

POINT MUTATIONS IN THE LUTEINIZING HORMONE RECEPTOR MRNA OF HOLSTEIN (*BOS TAURUS*) GRANULOSA CELLS – PARTIAL RESULTS

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Keywords: Bovine, Folliculogenesis, SNP

The final steps of follicular development and ovulation are LH dependent. Variations in the LH receptor (LHR) structure could be related to failures or deficient outcomes observed in cows undergoing reproductive protocols. The aim of this study was to identify variations in the mRNA of the LHR in mural granulosa cells recovered from dominant follicles of fertile Holstein cows. Cells from four previously selected cows were collected in vivo, washed in saline solution and kept in RNA Later (Ambion). RNA extraction were performed with "RNeasy Micro Kit" (Qiagen) and quantified by nano-spectrophotometry. Complementary DNA (cDNA) was produced using "SuperScript III kit" (Life Technologies). Nine primer sets were designed based on the *Bos taurus* sequence available in GenBank (NM_174381.1) and used in conventional PCR covering the whole transcript extension (2,106 base pairs). PCR products were purified using the "GFX PCR DNA and Gel Band Purification Kit" (GE Healthcare) prior to DNA sequencing reactions. Sequence chromatograms were obtained using MegaBACE 1000 DNA sequencer and sequences were analyzed using "DNA Baser software" (<http://www.dnabaser.com>). So far, eight SNP's were detected, from which five were found exclusively in one animal each, and three was constant in all four animals. With only one exception, all polymorphisms change amino acid sequence after translation. These polymorphisms can be related to hormone-receptor binding sites leading to a variety of reproductive responses. So far, the results of the present study suggest that SNPs in the LHR are also present among *Bos Taurus* breeds, and might be related to the selection for milk production. Financial Support: Embrapa, CNPq and FAPEMIG

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