

Sequence variability among ovine trophoblast interferon cDNA

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Recently a novel group of interferons (IFN) 172 amino acids in length and structurally related to the IFN- α family have been shown to be products of the trophoblast of certain ruminant species. They are important in triggering maternal responses to the presence of the peri-implantation stage conceptus in the uterus (1). Here, the cDNA representing six distinct mRNA for ovine trophoblast IFN have been cloned from a day 15–16 sheep conceptus library. The procedures were based on those described previously for the isolation of a single full-length clone (2).

The data reveal two distinct types of cDNA (a-type and b-type) and support previous evidence that the ovine trophoblast IFN belong to a multigene family. The a-type provides a potential site of N-glycosylation at codon 101 (asn⁷⁸), similar to the one on the cDNA for bovine trophoblast IFN (3). However, unlike bovine trophoblast IFN (4), ovine trophoblast IFN is not known

to be glycosylated. The b-type does not possess a potential site for N-glycosylation.

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A

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met ala phe val leu ser leu leu met ala leu val leu val
ACCTGAAGGTTCCCCCTGACCCCATCTCAGCCAGCCAGCCAGCCGATCTTCCCC ATG GCC TTC GTG CTC TCT CTA CTG ATG GCC CTG GTG CTG GTC
ser tyr gly pro gly gly ser leu gly cys tyr leu ser arg lys leu met leu asp ala arg glu asn leu arg leu leu asp arg
AGC TAT GGC CCA GGA GGA TCT CTG GGT TGT TAC CTA TCT CGG AAA CTC ATG CTG GAT GCC AGG GAG AAC CTC AGG CTC CTG GAC CGA
met asn arg leu ser pro his ser cys leu gln asp arg lys asp phe gly leu pro gln glu met val glu gly asp gln leu gln
ATG AAC AGA CTG TCA CCT CAT TCC TGT CTG CAG GAC AGA AAA GAC TTT GGT CTT CCC CAG GAG ATG GTG GAG GGC GAC CAG CTC CAG
lys asp gln ala phe ser val leu tyr glu met leu gln gln ser phe asn val phe his thr glu arg ser ser ala ala trp asn
AAG GAC CAG GCC TTC TCT GTG CTC TAC GAG ATG CTC CAG CAG AGC TTC AAC GTC TTC CAC ACA GAG CCG TCC TCT GCT GCC TGG AAC
thr thr leu leu glu gln leu cys thr gly leu gln gln gln leu asp his leu asp thr cys arg gly pro val met gly glu lys
AGC ACC CTC CTG GAG CAG CTC TGC ACT GGA CTC CAA CAG CAG CTG GAC CAC CTG GAC ACC TGC AGG GGT CCC GTG ATG GGA GAG AAA
asp ser glu leu gly lys met asp pro ile val thr val lys lys tyr phe gln gly ile his asp tyr leu gln glu lys gly tyr
GAG TCT GAA CTG GGA AAG ATG GAC CCC ATT GTG ACC GTG AAG AAG TAC TTC CAG GGC ATC CAT GAC TAC CTG CAA GAG AAG GGA TAC
ser asp cys ala trp glu ile val arg val glu met met arg ala leu thr ser ser thr thr leu gln lys arg leu thr lys thr
AGC GAC TGC GCC TGG GAA ATC GTC AGA GTC GAG ATG ATG AGA GCC CTC ACT TCA TCA ACC ACC TTG CAA AAA AGG TTA ACA AAG AGC
gly gly asp leu asn ser pro end end
GGT GGA GAT CTG AAC TCA CCT TGA TGA CTCTTGCCGACTAAGATGCCACATCACCCTCETACACCCGCTGTGTTTCATTTCAGAAGACTCTGATTTCTGCTCCAGC
CACCAAAATTCATTGAATTACTTTAGCTGATCTTTGTCAGTAGTAAAAAGCAAGTAGATATAAAAGTATTCAGCTGTAGGGCATGAGTCTGAAATGATGCCCTCCCTGATGTT
ATCTGTGTGCTGATTTATTATACCTTCTGCTGATTTAACTACTTAAAAATATTAGGAAATTTGTTGTTACATTTCATCTGTACATCATATTAATAATTTCTAAACAAAAA

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B

amino acid:	5	6	12	16	24	25	55	67	69	72	76	78	83	100	101	102	107	112	113	114	128	154	165		
aa of oTP-1 p6:	arg	lys	arg	arg	leu	ser	ser	val	his	arg	ala	asn	glu	arg	gly	pro	lys	gly	lys	met	his	ser	thr		
a type	oTP-1 p6	CGG	AAA	AGG	AGG	CTG	TCA	TCT	GTC	CAC	CGC	GCC	AAC	GAG	AGG	GGT	CCC	AAA	GGA	AAG	ATG	CAT	TCA	ACG	
	oTP-1 p12	
b type	oTP-201	+GA	.G.A.	..C	..C	C..	C..	T..	.A.	...	G..AA	G..	..T	..C	...	T..	GT.	.T.
	oTP-1 p3	.A.	.G.A.	..C	..C	C..	C..	T..	.A.	...	G..	..CAA	G..	..T	..C	...	T..	GT.	.T.
	oTP-1 p5	.A.	.G.A.	..C	..C	C..	C..	T..	.A.	..T	G..AA	G..	..T	..C	...	T..	GT.	.T.
	oTP-1 p7	.A.	.G.A.	..C	..C	C..	C..	T..	.A.	...	G..	..CAA	G..	..T	..C	...	T..C	GT.	.T.
	oTP-1 p8	.A.	.G.A.	..C	..C	C..	C..	T..	.A.	...	G..	..CAA	G..	..T	..C	...	T..	GT.	.T.
aa changes:	+glu	arg	lys	lys	*	*	pro	leu	tyr	his	*	asp	asp	*	asp	gln	glu	*	asn	val	tyr	val	met		
	gln																								

Figure 1A. Nucleotide and predicted amino sequences of ovine trophoblast interferon clone oTP-1 p6. The region coding for the mature protein and the polyadenylation sequence are underlined. **B.** Comparisons of the nucleotide and predicted amino acid differences in the open reading frame for the mature protein in six cDNA representing two types of mRNA (a and b types). Silent nucleotide changes are indicated by an asterisk.