A meta-analysis suggests that the culture environment affects mRNA translation in bovine oocytes

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Application Refining culture environment to support mRNA translation may improve egg quality.
Introduction Upon removal from antral follicles, fully-grown oocytes resume meiosis and fertilize in vitro. However, embryo development is lower compared to in vivo matured oocytes. Such loss of performance is likely caused by two main factors: 1) skipping final differentiation, also known as 'oocyte capacitation', occurring during follicular dominance and 2) inability of fully recreating a microenvironment that supports oocyte maturation. Given that resumption and completion of meiosis I is largely driven by post-transcriptional mechanisms and that the epidermal growth factor (EGF) network partially regulates maternal mRNA translation in mice, we conducted a meta-analysis in the attempt of better elucidating how the culture environment affects translation in bovine oocytes.
Material and Methods Isolation of polysome-associated mRNAs requires high amount of starting material. Therefore we exploited deposited datasets to gain information on 1) mRNAs polysome association in immature (GV) and mature (MII) bovine oocytes (GSE56603); 2) extent of amplification of polyadenylated mRNAs in GV and MII bovine oocytes (GSE61717); 3) mRNAs polysome association in MII mouse oocytes upon activation of the EGF network (GSE46640). A comparison between the datasets was conducted to identify translation patterns that are affected by maturation and by EGF-like growth factors. Since there was no suitable dataset on bovine oocytes to inform on the latter, a mouse dataset was used. GEO-retrieved datasets were re-analyzed using R-Studio. Differential expression was determined using edgeR (Bioconductor – Software packages). AdjP<0.05 and LogFC>2 were considered.
Results Twenty-seven transcripts were differentially associated to the polysomes in MII compared to GV bovine oocytes, and only one was common to the 320 transcripts overexpressed in response to EGF network. Therefore we included a second bovine dataset (GSE61717), which preferentially identifies polyadenylated, and therefore translated, mRNAs. However, also in this case the overlap between maturation-induced and EGF network-induced differences was minimal. To test if the failure to detect overlap was due to inter-specificity, we compared intraspecifically the polysome-associated and polyadenylated transcripts. Notably, while the overlap was still limited for MII oocytes, all the mRNAs preferentially associated to the polysome in GV were also overexpressed in the polyadenylated dataset at the same stage, indicating that the two experimental approaches yield comparable results for immature oocytes, but this homogeneity is somehow lost with in vitro maturation (IVM).
Conclusion This meta-analysis represents indirect evidence that IVM may lower egg quality by disrupting the oocyte translational program.
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