Gene networks during the first wave of spermatogenesis

A. Sironen[2], A. Laiho[1], N. Kotaja[3], A. Gyenesei[1], J. Vilkki[2],

[1] The Finnish Microarray and Sequencing Centre, Turku Centre for Biotechnology, University of Turku and Åbo Akademi University, Tykistökatu 6, FI-20520 Turku, Finland; [2]Agrifood Research Finland, Biotechnology and Food Research, Animal Genomics, FI-31600 Jokioinen, Finland; [3]Department of Physiology, Institute of Biomedicine, University of Turku, FI-20520 Turku, Finland

Objective

In this study we used the SOLiD 4 sequencing platform to investigate the gene expression patterns at five different time points during the first wave on murine spermatogenesis.

Design

We have used samples of time points, which correspond to specific cell content in the testis; at post natal day (PND) 7 only somatic cells and spermatogonia are present in the testis, at PND 14 early spermatocytes appear, at PND 21 late spematocytes, at PND 28 round spermatid have developed and finally at PND 28 elongating spermatids.

Materials and Methods

Whole testes from two C57BL/6NHsd mice of each time point were collected for RNA extraction. Protocols provided by Invitrogen were used for library construction for SOLiD 4 sequencing and LifeScope v2.1 for mapping the reads. Different analysis pipelines (Limma, DEseq, Cufflinks) were used for identification of differentially expressed genes and isoforms. In addition, clustering of the data was introduced in order to identify gene clusters.

Results

Our data emphasizes the importance of correct timing of gene expression within biological processes. In total over 26 000 genes were expressed in the testis and Cufflinks identified isoforms for 57% of these genes. Differential promoter and transcription start site usage appears to play a role in regulation of gene expression during spermatogenesis. Clustering of the data resulted in 34 different clusters based on the changes in expression pattern.

Conclusions

Transcriptomic analysis of testis tissue samples is highly informative due to the large number of expressed genes and identified isoforms. Our study provides a very valuable basis for investigation of factors contributing to male fertility.

Support

This study was supported by the Academy of Finland.