The Analysis of Seminal Plasma Proteins by Two-Dimensional Polyacrylamide Gel Electrophoresis (2-DE) in Hanwoo (Korean Native Cattle)

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ABSTRACT

This study was to evaluate the protein profile of seminal plasma using 2-DE in Hanwoo. Seminal plasma was harvested from five mature Hanwoo, and seminal plasma protein was extracted by M-PER Mammalian Protein Extraction Reagent. Proteins were refined by clean-up kit and quantified by Bradford method until total protein was 300 μ l. Immobilized pH gradient (IPG) strip was used 18 cm and 3~11 NL. SDS-PAGE was used 12% acrylamide gel. Each gels were visualized by comassie brilliant blue and silver staining. These spots were analyzed by MALDI-TOF MS and searched on NCBInr. The result, 20 proteins of 36 protein spots were searched through peptide sequencing on the NCBInr. 8 proteins profiled by 2-DE were proved through previous bovine studies and the name of each protein was albumin, nucleobindin, clusterin, TIMP-2, spermadhesin Z13, spermadhesin-1 and BSP proteins (BSP 30 kDa and BSP A1/A2). 12 new proteins were ATP synthase, protein MAK16 homolog, Transmembrane protein 214, E3 ubiquitin-protein ligase BRE1A, dual serine/threonine and tyrosine protein kinase, tissue factor pathway inhibitor 2, alpha-actinin-4, RUN domain-containing protein 3B, catenin alpha-1, protein-glutamine gamma-glutamyltransferase 2, plakophilin-1 and inter-alpha-trypsin inhibitor heavy chain H1 has not been previously described in the bovine seminal plasma study. These proteins may be contribute to define the type of proteins affecting fertility of male and improve the fertilizing ability of semen in Hanwoo.

(Key words: seminal plasma, 2D-PAGE, MALDI-TOF, Korean native cattle, proteins)

INTRODUCTION

Seminal plasma, an amorphous material existing in semen, comprises fluids from the testis and epididymis, and secretions from the sexual accessory glands of male reproductive tract. Seminal plasma contains proteins, lipids, carbohydrates, enzymes, vitamins, hormones, and trace elements, and becomes a micro-environment for spermatozoa survival after ejaculation (Chiu and Chamley, 2003; Miro et al., 2005; Troedsson et al., 2005; Cardozo et al., 2006). Seminal plasma contains a variety of biochemical components, some of which are relatively specific for the regulation of sperm function (Strzezek et al., 1992). The protein composition of seminal plasma has important effects on sperm motility (Sa'nchez-Luengo et al., 2004), viability and fertilization (Brandon et al., 1999).

Two-dimensional polyacrylamide gel electrophoresis (2-DE) is a valuable tool for the separation and characterization of

proteins from complex biological samples. Many proteins from seminal plasma of various species have been described and characterized and 2-DE has been widely used for their separation and analysis from bovine (Jobim *et al.*, 2004), equine (Brandon *et al.*, 1999), ram (Jonbim *et al.*, 2005), boar (Sanz *et al.*, 1993), ovine (Cardozo *et al.*, 2006) and human (Ding *et al.*, 2007).

However, seminal plasma proteins in Hanwoo are still poorly understood. Also, in previous bovine studies with 2-DE, a total of 25 spots was found in bovine seminal plasma (Jobim *et al.*, 2004). The seminal plasma protein profile, using 2-DE, has not been described yet in Hanwoo. Therefore, the objective of this study was to evaluate the protein profile of seminal plasma using 2-DE in Hanwoo.

MATERIALS AND METHODS

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1. Sample Collection and Processing

Semen from five mature Hanwoo were collected by artificial vagina. Seminal plasma was harvested from 1 ml of semen by centrifugation at $10,000 \times g$ for 30 min at $4^{\circ}\mathbb{C}$. The resultant supernatant was centrifuged again, and seminal plasma was kept at $-80^{\circ}\mathbb{C}$ for freeze drying. Seminal plasma protein was extracted from the freeze dried seminal plasma powder using freeze dryer by M-PER Mammalian Protein Extraction Reagent (Thermo, USA). Proteins were refined by clean-up kit (GE Healthcare, USA), and protein content was quantified with μ 300 μ g using Bradford's method.

2. Two Dimension Electrophoresis (2-DE)

Isoelectrofocusing (IEF) was performed with IPGphor unit (Amersham Biosciences, USA) using precast 18 cm pH 3~11 nonlinear IPG gel strips (Amersham Biosciences). 300 μ g of total proteins were mixed with the rehydration solution (7 M urea, 2 M thiourea, 4% w/v CHAPS, 50 M DTT and trace of bromophenol blue) to the total volume of 250 ml and incubated for 16 hr at room temperature (RT). Then, IEF was performed at 250 V for 2 hr, 8,000 V for 3 hr, and finally until total 60,000 V. After IEF separation, the gel strips were immediately equilibrated in the equilibrium buffer containing 50 mM Tris-HCl, pH 8.8, 6 M urea, 30% v/v glycerol, and 2% w/v SDS. The second dimension separation was carried out in 12% SDS-PAGE gels. Then, electrophoresis was performed using Protean II xi 2-D cell (Bio-Rad, USA) with 25 mA until the bromophenol blue reached the bottom of the gel.

3. Protein Stain

Gels were immersed in a solution of 0.1% Comassie Brilliant Blue R-250 (Sigma, USA), 45% methanol, 10% acetic acid and 45% water, and were stained overnight. The gels were destained in a mixture of 30% methanol, 10% acetic acid and 60% water.

Silver Staining Kit (GE Healthcare, USA) was used in 2-DE gels. The gels were fixed in 40% ethanol and 10% acetic acid for 30 min, sensitized in ethanol glutardialdehyde (25% w/v), sodium thiosulphate (5% w/v), and sodium acetate (17 g) for 30 min followed by 3 times washing with water for 15 min in each time. Then, the gels were immersed in silver nitrate (2.5% w/v) and formaldehyde (37% w/v) for 20 min, developed with sodium carbonate (6.25 g) and formaldehyde (37% w/v) for $2\sim5$ min, and stopped in EDTA-Na₂-2H₂O.

4. Proteomic Analysis by MALDI-TOF

The Comassie brilliant blue stained gel was scanned with the Image Scanner (Amersham Biosciences) and analyzed with the Phoretix Expression software v.2005 (Nonlinear Dynamics, UK). Destaining and in-gel trypsin digestion of the protein spots were performed as described previously. Xcise (Shimadzu Biotech Co, Japan), the automatic sample preparation system, was used for in-gel digestion, desalting, and plating. The desalting was performed with ZipTip C18 (Millipore, USA) and the plating with the 4-hydroxy- α -cyano-cinnamic acid (HCCA) matrix solution onto a MALDI-TOF MS plate. In-gel digested peptides were analyzed with MALDI-TOF MS spectrometer, Ultraflex-TOF/TOF (Bruker Daltonics, Germany). Peptide mass fingerprinting (PMF) ion search was performed using MASCOT 2.0 software and NCBInr protein databases.

RESULTS

This study have analyzed seminal plasma protein from Hanwoo using the 2-DE method. The distribution of Hanwoo seminal plasma proteins on Comassie Brilliant Blue (CBB) and silver stained gels are shown in Fig. 1. A total of 36 CBB-stained spot and 71 silver-stained spots were identified on the each gel by image analysis.

The identified 36 CBB stained protein spots were analyzed by MALDI-TOF MS. The protein was identified using the NCBInr database, and the result is shown in Table 1. The 20 proteins of 36 protein spots were searched through peptide sequencing on the NCBInr database after MALDI-TOF MS analysis. Spot No. 1 and 3, 6 and 17, 9 and 10, 12~16, 19~21, 23 and 31, 24 and 25, 27 and 28, finally 43~45 and 60 spots were confirmed with each same protein.

DISCUSSION

This study was performed for a comprehensive protein profile of seminal plasma from Hanwoo (Korean Native Cattle) using the 2-DE. And, 2-DE spots were visualized through CBB and silver stain (Fig. 1). Most of all, we selected that CBB stained spots has relatively large protein in spot than silver stained spots for effective protein analysis by MALDI-TOF. The result, 20 proteins of 36 protein spots were searched through peptide sequencing on the NCBInr database and MALDI-TOF MS (Table 1). 8 of 20 proteins profiled by 2-DE were proved through previous bovine studies (Jobim et al., 2004; Moura et

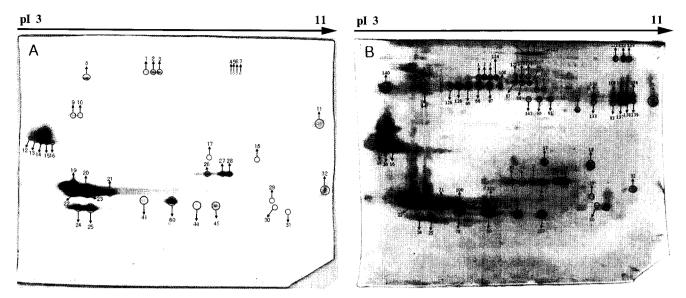


Fig. 1. Two-dimensional polyacrylamide electrophoretic gel of Hanwoo seminal plasma proteins. Two-dimensional 12% SDS-PAGE gel stained with CBB A and silver B. A: red circle was CBB stained spots; B: blue circle was only silver stained spots, red circle was indicated with spots both at CBB and silver. 300 μg of total protein was loaded to the 2-DE gel electrophoresis. First dimension used 18 cm, pl 3~11 NL strip and second dimension used 12% acrylamide gel.

al., 2007), and the name of 8 proteins was albumin, nucleo-bindin, clusterin, TIMP-2, spermadhesin Z13, spermadhesin-1 and BSP proteins (BSP 30 kDa and BSP A1/A2).

Protein spot 1, 3 probably corresponds to albumin, which is binds to sperm, and may also influence capacitation through its ability to modulate membrane cholesterol (Visconti and Kopf, 1998). Protein spot 12~16 and 19~21, 23, 31 corresponds to the complex of BSP proteins (BSP 30 kDa and A1/A2) present in seminal plasma, BSP 30 kDa are known to induce cholesterol efflux from the sperm membrane (Manjunath and Th'erien, 2002), and along with its ability to mediate sperm capacitation. BSP A1/A2 previously called PDC 109 is the main heparin binding protein in bovine seminal plasma; it bound specifically to sperm choline-phospholipids during ejaculation and promoted capacitation by cholesterol and phospholipids efflux (The'rien et al., 1999).

Protein spot 24, 25 corresponds to acidic seminal fluid protein (aSFP) is known to inhibit oxidative stress (Schoneck *et al.*, 1996). Bovine aSFP shares identity with proteins of protein spot 43~45, 60 corresponds to the spermadhesin family (Romao *et al.*, 1997). Binding of aSFP to ejaculated sperm occurs, but it is lost after capacitation (Dostolova *et al.*, 1994), suggesting that unlike porcine spermadhesins (Caballero *et al.*, 2004, 2005), bovine aSFP does not participate in sperm-oocyte interaction. Protein spot 9 and 10 corresponds to clusterin are

similar to those reported in the cauda epididymis fluid of bulls (Ibrahim et al., 1999). Clusterin is a multifunctional constituent of the seminal plasma and it can prevent oxidative damage to the sperm (Reyes-Moreno et al., 2002), bind and agglutinate abnormal spermatozoa in bulls (Ibrahim et al., 1999) and humans (O"Bryan et al., 1994) and act like a chaperone, protecting sperm from the toxic effects of protein precipitation (Humphreys et al., 1999; Wilson and Easterbrook-Smith, 2000). Clusterin has the ability to inhibit complement-induced sperm lysis (Ibrahim et al., 1999). Protein spot 27 and 28 corresponds to TIMP-2 associates with bovine and human sperm membranes (McCauley et al., 2001; Bechman-Shaked et al., 2002) and inhibitors of Metalloproteinases (MMPs) released from the sperm during acrosome reaction facilitate sperm-egg fusion in hamsters (D'1az-Perez and Meizel, 1992), and TIMPs interfere with gamete fusion in mice (Correa et al., 2000). Protein spot 8 corresponds to nucleobindin has been found secreted by bone cells and odontoblasts and as a structural element of their respective extracellular matrices (Petersson et al., 2004; Somogyi et al., 2004; Moura et al., 2007). However, those functions on sperm physiology are still unknown.

The spot No. 2, $4\sim7$, 11, 17, 18, 22, 26, 29, 30 and 32 identified in the 2-DE gels has not been previously described in the seminal plasma studies. Those are new proteins expressed in the seminal plasma fluid. Protein spot 2 corresponds to the

Table 1. Information of the polypeptide analysed in seminal plasma from Hanwoo

Spots No.	Protein name	Accession No.	Coverage (%)	MW (Da)	pI
1, 3	Serum albumin	P02769	10.4	69294	5.8
2	ATP synthase subunit beta, mitochondrial	P00829	11.2	54806	6.2
4	Protein MAK16 homolog	Q1RML7	17.1	35289	5.3
5	Transmembrane protein 214	A4FV45	11.5	77017	9.4
6, 17	E3ubiquitin-protein ligase BRE1A	A2VDP1	4.9	113659	5.7
7	Dual serine/threonine and tyrosine protein kinase	Q4TVR5	4.7	104805	6.4
8	Nucleobindin-1	Q0P569	28.3	54983	5.1
9, 10	Clusterin	P17697	15.7	51114	5.7
11	Tissue factor pathway inhibitor 2	Q7YRQ8	36.8	26675	9.1
12, 13, 14, 15, 16	Seminal plasma protein BSP-30 KDa	P81019	41.5	21269	5.7
18	Alpha-actinin-4	A5D7D1	6.7	104929	5.3
19, 20, 21, 23, 31	Seminal plasma protein PDC-109	P02784	32.8	15481	4.9
22	RUN domain-containing protein 3B	Q08E29	16.1	47034	5.3
24, 25	Spermadhesin-1	P29392 (2.72e+9)	73.9	15036	5.1
26	Catenin alpha-1	Q3МНМ6	8.5	100134	5.9
27, 28	Metalloproteinase inhibitor 2	P16368	30.9	24355	7.4
29	Protein-glutamine gamma-glutamyltransferase2	P51176	10.6	77113	5.1
30	Plakophilin-1	Q28161	5.5	80181	9.2
32	Inter-alpha-trypsin inhibitor heavy chain H1	Q0VCM5	4.1	101238	7.0
43, 44, 45, 60	Spermadhesin Z13	P82292	46.6	13383	5.6

ATP synthase isolated from bovine heart mitochondria (Bos taurus) is the best characterized ATP synthase biochemically and structurally. Beef heart is used as a source of the enyzme because of the high concentration of mitochondria in cardiac muscle (Zoleo et al., 2007). The spot No. 5 corresponds to Transmembrane protein 214, these proteins are present in the inner membranes of bacterial cells or the plasma membrane of eukaryotes, and sometimes in the outer membranes, and which may reflect their common evolutionary origin and similar folding mechanism (Almén et al., 2009). Protein spot 6 and 17 corresponds to E3 ubiquitin-protein ligase BRE1A, those are this is a ubiquitin ligase required for the ubiquitination of histone H2B and the methylation of histone H3 (Yamashita et al., 2004). Protein spot 32 corresponds to Inter-alpha-trypsin inhibitor heavy chain H1 is function as protease inhibitors (Zhuo et al., 2004). Other unknown proteins in bovine seminal plasma are the Protein spot No. 2 (Protein MAK16 homolog), 7 (Dual serine/threonine and tyrosine protein kinase), 11 (Tissue factor pathway inhibitor 2), 18 (Alpha-actinin-4), 22 (RUN domain-containing protein 3B), 26 (Catenin alpha-1), 29 (Protein- glutamine gamma-glutamyltransferase 2) and 30 (Plakophilin-1).

In conclusion, this study is protein profile of seminal plasma from Hanwoo using the 2-DE, and we found that 12 new proteins has not been previously described in the bovine seminal plasma study. So far, this the role of those proteins on the fertility of the male Hanwoo are still unknown. Therefore, we suggest that additional research are necessary to define the types of proteins affecting fertility of male and the mechanisms of their actions. Additional research may contribute to the development of strategies to improve the fertilizing ability of semen in Hanwoo.

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