Endometrial gene expression of inflammatory cytokines and serum amyloid A in mares resistant or susceptible to persistent endometritis


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The objective of the study was to evaluate the endometrial gene expression of inflammatory cytokines (IL-1β, IL-1RA, IL-6, IL-8, IL-10, TNFα) and serum amyloid A (SAA) in response to inoculation of 10^5 CFU *Escherichia coli* in mares resistant or susceptible to persistent endometritis, respectively.

Mares were classified as resistant or susceptible based on their clinical response to uterine inflammation and endometrial quality. Endometrial biopsies were recovered 3, 12, 24 and 72 hours (h) post-inoculation. Relative gene expression analyses were performed by quantitative real-time PCR using SYBR green and specific primers.

Resistant mares initially (3 h) showed an up-regulated endometrial gene expression of IL-1β, IL-6, and IL-8 (p<0.05) after *E. coli* inoculation compared to estrous baseline levels. The susceptible mares showed increased gene expression of IL-6 and IL-1RA (p<0.05) 3 h after bacterial challenge. Susceptible mares showed a sustained and prolonged inflammatory response with increased gene expression levels of IL-1β (p<0.01), IL-8 (p<0.01) and IL-1RA (p<0.001) at the end of the study period (72 h) compared to resistant mares. Endometrial mRNA transcripts of IL-1β and IL-1RA were significantly elevated in mares with heavy uterine bacterial growth (p<0.05).

The current investigation suggests that endometrial mRNA transcripts of pro-inflammatory cytokines as a response to endometritis are finely regulated in resistant mares, with an initial high expression level followed by normalization within a short period of time. Susceptible mares had a prolonged expression of pro-inflammatory cytokines, supporting the hypothesis that an unbalanced endometrial gene expression of inflammatory cytokines might play an important role in the pathogenesis of persistent endometritis.

**Keywords:** Infectious endometritis, endometrial inflammatory response