Transcriptome analysis of the adult human Klinefelter testis and cellularity-matched controls reveals disturbed differentiation of Sertoli- and Leydig cells article - DTU Orbit (15/11/2018)

The most common human sex chromosomal disorder is Klinefelter syndrome (KS; 47,XXY). Adult patients with KS display a diverse phenotype but are nearly always infertile, due to testicular degeneration at puberty. To identify mechanisms causing the selective destruction of the seminiferous epithelium, we performed RNA-sequencing of 24 fixed paraffin-embedded testicular tissue samples. Analysis of informative transcriptomes revealed 235 differentially expressed transcripts (DETs) in the adult KS testis showing enrichment of long non-coding RNAs, but surprisingly not of X-chromosomal transcripts. Comparison to 46,XY samples with complete spermatogenesis and Sertoli cell-only-syndrome allowed prediction of the cellular origin of 71 of the DETs. DACH2 and FAM9A were validated by immunohistochemistry and found to mark apparently undifferentiated somatic cell populations in the KS testes. Moreover, transcriptomes from fetal, pre-pubertal, and adult KS testes showed a limited overlap, indicating that different mechanisms are likely to operate at each developmental stage. Based on our data, we propose that testicular degeneration in men with KS is a consequence of germ cells loss initiated during early development in combination with disturbed maturation of Sertoli- and Leydig cells.

General information
State: Published
Organisations: Department of Bio and Health Informatics, DTU Multi Assay Core, Aarhus University, Copenhagen University Hospital, University of Copenhagen
Number of pages: 14
Publication date: 1 Jun 2018
Peer-reviewed: Yes

Publication information
Journal: Cell Death & Disease
Volume: 9
Issue number: 6
Article number: 671
ISSN (Print): 2041-4889
Ratings:
Web of Science (2018): Indexed yes
Scopus rating (2017): CiteScore 5.44 SJR 2.536 SNIP 1.497
Web of Science (2017): Impact factor 5.638
Web of Science (2016): Impact factor 5.965
Scopus rating (2015): CiteScore 5 SJR 2.501 SNIP 1.229
Web of Science (2015): Impact factor 5.378
Scopus rating (2014): CiteScore 4.63 SJR 2.49 SNIP 1.141
Web of Science (2014): Impact factor 5.014
Scopus rating (2013): CiteScore 5.07 SJR 2.491 SNIP 1.274
Web of Science (2013): Impact factor 5.177
Scopus rating (2012): CiteScore 5.61 SJR 1.381 SNIP 1.202
Web of Science (2012): Impact factor 6.044
Scopus rating (2011): CiteScore 4.29 SJR 1.222 SNIP 0.619
Web of Science (2011): Impact factor 5.333
Web of Science (2010): Impact factor
Original language: English
Electronic versions:
winge_et_al_2018.pdf
DOIs:
10.1038/s41419-018-0671-1

Bibliographical note
This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. The images or other third party material in this article are included in the article’s Creative Commons
license, unless indicated otherwise in a credit line to the material. If material is not included in the article’s Creative Commons license and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this license, visit http://creativecommons.org/licenses/by/4.0/.

Source: Scopus
Source-ID: 85047620969
Research output: Research - peer-review > Journal article – Annual report year: 2018