

Global analysis of *Mycoplasma hyopneumoniae* proteome: comparing virulent and avirulent strains

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Following the previous report of a proteomic survey of the pathogenic 7448 strain of the *Mycoplasma hyopneumoniae* swine pathogen, we performed a comparative protein profiling of three *M. hyopneumoniae* strains, namely the non-pathogenic J strain and the pathogenic strains 7448 and 7422. In 2DE comparisons, we were able to identify differences in expression levels between strains for 67 proteins, including cases of over-expression of cytoadherence-related proteins in pathogenic strains. 2DE immunoblot analyses allowed the identification of differential proteolytic cleavage patterns of the P97 adhesin in the three strains. For more comprehensive protein profiling, an LC-MS/MS strategy based on a modified multidimensional protein identification technology was used. Overall, 231 different proteins were identified, corresponding to 35% of the *M. hyopneumoniae* genome coding capacity, and experimental validation for at least 36 hypothetical genes was provided. Partially overlapping profiles of identified proteins were observed for strains J, 7448, and 7422, with 81 proteins identified only in one strain, 54 proteins identified in two of them, and 96 proteins identified in all strains. The functional classification of identified proteins was suggestive of physiological differences between the non-pathogenic and the pathogenic strains, with the first being richer in proteins classified as involved with cellular processes, and the latter being richer in proteins of the class of poorly characterized proteins (which includes adhesion molecules). Also, application of the exponentially modified protein abundance index demonstrated significant differences in the expression levels of proteins detected in more than one strain, confirming over-expression in one or two of the strains for 64 proteins.

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