Comparative Proteomics Analysis of Two Strains of *Neisseria meningitidis* Serogroup B and *Neisseria lactamica*

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Introduction

Neisseria meningitidis serogroup B (NmB) is cause of lifethreatening bacterial meningitis worldwide, especially among infants and young adults (1). Unlike the other serogroups of *N. meningitidis* (A, C, Y and W135), the B capsular polysaccharide serogroup is poorly immunogenic; thus, there is no effective vaccine based on capsular polysaccharides against NmB (2). *Neisseria lactamica* is a harmless commensal species and is more frequently colonized in the upper respiratory tract of infants and young children when compared to adults (3). Previous studies have shown that colonization with *N. lactamica* during early childhood will protect the host against colonization with *N. meningitidis* by natural immunity, which is thought to be due to shared common antigens (4,5). The main aims of this study were to determine whole proteome profiles of *N. lactamica* strains and to compare them with whole proteome profile of a reference strain of NmB for identification of some of common proteins between the two species.

Methods

We compared the whole proteomic profiles of *N. lactamica* strains and a reference strain of NmB. Lysates from bacterial strains were resolved by two-dimensional gel electro-phoresis (isoelectric focusing (IEF)/SDS-PAGE) (2DE), followed by Coomassie Brilliant blue staining. Some of the protein spots were excised from the gel and subjected to matrix-assisted laser desorption/ionization-tandem time-of-flight mass spectrometry (MALDI-TOF/TOF MS) analysis.

Results

The analysis of Coomassie-stained gels using ImageMaster 2D Platinum software identified approximately 800 reproducible protein spots in the range of p*I* 4.5 - 9.5 and *M*r of 8 - 100 kDa for each 2-DE gel of the studied bacterial strains (Figure 1).

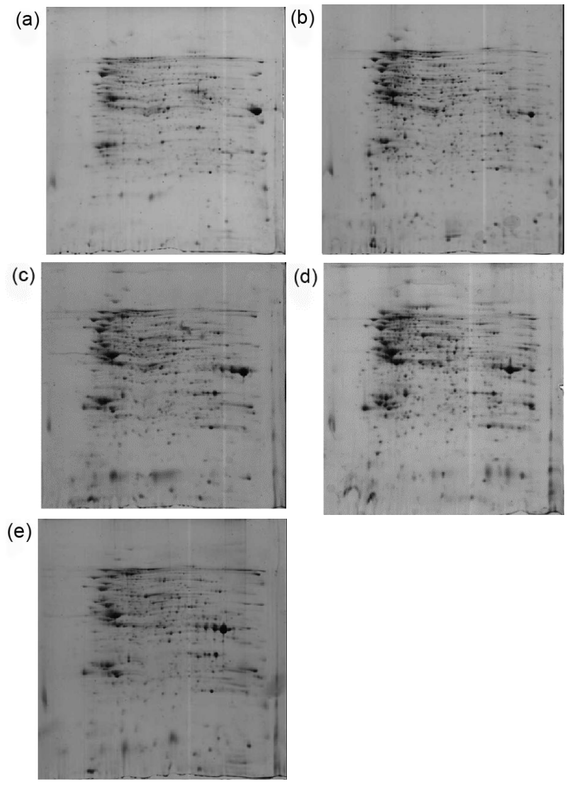

Figure 1. Representative 2DE proteome map of a total protein extract stained with colloidal coomassie brilliant blue G-250. *N. meningitidis* serogroup B ATCC 13090 (a) *N. lactamica* ATCC 23970 (b) *N. lactamica* NL1 (c) *N. lactamica* NL2 (d) and *N. lactamica* NL3 (e).

By comparing proteome maps of 2DE gels, more than 200 common protein spots were recognized between the two species. Forty-seven common protein spots between the studied bacterial strains were identified by MALDI-TOF/TOF-MS (Figure 2). As shown in Figure 3, the database search result using MASCOT and also protein sequence indicate the identity of the protein spot as phosphoglyceromutase.

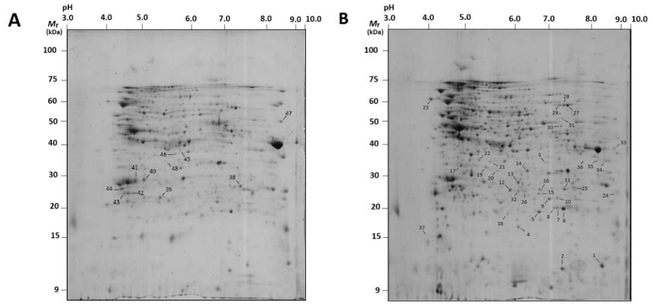

Figure 2. Numbered protein spots indicate common proteins identified by MALDI-TOF/TOF MS analysis. (**A**) 2DE gel related to the NmB (**B**) 2DE gel related to the reference strain of *N. lactamica*.

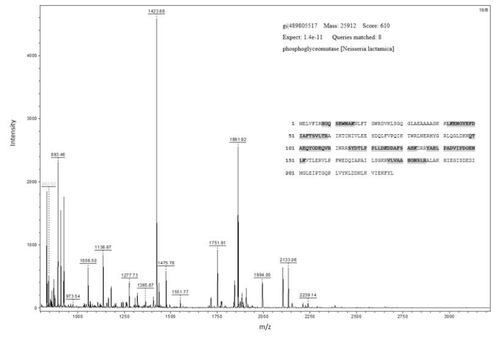

Figure 3. MALDI-TOF/TOF mass spectrum of the in-gel digested spot no. 15. The mass signals implicate the identity of the spot as phosphor-glyceromutase with sequence coverage: 37%.

The results indicated that among the protein spots identified by MOLDI-TOF/TOF mass spectro-metry, the groups of proteins included Cell surface, energy metabolism, amino acid transport and metabolism, coenzyme metabolism, defense, multifunctional cellular processes, DNA, RNA and protein synthesis, ribosomal structure, regulatory functions, replication, transcription, translation, unknown and hypothetical proteins with unknown function (data not shown). We found that *N. lactamica* strains have a proteome profile somewhat similar to each other and slightly different with NmB.

Conclusions

These results show the usefulness of proteome analysis in successful identification of the common proteins between *N. lactamica* strains and NmB. This proteomics analysis is the starting point in the path of knowledge development about whole proteome profiles of *N. lactamica* strains.

References

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