

Accepted Manuscript

Quantitative proteomic profiling indicates the difference in reproductive efficiency between Meishan and Duroc boar spermatozoa

Li Xinhong, Linqing Zhen, Jieli Fu, Lirui Wang, Qiangzhen Yang, Peifei Li, Yuhua Li



PII: S0093-691X(18)30170-5

DOI: [10.1016/j.theriogenology.2018.04.025](https://doi.org/10.1016/j.theriogenology.2018.04.025)

Reference: THE 14529

To appear in: *Theriogenology*

Received Date: 6 February 2018

Revised Date: 25 April 2018

Accepted Date: 25 April 2018

Please cite this article as: Xinhong L, Zhen L, Fu J, Wang L, Yang Q, Li P, Li Y, Quantitative proteomic profiling indicates the difference in reproductive efficiency between Meishan and Duroc boar spermatozoa, *Theriogenology* (2018), doi: 10.1016/j.theriogenology.2018.04.025.

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

Quantitative Proteomic Profiling Indicates the Difference in Reproductive Efficiency between Meishan and Duroc Boar Spermatozoa

Li Xinhong, Linqing Zhen, Jieli Fu, Lirui Wang, Qiangzhen Yang, Peifei Li, Yuhua Li

Shanghai Key Laboratory of Veterinary Biotechnology, School of Agriculture and Biology, Shanghai Jiao Tong University, Shanghai 200240, China

ABSTRACT

The reproductive efficiency of Meishan pigs is higher than that of Duroc pigs, but the underlying molecular mechanism for this disparity remains unclear. No systematic quantitative proteomics studies, comparing global proteins in Meishan and Duroc boar spermatozoa have been reported. Therefore, we applied iTRAQ labeling coupled with mass spectrometry, and analyzed the differences in proteins between Meishan and Duroc sperm. In the present study, a total of 1597 proteins were quantified. Of these proteins, 190 showed statistically significant fold changes between Meishan and Duroc spermatozoa. Bioinformatics analysis revealed that these differentially abundant proteins were primarily involved in energy metabolism, sperm motility, capacitation and sperm-oocyte binding. Remarkably, SPAG6, ACR, LDHC, CALM, ACE and ENO1 which are positively related to high litter size, were more abundant in Meishan spermatozoa than in Duroc spermatozoa. Moreover, APOA1, NDUFS2 and RAB2A which are negatively related to farrowing rates, were less abundant in Meishan spermatozoa than in Duroc spermatozoa. Interestingly, essential enzymes in Glycolysis/Gluconeogenesis, such as HK1, ALDH2, LDHA and LDHC, were markedly up-regulated in Meishan spermatozoa compared to

Download English Version:

<https://daneshyari.com/en/article/8426637>

Download Persian Version:

<https://daneshyari.com/article/8426637>

[Daneshyari.com](https://daneshyari.com)