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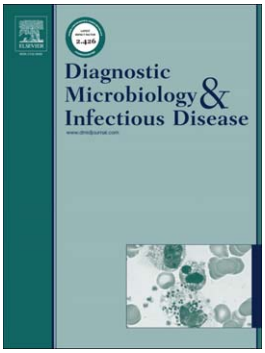

A Proteomics Approach to the Identification of Plasma Biomarkers for Latent Tuberculosis Infection

Xia Zhang, Fei Liu, Qi Li, Hongyan Jia, Liping Pan, Aiying Xing, Shaofa Xu, Zongde Zhang

PII: S0732-8893(14)00165-5
DOI: doi: 10.1016/j.diagmicrobio.2014.04.005
Reference: DMB 13600

To appear in: *Diagnostic Microbiology and Infectious Disease*

Received date: 6 December 2013
Revised date: 18 April 2014
Accepted date: 21 April 2014

Please cite this article as: Zhang Xia, Liu Fei, Li Qi, Jia Hongyan, Pan Liping, Xing Aiying, Xu Shaofa, Zhang Zongde, A Proteomics Approach to the Identification of Plasma Biomarkers for Latent Tuberculosis Infection, *Diagnostic Microbiology and Infectious Disease* (2014), doi: 10.1016/j.diagmicrobio.2014.04.005

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A Proteomics Approach to the Identification of Plasma Biomarkers for Latent Tuberculosis Infection

Running title: Proteomics in Latent Tuberculosis Infection

Xia Zhang, Fei Liu, Qi Li, Hongyan Jia, Liping Pan, Aiying Xing, Shaofa Xu*, Zongde Zhang*

Department of Beijing Key Laboratory of Drug Resistance Tuberculosis Research, Beijing Chest Hospital, Capital Medical University, Beijing Tuberculosis and Thoracic Tumor Research Institute, Beijing, China

*****Corresponding authors. Shaofa Xu is to be contacted at Tel: +86-10-89509155; Fax: +86-10-69546819. Zongde Zhang, Tel: +86-10-89509365; Fax: +86-10-69546819.

Email address: shaofaxu8950@126.com (S. Xu), zhang2001512@126.com (Z. Zhang).

ABSTRACT

A proteomic analysis was performed to screen the potential latent tuberculosis infection (LTBI) biomarkers. A training set of spectra was used to generate diagnostic models, and a blind testing set was used to determine the accuracy of the models. Candidate peptides were identified using nano-liquid chromatography-electrospray ionization–tandem mass spectrometry. Based on the training set results, three diagnostic models, recognized LTBI subjects with good cross-validation accuracy. In the blind testing set, LTBI subjects could be identified with sensitivities and specificities of 85.20% to 88.90% and 85.7% to 100%, respectively. Additionally, 14 potential LTBI biomarkers were identified and all proteins were identified for the first time through proteomics in the plasma of healthy, latently infected individuals. In all, proteomic pattern analyses can increase the accuracy of LTBI diagnosis, and the data presented here provide novel insights into potential mechanisms involved in

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