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TITLE

COMPARATIVE PROTEOMIC ANALYSIS OF THREE MYCOPLASMA HYOPNEUMONIAE STRAINS USED AS BACTERINS IN COMMERCIAL VACCINES

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CONTENT

Background and Objetives. Commercial vaccines against M. hyopneumoniae (Mhyo) are bacterins based on different strains. Although proteomic variability among Mhyo strains has been described, comparison between the strains used in bacterins has not been performed. Therefore, this study aimed to describe and compare the proteomic profiles of three Mhyo strains used in commercial vaccines.
Material & Methods. Three Mhyo isolates corresponding to commercial vaccines were cultured: 1) strain 2940 (isolated in the late 1990s), 2) the reference strain (RS) J (SJ, ATCC©25934™) and 3) strain 11 (S11, ATCC©25095™), both isolated in the early 1960s. Bacterial pellets were obtained from cultures by centrifugation. A triplicate of each extract was digested with tripsin by FASP and analyzed by LC-MS/MS in a high resolution LTQ-Orbitrap XL mass spectrometer. Proteins were identified by database search using Proteome Discoverer and a quantitative label-free study was done using Progenesis QI and DanteR. A statistical analysis from normalized data was carried out taking the most recent isolated strain (2940) as control condition. Proteins with p-value<0.05 and ratio (reporter ion value in study condition/reporter ion value in control) >1.2 or <0.8 were considered differentials.
Results. Around 400 proteins were identified per strain. From these proteins, 143 and 180 were found differentially in the comparison S11/2940 and SJ/2940, respectively. Such data defined a group of 235 differentially detected proteins with 92 common proteins in both comparisons. The ten most differentially identified proteins in S11/2940 were predicted as unknown (5), cytoplasmic (4) and extracellular (1) proteins. Similarly, SJ/2940 comparison showed unknown (6), cytoplasmic (3) and extracellular (1) proteins.
Discussion & conclusion. Differences on proteomic profiles from the studied vaccine strains were detected. Further investigations are needed to elucidate the role of such proteins differentially present in the three strains.