Epidemiological survey of coxiella burnetii specific antibodies in sheep, goats a...

Science, Epidemiology

In the current study, PCR was employed on vaginal swab to diagnose Q fever as one of the routes of discharge of C. burnetii is the vaginal mucus.

Infected ticks are playing a major part in the transmission of C. burnetii among livestock. Camels are the main source of C. burnetii in in Saudi Arabia. The possibility of spreading of the infection from camel to sheep and goats is high as these animals grazing together. In livestock, C. burnetii infection is mainly subclinical and the only prominent sign is abortion. Abortion rates can reach up to 80%. The evident increase of serum proinflammatory cytokines (TNF-α, IL-1β, IL-6) reported in the infected animals in this study indicates the promotion of monocytes and macrophages to secret proinflammatory cytokines. Cytokines are involved in elimination process of C. burnetii in infected. The species variations recorded in the concentration of cytokines possibly attributed to variation within cytokine genes.

Hp and SAA are the key acute phase proteins in ruminant, which synthesized in the hepatocytes. This protein varies in concentration during infections, inflammation, surgical trauma and stress. The study confirmed that Hp and SAA were significantly increased in Coxiella burnetii infected sheep, goats and she-camels. Probably, the significantly elevated proinflammatory cytokines recorded in this study mediated the significant increase of Hp and SAA. Hp binds the free hemoglobin, thus preventing the bacteria from iron required for their growth. SAA bind to Gram-negative bacteria cause opsonisation of the target microorganism. The species variations in Hp and

SAA concentrations reported in this study supposed to inherit differences in production and in the rates diffusion of these APPs from the circulation.

Moreover, the concentrations of Hp indicate the severity of the infection and underlying tissue injure. Parallel to the results of Cecilian et al, 2002; Ganheim et al., 2003 and Petersen et al., 2004, El-Bahr and El-Deeb, 2016, a very low concentration of HP and SAA was reported in the current study in healthy animals.

Oxidative stress has been recorded in various infectious or non-infectious diseases of domestic animals. The oxidative stress can be determined by measuring of oxidant and antioxidant activity. Lipids are liable to oxidation and lipid peroxidation products are potential biomarkers for oxidative stress. MDA is one of the final products of polyunsaturated fatty acids peroxidation in the cells. An increase in free radicals causes overproduction of MDA. The significant increase of MDA in infected sheep, goats and she-camels recoded in the current study indicate the excessive lipid peroxidation. This may be due to reduced accessibility of antioxidants or over generation of ROS. The exhaustion of SOD, GSH and CAT in cells protection against oxidative stress may justify the reported low concentration of these enzymes in infected animals. As Hp, SAA, TNF-α, IL-6, IL-β, and MDA had the maximum sensitivity and specificity so they are suitable indicators for APPs, cytokines responses and oxidative stress changes in Coxiella burnetii infected sheep and goats. The better degree of sensitivity and specificity of Hp and MDA reported in Coxiella burnetii infected she camels, recommended them to be sensitive markers for the disease in this species.

We can conclude that acute phase proteins, cytokines and oxidative stress markers considered of being indicative biomarkers of naturally occurring Q fever in sheep, goats and camels. Moreover, these biomarkers may have a significant role in the diseases pathogenesis in these animals.