

JOINT EVENT

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**Isobaric tags for relative and absolute quantitation labelling-based proteomic analysis of *Mycoplasma mycoides*, causative agent of contagious bovine pleuropneumonia**

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Contagious bovine pleuropneumonia (CBPP), an endemic disease, is still threatening cattle health. A Proteomics study of *mycoplasma mycoides* is rarely known. This study screened the differentially expressed proteins (DEPs) between standard strains (PG45) and field isolate strains (HN12, Henan Province, China) using isobaric tags for relative and absolute quantitation labeling (iTRAQ). A total of 447 proteins were identified, 66 DEPs were quantified, 25 of which were up-regulated and 41 down-regulated between the two strains. Bioinformatic analysis revealed that these DEPs are involved in a wide variety of biology process played roles in *Mycoplasma mycoides*. Functional and KEGG pathway analysis revealed that the differential identified protein were related to bacterial secretion system, ABC transporters, HIF-1 signaling pathway, protein export, RNA degradation, mismatch repair, DNA replication, homologous recombination, aminoacyl-tRNA biosynthesis, ribosome, tyrosine metabolism, pentose phosphate pathway, glycolysis/gluconeogenesis, carbon fixation in photosynthetic organisms, oxidative phosphorylation, photosynthesis. This is the first comparative proteomic report on standard strains (PG45) and field isolate strains. These identified protein data will provide new view valuable information for understanding the molecular mechanisms of *Mycoplasma mycoides*. And these proteins may potentially act as bio-markers for diagnosis, vaccine or predict developmental competence of *Mycoplasma mycoides*.

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