Original study

# Plasma proteomic profiles of healthy and mastitic cows – host responses to bovine mastitis

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# Abstract

Mastitis is the most common disease in dairy cows and has resulted in a tremendous economic loss in dairy industry. In the present study, differentially expressed proteins (DEP) were identified among healthy, moderate and severe mastitic cows by proteomic profiling. The health status of cows was closely determined by the somatic cell count (SCC). Differentially expressed proteins were resolved using the two-dimensional gel electrophoresis (2-DE) with the pH 4-7 non-linear DryStrips. Subsequently, 8 protein spots, which altered more than 3-fold, were isolated and identified with the matrix-assisted laser desorption/ionisationtime of flight mass spectrometry (MALDI TOF/TOF MS). The identified spots were split into four proteins: α-2-HS-glycoprotein, serum albumin, transthyretin (TTR) and haptoglobin, respectively. Compared with the healthy cows, the expression of haptoglobin was upregulated in mastitic cows, and the others were down-regulated. Moreover, the proteomic data were consistent with the results of Western blot. All of the identified DEPs were acute phase proteins, which acted together and represented the consequence of serial cascades after mastitic infection. More importantly, the  $\alpha$ -2-HS-glycoprotein was novel identified corresponding to the bovine mastitis in Chinese Holstein dairy cows. Taken together, our results indicate that the host responses may play an important role in the pathogenesis of mastitis and provide the potential diagnostic indicator of the underlying mastitis in dairy cows.

Keywords: bovine mastitis, DEP, host response, 2-DE

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## Introduction

Mastitis is defined as an inflammation of the mammary gland that is usually caused by microbial infections and resulted in destruction of the milk secreting cells, which contributed to a permanent loss of productive ability consequently (Long *et al.* 2001). The bovine mastitis has a relatively high incidence worldwide and has been recognized as the most costly disease in the dairy industry (Huijps *et al.* 2008). It commonly occurs in response to intramammary bacterial infections, but also to intramammary mycoplasmal, fungal or algal infections. Depending on the duration of infection and appearance onset of clinical symptoms, mastitis could be assigned to clinical and subclinical bovine mastitis.

Somatic cell count (SCC) is one of the main indicators of milk quality, and also considered as a trait for mastitis resistance. In one individual, the SCC of 100×10<sup>3</sup> cells/mL or less indicated an 'uninfected' cow, and there are no significant production losses. General agreement on the threshold SCC of 200×10<sup>3</sup> would determine whether a cow is infected with mastitis. Cows infected with mastitis have an SCC of 300×10<sup>3</sup> or greater. Meantime, the California Mastitis Test (CMT) is a simple cow-side indicator of the somatic cell count of milk. It disrupted the cell membrane of any cells present in the milk sample, allowing the DNA in those cells to react with the test reagent, forming a gel (Whyte *et al.* 2005). Somatic cell count and CMT were implemented in the routine stock evaluation in many countries. Many QTLs affecting SCC had been identified in the telomeric regions of BTA18 (Kühn *et al.* 2003, Xu *et al.* 2006, Kühn *et al.* 2008, Thomsen *et al.* 2011). Furthermore, a genome-wide significant QTL for clinical mastitis was detected (Schulman *et al.* 2004).

In this study, global views of the DEPs corresponding with healthy, moderate and severe mastitis were profiled by 2-DE. The identical spots with altered dosages which were expected to be relative to bovine mastitis were further identified by MALDI TOF/TOF MS and validated by western blot. Ultimately, the proteomic information in the plasma will highlight the pathophysiology of bovine mastitis and be helpful to identify potential targets for mastitis diagnosis and therapies.

# Material and methods

#### Plasma isolation and protein preparation

Mammary quarter foremilk samples were tested using CMT and SCC A total of 20 Holstein dairy cows were selected for study [10 healthy cows (CMT negative,  $SCC \le 200 \times 10^3$ ), 5 moderate mastitic cows (CMT positive,  $SCC < 2000 \times 10^3$ ) and 5 severe mastitic cows (CMT positive,  $SCC < 2000 \times 10^3$ ). Blood samples were acquired by jugular venipuncture in 6 mL K<sub>2</sub>EDTA Vacuum Blood Collection Tubes (BD Diagnostics, USA). Blood plasma was obtained by horizontal centrifugation at  $1000 \times g$  for  $10 \min$  at  $4^{\circ}$ C. Then plasma was pooled with equivalent volume according to healthy, moderate and severe mastitic cows, separately. The supernatant phase was collected with pooled plasma centrifugation at  $2400 \times g$  for  $15 \min$  and aliquot stored in liquid nitrogen.

## Two-dimensional electrophoresis (2-DE)

Isoelectric focusing (IEF) was performed using 17 cm, nonlinear, pH 4-7 DryStrips (Bio-Rad Laboratories Inc., Hercules, CA). Five  $\mu$ L of plasma with 10  $\mu$ L of 10 % sodium dodecyl sulphate (SDS) and 2.3 % dithiothreitol (DTT) were heated at 95 °C for 5 min. DryStrips were rehydrated in 400  $\mu$ L of the rehydration buffer with 4  $\mu$ L of the treated sample (Alonso-Faust *et al.* 2012). Gels were stained using the silver staining method (Sinha *et al.* 2001). All gels were scanned using Powerlook 2100XL (UMAX Technologies, Inc., Taiwan).

## Image analysis

The images of 2-DE gels were measured by the PDQuest software version 7.1 (Bio-Rad Laboratories). Three repetitive gels from each type of pooled plasma were analysed as one match-set to generate the master gel. Relative intensity of each matched spot on the master gel was compared with those from the healthy, moderate and severe mastitic cows. The protein spots with a 3-fold altered expression were cut, extracted and identified according to the well-established protocol (Yan *et al.* 2006).

## Western blot detection

In an attempt to validate the proteomic results, western blot was performed with the specific antibodies for alpha-2-HS-glycoprotein, haptoglobin and TTR, respectively. After CMT and SCC test, one healthy (SCC=200×10<sup>3</sup>) and two mastitic cows (SCC=5 985×10<sup>3</sup> and 1 325×10<sup>3</sup>) were analysed. Total plasma protein concentration was precisely determined by the DC protein assay kit using gamma globulin as a standard (500-0111, Bio-Rad, Richmond, CA). One  $\mu$ L plasma sample (diluted 1:4) with 9  $\mu$ L loading buffer (600 mM pH 6.8 Tris-Hcl, 10% SDS, 50% sucrose, 10 mM DTT) heated for 5 min, was separated by 12% SDS/PAGE and then transferred to 0.45  $\mu$ m polyvinylidene fluoride membranes (Millipore, Bedford, MA) at 100 V for 1 h with cooling. The membranes were treated with antibody followed by washing with PBS-T and exposuring with ECL mixture. Film was scanned and the density of the protein band was quantified by Quantity One software (Bio-Rad, Laboratories).

# Results

## Two-dimensional proteome maps of bovine plasma

In our study, 173-233 distinct spots were detected with a molecular mass ranging from 100 kDa to 20 kDa and with the pH scale from 4 to 7. The representative plasma 2-DE profiles of plasma proteins were shown in Figure 1. There were 173 matched spots corresponding to healthy, moderate and severe mastitic cows, representing the 80.6% identical spots in the 2-DE gels. These protein spots were remained for further analyses.

## Identification of differentially expressed proteins

Densitometry comparison of protein spots among healthy, moderate and severe mastitic cows were analysed with PDQuest 7.1 (Bio-Rad, Hercules, CA, USA), overlapped spots were not recognized. The expressions of 8 spots were altered more than 3-fold whereat 6 protein

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Spots No.	Protein name	Acc. No.	Source	Protein score	Matched Peptides <sup>1</sup>	Sequence coverage <sup>2</sup> (%)	Experimental pI/MW	Expression level (mastitic/healthy)
-	alpha-2-HS-glycoprotein	NP_776409	Bos taurus	356	10	32	5.26/38394.4	<b> </b> →
2	alpha-2-HS-glycoprotein	NP_776409	Bos taurus	361	10	36	5.26/38394.4	
	albumin	P02769	Bos taurus	476	13	25	5.82/69248.4	
4	albumin	P02769	Bos taurus	308	10	21	5.82/69248.4	
5	albumin	P02769	Bos taurus	602	17	34	5.82/69248.4	
9	transthyretin	NP_776392	Bos taurus	92	4	31	5.91/15717	
7	haptoglobin	CAC0053	Bos taurus	367	10	26	9.76/11232.2	
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Table 1

<sup>1</sup>The number of matched peptides in the database search. <sup>2</sup>The total coverage of the matched peptides in relation to the full-length sequence.



spots showed a down-regulation and 2 protein spots displayed an over-expression in both moderate and severe mastitic cows. After MALDI-TOF/TOF MS, 6 protein spots (Spots 1-6) corresponded to 3 proteins: fetuin, TTR and serum albumin were identified, while the over-expressed spot (Spot 7) was haptoglobin (Table 1). Spot 8 was failed to be identified.

#### Western blot analysis

Fetuin and TTR were detectable at the 59 kDa and 43 kDa immunoreactive bands, respectively. The expression of fetuin was down-regulated in health cows, which was approximately 2-times lower than that in both moderate and severe mastitic cows. Transthyretin was also down-regulated in mastitic cows. Compared to the healthy group, the haptoglobin was detectable as one over 120 kDa immunoreactive band and showed marginally significant 1.72- and 1.43-fold increases in moderate and severe mastitic groups, respectively (Figure 2).



#### Figure 2

The DEPs was validated by western blot. (a) The representative image of DEPs. The values in parenthesis are the relative normalized intensities compared to those in healthy cows. (b) The internal control was indicated by the 2-DE gels using 1  $\mu$ L total plasma protein.

# Discussion

#### Protein down-regulated in the plasma of mastitic cows

Spots 1 and 2, alpha-2-Heremans-Schmid Glycoprotein

α-2-HS-glycoprotein, also called fetuin, is a secreted plasma protein that is expressed in hepatocytes, monocyte/macrophages and bone. Fetuin influenced the resolution of inflammation through enhancing the phagocytosis in foreign particles and apoptotic cells by macrophages (Wang *et al.* 1998, Jersmann *et al.* 2003), suggesting a positive role in the recovery phase of acute inflammatory responses (Lord *et al.* 2003). The hepatic mRNA levels of fetuin in human and rat transiently fell during the acute phase of a systemic inflammation (Ruminy *et al.* 2001).

#### Spots 3 to 5, serum albumin

Serum albumin was a negative acute-phase protein, with antioxidant function (Roche *et al.* 2008). The concentration of serum albumin increased due to increased capillary permeability in infected quarter milk (Nicholson *et al.* 2000). Rezamand *et al.* (2007) found that Holstein and Jersey dairy cows had greater albumin concentrations than animals with extra intramammary infection (IMI). The mean albumin concentration in blood decreased significantly during the acute-phase period by radial immunodiffusion, and the lowest level was found in Holstein-Friesian heifers infected with *Escherichia coli* after 12 h (Van Merris *et al.* 2004). However, the level of serum albumin was not altered in blood of Finnish Ayshire cows with *Escherichia coli* mastitis under the same protocols (Raulo *et al.* 2002).

#### Spot 6, transthyretin (TTR or prealbumin)

Transthyretin was related to the transport of thyroid hormones and retinol, which was affected by inflammation and malnutrition (Myron *et al.* 2007). It also was an inhibitor of monocyte and endothelial cell IL-1 production, thus, presenting anti-inflammatory properties (Borish *et al.* 1992). During inflammation status, the altered level of TTR was proposed to be a result of the change of some small molecules binding to endocrine proteins (Bernstein 2009). The concentrations of TTR and plasma retinol binding protein (RBP) were related to the infection rate of M. paratuberculosis in cattle (Seth *et al.* 2009).In Holstein and Jersey dairy cows with extra IMI, the plasma concentrations of TTR at week 1 postpartum were lower than those in cows without IMI (Rezamand *et al.* 2007).

#### Protein up-regulated in the plasma of mastitic cows

#### Spot 7, haptoglobin

Haptoglobin was a haemoglobin binding protein and also played an anti-inflammatory role (Quaye 2008). Haptoglobin had been reported to be a useful indicator of bovine bacterial infection. It also was synthesized in mammary gland (Thielen *et al.* 2007), and its concentration increased 200-fold locally in infected quarters (Mitterhuemer *et al.* 2010), which started to rise 24 h after *E. coli* inoculation and peaked at 60-68 hours (Suojala *et al.* 2008). Chronic purulent infections continuously induced the production of haptoglobin, whereas short-lived coliform infections might only trigger a temporary haptoglobin response (Petersen *et al.* 2004).

#### Potential novel indicator for mastitis

The  $\alpha$ -2-HS-glycoproteinwas identified previously in 2-DE of mastitis whey and milk, which accounted for the leakage of serum proteins (Anderson *et al.* 2002, Smolenski *et al.* 2007). However, the identification of  $\alpha$ -2-HS-glycoprotein in blood plasma has not been reported yet in mastitic cows. In our study, the level of  $\alpha$ -2-HS-glycoprotein in plasma was related to the morbidity of mastitis and verified by western blot. Thus, we suggest that  $\alpha$ -2-HS-glycoprotein based screening test may be used to monitor progression of the bovine mastitis.

In conclusion, in the study, all of the DEPs were acute phase proteins. Their altered expressions in plasma revealed the host defence to inflammation. To minimize the damage of mammary tissue caused by bacterial toxins and reactive oxygen species released from neutrophils, inflammatory response needs to be regulated by systemic factors (Burvenich *et* 

*al.* 2007, Paap *et al.* 2002). It had been reported that the host defence status was a cardinal factor determining the outcome of the disease in *E. coli* mastitis (Burvenich *et al.* 2003). Our data will highlight the pathophysiology of bovine mastitis and be helpful to identify potential targets for mastitis diagnosis in future.

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