

Proteomic Analysis of Total Proteins from *Mycoplasma synoviae* and
Mycoplasma hyopneumoniae

¹Tavares, C.P., ¹Menegatti, A.C.O., ¹Couto, M.S.R., ¹Vernal, J., ²Klein, C. S.,
²Rebelatto, R., ¹Terenzi, H.

¹Lab. de Expressão Gênica, Departamento de Bioquímica, CCB, UFSC, Santa
Catarina

²Lab. De Sanidade Animal-EMBRAPA Suínos e Aves-Santa Catarina
jvernal@yahoo.com/ hterenzi@ccb.ufsc.br

Mycoplasma synoviae and *Mycoplasma hyopneumoniae* are obligate parasites members of the class Mollicutes, and the smallest known prokaryotes with self-replication ability. These prokaryotes have a reduced genome size and reduced biosynthetic machinery, being responsible for significant economic impact on animal production. *M. synoviae* is responsible for an upper respiratory tract disease of chickens and turkeys. *M. hyopneumoniae* is the infective agent of enzootic pneumonia in swines. Both organisms increase the susceptibility to secondary infections. Recently, the genome sequences of *M. synoviae* strain 53 and *M. hyopneumoniae* strain 7448 have been reported. In this work a preliminary two-dimensional gel electrophoresis (2-DE) proteomic analysis of these organisms is described and the repertoire of proteins identified by MS obtained is shown. The proteome maps were constructed in combination with mass spectrometry (MALDI-TOF MS). So far, proteins from about 630 spots from *M. synoviae* and 157 spots from *M. hyopneumoniae* were characterized with MS by determining the molecular weights and partial sequences of their tryptic peptides. The molecular mass (MW) and the isoelectric point (pI) of each protein were experimentally determined and compared with gene-deduced MW/pI coordinates obtained from MASCOT NCBI database (<http://www.matrixscience.com/>). There were identified 267 protein spots from *Mycoplasma synoviae* which correspond to 110 different polypeptides, and 43 protein spots from *Mycoplasma hyopneumoniae* corresponding to 24 different proteins. Based on the Clusters of Orthologous Groups (COG) functional classification, the identified proteins were assigned to different groups according to their functions.

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