindl11 sites of plasmid pPTH-AA-Eco, and was used in the substitution of the existing sequences in other plasmids Plasmid PTH-A PTH-AA-Eco, with the new insert, didn't produce more immunocative PTH than its precursor plasmid pPTH-AA (1-84) and PTH-(8-84), with the short analog anounting to 80-901 of the immunoreactive from pPTH-G, yielded immunoreactive PTH at 25 mg/l (Table 2). Upon analysis described below, the PTH products were exhibited to be PTH-(1-64) and PTH-(8-84), with the short analog anounting to

(s-84), with the short analog amounting to 80-90% of the immunoreactive mixture. The "E. coli-like" codon degeneracy was then extended further upstream to positions +8 and +18, and its effect on expression was investigated. Initially a precurser plasmid pPTH-(29-84)-Eco was constructed via ligation of the "E. coli-like" PTH-(29-84) insert with the identically linearized plasmid pUCS. The resultant plasmid pPTH-(29-64)-Eco was cut at EcoRI and PsII sites for the subsequent construction of two plasmids pPTH-A-Eco(18-64) and PFIH-A-Eco(18-64) via the crossover linker approach already described in the synthesis of pPTH-A. Expression of transformants with both plasmids yielde PTM-(18-64) at 1 PTH-A-Plasmid pPTM-CompE-Eco (Table 2), Plasmid pPTM-CompE-Eco (Table 2), with another adenine-containing degenerate codon AGC for Ser-1 and 3, produced PTM-(18-64) at 12 me/1 during expression.

Table 2. Expression of PTH genes possessing different amino-terminal nucleotide sequences in *E. coli* strain Y1091.

PTH gene	N-term		inal cod		ing sequences ¹	
-containing	PTH ^a mg/1	1	2	3	4	5
plasmids	(% protein)	Ser	Val	Ser	Glu	Ile
pPTH-AA-Eco	20 (2.5)	TCA	GTA	TCA	GAA	ATA
pPTH-wA-Eco ^C	15 (2)					
pPTH-A-Eco(18-84)d	14					
pPTH-A-Eco(8-84)	7					
pPTH-CompE-Eco	12	AGC		AGC		
pFTH-GG-Eco	25 ^f	G	G	G	G	
pPTH-hA-Eco	0.39	т	G	AGT		

Estimated by the Allegro RIA. Values in parenthesis () were percentage of bacterial protein, calculated by integrating the areas under the peak after densitemetric scanning of gel. Nucleotide sequence encoding the PTH-(1-5) region of pPTH-AA-Eco is presented. For other plasmids, only nucleotides different from pPTH-AA-Eco were presented in this Table. Codon differences in other regions are stated individually. GTA-21 and TTA-24. CGT-20, 25, CTG-24 and AAA-27. AAC-10, CTG-11, 15, 24, AAA-13, 26, 27, CGT-20, GTG-21 and CGC-25. Mixture of PTH-(1-84) and PTH-(8-84). See Fig. 4. Nature of the immunoreactive PTH not determined.

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Gel electrophoresis and immunoblotting. Gel electrophoresis of a lysate of clone Y1091:pFTH-AA-Eco revealed a new polypeptide with the same mobility as a synthetic sample of human FTH (Figure 3). Western blotting with antibody specific to FTH-(1-17) or FTH-(69-84) confirmed the new polypeptide as FTH-(1-84) [Figure 4]. Short analogues, such as FTH-(18-84), were not detected. Exclusive production of FTH-(1-84) was also confirmed in transformants possessing plasmids pFTH-AA, pFTH-CompE, pFTH-WA-Eco (Table 1), pFTH-A-Eco(18-84), pFTH-A-Eco(18-84), and pFTH-CompE-Eco (Table 2), figure 4). Gel electrophoresis of a lysate of clone Y1091:pFTH-GG-Eco indicate mainly a new polypeptide more mobile than the synthetic human FTH (Figure 3), and it was eventually identified as FTH-(18-84). Western blotting with nati PTH-(1-17) antibodies showed a dramatic loss of immunreactivity of PTH-(8-84) in this lysate (Figure 45), caused by the absence of the PTH-(1-7) region. Identitical immunreactive was also observed in transformant possessing plasmid pFTH-GG (Figure 4). Core Western blots therefore confirmed the failure of the Allegro Intact PTH RIA to exclude the FTH-(8-84) fragment in the estimation of FTM.

in the estimation of FTM. Extraction and purification of recombinant PTM. The acidic extraction of E. coli Y1091:pTM-AA-Eco enriched PTM-(1-84) to 10% of the total protein (60% recovery) (Rabbani et al., 1988). The extract was processed through column chromatography on cation exchanger (58) recovery) (Figure 58), to yleid further purifies through reverse phase chromatography (Figure 58), to yleid capability of separation of intact PTM, the unprocessed fMc-PTM, and analogue PTM-(8-64) in a gradient of acetonitrile in 0.1% TFA (Rabbani et al., 1988), revealed intact PTM as the only PTM-moleck From 2 liters of culture medium, 6 mg of the recombinant intact PTM was obtained after lyophilization, with an overall recovery of 15%. Its purity was confirmed by gel electrophoresis (Figure 3), Western blots (Figure 4), and analytical MPLC on C18 silica in the presence of 0.1% heptafluoroacetic acid (Rabbani et al., 1988) or TFA.

 $\label{eq:Characterization. Amino acid composition analysis of the purified intact PTH was identical to the expected value for human PTH-(1-84) (Table 3).$

Table 3. Amino acid composition of the purified recombinant intact PTH.

Amino	Residues/mol determined			nearest		
acid	24h	48h	72h	integer	PTH-(1-84	
Asx	10.00	10.00	10.00	10 ^a	10	
Thr	0.82	0.82	0.80	1.	1	
Ser	6.08	5.46	4.90	7 ^b	7	
Glx	11.20	11.20	11.23	11	11	
Pro	3.00	2.89	2.87	3	3	
Gly	3.94	3.98	3.90	4	4	
Ala	7.00	6.99	7.03	7	7	
Cys	0.00			0	0	
Val	7.97	8.04	7.86	8	8	
Met	1.95	1.86	1.80	2	2	
Ile	0.98	0.98	0.95	1	1	
Leu	9.77	9.75	9.62	10	10	
Tyr	0.00	0.00	0.00	0	0	
Phe	0.99	1.04	1.03	1	1	
His	4.04	4.09	4.06	4	4	
Lys	9.07	9.04	9.01	9	9	
Arg	4.95	5.03	4.97	5	5	
Trp	1.06			1	1	
Total				84	84	

a 10 Asx residues/mol is assumed. ^b Extrapolated value of 6.7 at zero time.

In repeated analyses, values of 1.95, 1.91, 2.07 and 2.09 were obtained for the number of methionine residues after hydrolysis of 24 h (Table 3), thus generally consistent to the predicted value of 2 for the processed intact FTH (Nendy et al., 1981). No methionine sulfoxide has been observed in the hydrolysed residues of FTH. Sequencing analysis of the purified intact FTH confirmed that the 40 method of the sequencing other regions, the recombinant intact FTH (Hendy et al., 1981). For sequencing other regions, the recombinant intact FTH vas initially digested with endoproteinase App-M, which has been reported to cleave specifically at the amino-terminus of the aspartic acid residues. After revealed an 11 amino acid sequence, identical to the FTH-(74-84) terminus (Hendy et al., 1981). The amino-acid sequence of the analogue FTH-(8-84) was also established by the same analysis. Tonspray mass spectrum of recombinant PTH-{1-84} predominantly showed the molecular ions possessing different number of H charge (Figure 6). Calculation based on different molecular ions yielded an average molecular mass of 9425.66 ba. The abhence of other unidentified lons generally confirmed purity of this sample.

Bioassays. The purified recombinant intact PTH was compared with synthetic samples of intact PTH and fragment PTH-(1-34) in an adenylate cyclase bloassay (Figure 7). The recombinant intact PTH stimulated adenylate cyclase in osteosarcoma cells with a $k_{\rm acc}$ value (half maximum stimulation) of 1.6 mM, as compared to 3.8 mM for the synthetic intact PTH (Wingender et al., 1989; Rabbani et al., 1989), and 0.59 mM for the more potent short fragment PTH-(1-34). The smaller $k_{\rm acc}$ of the recombinant PTH, as compared to the synthetic standard, indicated a higher potency of the former.

1 2 3 4 5 6 7 8 9 10 Met Ser Val Ser Glu Ile Gln Leu Met His Asn PlAA crossover linker 5'ACAA TIT CAC \underline{AGG} GG AAA CAGJCT ATG TCA GTA TTA GGA ATA CAA TTA ATG CAJT AAT ITG TC GTA TTA GTT AAT TAC GT A TTA \underline{CAJT} AAT TAC GT A TTA \underline{CAJT} PAA

Figure 1. Oligonucleotides COL-1, PIAA, P2B, P3, P6, P7B and P8AA for the construction of the PTH-(1-28) region of plasmid pPTH-AA. After phosphorylation, the oligonucleotides were ligated to the Psti end of the EcoRI/PstI-cut plasmid pPTH-84. In vivo intramolecular recombination between crossover linker COL-1 and the lacZ ribosome-binding site of the plasmid yielded plasmid pPTH-AA.

28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 P103b 5'-G GAC GTT CAC AAT TTC GTT GCG CTG GGC GCT CCG CT]G GCA CCG CGT GAC GCT AAG GCA CGC GAA GGC GAA CGC GAA GGC GA C CGT GGC GCA CGC GCA GGC GA C CGT GGC GCA CTG CGA PS01

P203

Ter

TAA AGA TCT TGA ATT TCT AGA AC<u>T TCG A</u>-5' *Bin*dIII

Figure 2. Oligonucleotides P103b, P104, P105, P106, P201, P202, P203 and P204a for the construction of the PTH-(29-84) region of plasmid pPTH-AA-Eco. After phosphorylation, the oligonucleotides were ligated to the PstI/HindIII-cut plasmid pPTH-AA to yield plasmid pPTH-AA-Eco.



Figure 3. SDS-PAGE of PTH expressed in E. coli. SDS whole cell lysate (from 40 µl culture), purified recombinant intact PTH and synthetic intact PTH (both 800ng) were electrophoresed on a 18% gel with subsequent Coomassie Blue staining. Lane a, negative control lysate of Y1091;pUCS; b, lysate of Y1091;pUCS; c, lysate of Y1091;pUCS; d, lysate of Y1091;pUCS; c, lysate of Y1091;pUCS; d, lysate of Y1091;pUCS; d, lysate of X1091;pUCS; d, lysate of X1091;pUCS; d, lysate of the synthetic PTH; e, synthetic PTH; f, purifiel recombinant PTH. Note change of mobility of synthetic PTH when mixed with relate in lane d. The positions of intact PTH, analogue PTH-(8-84) and molecular weight standards are indicated on left.



Figure 4. SDS-PAGE and immobiliting of PTH expressed in *E. coli*. SDS whole cell lysate (from 24 µl culture), purified recombinant intact PTH, and synthetic intact PTH (both 400 ng) were electrophoresed on a 18% gel. Protein contents were electrotransfered to two nitrocellulose membranes which sandwiched the gel (200 milliamp, 15 min and then current reversed for 45 min). The membranes were immunoblotted separately with the anti PTH-(69-84) antibodies (panel A), and the anti PTH-(1-17) antibodies (panel B). Lane a, negative control lysate of JM1031:pPTH-GGE (, lysate of Y1091:pPTH-GGE (, lysate of Y1091:pPTH-GGE (, lysate of Y1091:pPTH-GGE (), lysate of Y1091:pPTH-A) e, lysate of Y1091:pPTH-A) e, in the positions of intact PTH, analogue PTH-(8-84) and molecular weight standards are indicated on left.



Figure 5. Purification of recombinant PTH. Panel A, chromatogram of the acidic cell extract on cation exchanger Mon S, with concentration of PTH (\bullet) in collected fractions (1 ml) estimated. Panel B, chromatogram of subsequent HPLC purification on C₁₈ silica, with PTH-containing peak (stippled) indicated.



Figure 6. IonSpray mass spectrum of purified recombinant PTH-(1-84). The m/z value and z the number of H⁴ charges (in parenthesis) of each molecular ion were indicated. Molecular mass is calculated by the formula of $(m/z \ x \ z) - z$ in four most prominent peaks. Molecular mass of 9424.90, 9425.91, 9426.91 and 9424.92 Davas obtained, with an average of 9425.65 Da.



Figure 7. Adenylate cyclase assay of the recombinant intact PTH. The osteosarcoma cell (UNR 106) bioassay of purified recombinant intact PTH (O), synthetic intact PTH (\oplus) and PTH-(1-34) (\oplus) was carried as described.