Comparative Proteomic Analysis of *B. henselae* Houston and *B. henselae* Marseille by Two-dimensional Gel Electrophoresis

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Objective To compare the protein difference between *B. henselae* Houston and *B. henselae* Marseille by two-dimensional gel electrophoresis. **Method** Protein samples were prepared by vorterx, ultrasonic treatment, and centrifugation. Protein concentrations were determined by Bradford method. Protein difference was compared by the first IEF and the second SDS-polyacrylamide gel electrophoresis. **Results** Protein concentrations in samples of *Bartonella henselae* Houston and *Bartonella henselae* Marseille were 2.117 μ g/µL and 2.200 μ g/µL respectively. Sample protein of *40* μ g for IPG strips loading was perfect. The results of 2-DE in pH 4 to 7 IPG strips showed that the total protein spots of *Bartonella henselae* Houston and *Bartonella henselae*. **Conclusion** The procedure of 2-DE may prove successful for the proteomic analysis of *Bartonella henselae*. Bartonella henselae Houston and Bartonella henselae. Bartonella henselae Houston and Bartonella henselae.

Key words: Protein; B. henselae; Two-dimensional gel electrophoresis

INTRODUCTION

The species name of B. henselae was first proposed in 1992^[1]. It is a gram-negative, oxidasenegative, fastidious, aerobic, rod-shaped and slowgrowing bacterium. Improvements in the techniques used to isolate B. henselae and new methods for the identification and detection of the organism have to further determine enabled us clinical manifestations of infections including cat scratch disease (CSD)^[2-5], BA^[6], D)^[2-5], BA^[6], peliosis hepatitis^[6], endocarditis^[8-9], and neurological septicemia^[7]. disorders^[10].

In 1996, Drancourt *et al.* ^[11] reported a new serotype of *B. henselae* named Marseille, which is also a new genotype. The authors found that two isolates of *B. henselae*, from a patient with endocarditis and a patient with CSD, are genetically different from all previously isolated strains by sequence analysis of the 16S rRNA-encoding gene. Investigators in the Netherlands^[12] also demonstrated

two restriction fragment length polymorphism (RFLP) patterns of B. henselae DNA in samples from CSD patients, which are shown by analysis of the 16S-23S rRNA gene spacer PCR fragments and 16S rRNA gene PCR products digested with AluI. The presence of two genotypes is later confirmed in France and Germany^[13-16] based on sequencing of the 16S rRNA-encoding gene. Based on 16S rRNA gene differences, genotypes I and II are proposed. Bartonella henselae Houston is genotype I, and Bartonella henselae Marseille is genotype II. The reports of previous studies are concentrated on culturing, gene sequence analysis by PCR method, serological diagnosis and prevalence of Bartonella henselae. Few studies about protein difference between the two genotypes are reported. So we studied protein difference between B. henselae Houston and B. henselae Marseille with the methods of 2-dimensional gel electrophoresis. The results of these studies are described herein.

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MATERIALS AND METHODS

Chemicals

Chemicals were purchased from Merck-Eurolabo (Leuven, Belgium), except for CHAPS, sodium dodecyl sulfate, potassium ferricyanide, urea, and trifluoroacetic acid (TFA), which were from Sigma-Aldrich (Steinheim, Germany). Dithiothreitol (DTT) was from Serva (Heidelberg, Germany), Tris were from ICN (Aurora, OH, USA), and sodium thiosulfate and ammonium hydrogen carbonate were from UCB (Brussels, Belgium).

Bacterial Cultures

B. henselae Houston and *B. henselae* Marseille were obtained from Unite des Rickettsies of Universite of Mediterrance, Faculte de Medecine, Marseille, France. The two *Bartonella* strains were grown on Columbia sheep blood agar (BioMerieux, Marcy l'Etoile, France) at 37° C in a 5% carbon dioxide incubator, harvested after 8 days of culture, suspended in deionized water and stored at -70° C.

Sample Protein Preparation

One mL of the above lyophilized bacteria of *Bartonella henselae* Houston and *Bartonella henselae* Marseille was dissolved in 3 mL solubilization mixture containing 7 mol/L urea, 2mol/L thiourea, 4% CHAPS (W/V), vortexed on ice with ice-cold reagents for 30 min, ultrosonic treatment lasted for 1 min by output power 600 W, then 100 000 \times g centrifugation for 30 min at 4°C. The pellets were discarded and the supernatant was collected for protein determination.

Total Protein Determination

Protein was quantified by the Bradford method using the BioRad protein assay (BioRad, Richmond, CA, USA) with bovine serum albumin as a standard. All samples and bovine serum albumin standards contained 10 μ L of a 10:1 (vol/vol) mixture of sample buffers 1 and 2.

Isoelectrofocusing

Eighteen-centimeter immobilized pH gradient (IPG) strips (pH 3 to 10, 4 to 7) were rehydrated overnight at room temperature with 360 μ L of sample containing protein. Isoelectric focusing (IEF) was conducted at 20°C for 7 h (1 V, 1 min; 500 V, 30 min; 3500 V, 6.5 h).

SDS-polyacrylamide Gel Electrophoresis

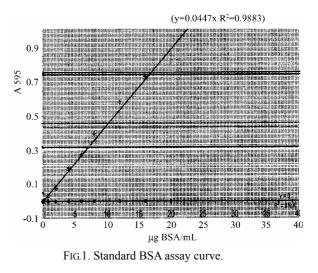
After IEF, each IPG strip was washed for 15 min

in 10 mL of equilibration buffer 1 (6 mol/L urea, 133 mmol/L DTT, 30% glycerol, 50 mmol/L Tris-acetate, pH 7.0) and then for 15 min in 10 mL of equilibration buffer 2 (6 mol/L urea, 2.5% iodoacetamide, 30% glycerol, 50 mmol/L Tris-acetate, pH 7.0). The IPG strips were loaded onto 10% precast Duracryl gels (22 cm by 23 cm by 1 mm; Tris/Tricine/SDS chemistry). Electrophoresis was carried out for 5 to 6 h (500 V; 14 000 to 20 000 mW/gel) at 15°C. All subsequent operations were carried out in an automated staining apparatus by silver staining method. At last, the gels were scanned with ImageScanner II and saved in the computer. Total protein spots were analyzed by the software of ImageMaster Labscan v 3.00.

RESULTS

Total Protein Concentration Determination

The protein concentration of samples was assayed using Bradford method, and the standard BSA assay curve is shown in Fig.1. The results showed that the protein concentration of samples of *Bartonella henselae* Houston and *Bartonella henselae* Marseille was 2.117 μ g/ μ L and 2.200 μ g/ μ L respectively.



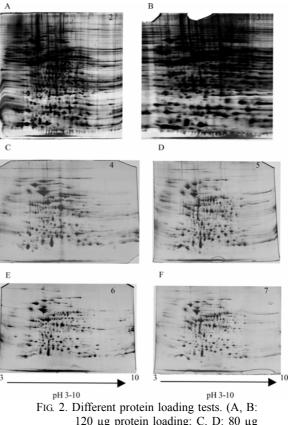
Comparison of 2-DE in Different Protein Load Condition

Eighteen-centimeter immobilized pH gradient (IPG) strips (pH 3 to 10) were rehydrated overnight at room temperature with 350 μ L of sample containing total protein of 40 μ g, 80 μ g, 120 μ g respectively, and then isoelectric focusing (IEF), sodium dodecyl sulfate poly acrylamined gel

electrophoresis (SDS-PAGE), and silver staining were carried out. The results showed that the 120 μ g sample protein for IPG loading (Figs. 2A, 2B) was too much, and the spots on gels were not separated well and overlapped, and that the background was dark. Sample protein of 80 μ g for IPG loading (Figs. 2C, 2D) was better than that of 120 μ g for IPG loading, but the background was still dark and the spots were overlapped. The spots on gels were clear and separated well if the IPG strips were loaded with sample protein of 40 μ g (Figs. 2E, 2F). Consequently, the sample protein of 40 μ g for IPG strip loading was perfect in the following experiments.

Comparison of 2-DE in Protein Spot

The results of 2-DE in pH 4 to 7 IPG strips are shown in Figs. 3A, 3B. The total protein spots of *Bartonella henselae* Houston and *Bartonella henselae* Marseille were 375 and 379 respectively. Five protein spots of *Bartonella henselae* Marseille could not be found on the gel of *Bartonella henselae* Houston. Seven protein spots of *Bartonella henselae* Houston could neither be found on the gel of *Bartonella henselae* Marseille. Furthermore, the spot difference was found to be about at 60 000 Da. No other spot difference could be found on the gel. 95% spots were the same between the two strains of *Bartonella henselae*.



 Directin protein loading; C, D: 80 μg protein loading; E, F: 40 μg protein loading).

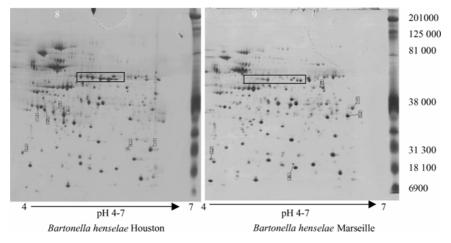


FIG. 3. Protein spots of Bartonella henselae Houston (A) and Bartonella henselae Marseille (B).

DISCUSSION

With the current interest in proteomics, two dimensional gel electrophoresis (2-DE) has emerged as a powerful technique for the separation and characterization of proteins and elucidation of protein-gene linkages^[17]. In order to gain clear and separated good spots in gels of 2-DE, preparation of

protein samples is a crucial step^[18]. By studying different protein load conditions, the best sample protein for IPG strip loading has been found. Clear and separated good protein spots on gels were gained when the IPG strips were loaded with sample protein of 40 μ g (Figs. 2C, 2D). So in this research, the protein samples of *Bartonella henselae* Houston and

Bartonella henselae Marseille were prepared successfully. The solubilization mixture containing 7 mol/L urea, 2 mol/L thiourea, 4% CHAPS (W/V) and ultrosonic treatment were suitable conditions for protein sample preparation of Bartonella henselae. Protein spots of Bartonella henselae Houston and Bartonella henselae Marseille were compared with 2-DE method, 5% protein spot difference was found and proved that Bartonella henselae Houston and Bartonella henselae Marseille were different genotypes. The result is consistent with sequencing analysis of the 16S rRNA-encoding gene. In addition, the procedure of 2-DE may prove useful for the proteomic analysis of Bartonella henselae. So the research is significant for vaccine development against cat scratch disease by peptide sequencing of the antigenic proteins in the future.

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