Additions & Corrections

Vol. 12 (2013) 2081–2095

Analysis of the Secretome and Identification of Novel Constituents From Culture Filtrate of Bacillus Calmette-Guerin Using High-resolution Mass Spectrometry

Jianhua Zheng, Xianwen Ren, Candong Wei, Jian Yang, Yongfeng Hu, Liguo Liu, Xingye Xu, Jin Wang, and Qi Jin

The original article (Molecular & Cellular Proteomics 12: 10.1074/mcp.M113.027318) failed to cite the article Bell, et al., 2012 J Proteome Res 11, 119–130.

Page 2081, abstract: In the sentence on line 23, “There are 103 secreted proteins that have not been reported in previous studies on the mycobacterial secretome and are unique to our study,” the word “the mycobacterial” should be revised to “BCG”.

Page 2082, left column: In the end of first paragraph, the following sentence should be added. “Bell et al. used a variety of methods to study M. tuberculosis proteins by LC-MS and created a comprehensive resource by characterizing all M. tuberculosis subcellular fractions. In total 398 proteins were included in the CF fraction with high probability (74)”.

Page 2082, right column: In the sentence on line 10, “We found 103 secreted proteins that have not been reported in previous studies on the mycobacterial secretome and that are unique to our study”, the word “the mycobacterial” should be revised to “BCG”.

Page 2086, left column, the third paragraph: Since we integrated the identification data in CF fraction of M. tuberculosis from Dr. Hess work, some data in the “Comparisons with Other Studies on the Mycobacterial Secretome” paragraph should be revised accordingly. The first six sentences, “To investigate the secreted proteins in CFs, a number of mycobacterial secretome studies have been undertaken (8, 11–14, 25–34, 74). Table I summarizes the major studies on the mycobacterial secretome performed to date. These studies focused on CFs of different mycobacterial substrains, including BCG variants. Combining all of the data from the studies published to date, there are 397 proteins that have been reported in different mycobacterial culture filtrates. Among them, 148 proteins were considered to be secreted proteins, including classical and leaderless secreted proteins or lipoproteins. We compared the proteins identified in our study with those identified in previous studies and found that 82 of the secreted proteins were previously reported. Therefore, there are 103 secreted proteins that have not been reported previously and are unique to our study”, should be revised like this: “To investigate the secreted proteins in CFs, a number of mycobacterial secretome studies have been undertaken (8, 11–14, 25–34, 74). Table I summarizes the major studies on the mycobacterial secretome performed to date. These studies focused on CFs of different mycobacterial substrains, including BCG variants. Combining all of the data from the studies published to date, there are 592 proteins that have been reported in different mycobacterial CFs. Among them, 179 proteins were considered to be secreted proteins, including classical and leaderless secreted proteins or lipoproteins. We compared the proteins identified in our study with those identified in previous studies in mycobacterial secretome and found that 113 of the secreted proteins were previously reported. Therefore, there are 72 secreted proteins that have not been reported previously in mycobacterial secretome. Comparing with BCG secretome, 103 secreted proteins have not been reported previously in CFs of BCG and are unique to our study”.

Page 2093, left column: In the sentence on line 15 in CONCLUSIONS section, “These data represent the largest number of mycobacterial secreted proteins reported in a single study, and some of these proteins might be potential candidates for vaccination and therapeutics”, the word “mycobacterial” should be revised to “BCG”.

Molecular & Cellular Proteomics 12:10.1074/mcp.A113.027318, 3987–3988, 2013.

REFERENCE

1. (74) Bell, C., Smith, G. T., Sweredoski, M. J., and Hess, S. (2012) Characterization of the Mycobacterium tuberculosis proteome by liquid chromatography mass spectrometry-based proteomics techniques: a comprehensive resource for tuberculosis research. J Proteome Res 11, 119–130

We suggest that subscribers photocopy these corrections and insert the photocopies at the appropriate places where the article to be corrected originally appeared. Authors are urged to introduce these corrections into any reprints they distribute. Secondary (abstract) services are urged to carry notice of these corrections as prominently as they carried the original abstracts.
| Year | Title | No. of identifications | No. of secreted proteins | Analysis method and instrument used | Reference |
|------|-------|------------------------|--------------------------|-----------------------------------|-----------|
| 1997 | Definition of Mycobacterium tuberculosis culture filtrate proteins by two-dimensional polyacrylamide gel electrophoresis, N-terminal amino acid sequencing, and electrospray mass spectrometry | 32 | n.d. | 2-DE and TSQ-700 quadrupole MS | (25) |
| 1999 | Comparative proteome analysis of Mycobacterium tuberculosis and Mycobacterium bovis BCG strains: towards functional genomics of microbial pathogens | 263 | 54 | 2-DE and MALDI-TOF (Voyager Elite MS) | (26) |
| 2000 | Toward the proteome of Mycobacterium tuberculosis | 288 | 49 | 2-DE and MALDI-MS | (27) |
| 2001 | Mapping and identification of Mycobacterium tuberculosis proteins by two-dimensional gel electrophoresis, microsequencing and immunodetection | 61 | 14 | 2-DE and microsequencing, immunodetection | (28) |
| 2002 | The application of proteomics in defining the T cell antigens of Mycobacterium tuberculosis | 30 | n.d. | 2-DE and LCQ-ESI-MS | (29) |
| 2003 | Comparative proteome analysis of culture supernatant proteins from virulent Mycobacterium tuberculosis H37Rv and attenuated M. bovis BCG Copenhagen | 137 | 42 | MALDI-MS PMF, ESI-MS/MS or CapLC-ESI-MS/MS | (8) |
| 2003 | Comparative proteome analysis of culture supernatant proteins of Mycobacterium tuberculosis H37Rv and H37Ra | 5 | n.d. | 2-DE-MALDI-TOF MS | (31) |
| 2003 | Identification of novel proteins in culture filtrates of Mycobacterium bovis bacillus Calmette-Guerin in the isoelectric point range 6–11 | 12 | n.d. | 2-DE and MALDI-TOF (Voyager Spec MS) | (12) |
| 2004 | Comparative proteome analysis of culture supernatant proteins from Mycobacterium tuberculosis H37Rv | 8 | 4 | 1-DE and MALDI-MS and ESI-MS/MS (Voyager Elite) | (10) |
| 2007 | Comprehensive analysis of exported proteins from Mycobacterium tuberculosis H37Rv | 257 | 159 | 2-DE and MALDI-TOF MS; LC coupled MS/MS | (11) |
| 2009 | Immunoproteomic identification of secretory and subcellular protein antigens and functional evaluation of the secretome fraction of Mycobacterium immunogenenum, a newly recognized species of the Mycobacterium cheloneae-Mycobacterium abscessus group | 33 | 4 | 2-DE and MALDI-TOF | (33) |
| 2009 | Mycobacterium tuberculosis glycoproteomics based on ConA lectin affinity capture of mannosylated proteins | 41 | 31 | 2-DE, Ligand Blotting and Immunoblotting, LC-3200 Q TRAP-MS | (32) |
| 2010 | The secretome of a recombinant BCG substrain reveals differences in hypothetical proteins | 9 | n.d. | 2DE-3200 Q-TRAP-MS/MS | (13) |
| 2010 | Descriptive proteomic analysis shows protein variability between closely related clinical isolates of Mycobacterium tuberculosis | 101 | n.d. | 2-DE,iTRAQ-labeled and LTQ-MS | (34) |
| 2011 | Proteomic profile of culture filtrate from the Brazilian vaccine strain Mycobacterium bovis BCG Moreau compared to M. bovis BCG Pasteur | 101 | 53 | 2-DE and MALDI-TOF/TOF (4700 Proteomics Analyzer) | (14) |
| 2012 | Characterization of the Mycobacterium tuberculosis proteome by liquid chromatography mass spectrometry-based proteomics techniques: a comprehensive resource for tuberculosis research | 398 | n.d. | LC and ESI-MSMS (LTQ-Orbitrap Classic) | (74) |
| 2013 | Analysis of the secretome and identification of novel constituents from culture filtrate of bacillus Calmette-Guerin using high-resolution mass spectrometry | 239 | 185 | 1-DE and ESI-MSMS (LTQ-Orbitrap Velos) | This study |

ESI, electrospray ionization; PMF, peptide mass fingerprint; n.d., no data.