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Data Article

Transcriptomes of bovine ovarian follicular and luteal cells

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ABSTRACT

Affymetrix Bovine GeneChip® Gene 1.0 ST Array RNA expression analysis was performed on four somatic ovarian cell types: the granulosa cells (GCs) and theca cells (TCs) of the dominant follicle and the large luteal cells (LLCs) and small luteal cells (SLCs) of the corpus luteum. The normalized linear microarray data was deposited to the NCBI GEO repository (GSE83524). Subsequent ANOVA determined genes that were enriched (≥ 2 fold more) or decreased (≤ -2 fold less) in one cell type compared to all three other cell types, and these analyzed and filtered datasets are presented as tables. Genes that were shared in enriched expression in both follicular cell types (GCs and TCs) or in both luteal cells types (LLCs and SLCs) are also reported in tables. The standard deviation of the analyzed array data in relation to the log of the expression values is shown as a figure. These data have been further analyzed and interpreted in the companion article “Gene expression profiling of

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ovarian follicular and luteal cells provides insight into cellular identities and functions" (Romereim et al., 2017) [1].

Specifications Table

Subject area	*Biology*
More specific subject area	*Reproductive Physiology*
Type of data	*Tables, figure*
How data was acquired	*RNA Microarray*
Data format	*Normalized, analyzed, filtered*
Experimental factors	*Isolation of four ovarian somatic cell types*
Experimental features	*A comparative transcriptome analysis of the granulosa cells and theca cells of the ovarian follicle versus the large and small luteal cells of the corpus luteum provides cell type markers, functional insight, and support for the differentiation lineage model describing where the luteal cells originate.*
Data source location	*Lincoln and Omaha, NE, USA*
Data accessibility	*Filtered dataset is present as tables in this article, raw data is in the public NCBI repository GEO* GSE83524. http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE83524

Value of the data

- The follicular GC and TC transcriptome data can be compared to previously published bovine gene expression analyses for corroboration [2,3] and are valuable in metadata analyses investigating GC and TC transcriptomes at different stages or in different species.
- There are no previously published transcriptomes available for large luteal cells (LLC) and small luteal cells (SLC). Therefore, the luteal cell gene expression data allow novel insight into these two cell types.
- Lists of identified genes that are specifically enriched in each somatic ovarian cell type can inform future physiological research on the functions of the ovarian somatic cells.

1. Data

- The normalized linear microarray data are available at the NCBI GEO repository: GSE83524 at http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE83524
- Fig. 1: A graph depicting the frequency of log-intensities (A–D) and standard deviation versus log-intensity (E–H) of the microarray data for each cell type as well as the average standard deviation versus log-intensity for all of the microarray data (I).

All tables listed below contain the Affymetrix probeset ID, gene symbol, description of the gene, fold changes, and relevant normalized linear microarray data. There are four microarray replicates for the GC cell type and three replicates for the TCs, LLCs, and SLCs.