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# 1 Expression of acute phase proteins and inflammatory cytokines 2 in mouse mammary gland following *Staphylococcus aureus* 3 challenge and in response to milk accumulation

4 Sasan Nazemi<sup>1\*</sup>, Bent Aalbæk<sup>2</sup>, Mads Kjelgaard-Hansen<sup>1</sup>, Sina Safayi<sup>3</sup>, Dan Arne Klærke<sup>1</sup> and  
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10 Received 14 April 2014; accepted for publication 21 July 2014

11 We used a mouse model of pathogenic (*Staphylococcus aureus*) and non-pathogenic (teat sealing)  
12 mammary inflammation to investigate mRNA expression of several inflammatory cytokines and acute  
13 phase proteins (APP) in mammary tissue and liver, and the appearance of some of these factors in  
14 plasma and milk. The expression levels of IL1 $\beta$  and TNF $\alpha$  were markedly up-regulated in *Staph.*  
15 *aureus*-inoculated mammary tissue at 72 h, whilst IL6 was up-regulated to a lesser extent in a way  
16 which was not confined to the inoculated glands. APP expression was up-regulated at 48 and 72 h in  
17 both *Staph. aureus*-inoculated and teat-sealed mammary glands. These differences between cytokine  
18 and APP expression provide additional support for the contention that APPs are produced within the  
19 mammary tissue itself during inflammation, rather than in associated immune cells. We propose that  
20 measurement of cytokines and APP in combination might provide a tool for diagnostic discrimination  
21 between mastitis caused by pathogenic invasion and milk accumulation, and hence allow for better  
22 targeting of antibiotic therapy. In comparison with mammary expression, expression of cytokines in  
23 liver tissue was up-regulated to a similar or lesser extent, whilst expression of APP was up-regulated to  
24 a much greater extent. The first appearance of increased cytokine and APP concentrations in plasma  
25 and of milk amyloid A (MAA) in milk occurred in advance of the measurable up-regulation of  
26 expression, hence their origin cannot be stated with certainty.

27 **Keywords:** Mouse, mammary gland, APP, cytokines, *Staphylococcus aureus*, mastitis.

28  
29 Pathological inflammation of the mammary gland, mastitis,  
30 is one of the most costly diseases in the dairy industry, caus-  
31 ing both direct and indirect losses (Seegers et al. 2003;  
32 Bannerman, 2009; Cha et al. 2011). The pathogenicity and  
33 involvement of *Staphylococcus aureus* as a causative factor  
34 in intramammary infection (IMI) has been widely discussed  
35 (Bayles et al. 1998; Hensen et al. 2000; Schukken et al.  
36 2011) as has its relevance as a major cause of chronic  
37 subclinical mastitis. Defining and establishing better and  
38 more reliable diagnostic biomarkers for earlier detection of  
39 clinical mastitis would be immensely valuable (Eckersall  
40 1995; Eckersall & Bell, 2010) but so would better methods  
41 for diagnosing subclinical mastitis (Akerstedt et al. 2011).

The mammary gland is also subject to inflammatory re- 42  
sponses not attributable to microbial invasion. This is most 43  
evident at the end of lactation when milk accumulation 44  
causes increased intramammary pressure leading to an 45  
inflammatory acute phase response (Stein et al. 2004), 46  
disruption of the mammary epithelium, apoptosis and 47  
extensive tissue remodelling (Quarrie et al. 1996; Theil 48  
et al. 2005). Non-pathogenic mammary inflammation may 49  
also occur to some extent during the normal filling of the 50  
gland between milkings/sucklings, especially if the latter is 51  
delayed for some reason (Lacic et al. 2011). In many cases 52  
the aetiology of mammary inflammation is not easy to 53  
determine. For instance, many breastfeeding practitioners 54  
consider that human mastitis rarely involves a pathogen, 55  
but is due to ‘blocked ducts’ and hence milk accumulation 56  
(Kvist, 2013). The use of antibiotic therapy to treat human 57  
mastitis varies greatly from country to country (Scott et al. 58

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59 2008) whereas the majority of bovine mastitis is treated by  
60 antibiotic, often without direct evidence of infection (and  
61 hence unnecessarily: Roberson, 2012). There is a diagnostic  
62 need across species to be able to distinguish between  
63 infectious mastitis and 'physiological inflammation'.

64 The involvement of different cytokines and acute phase  
65 proteins (APPs) has been reported in different inflammatory  
66 responses including mastitis (see Murata et al. 2004 for  
67 review). Tissue damage, including mastitis, induces an acute  
68 phase response (APR) which mostly comprises the release of  
69 inflammatory mediators from tissue macrophages at the  
70 damaged site (Koj, 1996). As a result, mastitic milk contains  
71 elevated levels of cytokines (Peli et al. 2003). APPs are also  
72 found in milk. Colostrum was shown to contain high levels of  
73 mammary-associated serum amyloid A3 (SAA3: McDonald  
74 et al. 2001) which was later also found, together with  
75 haptoglobin (HP) in naturally occurring and experimentally  
76 induced mastitis (Nielsen et al. 2004; Eckersall et al. 2006).  
77 A third APP,  $\alpha$ 1-acid glycoprotein (AGP) is also present in  
78 colostrum and mastitic milk (Cecilian et al. 2005; Eckersall  
79 et al. 2007). Systemic as well as local production of APPs  
80 is believed to play an important role in host defence (see  
81 Eckersall & Bell, 2010 for review).

82 Using mice as a model for infectious mastitis has been  
83 well established for several decades (Chandler, 1970;  
84 Anderson, 1977) and more recently has been used for  
Q4 85 *Staph. aureus* mastitis (Brouillette & Malouin, 2005a;  
86 Brouillette et al. 2005b; Hu et al. 2010). However, the  
87 murine APR has not been characterised, nor has pathogenic  
88 inflammation been compared with non-pathogenic. The  
89 objective of this study was to establish a mouse model to  
90 allow comparison of the APR in response to infusion of  
91 *Staph. aureus* and to accumulation of milk caused by teat  
92 sealing. Cytokines included for study were IL1 $\beta$ , IL6 and  
93 TNF $\alpha$ , and APPs were AGP, SAA3 and HP. We focused at  
94 both local and systemic level, measuring mammary tissue  
95 gene expression with qRT-PCR (real-time quantitative PCR)  
96 and analysing milk and blood plasma using commercially  
97 available ELISA and Multiplex immunoassays. The research  
98 addresses two hypotheses: firstly, that acute phase proteins  
99 present in milk are in part or wholly of local (mammary)  
100 origin; and secondly, that the profile of APP production will  
101 differ between pathogenic inflammation and inflammation  
102 caused by milk accumulation.

## 103 Material and methods

### 104 Animals

105 The experiment was performed according to the guidelines  
106 of the European Convention for protection of Vertebrate  
107 Animals and Animal Experimentation Act under Danish  
108 national legislation and conducted at Technical University  
109 of Denmark (DTU), (License Number: 2012-15-2934-  
110 00587). NMRI outbred mice (male around 35 g and female  
111 around 25 g) were purchased from two different companies,  
112 Taconic and Harlan, from Denmark and Netherlands,

respectively, in order to establish our own breeding colonies. 113  
Experimental mice were fed fortified breeding diet (Altromin 114  
Spezialfutter GmbH&Co.KG, Germany) ad libitum. Females 115  
were placed singly with males and examined daily for the 116  
presence of a vaginal plug. Pregnant mice were transferred 117  
into single cages and provided with nesting material. Follow- 118  
ing parturition the number of pups was adjusted to 10 119  
(Shipman et al. 1987) to ensure a constant suckling stimulus. 120

### Experimental procedure 121

Lactating mice were used on day  $7 \pm 2$  of lactation. General 122  
anaesthesia was induced with isoflurane (IsoFlo Vet, Orion 123  
Pharma Animal Health) and continued with hypnorm/ 124  
dormicum (VetPharma Ltd/Dormicum 5.5 mg/ml ROCHE) 125  
0.075 ml/10 g/mouse. Individual teats were cleaned with 126  
70% ethanol and visualised through a binocular stereo- 127  
microscope. A Nanofil™ 100- $\mu$ l microinjection syringe 128  
(World Precision Instruments Inc, SG2 7EG UK) attached 129  
to a micromanipulator was carefully positioned such that the 130  
tip of a blunt 36-g needle attached to the syringe was close to 131  
the tip of the teat, which was then carefully lifted onto the 132  
needle using microforceps. Once the needle was located 133  
within the teat the contents of the syringe were carefully dis- 134  
charged through the teat into the gland. A total of 36 mice 135  
were inoculated in this way. In each mouse, the fourth and 136  
fifth inguinal glands on one side were infused with 100  $\mu$ l of 137  
*Staph. aureus* suspension whilst the two contralateral in- 138  
guinal glands were infused with 100  $\mu$ l of normal saline 139  
vehicle. The second and third thoracic glands on one side 140  
were sealed with tissue adhesive (Loctite super glue uni- 141  
versal) whilst the contralateral glands were untreated as 142  
control. The treatment sides were randomised between 143  
mice, and in each mouse the pathogen and sealing treat- 144  
ments were made on opposite sides. Following inoculation 145  
the mouse was kept separated from its pups for 4 h in order to 146  
obtain better colonisation of the bacteria. 147

### Bacterial strain 148

*Staph. aureus* AO35 was obtained from an infected cow and 149  
kindly provided by our colleague, Dr Arshnee Moodley, at 150  
the Department of Veterinary Disease Biology, Copenhagen 151  
University, Denmark. The isolate was propagated in 10 ml of 152  
Luria-Bertani (LB) broth for 18 h at 37 °C, sedimented by cen- 153  
trifugation and re-suspended in sterile isotonic saline. The 154  
viable count was made by counting the number of colonies 155  
formed on the LB agar medium, inoculated with 10- $\mu$ l 156  
volumes of tenfold dilution and incubated at 37 °C for 24 h. 157  
The suspension was then diluted with sterile isotonic saline 158  
to obtain a suspension containing 10 000 cfu/ml. The bac- 159  
terium was successfully re-isolated from the infused mice 160  
(data not shown). 161

### Sampling 162

The 36 inoculated mice were divided into 6 groups of 6 mice 163  
for sample collection at 0 (control), 4, 10, 24, 48 and 72 h 164

**Table 1.** Primer sequences used for real-time PCR reactions

Gene	Sequence	Amplicon (bp)	NCBI ref. sequence
IL1 $\beta$		355	NM_008361.3
Forward	5'GTGTCTTTCCCGTGGACCTT 3'		
Reverse	5'TGGGTGTGCCGTCCTTCATT 3'		
IL6 $\dagger$		453	NM_010551.3
Forward	5'ACACCACTACAGCCCAACAC 3'		
Reverse	5'TTGACCCAGGAGACCAGAAAATC 3'		
SAA3 $\ddagger$		363	NM_011315.3
Forward	5' AGCCTTCCATTGCCATCATTCTT 3'		
Reverse	5' AGTATCTTTTAGGCAGGCCAGCA 3'		
HP		180	NM_017370.2
Forward	5' TGGGGTCCAGCCTATCTTGA 3'		
Reverse	5' ACACCATACTCAGCGACAGC 3'		
AGP		108	NM_008768.1
Forward	5' GGAAGCTCAGAACCCAGAACA 3'		
Reverse	5' CTGAAAGCTGCACCCATGAAA 3'		
TNF $\alpha$		261	NM_013693.2
Forward	5'AAGAGGCACTCCCCAAAAG 3'		
Reverse	5'CTTGGTGGTTGCTACGACG 3'		
Rpl13a		140	NM_009438.5
Forward	5'TTGTGGCCAAGCAGGTACTTC 3'		
Reverse	5'TCGGGAGGGGTGGTATT 3'		

$\dagger$ IL6 reverse primer sequence was from Wang et al. (2008)

$\ddagger$ SAA3: Villalba et al. (2012)

165 after inoculation. Mice were anaesthetised and injected  
 166 with 0.15 iu oxytocin (Oxytocin-S 0.18 mg/ml, Intervet)  
 167 IP for milk sample collection into micro-capillary, non-  
 168 heparinised tubes. Milk samples were obtained from the  
 169 three treatments (inoculated, vehicle infused and control  
 170 glands) at 0, 4, 10, 24 and 48 h. Owing to extreme inflam-  
 171 matory response at the bacterial infused gland at the 72-h  
 172 group samples could not be reliably collected. Blood  
 173 samples were collected by cardiac puncture and 22-gauge  
 174 needles, stored at 4 °C overnight then centrifuged at 1500 g  
 175 at 4 °C for 10 min for serum collection. Blood sera and  
 176 milk samples were stored at –80 °C for further analysis.  
 177 The anaesthetised mouse was then sacrificed by cervical  
 178 dislocation for tissue sampling. Control, *Staph. aureus*-  
 179 inoculated, vehicle-infused and teat-sealed mammary  
 180 tissues were quickly collected and divided into two pieces;  
 181 a larger portion for flash freezing with liquid nitrogen and  
 182 storing at –80 °C, and a smaller portion fixed in 4% PFA  
 183 (v/v) (paraformaldehyde) for 24 h followed by transferring  
 184 into 70% ethanol for 3 d before paraffin embedding.

## 185 RNA preparation

186 Frozen mammary glands and livers were cut into smaller  
 187 pieces of 20–25 mg on dry ice. Tissues were homogenised  
 188 with Trizol (Life Technologies Europe BV, 2850 Naerum,  
 189 Denmark) and frozen stainless steel beads (5 mm Qiagen  
 190 Cat.no 69989) with TissueLyser II from Qiagen (Cat.no  
 191 85300). They were then centrifuged for 10 min at 4 °C and  
 192 transferred into MaXtract High Density 1.5-ml tubes (Qiagen  
 193 Cat.no 129046); final isolation was performed by using SV

Total RNA isolation system kit from Promega (Naka, 194  
 Sweden) according to the guidelines. RNA yield was after- 195  
 wards checked by NanoDrop ND-1000 Spectrophotometer 196  
 and the quality of RNA was determined by using Aligent 197  
 2100 Bioanalyzer System (Aligent Technologies). 198

## cDNA synthesis, primer design and qRT-PCR

199

Isolated RNA transcribed to cDNA by using 5 $\times$  MMLV 200  
 reverse transcriptase, dNTP, random hexamer primer, 201  
 RN-ase inhibitor and MMLV enzyme by adding H<sub>2</sub>O up to 202  
 25  $\mu$ l cocktail in total (Promega, Nacka, Sweden). The cDNA 203  
 was stored at –20 °C for short periods and –80 °C for longer 204  
 times and also diluted to a concentration of 4 ng/ $\mu$ l before 205  
 quantification. 206

Three reference genes, RPL13A (ribosomal protein L13a), 207  
 HPRT (hypoxanthine-guanine phosphoribosyltransferase) 208  
 and GAPDH (glyceraldehyde 3-phosphate dehydrogenase) 209  
 were selected (Han et al. 2010). RPL13A was selected as the 210  
 most stable reference gene for normalisation of the data. 211  
 Target and reference genes were tested for genomic DNA on 212  
 2% agarose gel, standard curves were obtained, and accept- 213  
 ance efficiency range was set to 1.8–2 with satisfactory 214  
 melting curves. Products were sent for DNA-sequencing at 215  
 TAG Copenhagen A/S, Denmark. Samples were run in 216  
 triplicate with inter-plate calibrators using LighCycler<sup>®</sup> 480 217  
 machine (SYBr green 1 master mix) from Roche Applied and 218  
 Diagnostics (Hvidovre, Denmark) 10  $\mu$ m for each primer in a 219  
 10- $\mu$ l reaction mixture containing 2  $\mu$ l of total cDNA 220  
 (Rahbek et al. 2014). Primer sequences are listed in Table 1. 221

## 222 Serum cytokine, APP and milk amyloid A concentrations

223 Serum concentration of IL1 $\beta$ , IL2, IL6, IL10 and TNF $\alpha$  were  
 224 measured with a Mouse Magnetic Cytokines/Chemokines  
 225 panel, MICYTOMAG-70 MILLIPLEX Map, Millipore by  
 226 Luminex 200. The assay was provided with calibration and  
 227 standards. The observed assay response from calibrators  
 228 and controls were acceptable and showed the accuracy of  
 229 the measurements. The samples were run in one batch and  
 230 all samples were assayed in duplicate.

231 SAA and HP concentrations were measured by com-  
 232 mercially available ELISA kits. Murine serum amyloid A  
 233 (SAA) (TP-802M), pre-coated microplate and haptoglobin  
 234 (HP) (TP-801) Tridelta (Development Ltd, Ireland) assays  
 235 were used for APP measurement in serum samples and by  
 236 following the manual instruction, both kits were provided  
 237 with their calibrators. Concentration of mouse milk amyloid  
 238 A (MAA) was also determined by using a kit from Tridelta  
 239 (Development Ltd, Ireland) (TP-807). This ELISA kit was also  
 240 pre-coated and provided with the calibrators. Concentra-  
 241 tions in blood sera and milk samples were determined using  
 242 BioTek ELx800 Absorbance Microplate Reader $\text{\textcircled{R}}$  by reading  
 243 at both 450 and 630 nm, and calculated by Gen5 software.  
 244 Samples were assayed in duplicate and samples with higher  
 245 concentration than the standards were re-diluted and re-  
 246 analysed in order to obtain their concentration values within  
 247 the range of the standard curves.

## 248 Statistical analysis

249 Relative gene expression analysis was implemented based  
 Q5 250 on Pfaffl (2001) and statistical analysis of all data was per-  
 251 formed by using the mixed procedures in SAS (version 9.3,  
 252 SAS Institute Inc. 2010). Variables in the statistical model  
 253 included the group, treatment and their interaction as fixed  
 254 effects, and the factors such as animal, gland side within  
 255 a row in the animal as random effects, as shown in the  
 256 following model:

$$Y = \mu + \alpha_i + \beta_j + \alpha\beta_{ij} + \gamma_k + \rho_{lm} + \varepsilon_{ijklm},$$

257 where  $Y$  = the dependent variables,  $\mu$  = the overall means,  
 258  $\alpha_i$  = group ( $i$  = control, right or left),  $\beta_j$  = treatment ( $j$  = control,  
 259 staph, sealed or saline),  $\alpha\beta_{ij}$  = interaction between group and  
 260 treatment,  $\gamma_k$  = random effect of animal ( $l$  = 1, 2, ... and 35),  
 261  $\rho_{lm}$  = random effect of gland side within a row ( $l$  = left or right;  
 262  $m$  = gland number),  $\varepsilon_{ijklm}$  = random variation which was  
 263 assumed to be normally distributed with a variance  $\sigma^2$  and  
 264 a mean of zero. For expression analysis between control  
 265 glands and liver samples, variables in the statistical model  
 266 included the group (control gland and liver), treatment  
 267 (control, 4, 10, 24, 48 and 72 h) and their interaction as fixed  
 268 effects, and the factor animal (1, 2, ... and 35) as random  
 269 effect. For analysis of mouse milk amyloid A (MAA) data,  
 270 group (control, 4, 10, 24 and 48 h), treatment (control, *Staph.*  
 271 or saline) and their interaction were included as fixed effect  
 272 and animal (1, 2, ... and 30) as random effect. For analysis of  
 273 serum amyloid A (SAA) ELISA, colorimetric haptoglobin and

mouse MAGNETIC cytokines assays, group (control, 4, 10, 274  
 24, 48 and 72 h) was included as fixed effect and animal 275  
 (1, 2, ... and 35) as random effect. Before performing the final 276  
 statistical analyses, data were checked for outliers based on 277  
 residual plots. One mouse from the 24-h group was ex- 278  
 cluded from the whole study. 279

Presented results are expressed as least squares 280  
 means  $\pm$  SEM for the graphs and the significance levels for 281  
 overall effects in table. The PDIF option in SAS was used to 282  
 generate comparisons between treatment means. The level 283  
 of significance was set at  $P < 0.05$  and graphs were made 284  
 with SigmaPlot 12.0. 285

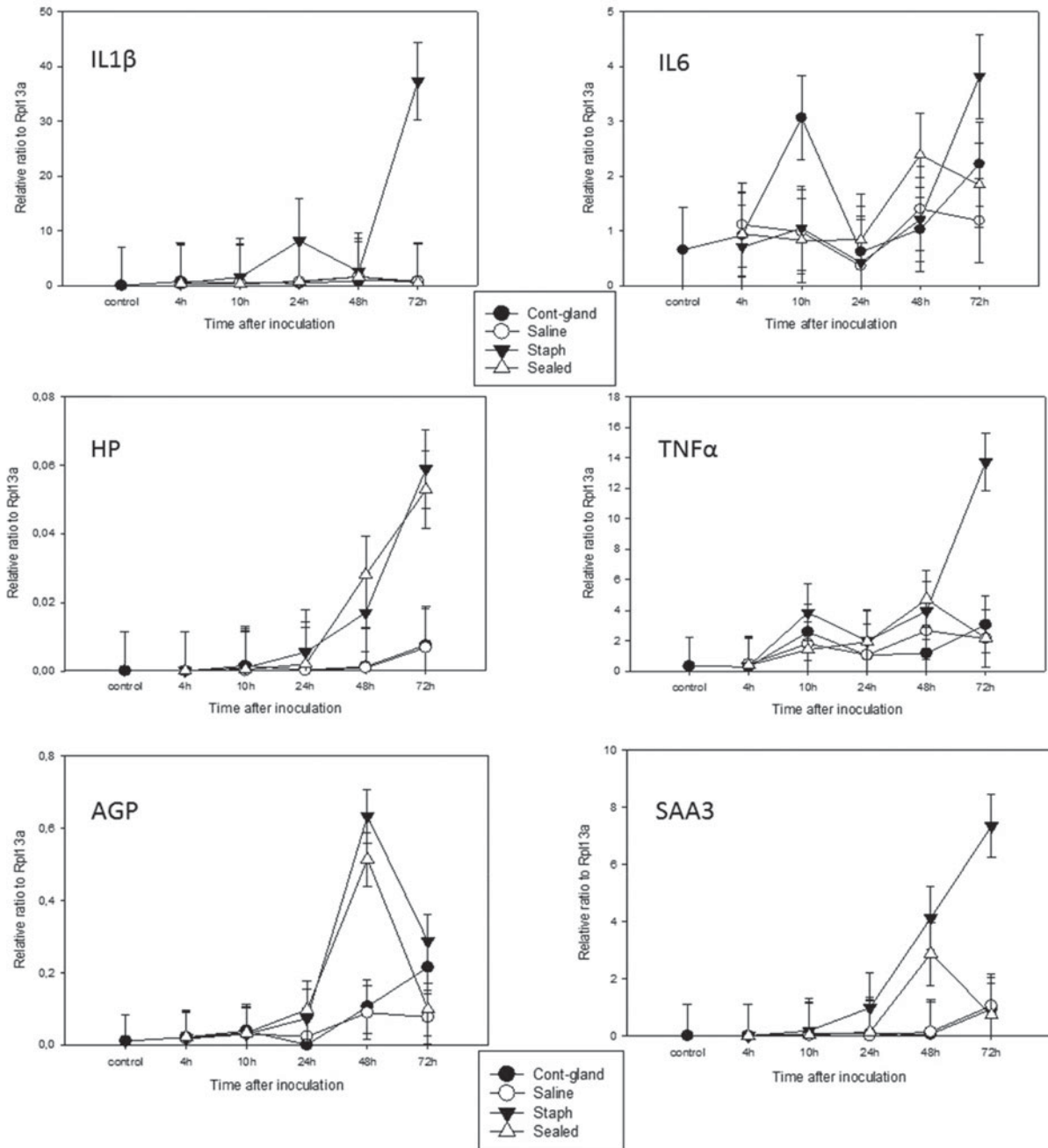
## Results

### Mammary gland mRNA expression analysis

Data for mammary gland expression of the three cytokines 288  
 IL1 $\beta$ , IL6, and TNF $\alpha$  are in Fig. 1 and significance levels for 289  
 the overall effects of time after inoculation and treatment are 290  
 in Table 2. 291

Relative to the reference gene RPL13A, IL1 $\beta$  expression 292  
 remained at pre-inoculation level until 24 h, when there was 293  
 a small (non-significant) and transient increase in glands 294  
 infused with *Staph. aureus*. A much larger and significant 295  
 ( $P < 0.05$  vs. control) increase occurred in the same treatment 296  
 at 72 h, whilst all other treatments (including sealed glands) 297  
 showed no increase (Fig. 1, IL1 $\beta$ ). When statistical analysis 298  
 was restricted to the *Staph. aureus* glands, there was a 299  
 significant effect of time after inoculation ( $P < 0.05$ ) but 300  
 when all treatments were included there was no significant 301  
 effect (Table 2). A different pattern was observed for IL6. 302  
 There was a small but significant ( $P < 0.05$ ) increase in 303  
 overall IL6 expression with time after inoculation, but whilst 304  
 the eventual increase was numerically greatest in *Staph.* 305  
*aureus*-inoculated glands, there was no significant difference 306  
 between the treatments at any time point (Fig. 1, IL6). 307  
 Changes in TNF $\alpha$  were similar to IL1 $\beta$  in that there was a 308  
 large and significant increase in the *Staph. aureus*-treated 309  
 glands at 72 h ( $P < 0.05$  vs. control) but in this case there was 310  
 an overall effect of time after inoculation ( $P = 0.01$ , Table 2) 311  
 indicating that the increased expression was not restricted to 312  
 the *Staph. aureus* glands. Nevertheless, there was a sig- 313  
 nificant treatment effect. 314

Mammary expression of the three APP, HP, AGP and 315  
 SAA3 are in Fig. 1 (HP, AGP and SAA3). HP was expressed at 316  
 low levels compared with the cytokines and other APP; 317  
 nevertheless, there was a clear increase in expression with 318  
 time after inoculation ( $P < 0.001$  overall). In contrast to the 319  
 cytokine patterns, this increase occurred to approximately 320  
 equivalent extents in *Staph. aureus*- and teat-sealed glands, 321  
 where it was evident at both 48 and 72 h. At 72 h there were 322  
 small increases in expression in control and vehicle glands, 323  
 but the difference between treatment groups was significant 324  
 ( $P < 0.05$ ). Expression of AGP was significantly affected by 325  
 time after inoculation ( $P < 0.001$ ) and by treatment ( $P < 0.01$ ) 326  
 with the main effect being a parallel large increase in 327



**Fig. 1.** Relative expression of IL1 $\beta$ , IL6, TNF $\alpha$ , HP, AGP and SAA3  $\pm$ SE between four treatments within time intervals for mammary glands.

328 *Staph. aureus*- and teat-sealed glands at 48 h, followed by a  
 329 decrease. There was a clear tendency for expression to  
 330 increase at 72 h in control and vehicle glands; hence, there  
 331 was a significant interaction between time and treatment  
 332 effects ( $P < 0.001$ ). Expression of SAA3 also increased with  
 333 time after inoculation ( $P < 0.01$  overall) and in response to  
 334 treatments ( $P < 0.01$  overall). Initially, there was a parallel  
 335 increase in *Staph. aureus*- and teat-sealed glands at 48 h, but  
 336 in the former this increase was sustained to 72 h whereas in  
 337 the latter there was a decline after 48 h.

*Liver mRNA expression analysis*

338

339 Expression levels of cytokines and APP in liver and control  
 340 mammary gland tissue are compared in Fig. 2. Based on  
 341 expression relative to RPL13a, expression of the three cyto-  
 342 kines was higher or similar in mammary tissue compared  
 343 with liver, whilst expression of the three APPs was much  
 344 lower in mammary gland compared with liver. Hepatic  
 345 expression of all three cytokines and all three APPs increased  
 346 significantly with time after inoculation (Table 2). The time



**Table 2.** Significance levels for overall effects. Data are shown in Figs. Figs. 1–3 and the statistical models used are described in the text. Mammary gland expression of cytokines and APP was analysed for effects of time after inoculation/teat sealing and for treatment effects comparing *Staphylococcus aureus* inoculation, vehicle infusion, teat sealing and no treatment. Liver expression and appearance of cytokines and APP in plasma and milk were analysed only for time after inoculation/teat sealing. NS: not significant. nd: not determined

	Mammary gland expression			Liver expression	Plasma concentration	Milk concentration
	Time	Treatment	Interaction			
IL1 $\beta$	NS	NS	NS	$P < 0.05$	nd	nd
IL6	$P < 0.05$	NS	NS	$P < 0.05$	$P < 0.001$	nd
TNF $\alpha$	$P = 0.01$	$P < 0.05$	NS	$P < 0.01$	nd	nd
HP	$P = 0.001$	$P = 0.05$	NS	$P < 0.001$	$P < 0.001$	nd
AGP	$P < 0.001$	$P < 0.01$	$P < 0.001$	$P < 0.001$	nd	nd
SAA3/MAA	$P < 0.01$	$P < 0.01$	NS	$P < 0.001$	$P < 0.001$	$P < 0.05$

347 course of increased hepatic expression of IL6 and TNF $\alpha$  was  
348 parallel in liver and control mammary tissue, whereas IL1 $\beta$   
349 increased at 72 h in liver only. Hepatic expression of HP,  
350 AGP and to a lesser extent SAA3 increased at 48 h, and all  
351 three increased further at 72 h.

### 352 Blood serum and milk analysis

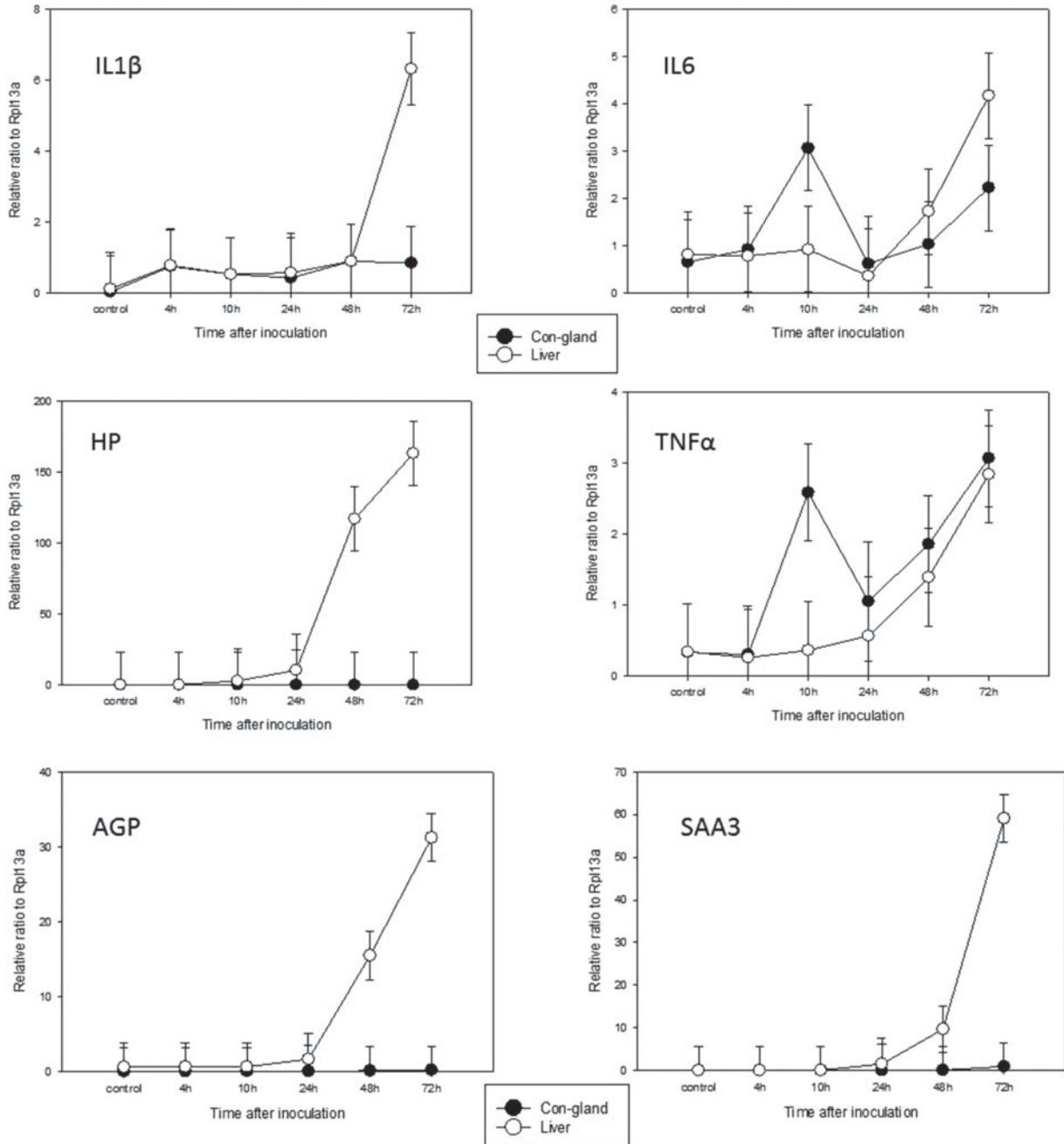
353 IL6, HP and SAA serum concentrations were quantified  
354 using a cytokine panel and commercially available ELISA  
355 kits. Data are in Fig. 3 and significance levels in Table 2. All  
356 three markers gradually and significantly increased begin-  
357 ning after 10 h. IL6 concentrations were very much lower  
358 than either of the APPs, with HP present at much higher  
359 levels than SAA. MAA was detected in milk from *Staph.*  
360 *aureus*-inoculated glands at 24 and 48 h and from vehicle-  
361 infused glands at 48 h, although at levels approximately  
362 5-fold lower than in inoculated glands.

### 363 Discussion

364 Using a novel model that compares pathogenic and non-  
365 pathogenic inflammation we have characterised the local  
366 response to mammary inflammation in mice, and have  
367 demonstrated increased expression of various inflammatory  
368 cytokines and APPs. We have shown that the response to  
369 pathological inflammation (infection with *Staph. aureus*) is  
370 different from the response caused by 'physiological inflam-  
371 mation' (due to milk accumulation). The expression of  
372 inflammatory cytokines was increased only in individual  
373 glands inoculated with the pathogen, whereas APP ex-  
374 pression was increased in both pathogen-inoculated and  
375 teat-sealed glands. The time course of the APP response was  
376 similar for the two inflammatory states, with the exception  
377 that SAA3 remained elevated beyond 48 h in pathologically  
378 inflamed glands, but not in physiologically inflamed.

379 Milk contains a great many bioactive factors, but the  
380 mammary gland is a complex structure, hence in many cases  
381 the precise origin of these factors (including cytokines and  
382 APPs) has not been totally elucidated. Proteolytic

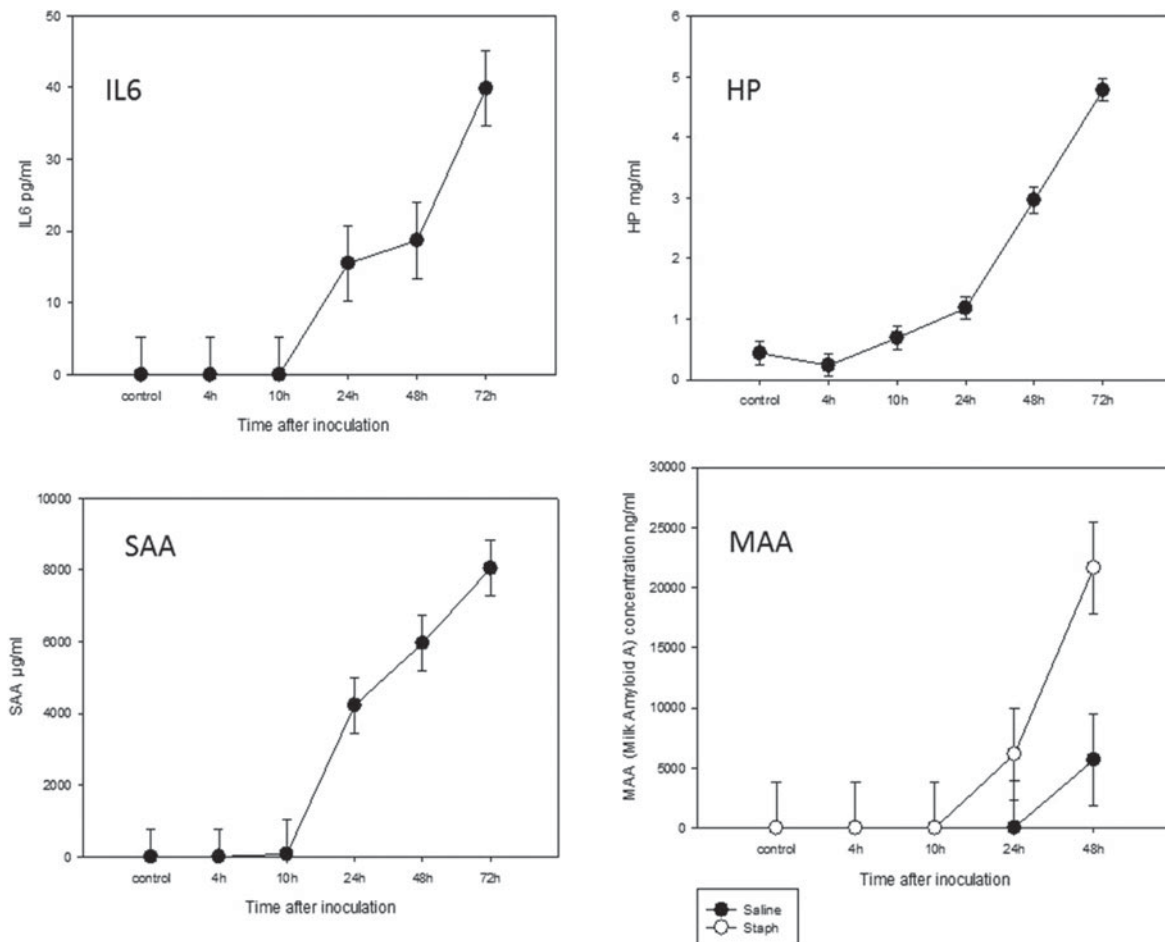
breakdown of synthesised protein (largely caseins) during  
storage, transcellular trafficking and secretion of intact  
molecules from plasma to milk, paracellular transfer of mol-  
ecules through 'leaky' tight junctions and de-novo synthesis  
and secretion by mammary epithelial cells are all possible  
sources of proteins and peptides in milk. It must also be  
recognised that detection of mammary expression of a  
particular protein does not necessarily imply production by  
mammary secretory cells, since the tissue is very highly  
vascularised. Where cytokines are concerned, it is important  
to recognise that mastitic milk contains very large numbers  
of neutrophils and other immune cells, and whilst mammary  
epithelial cells have been shown to synthesise certain  
cytokines (Goldman et al. 1996) it is likely that the majority  
of cytokines in mastitic milk will be derived from immune  
cells of one sort or another. The situation is less clear for  
APPs. On the basis of milk/plasma profile comparison and  
expression within mammary tissue, Eckersall et al. (2006)  
proposed that MSAA3 was a specific product of mammary  
tissue, and our data support that conclusion. Pedersen et al.  
(2003) used a bovine *Streptococcus uberis* model and  
observed a marked increase in milk HP without a con-  
comitant increase in plasma levels, and Hiss et al. (2004)  
observed expression of HP in mammary tissue after  
endotoxin challenge. Nevertheless, Lai et al. (2009) consider  
that neutrophils are the major source of HP in mastitic milk,  
although they also showed epithelial expression. Expression  
of AGP in mammary tissue has been shown (Cecilianani et al.  
2005, 2007), but the same group subsequently demonstrated  
that bovine neutrophils also express AGP (Rahman et al.  
2008). To our knowledge, AGP has not previously been  
investigated in relation to mastitis. Our expression data  
provide additional indirect evidence for production of all  
three APPs by mastitic mammary tissue, as opposed to im-  
mune cells contained within the sample. Although we did  
not measure immune cells in our milk (or tissue) samples, the  
fact that cytokine levels increased in the *Staph. aureus*-  
challenged glands but not appreciably in the teat-sealed  
glands leads us to suggest that the number of immune cells  
was probably greater in the former than the latter. In support  
of this, Brouillette et al. (2004) observed marked infiltration



**Fig. 2.** Relative expression of IL1 $\beta$ , IL6, TNF $\alpha$ , HP, AGP and SAA3  $\pm$ SE between control glands and liver samples within time intervals.

424 of polymorphonuclear monocytes 12 h after inoculation  
 425 with *Staph. aureus* in a mouse mastitis model. Despite this  
 426 likely difference in immune cells, the expression of HP and  
 427 AGP was identical in the two scenarios, and the expression  
 428 of SAA3 was very similar prior to 72 h. This time-point has  
 429 physiological relevance for the mammary involutionary  
 430 process in mice. Sorensen & Knight (1997, unpublished  
 431 data) showed that murine lactation could be 'rescued' by  
 432 resuckling after periods of non-suckling of up to 72 h, but not  
 433 thereafter. Stein et al. (2004) demonstrated a biphasic

immune response in involving mouse mammary tissue, 434  
 with an initial and rapid acute phase response followed by 435  
 significant infiltration of neutrophils and macrophages only 436  
 after day 4, providing additional confirmation that our data 437  
 are most likely to represent actual mammary expression. At 438  
 the same time, it is important to recognise that our current 439  
 model represents involution due entirely to local factors 440  
 within the gland, since the systemic suckling stimulus was 441  
 maintained throughout. From a diagnostic point of view our 442  
 model is appropriate; detecting non-pathogenic mastitis due 443



**Fig. 3.** Concentration of SAA, HP and IL6 in blood serum  $\pm$  SE between groups. MAA concentration  $\pm$  SE between control group, saline and staph injected groups within time intervals.

444 to milk accumulation in the context of bovine or human  
 445 lactation would be done when milking or suckling was  
 446 continuing. On the basis of our data, we can propose that the  
 447 combination of cytokine and APP measurement might allow  
 448 for discrimination between pathogenic and non-pathogenic  
 449 mastitis. Such discrimination is important, since the former  
 450 would be likely to respond to antibiotic treatment whereas  
 451 the latter would not.

452 The normal course of events in an inflammatory response  
 453 is for local signals originating at the site of inflammation to  
 454 subsequently activate hepatic cytokine and APP production  
 455 (Yoshioka et al. 2002). We observed increased mammary  
 456 expression of IL6 at 10 h, but the significance of this obser-  
 457 vation is uncertain because it was only in the control gland.  
 458 Plasma levels of IL6 increased at 24 h, but hepatic expression  
 459 remained low until 48 h. There was a generalised increase of  
 460 mammary TNF $\alpha$  expression at 10 h, but overall our data do  
 461 not shed significant light on the local signals that provide the  
 462 earliest indication of an infection. IL1 $\beta$  had the highest and  
 463 also earliest mammary expression response to *Staph. aureus*  
 464 and is probably worthy of more detailed study if an early  
 465 diagnostic tool is the target. Gunther et al. (2011) compared

*Escherichia coli* and *Staph. aureus* challenge of bovine MEC 466  
 in vitro and observed very marked and early stimulation of 467  
 TNF $\alpha$ , IL6 and IL1A in response to the former, but not the 468  
 latter. It is likely that early detection will be particularly chal- 469  
 lenging where *Staph. aureus* mastitis is concerned. Similar 470  
 conclusions have been drawn by others (Bannerman et al. 471  
 2004; Petzl et al. 2008). The plasma cytokine analysis that 472  
 we performed should have been capable of detecting 473  
 additional cytokines had they been present, which may 474  
 have been a methodological problem but could also have 475  
 indicated low responsiveness to *Staph. aureus*. The large 476  
 increase that we observed in plasma IL1 $\beta$  at 72 h was 477  
 accompanied by symptoms of systemic infection in some of 478  
 the mice, including lack of normal behaviour, grooming and 479  
 loss of appetite. Interpretation of our mammary data must 480  
 take these systemic responses into account. In quantitative 481  
 terms, we observed much greater expression of APP by liver 482  
 than by mammary gland, but the increased plasma levels of 483  
 APP were first observed at 24 h, in advance of both hepatic 484  
 activation and the major increases in mammary expression. 485  
 The one APP that we measured in milk, MAA was at much 486  
 lower concentration than SAA in blood, but these data are 487

not directly comparable since they were obtained using different antibodies. Kovacevic-Filipovic et al. (2012) have recently compared bovine milk and plasma SAA and observed rather similar concentrations during *Staph. aureus* mastitis, but on the basis of isoform distribution concluded that plasma SAA and M-SAA did not simply equilibrate through leaky tight junctions. Our data do not allow us to speculate on the relative importance of locally or systemically produced APP in local host defence within the mammary gland. Given the different degrees of up-regulation, it is possible that liver is the major site of APP production, acting in response to inflammatory cytokines produced by the mammary gland. However, this cannot be stated with certainty.

In conclusion, we observed different patterns of mammary expression of inflammatory cytokines and APPs in pathogenic vs. non-pathogenic mammary inflammation in a mouse model. This could potentially form the basis for differential diagnosis of the two conditions. Further research is needed to clarify the interrelationships between cytokine and APP production in mammary tissue and liver.

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