Co-expression and Sequence Determination of Estrogen Receptor Variant Messenger RNAs in Swine Uterus

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ABSTRACT : Steroid hormones and their receptors play an important role in reproductive process. Estrogen is intimately involved with pregnancy and its function is mediated through the estrogen receptor which has been chosen as a candidate gene to study litter size in pigs. In this study, we report that two estrogen receptor variants, designated pER-1 and pER-2 were co-expressed in the uteri of normal cycling Lan-Yu pig (*Sus vittatus*; a small-ear miniature in Taiwan) with the pER-1 expression level appeared to be several times higher than that of pER-2. These receptor variants were isolated using reverse transcription-PCR from the pig uteri and their sequences were determined. The pER-1 and pER-2 sequences, which are homologous to those found in other mammalian estrogen receptors, encode putative proteins consisting of 574 and 486 amino acids, respectively. A deletion in exon I was identified in both sequences, with deletion lengths of 63 bp in pER-1 and 327 bp in pER-2. The deletion in pER-1 is internal to that in pER-2 and both deletions resulted in a truncation of the B domain, which confers the transactivating activity of estrogen receptor protein. This result describes the existence of estrogen receptor variants with a deletion in exon I and implies the possibility that physiological functioning of an estrogen receptor may not require the presence of an intact B domain. *(Asian-Aust. J. Anim. Sci. 2003. Vol 16, No. 12 : 1716-1721)*

Key Words : Gene Expression, Estrogen Receptor, Pig, Reproduction

INTRODUCTION

Estrogen receptors (ER) belong to the superfamily of retinoic acid. vitamin D and steroid and thyroid hormone receptors (Green et al., 1986). The members of this family are ligand-induced transcription factors composed of functional modules that mediate DNA and hormone binding. dimerization and transcriptional activation (Kumar et al., 1987; Evans, 1988; Gronemeyer, 1991). ER and its hormone ligand, the female sex steroid 17-estradiol, play critical roles in the development of secondary female sexual characteristics, the establishment of female reproductive cycle, fertility, and pregnancy maintenance (King, 1991). Estradiol is also thought to be essential to embryonic and fetal development (Rothschild et al., 1996).

Estrogen regulates female reproductive functions and embryonic development primarily through the nuclear estrogen receptor-alpha (ER-alpha). Upon binding to the estrogen ligand, ER-alpha protein is activated and becomes a transcription factor that modulates the expression of target genes (Das et al., 1997; Rissman et al., 1997). In an ERalpha knockout mouse model, severe reproductive and behavior deficits have been observed. Both male and female mice became completely infertile and the induction of female sexual behaviors by estradiol and progesterone was diminished (Moffatt et al., 1998). Mice lacking the ER-

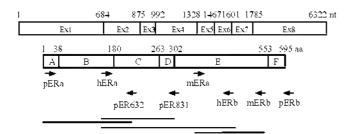
alpha also exhibited unsuccessful ovulation and the estrogen-induced epithelial mitogenesis in female reproductive organs was impaired (Cooke et al., 1998; Schomberg et al., 1999). The recently cloned estrogen receptor-beta (ER-beta), like ER-alpha, is a member of the steroid receptor superfamily (Kuiper et al., 1996), and low but detectable levels of ER-beta mRNA and protein have been detected in the rodent uterus and vagina (Couse et al., 1997; Kuiper et al., 1997; Saunders et al., 1997). However, the molecular mechanisms that regulate the transcriptional activity of ER-beta may be distinct from those of ER-alpha (Tremblay et al., 1997). Observation with mice lacking ERbeta indicated that ER-beta is essential for normal ovulation efficiency but is not required for female or male sexual differentiation, fertility or lactation (Krege et al., 1998).

The ER present in swine uteri is widely used for studying hormone binding, receptor dimerization, DNA binding, and phosphorylation (Lahooti et al., 1994; Le Goff et al., 1994). However, in contrast to numerous data collected and published on human. rat and mouse ER-alpha and ER-beta sequences and their variants (Green et al., 1986: Koike et al., 1987: Bokenkamp et al., 1994: Kuiper et al., 1996), porcine ER-alpha sequences have only recently been determined in a single strain (Bokenkamp et al., 1994) Sus scrofa or Large white, and information on the presence of ER-beta has not been reported. In this study, we report cloning and sequence determination of two co-expressed ER messenger RNA variants of ER-alpha from the uteri of Sus vittatus, or Lan-Yu pig. a species found in Taiwan. The Lan-Yu pigs are miniature wild pigs with small ear and black body. A comparison of the cDNA sequences of these two ER variant with those published for other species

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mERa:GGAGATTCTGATGATTGGTCT (Graham et al., 1990) mERb:CATCTCCAGGAGCAGGCTAT (Graham et al., 1990) pERa:TGCAGAGAATTCATGACCATGACC pERb:AGTCCGAATTCTCAGATTGTGGGTG hERa:GTGTCTGTGATCTTGTCC hERb:TCTGCCAAGGAGACTCGC pER632:TCTCTTGAAGAAGGCCTTACAG pER831:CAGATCTCATGTCTCCAG

Figure 1. Positions of various primers used to amplify ER-alpha mRNA from the uteri of Lan-Yu pig. The schematic representation of ER-alpha mRNA (top) and protein modified from Gotteland et al. (1995) shows the map position of the eight exons and six domains, respectively. The heavy lines represent the pig ER cDNA fragments amplified by individual primer sets.

revealed unexpected and novel exon I deletion.

MATERIALS AND METHODS

Materials

TRIzol reagent and superscript II reverse transcriptase were obtained from GibcoBRL Life Tech (Gaithersburg, MD, USA). The pCR-Script SK (+) and TA cloning kit used in this study were purchased from Stratagene (La Jolla, CA, USA) and Invitrogen (Leek, Netherlands), respectively.

Porcine uterine RNA isolation and reverse transcription-polymerase chain reaction (RT-PCR) assays

Lan-Yu pig (Sus vittatus; a small-ear miniature gilt (Mason, 1996)) uteri from four-month-old animals were obtained from the Department of Animal Sciences at the National Taiwan University, the location of conservation of Lan-Yu pigs, and stored at -80°C until use. The Lan-Yu pigs, also known as Yan-Yu small-ear miniature pigs or Taiwan small-ear miniature pigs become fertile earlier than Large White at 97±42 days of age. The length of pregnancy is 114 days in average for Lan-Yu pigs. The visible characteristics of Lan-Yu pigs included small and erect ear: straight tail; long and slightly concave face; very short legs with thick strong pasterns: stiff bristles; hanging belly and curving back and boars showing attack behavior under stress. Uterus RNA was prepared according to procedures described by Chomczynski and Sacchi (1987). For cDNA synthesis. 5 g of porcine uterus RNA was mixed with 4 l of 5X first strand buffer, 2 l of 0.1 M DTT, 1 l of 10 mM

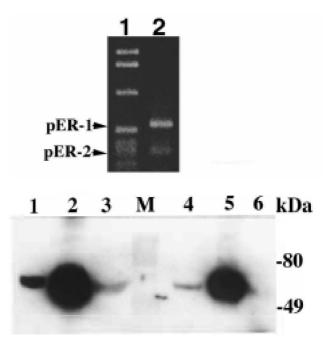


Figure 2. RT-PCR amplification of the 5' end of the ER-alpha cDNA from the uteri of Lan-Yu pig. Total RNA was prepared from pig uteri and amplified with primers pERa and pER632. 1 kb DNA marker (BRL GIBCO) was used as molecular weight markers in lane 1.

dNTPs and 11 (200 units) of reverse transcriptase in a total reaction volume of 20 l. Reaction mixtures were first incubated at 45°C for 1 h and then at 70°C for 15 min. Various pig ER cDNA fragments were amplified from a 100 l reaction mixture containing 1 X PCR buffer. 0.1 mM dNTPs, 0.5 g primers. 2.5 U Taq DNA polymerase. 1.5 l of RT product and a pre-determined concentration of MgCl₂ (4 mM for the primer sets of mERa/mERb and mERa/pERb; 3 mM for the primer set of hERa/hERb; 1 mM for the primer sets of hERa/pER632). Primers used in this study and the DNA fragments amplified are listed (Figure 1). Amplified DNA fragments were analyzed by agarose gel electrophoresis and their identification was confirmed by Southern blot analysis using a digoxigenin (DIG) labeled human ER cDNA probe.

Cloning and Sequencing of cDNA fragments

Amplified cDNA fragments were cloned either into the PCRII using a TA cloning kit or into the pCR-Script SK(+) after flushing the cDNA ends with cloned pfu DNA polymerase according to manufacture's suggestion (Stratagene, La Jolla, CA, USA). Both strands of the cloned cDNA fragments were sequenced using an ALF express DNA Sequencer (Pharmacia Biotech, Uppsala, Sweden).

RESULTS

Our strategy for cloning the ER from porcine uteri is

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Met Thr Met Thr Leu His Thr Lys Ala Ser Gly Met Ala Leu Leu His Ghn Jle Ghn Ala Asn Ghu Leu Glu Pro Leu Asn Arg Pro Ghn Leu Lys Ile Pro Leu Ghu Fro Leu Ghy 121 GAG GTG TAC GTG GAC AGC AGC AGC GAC GTG TAT AAC TAC CCC GAG GGC GCC GCC TAC GAC TTC AAC GCC GCG GCG TTC GGC GCC AAC GGC TTC GGG GGC GTC CAG CCG CTC CAG Glu Val Tyr Val Asp Ser Ser Lys Pro Ala Val Tyr Asn Tyr Pro Glu Gly Ala Ala Tyr Asp Phe Asn Ala Ala Ala Ala Ala Ala Asn Gly Leu Gly Leu Gly Phe Gln Pro Leu Asn 241 Val Ser Pro Ser Pro Leu Val Leu Leu His Pro Pro Cho Leu Ser Pro Phe Leu His Pro His Chy Chin Chin Val Pro Tyn Tyn Leu Chu An Chu Pro Ser Chy Tyn Ail Val 361 48 ACT COC TAC TOT OCA OTO TOC ANT GAC TAT GCC TCA GOC TAC CAT TAT OGA OTT TOO TOT TOC OAO OCC TOT AND OCC TTC TAC AND AGA AGT ATT CAA OGA CAT AAT OAC TAC ATO Thr Arg Tyr Cys Ala Val CysAsn Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met Cys CCA GCC ACC AAC CAG TGC ACA ATT GAT AAG AAC AGG AAG AGG AAG AGC TGT CAG GCC TGC CBG CTA CGC AAG TGC TAC GAA GTG GGC ATG ATA GAG GGG ATA CGG AAA GAC CGG AGA GGA Ala Thar Asn Gln Cys Thar Ile Asp Lys Asn Ang Ang Lys Ser Cys Ghn Ala Cys Ghn Leu Ang Lys Cys Tyr Glu Val Gly Mei Mei Lys Gly Gly Ile Gln Lys Asp Gin Ang Gly Pro ôlly Ang Met Leu Lys His Lys Ang Oth Ang Asp ôlly ôllu ôlly Ang Asn Glu Ala Val Pro Pro ôlly Asp Met Ang Ser Ala Asn Leu Thy Pro Ser Pro Leu Leu Ile Lys His Thr 841 Lys Lys Asn Sei Pro Val Leu Sei Leu Thi Ala Asp. Om Met He Sei Ala Leu Leu Glu Ala Olu Pro Pro He. He Tyi Sei Olu Tyi Asp. Pro Thi Arg. Pro Leo Sei Glu Ala Sei Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg Ghu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Leu Asp Leu Ser Leu His Asp Glu Val His Leu Leu Glu Cys 1081 AND OCCIDE CTA GAO ATO CTO ATO ATT OGT OTT OTO TOO AOO CAO CAO CAO COO A GOG AAO CTO CTO ITT OCT OCT AAC TTO CTO CTO AGO AAO CAO GAO GAA GITOT OTO GAO OGA ATO Ala Tap Leu Giu lie Leu Mei lie Giu Leu Val Tap Arg. Ser Mei Giu Has Pro Giu Lys. Leu Leu Phe Ala Pro Asin. Leu Leu Asip Arg. Asin. Giu. Giu Ju; Mei 1201 OTG GAG ATC TTT GAC ATG TTG CTG GCT ACA TCA TCT COC TTC CGT ATG ATG AAT CTC CAG GGA GAG GAG TTT GTG TGC CTC AAA TCC ATC ATT TTG CTT AAT TCT GGA GTG TAC ACG TTT Val Glu Die Phe Asp Met Leu Leu Als The Ser Ser Arg Phe Arg Met Met Ash Leu Gln Gly Glu Glu Phe Val Cys Leu Lys Ser Die Die Leu Leu Ash Ser Gly Val Tyi The Phe 1321 CTG TCC AGC ACC CTG AAG TCT CTG GAA BAG AAG GAC CAT ATC CAC CGT GTC CTG GAC AAB ATC ACA GAC ACC TTG ATC CAC CTG ATG GCC AAA GCG GGC CTG ACT CTG CAGCAG CAG CAC Ser Ser The Lew Lys Ser Lew Glu Glu Lys Asp His Ile His Aug Val Lew Asp Lys Ile The Asp Thr Lew Ile His Lew Met Ala Lys Ala Gly Lew The Lew Gle Gle 144L Gin 1561 Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser His Phe Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Asn Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu AND ATO CTA 040 000 CAO 000 MetLeu Asp Ala Hus Ang Leu Hus Ala Pro Thr Asn Leu Gly Gly Pro Pro Pro Glu Asp Met Ser Gln. Ser Gln Leu Ala Thr Ser Gly Ser Thr Pro Ser Hus Ser Leu Gln Met 1725 Ghi TAT TAC ATC ACG GGG GAG GCG GAG AAC TTC CCC ACC ACA ATC TGA Tyr Tyr Ile Thr Oly Olu Als Olu Asn Phe Pro The Thr Ile End В ATO ACC ATO ACC ACC AGO GTO GOO ATO GOO ATO GOO ATO CAO ATO CAO ACC GAO GAO GTO GAO CTO GAO CTO GAO GTO G His Thr Lys Ala Ser Gly Met Ala Leu Leu Gin Ile Gin Ala Asn Giu Leu Giu Pro Leu Asn Arg Pro Giu Leu Lys Ile Pro Leu Giu Arg Pro Leu Gly Met Thr Met Thr Leu 121 GAG GTO CCA AAT TCA GAT AAT CGG CBC CAG GBT GBC AGA GAB AGA TTB BCC AGC ACC AGT GAC AAG GGA AGC ATG GCC ATG GAA TCT GCC AAG GAG ACT CGC TAC TGT GCA ATG GCC AAG Val Pro Asn Ser Asp Asn Ang Ang Glu Gly Gly Ang Glu Ang Leu Ala Ser Thr Ser Asp Lys Gly Ser Mei Ala Mei Glu Ser Ala Lys Glu Thr Ang Tyr Cys Ala Val Cys Asn <u> Gilu</u> GAC TAT GCC TCA BGC TAC CAT TAT BGA GTT TGG TCT TBC BAB BGC TBT AAG BCC TTC TTC AAG AGA AGT ATT CAA GGA CAT AAT GAC TAC ATG TGT CCA BCC ACC AAC CAB TGC ACA ATT Asp Tyn Ala Ser Gily Tyr Hie Tyr Gily Val Typ Sen Cys Glu Gily Cys Lys Ala Phe Phe Lys Ang Sen Ile Glu Gily HisAsn Asp Tyn Met Cys Fro Ala Thr Asn Giln Cys Thr Ile 361 Asp Lys Asn Arg Arg Lys Ser Cys Ghn Ala Cys Arg Leu Arg Lys Cys Tyr Ghu Val Ghy Met Met Lys Ghy Ghy Ile Arg Lys Asp Arg Arg Ghy Ghy Arg Met Leu Lys His Lys Arg 481 Ghn Ang Asp Ang Ghy Ghu Ghy Ang Ann Ghu Ala Val Pro Pro Ghy Ang Met Ang Ser Ala Ann Leu Trp Pro Ser Pro Leu Leu Ile Lys Hus Thr Lys Lys Asa Ser Pro Val Leu Ser 601 CTE ACA GCC GAC CAG ATE ATE AGT GCC TTG TTE GAE GCT GAG CCC CCC ATA ATE TAT TEC GAG TAT GAT CCT ACE AGA CCC CTC AGT GAE GCT TCA ATE GTE GGC TTG CTG ACE AAC CTC Leu The Ale Asp Ohn Met He See Ale Leu Otu Ale Ohn Pro Pro Ille He Tyn Ser Ohn Tyr Asp Pro Thi Ale Pro Leu Ser Ohn Ale See Met Met Oly Leu Leu Thi Ash Leu 21 GCA GAC AGG GAG CTG GTA CAC ATG ATC AAC TGG GCA AAG AGG GTG CCA GGA TTT TTG GAT TTA AGC CTC CAT GAT CAA GTG CAT CTT CTG GAA TGT GCC TGG CTA GAG ATC CTC ATG ATT Ala Asp Aug Jhu Leu Val His Met Ile Ash Thp Ala Lys Ang Val Pro Jhy Phe Leu Asp Leu Sen Leu His Asp Gln Val His Leu Leu Jhu Cys Ala Thp Leu Jhu Ile Leu Met Ile 841 OGT OTT OTO TOO COO TOO ATO DAD CAO COA GOD AAG OTO CTO TIT GUT OTT AAC TTO UTO CTO DAC AGO AAC CAG GOC AAD TOT GTO GAD GOA ATO OTO GAD ATO TTI GAC ATO TTO CTO Giy Leu Val Trp Arg Ser Met Giu His Pro Giy Lys Leu Leu Phe Ala ProAsn Leu Leu Asp Arg Asn Gin Giy Lys Cys Val Giu Giy Met Val Giu Ile Phe Asp Met Leu Leu 961 1081 GAA GAG AAG GAC CAT ATC CAC CGT GTC CTG GAC AAG ATC ACA GAC ACC TTG ATC CAC CTG ATG GCC AAA GCG GGC CTG ACT CTG CAG CAG CAG CAC CGG CGT CTC GCG CAG CTC CTC CTC CTC Θю 1201 Lys Asp His He His Ang Val Leu Asp Lys He The Asp The Leu He His Leu Met Ala Lys Ala Gly Leu Thr Leu Oln Oln His Ang Ang Leu Ala Glin Leu Leu Leu lle Leu Sen His Phe ang His Met Sen Asn Lys Oly Met Olu His Leu Tyr Asn Met Lys Oys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Met Leu Asp Ala His Ang Leu CAC OCCICA ACCIAC UTCIGGIOGO CCA CCC CCG GAG GAC ATGIAGCICAG AGCICAG CTO GCC ACCITCG GGC TCA ACTICCA TCO CATITCC TTG CAA ATGITAT TAC ATGIAGCIGG GAG GCG GAG His Ala Pro Thr Am Leu Gly Giy Pro Pro Glu Asp Met Ser Gin Ser Gin Leu Ala Thr Ser Gly Ser Thr Pro Ser His Ser Leu Gin MetTyr Tyr Ile Thr Gly Glu Ala Glu 1441 1461

AAC TTO CCC ACC ACA ATO TOA Asti Phe Pro Thr. Thr. De End

Figure 3. DNA sequences and deduced amino acid sequences of the ER-alpha variants pER-1 (A) and pER-2 (B) in the uteri of Lan-Yu pig.

presented in Figure 1. Fragments of pig ER cDNA were amplified and cloned into appropriate plasmids. Surprisingly, two cDNA fragments encoding the N-terminal region of the ER protein were amplified using the primer set of pERa and pER632 (Figure 2). In addition to a DNA fragment of 600 bp (similar to the expected size of 632 bp). one minor DNA fragment of 300 bp was also amplified in the PCR products. The amount of the major DNA fragment, designated 5' end of the pER-1 appeared to be about four times that of the minor DNA fragment, designated 5' end of the pER-2 presented in the uterus RNA. All attempts to improve the specificity of the PCR technique failed to eliminate the pER-2 DNA fragment from the PCR products. Southern analysis using a human ER cDNA fragment as a probe revealed hybridization with both the major and minor DNA fragments (data not shown). Since the pER-1 and pER-2 cDNA fragments are potentially two variants of ER messenger RNA, the decision was made to clone and determine the sequences of both. By combining the sequences of amplified pig ER cDNA fragments, the lengths of pER-1 and pER-2 were determined (Figure 3). Fragment lengths were measured at 1.725 bp for pER-1 and 1.461 bp for pER-2. Both sequences were found to be highly homologous to those reported for other species (Figure 4).

A more detailed comparison of the pER-2 sequences with ER cDNA sequences from other mammals identified a 327 bp deletion from nucleotide 126 to 452. A putative protein of 486 amino acids with a deletion of 109 amino acid residue (from 43 to 151 aa) in the B domain of the ER protein was deduced from the sequences of pER-2. A deletion corresponding to the 193-255 bp region which was internal to the deletion in pER-2 was also observed in the pER-1 sequences. The pER-1 amino acid sequences was therefore deduced as consisting of 574 amino acids. with the B domain of the ER shortened by 21 amino acids (65-85 aa) compared to that reported by Bokenkamp et al. (1994) for the Large White pig species. A comparison with ER cDNA taken from Large White pig (*Sus scrofa*) revealed alterations in four bases which did not result in changes in amino acid sequences: at 264 (G/A). 606 (T/C). 1.602(T/C) and 1.692 (A/G).

DISCUSSION

Two ER-alpha messenger RNA variants with deletions in the exon I were identified in the uterus of Lan-Yu pigs. Their sequences were determined and compared with the

ftnbjolsx0 Human pER-1 pER-2 <i>S.scrifa</i> :: Rat :: Mouse	1 50 MTMTLHTKASGMALLHOIOGNELEPLNRPQLKIPLERPLGEVYLDSSKPA
51 Human pER-1 pER-2	100 VYNYPEGAAYEFNAAAAANAQVYGQTGLPYPPGSEAAAFGSNGLG :::::::::::::::::::::::::::::::::::
Rat :F Mouse	::::::::::::::::::::::::::::::::::::::
10 Human pER-1 pER-2 S. scrifa : : :	1 150 GFPPLNSVSPSPLMLLHPPPQLSPFLQPHGQQVPYYLENEPSGYTVREAG ::Q::::::::::::::::::::::::::::::::::
	.Q:;:::::::::::::::::::::::::::::::::::
Human pER-1 pER-2 S.scrifa::	PPAFYRPNSDNRRQGGRERLASTNDKGSMAMESAKETRYCAVCNDYASGY ::::::::::::::::::::::::::::::::::::

Figure 4. Comparison of the amino acid sequence of Lan-Yu pig ER-alpha variants with those from human, large white pig, mouse and rat. "-" indicated the absence of corresponding amino acid and ":" indicates that the same amino acid is present compared to the sequence of human ER.

ER cDNAs of other species. The major variant pER-1 contained a deletion of 63 nucleotide deletion and the minor variant pER-2 contained a 327 nucleotide deletion. Both variants stay in frame and code for a ER protein missing aa 65-85 and aa 43-151 in the B domain, respectively. The B domain of ER protein confers transactivation activity and is not as conserved as domains C (involved in DNA binding) or E (required for ligand binding).

To our knowledge, ER-alpha messenger RNA variants with deletions in exon I have not been previously reported. However, data has been published on observed deletions in exons 2-7 in various tumor tissues and established cell lines (Graham et al., 1990; McGuire et al., 1992; Koehorst et al., 1993; Pfeffer et al., 1993) and whether these ER variants are physiologically significant in terms of tumor progress remains unknown (Wang and Miksicek, 1991; Pfeffer et al., 1995). That the ER variants reported previously were resulted from a precise deletion of either a single exon (exons 2, 3, 4, 5, or 7), or two exons (exon 3 and 4) suggests an alternative splicing mechanism was involved. In addition to tumor tissues, Gotteland et al. also observed the presence of at least six ER messenger RNA variants in normal breast tissues (Gotteland et al., 1995). In the present study, we observed the co-expression of two ER messenger RNA variants in pig uteri. Unlike the previously described "exon-skipping" mutants, these variants most likely reflect changes in genomic ER sequence, especially since the two messenger RNAs do not correspond to the normal splicing patterns of ER mRNA. Detained genomic sequence characterization would facilitate the understanding of whether such changes take place in the ER gene. The putative proteins translated from these two pig ER RNAs observed in this study exhibit internal in-phase deletion in B domain and thus generated a in-frame truncation of the ER protein. Very few cases of truncated protein synthesis have been previously reported in the literature. A 46 and a 47 kDa with characteristics of ER protein were identified by Diaz-Chico et al. (1988) and Jozan et al. (1991). They suggested that these truncated proteins were generated by deletion in exons 3 and 4. A 80 k Da ER variant containing an in-frame duplication of exons 6 and 7 due to genomic rearrangement was reported by Pink et al. (1996). Graham et al. (1990) also described ER mutations that include two frame-shift/termination mutants plus an additional mutant with a large in-frame deletion spanning the hinge region and some of the hormone-binding domains (Gronemeyer, 1991). They suggest that these mutations were generated by chromosomal rearrangement. Whether similar mechanism is involved in generating the pER-1 and pER-2 varients requires further investigation.

The pER-1 and pER-2 fragments were the only two specific DNA fragments that could be detected via RT-PCR technique in this study and attempts at identifying the presence of non-deleted ER mRNA species were unsuccessful. Therefore, it appeared that either the nondeleted ER RNA is not expressed in pig uterus or its expression level is below detection limit used in the present experiment. In addition, the deletion in pER-1 did not appear to be an artifact that may occur using culture cells as starting materials since it was isolated from the uteri of normal cycling pig. In previous reports, Rothschild et al. studied the role of the ER gene on litter size in pigs and detected genetic difference at the ER among different pig species. They also suggested that such genetic difference is associated with litter size in pigs and ER is the best predictor of litter size differences (Rothschild et al., 1996). At farrowing, the average litter size of Lan-Yu pigs have been reported to be 4.71-5.89 and the survival rates of 8 week piglets at weaning was in the range of 84-91%. Therefore, it is interesting to speculate but remains to be studied the potential association for these ER variants occuring in Lan-Yu pig (a miniature) but not in Large White Pig or sheep (Madigou et al., 1996). In summary, the two ER variants from the uteri of Lan-Yu pig both contained an unusual exon I deletion. Although an affinity for estradiol is retained in the C-terminal half of the molecules (Murdoch et al., 1990) that appears to be intact in the two ER variants, it remains to be shown what effects these deletions. especially in pER-2, have on normal ER functions.

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