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Data Article

Data in support of peptidomic analysis of spermatozoa during epididymal maturation

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ABSTRACT

The final differentiation of the male germ cell occurs in the epididymal duct where the spermatozoa develop the ability to be motile and fertilize an ovum. Understanding of these biological processes is the key to understanding and controlling male fertility. Comparative studies between several epididymal maturation states could be an informative approach to finding sperm modifications related to maturation and fertility. Here we show the data from differential peptidomic/proteomic analyses on spermatozoa isolated from 4 epididymal regions (immature to mature stage) using a profiling approach based on MALDI-TOF mass spectrometry and, combined to top-down MS in order to identify peptidoforms and proteoforms. By this way, 172 *m/z* peaks ranging between 2 and 20 kDa were found to be

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modified during maturation of sperm. A total of 62*m*/*z* were identified corresponding to 32 different molecular species. The interpretation of these data can be found in the research article published by Labas and colleagues in the Journal of Proteomics in 2014 [1].

Specifications table

Subject area	Reproductive biology
More specific subject area	Peptidomic analysis of boar epididymal spermatozoa and molecular phenotypes at different maturation stages
Type of data	*Top down raw data and.csv tables with identified proteins*
How data was acquired	*Experiments performed on a LTQ Orbitrap Velos Mass Spectrometer (Thermo Fisher Scientific, Bremen, Germany)*
Data format	*Raw data* *.csv results tables of top-down identification*
Experimental factors	*Boar spermatozoa from 4 different regions of the epididymis*
Experimental features	*Epididymal spermatozoa peptidome* (*Sus scrofa*) *and investigation of the boar sperm maturation process*
Data source location	*N/A*
Data accessibility	*Data are available here and via the PRIDE partner repository with the dataset identifier PXD001303.*

Value of the data

- First description of peptidome/degradome of epididymal spermatozoa from boar (*Sus scrofa*).
- Molecular phenotypes distinguishing degrees of maturation of spermatozoa during the epididymal transit.
- First description of protease activities involved in maturation of epididymal spermatozoa.

1. Data

Mean peak values obtained from intact cells (IC), detergent-soluble extracts (SD) and detergent-insoluble extracts (ID) associated with immature (IC2, SD2, ID2) and mature epididymal spermatozoa (IC9, SD9, ID9) are shown in Supplementary Table 1. Only 172*m*/*z* peak values for which the fold-changes were >2 and which presented at least one significant difference between epididymal samples ($p<0.05$) are reported in this table. Some of them are identified. The variation index was calculated as the product of the absolute difference between the maximum (max) and minimum (min) peak intensity values multiplied by the fold-change (fold) between the two extreme values. The variations are expressed as linear decrease (LD) or linear increase (LI) when all the mean values for the four epididymal samples were significantly different from each other ($p<0.05$), expressed as increase (I) or decrease (D) when at least one of the mean values was not significantly different from the others, and intermediate (inter.) when at least one value was different. In the first column, *m*/*z* values in green correspond to *m*/*z* peaks observed only in IC analysis (a total of 135*m*/*z*). Rows with color in IC, SD and ID columns correspond to specific peaks for the sample preparation.