

LC-MS/MS BASED PROTEOMIC ANALYSIS OF THE SWINE PATHOGEN *MYCOPLASMA HYOPNEUMONIAE*

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Mycoplasma hyopneumoniae is an important pathogen for pigs, being the causative agent of enzootic pneumonia (EP). Recently, the genome sequences of three *M. hyopneumoniae* strains, one non-pathogenic (J) and two pathogenic (7448 and 232), have been reported. A preliminary and complementary proteomic analysis of the 7448 strain, by two-dimensional gel electrophoresis and MALDI-TOF MS, was also reported by our group. In this work, the *M. hyopneumoniae* proteomic analysis has been extended, by the use of a modified multidimensional protein identification technology (MudPIT). We were able to identify 94, 88 and 92 proteins, from strains J, 7448 and 7422, respectively. From the total of 167 identified proteins, 95 were detected in a single strain, being 28 for the 7448 strain, 30 for the 7422 strain, and 37 for the J strain. Only 35 proteins were shared by all strains, while 37 were shared by two of them. The repertoires of identified proteins of the two pathogenic strains are as different between them as they are from that of the non-pathogenic one indicating a significant interstrain variability. In the pathogenic strains, known adhesins are quantitatively more represented than in strain J, which protein expression profile is suggestive of a non-infective (with quantitatively less adhesins) proliferate lifestyle.
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