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

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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