

Functional genome research in reproductive biology and biotechnology ? a minireview

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Abstract :

Female infertility is an increasingly important problem in cattle, causing enormous costs and retarding genetic progress. Current attempts to improve fertility by genetic selection are inefficient due to the low heritability of the respective trait, i.e. the nonreturn-rate 90 days after first service (NRR 90). Thus novel phenotypic traits more closely related to fertility are urgently needed. Since a large proportion of pregnancy losses occur in the preimplantation period, the interaction between early embryos and their maternal environment is an attractive target for systematic investigations, which may uncover mechanisms underlying early embryonic death. Based on holistic transcriptome and proteome studies [Hiendleder et al. 2005, Wolf et al. 2006] we attempt to understand the quantitative biology of embryo maternal communication and the regulation of endometrial receptivity [Wolf et al. 2003]. A short-term goal is the development of array-based systems for the differential diagnosis of fertility problems and for evaluating the connection between metabolic disturbances and reproductive functions. A long-term goal is the identification of genetic variation affecting the fertility-related gene expression profiles in female reproductive tissues such as endometrium. The endometrium undergoes marked functional changes during estrous cycle and pregnancy. As the adjacent environment of the conceptus, it represents the maternal interface for embryo maternal communication, which is essential to maintain pregnancy. Transcriptome studies provide the unique opportunity to assess molecular profiles changing in response to endocrine or metabolic stimuli or to embryonic pregnancy recognition signals [reviewed in Bauersachs et al. 2008, Spencer et al. 2008].

Key Word :

cattle, cloning, endometrium, estrus, infertility, pregnancy, transcriptome

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