REGULATION OF LHR MRNA BINDING PROTEIN (LRBP) EXPRESSION IN BOVINE *CORPUS LUTEUM*

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INTRODUCTION AND OBJECTIVE

Luteinizing hormone (LH) plays an essential role in controlling physiological processes such as ovulation and luteal maintenance acting by LH receptor (LHR). Although studies report the importance of this receptor in luteal development in bovine species, the mechanisms of regulation of LHR expression in the bovine *corpus luteum* (CL) have not been completely elucidated. Studies described the regulation of the LHR by the LHR mRNA binding protein (LRBP) in granulosa cells during follicle development, but its role has not yet been described in luteal tissue in cattle.

MATERIAL AND METHODS

Thus, we aimed to quantify relative mRNA abundance of LHR and LRBP in bovine CL. For this, CL were morphologically classified into two stages of development: functional CL; characterized by well-developed vasculature, often visible at the apex, completely orange or yellow, and 1.6 to 2.0 cm in diameter; and CL in regression, characterized by no visible vasculature on the surface, pale yellow to white in color and less than 1 cm in diameter.

Functional CL (n=5)

Regressed CL (n=5)

Progesterone concentration

Immunolocation

RT-qPCR

Expression: LHCGR and LRBP
Endogenous control – (PPIA)

Relative expression was determined by the Pffafl's equation and means were compared by T test. Tissue progesterone concentration was also quantified in order to confirm luteal status. Differences were considered significant when P≤ 0.05.

For characterization of bovine CL status: a higher progesterone concentration in the functional CL (102.8 ± 11.4 ng/mL) was confirmed compared to CL in regression (12.38 ± 1.95 ng/mL; p<0.0001).

RESULTS

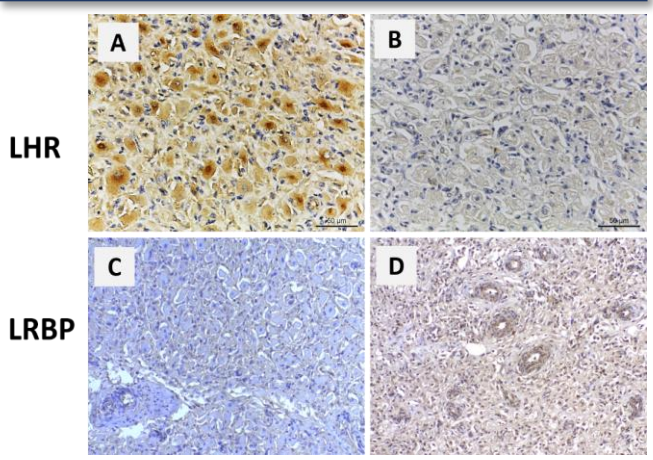

Fig. 1. Immunolocation of LHR (A and B) and LRBP (C and D) protein in the bovine corpus luteum. We highlight the strong immunoreactivity of LHR in functional CL (panel A) when compared to regressive CL (panel B) and conversely the lower reactivity of LRBP in functional CL (panel C) compared to regression CL (panel D).

The relative mRNA abundance of LHR was also higher in the functional CLs (0.55±0.14) when compared to the CLs in regression (0.01±0.0015; p≤0.05).

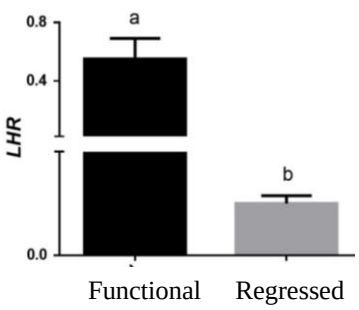

Fig. 2. Expression of LHR in functional or regressed bovine CLs.

The abundance of mRNA of LRBP was lower in functional CLs (0.14±0.01) when compared to CLs in regression (0.70±0.09; p≤0.05).

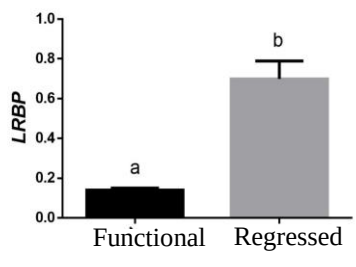

Fig. 3. Expression of LRBP in functional or regressed bovine CLs.

CONCLUSION

We concluded that there is *LRBP* expression in bovine CLs and it is regulated during luteal regression. Furthermore, we suggest that the suppression of *LHR* expression during luteal regression could be, in part, due to the increase in *LRBP* expression.