Gene expression patterns in mammary gland parenchyma and lining epithelial cells (CLEC) of dairy cows infected with bacteria

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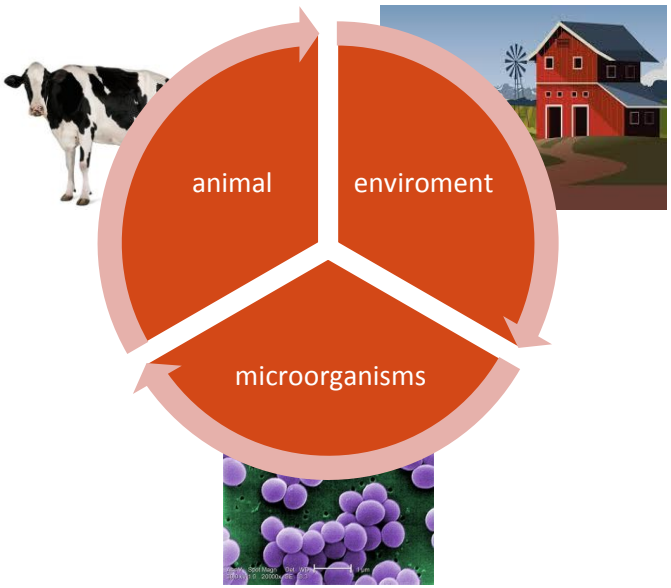
Mammary gland inflammation



Results:

- Losses in milk production
- Premature culling
- Additional work on farms
- Veterinary services
- Drugs

<u>The animal welfare deterioration and huge economic losses</u>

The reasons of this state:

- environmental:
  -milking hygene, milking eqipment, microclimate, nutrition, maitaining conditions

- microorganisms – pathogenic and enviromental:
  - *Staphylococcus aureus*
  - *Staphylococcus epidermidis*
  - *Escherichia coli*
  - *Mycoplasma* spp.

- individual predisposition of each cow:
  -age, disease resistance, lactation phase, udder construction, productivity, other diseases

Mammary gland parenchyma vs. cisternal lining epithelial cells

Mammary gland parenchyma

- milk production, but also immune cell recruitment after bacterial infection detection such, as:
  - cytokines
  - chemokines
  - host defense peptides

huge enzymatic role in response to bacterial infection

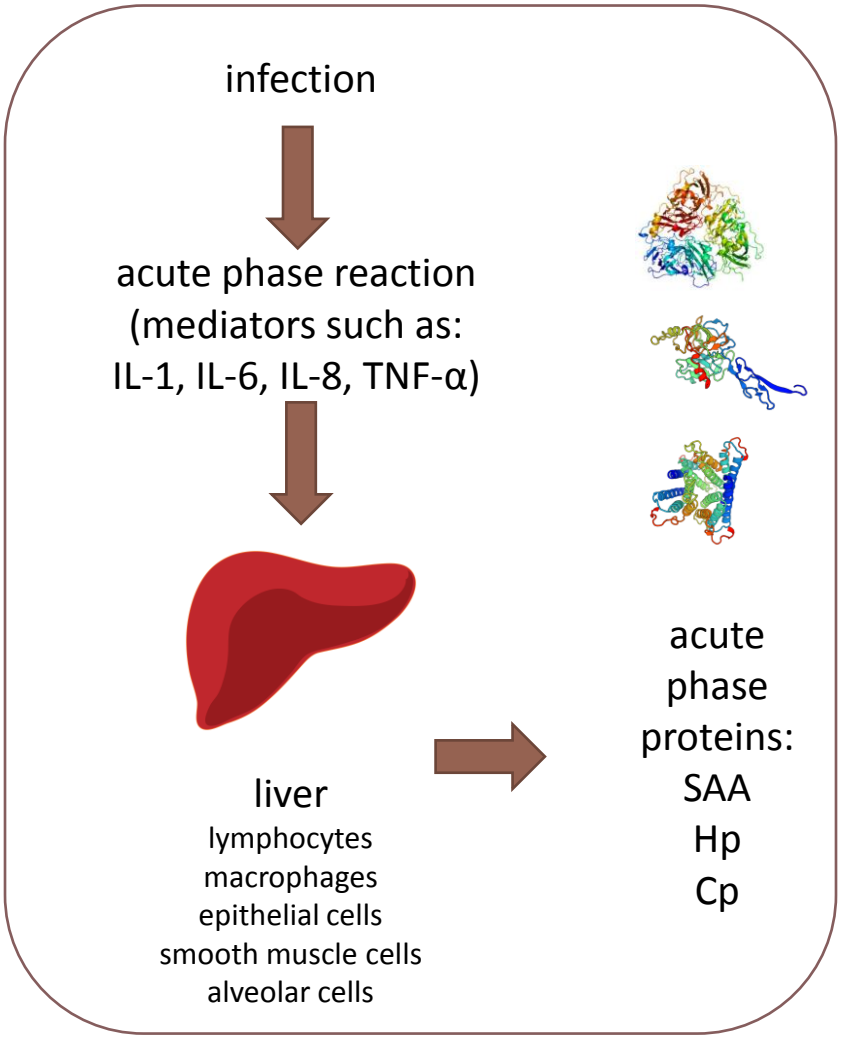
Cisternal lining epithelial cells

- first line of defense against microorganisms
- mechanical barrier against bacterial invasion
- rich in keratin – produces keratin plug

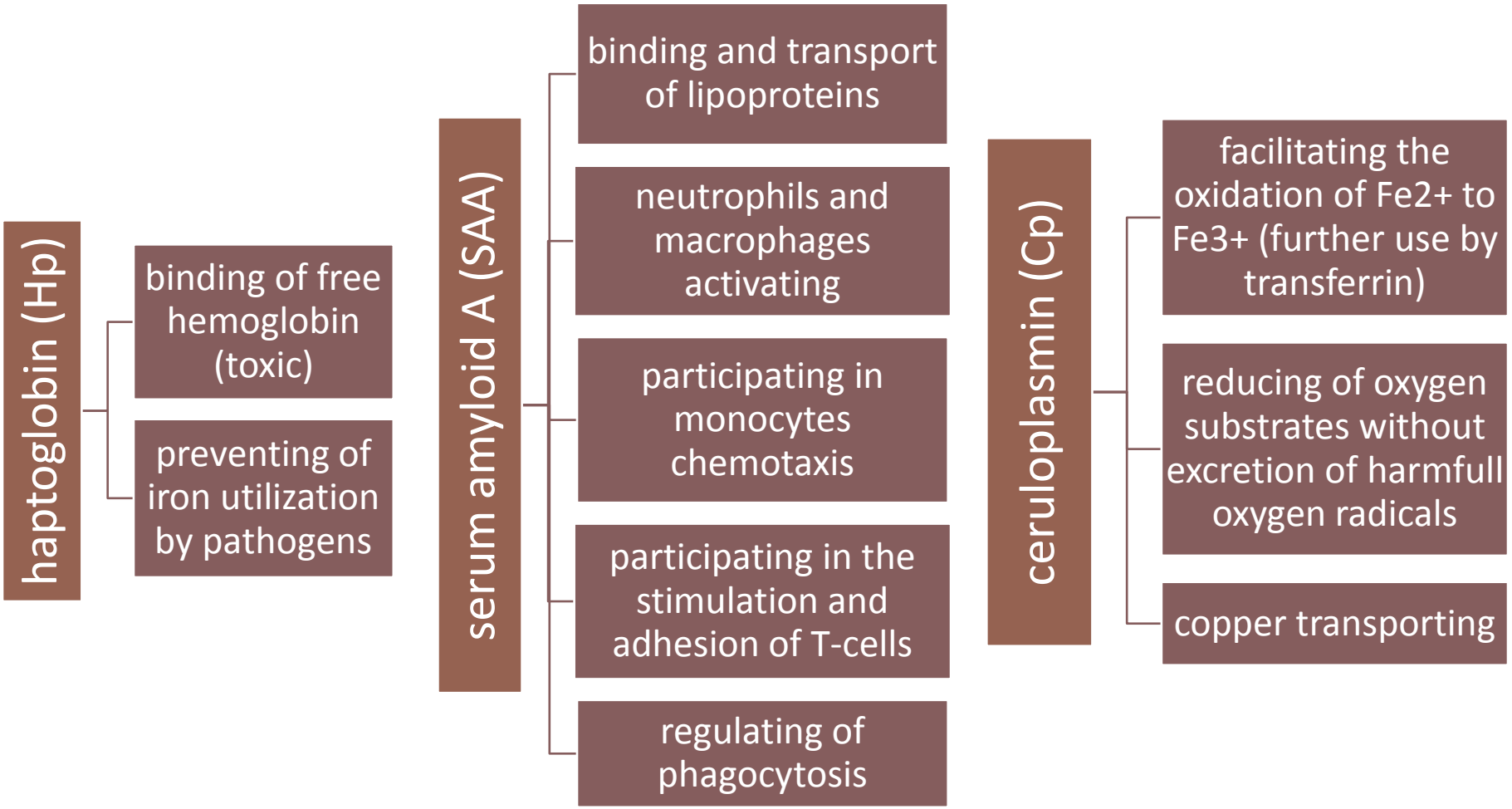
enzymatic role?

Acute phase proteins (APPs)

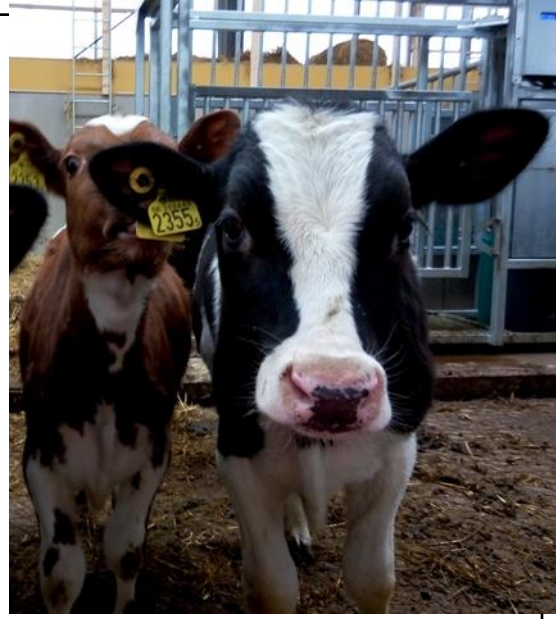
- heterogeneous group of proteins regarding their structure, function or mode of action
- pro- or anti-inflammatory properties
- changes in production:
  - as a result of complement system activation
  - as a result of pro-inflammatory mediators release
- concentration of APPs as a trauma response
  - increasing (positive APPs, e.g. SAA, Hp or Cp)
  - decreasing (negative APPs, e.g. albumins)



Selected proteins:



The aim of this study was:



- expression level of selected acute proteins genes (*Hp*, *Cp*, *SAA*) analysis in mammary gland epithelial tissue (parenchyma) and cisternal lining epithelial tissue depending on health status of the dairy cow

- comparison of selected acute phase proteins expression levels between secretory and cisternal lining epithelial tissue in mammary gland depending on the health status of the animal

Samples

- 51 udder samples collected from 40 Polish Holstein-Friesian cows of Black-and-White variety suffering from chronic and recurrent mastitis

- microbiological analysis:
  - coagulase-positive staphylococci (CoPS, N=25)
  - coagulase-negative staphylococci (CoNS, N=13)
  - free form bacteria (N=13)

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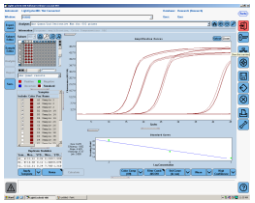
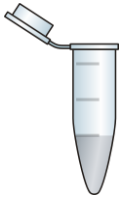
Methods



collecting samples → RNA isolation → reverse transcription reaction → qPCR reaction → result analysis → statistical analysis



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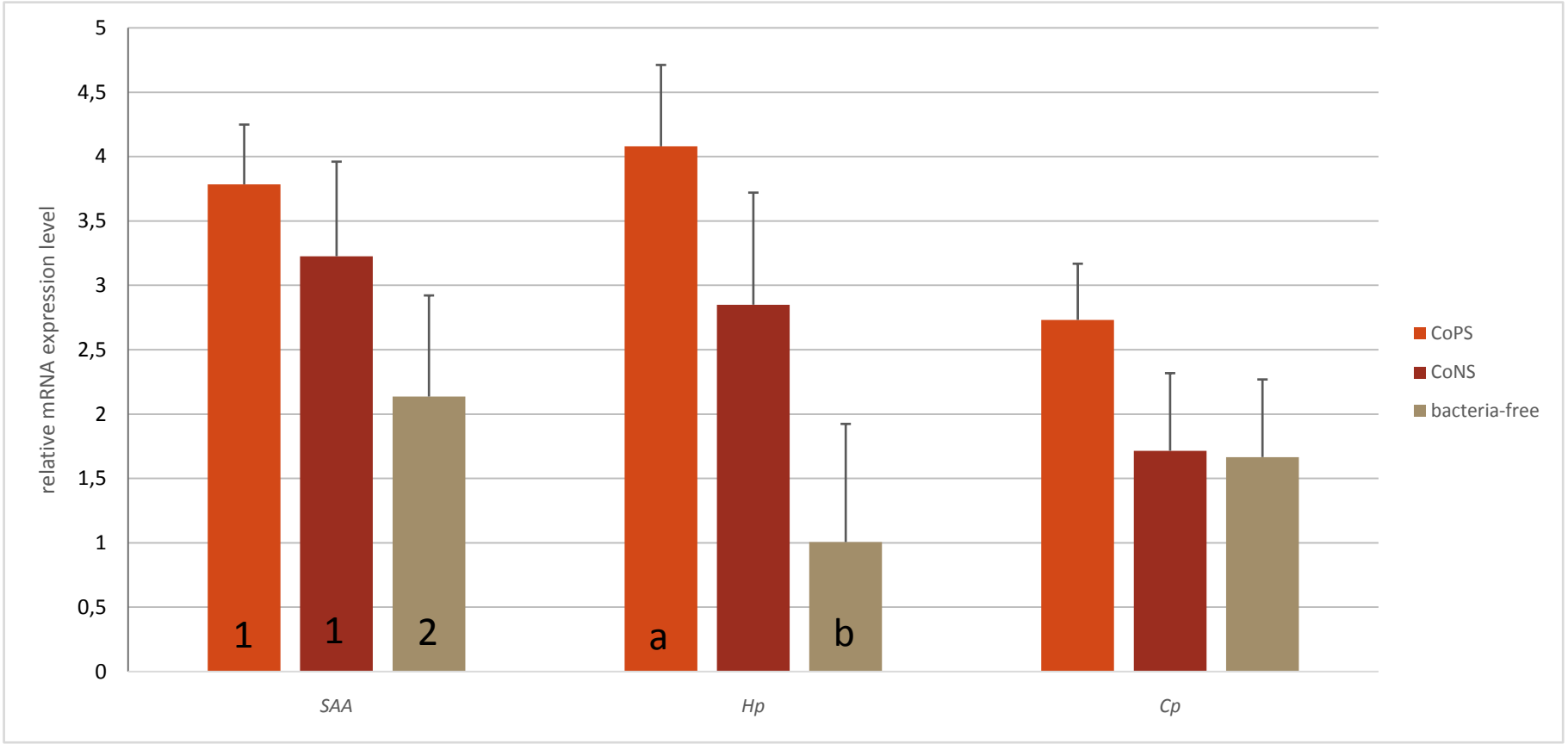
Results

mRNA expression levels of *SAA, Hp, Cp* in mammary gland parenchyma

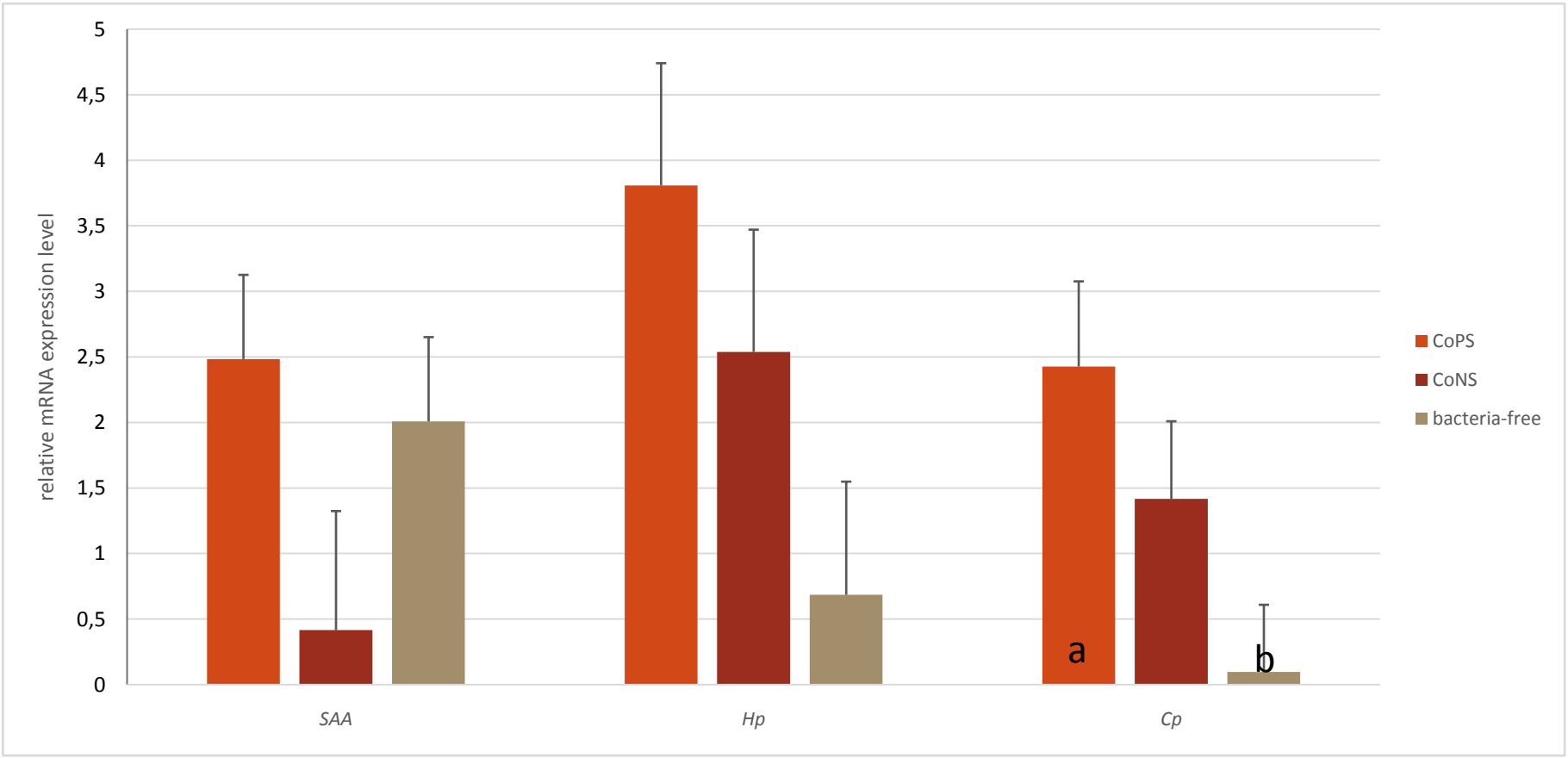


0.05<p≤0.1

p≤0.05

Results

mRNA expression levels of *SAA, Hp, Cp* in cisternal lining epithelial cells

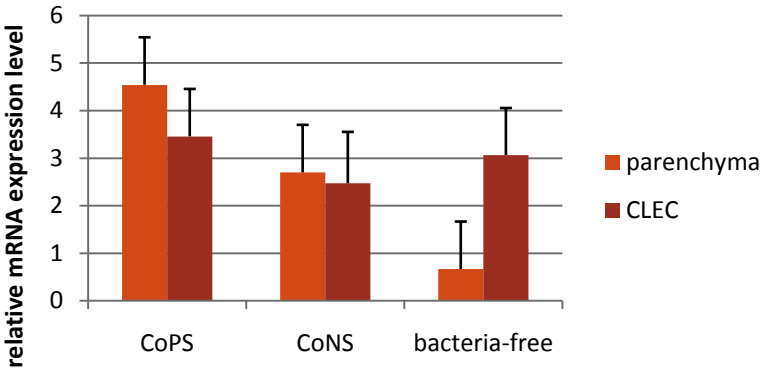


p≤0.05

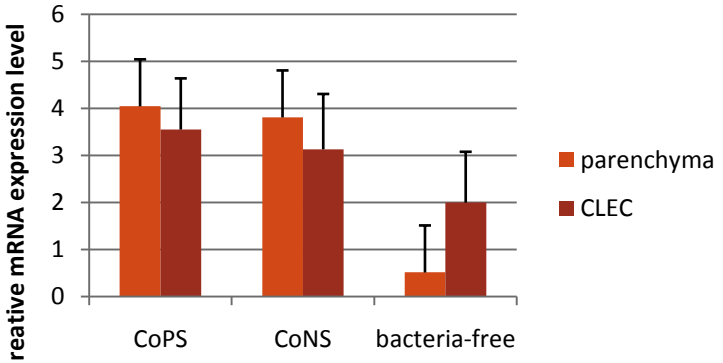
Results

mRNA expression levels of *SAA, Hp, Cp* genes
mammary gland parenchyma vs. cisternal lining epithelial cells

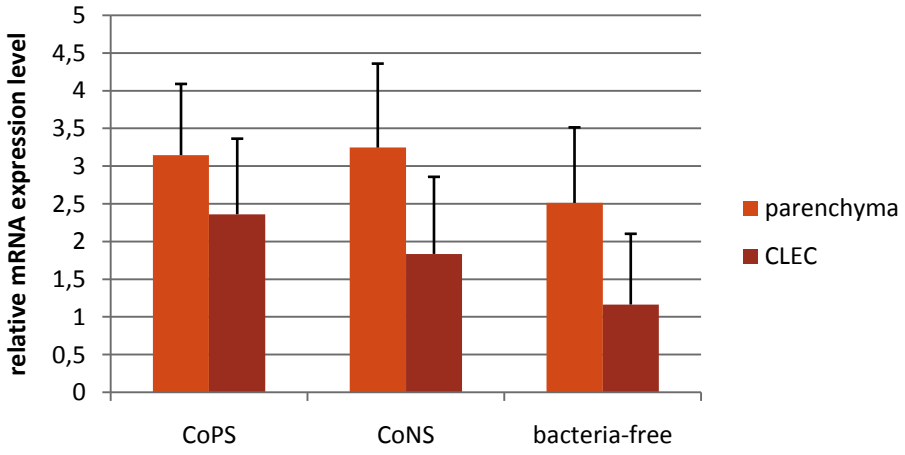
SAA



Hp



Cp



Summary

- Higher expression levels of ***Hp, SAA*** genes in CoPS infected mammary gland parenchyma compared to bacteria-free ones were stated
- Higher expression level o ***Cp*** gene in CoPS infected samples of CLEC compared to the bacteria-free samples was noticed
- No differences in APP expressions between **CLEC** and **parenchyma** were stated, which suggests similar immunological answer of both analysed tissues regarding these APPs
- **Both types of bacteria** arouse similar immunological answer of the both studied tissue testifying to their similar pathogenicity

Thank you for attention

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