

Sequence of the porcine transforming growth factor-beta precursor

Rik Derynck and Lucy Rhee

Department of Molecular Biology, Genentech, Inc., 460 Point San Bruno Boulevard, South San Francisco, CA 94080, USA

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A lambda gt-10-based cDNA library derived from polyadenylated porcine ovary mRNA (1) was screened by hybridization to the human transforming growth factor-beta (TGF-beta) cDNA insert of lambda BC1 (2). Two strongly hybridizing recombinant cDNA phage were sequenced (3,4) and their cDNA sequences were in absolute agreement. The longest cDNA insert contained in lambda pigbeta1 is 1,604 bp and encodes the complete porcine TGF-beta precursor (Fig. 1). Comparison of the deduced amino acid sequences for the human (2), murine (5) and porcine TGF-beta precursors shows that the N-terminal third of the precursor is virtually identical while the middle third is somewhat less conserved. The C-terminal third of the precursor which comprises the mature TGF-beta monomer sequence is again very conserved. The RGD sequence (residues 244-247) which could play a role in cellular adhesion is present in all three precursors (6,7). The polypeptide sequence of the mature human and porcine TGF-beta is identical. The porcine precursor sequence contains only two potential N-glycosylation sequences instead of the three corresponding sequences in the human and murine TGF-beta precursors.

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REFERENCES 1. Mason,A.J. et al. (1985) Nature 318, 659-663. 2. Derynck,R. et al. (1985) Nature 316, 701-705. 3. Sanger,F. et al. (1977) Proc. Natl. Acad. Sci. USA 74, 5463-5467. 4. Messing,J. et al. (1981) Nucl. Acids Res. 9, 309-321. 5. Derynck,R. et al. (1986) J. Biol. Chem. 261, 4377-4379. 6. Pierschbacher,M.D. and Ruoslahti,E. (1984) Nature 309, 30-33. 7. Pierschbacher,M.D. and Ruoslahti,E. (1984) Proc. Natl. Acad. Sci. USA 81, 5985-5988.

1 CGACTCCCGGAGAACTTGACCCCAAGCTCGGGGCGACCCCCCTGCACACTTCCCACTTCAGCCCTCTGCTGAGCCCTGCGCATCAAGACCCCT
101 TCTCGGATCCGGGAGACGGAATCTGTCTCAGACACTGCTCAGCTTTCTTATTCAGAGACCACCACCTCTGGTACCAAGATCGCCCATCTCGGTTTTTTC
201 CGTAGGATACCGAGAACCCACCATCATGAGAGCCCTCCCTTCCACCTCTGCTCTCTGCTTCTCCCTGAGAGCTCAACTTCCCTCCACCCCAAGATCTCTCTA
301 CCTTTTCTGGGAGACCCCTCAGCCCTTGAGGGGCGGGGCGCTCCCTCTTCTACCCAGCCGCTCGCACTCTCGGCTGTGCGGGGGCGCCGCTCTC
Met Pro Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu Trp Leu Val Leu Thr Pro Gly
401 CCC ATG CCG CCT TCG GGG CTG CCG CTC TTG CCG CTG CTG CTG CCG CTG CTG TGA GTG CTG ACG CCT GGC
Arg Pro Ala Ala Gly Leu Ser Thr Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Ile Gly Ala Ile
476 CGG CCG GCC GCG GGA CTG TCC ACC TGC AAG ACC ATC GAC ATG GAG CTG GTG AAG CCG AAG CCG ATC GAG GCC ATT
50 Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser Gln Gly Asp Val Pro Pro Gly Pro Leu Gly
551 CGC GGC CAG ATT CTG TCC AAG CTT CCG CTC GCC AGC CCC CCG AGC CAG GGG GAG CTG CCG CCC GGC CCG CTG CCT
Glu Ala Val Leu Ala Leu Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Arg Pro Glu Pro
626 GAG GCC GTA CTG GCT CTT TAC AAC AGT ACC CCG GAC CCG GTA GCC GGG GAA AGT GTC GAA CCG GAG CCC GAG CCA
100 Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe
701 GAG GCG GAC TAC TAC GCC AAG GAG GTC ACC CCG GTG CTA ATG GTG GAA AGC GGC AAC CAA ATC TAT GAT AAA TTC
Lys Gly Thr Pro His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val Pro Glu Pro Val Leu
776 AAG GGC ACC CCC CAC AGC TTA TAT ATG CTG TTC AAC ACG TCG GAG CTC CCG GAA GCG GTG CCG GAA CCT GTA TTG
150 Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr
851 CTC TCT CCG GCA GAG CTG CCG CTG CTG AGG CTC AAG TTA AAA GTG GAG CAG CAC GTG GAG CTA TAC CAG AAA TAC
Ser Asn Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Ala Pro Ser Asp Ser Pro Glu Trp Leu Ser Phe Asp
926 AGC AAT GAT TCC TGG CCG TAC CTC AGC AAC CCG CTG CTG GCC CCC AGT GAC TCA CCG GAG TGG CTG TCC TTT GAT
200 Val Thr Gly Val Val Arg Gln Trp Leu Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Cys Ser
1001 GTC ACC GGA GTT GTG CCG GAG TGG CTG ACC CCG AGA GAG GCT ATA GAG GGT TTT CCG CTC AGT GCC CAC TGT TCC
Cys Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn Ser Gly Arg Arg Gly Asp Leu Ala Thr
1076 TGT GAC AGC AAA GAT AAC ACA CTC CAC GTG GAA ATT AAC GGG TTC AAT TCT GGC CCG GGG GAT GAG CTG GCC ACC
250 Ile His Gly Met Asn Arg Pro Phe Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His Ser Cys
1151 ATT CAC GGC ATG AAG CCG CCC TTC CTG CTC ATG GCC ACC CCG CTG GAG AAG GGC CAG CAC CTG CAC AGC TCC
Arg His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr
1226 CCG CAC CCG CGA GGC CTG GAT ACC AAC TAC TGC TTC AGC TCG ACG AAG AAG TCG TGC TGC CCG CAG CTG TAC
1301 ATT GAC TTC CCG AAG GAC CTG GGC TGG AAG TGG ATT CAT GAA CCC AAG GGC TAC CAT GCC AAT TTC TGC CTG GGG
Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly
1376 CCC TGT CCC TAC ATC TGG AGC CTA GAC ACT CAG TAC AGC AAG GTC GCT CTG TAC AAC CAG CAC AAC CCG GGC
Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro
1451 GCG TCG GCG GCG CCG TGC TGC GCG CAG GCG CTG GAG CCA CTG CCC ATC GTC TAC TAC GTC GGC CCG AAG CCC
Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
1526 AAG GTG GAG CAG CTG TCC AAC ATG ATC GTG CGT TCC TGC AAG TGC AGC TGA G6CCCCCCCCCAGCCCGCCCGCCAC