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Cloning and Expression of a Metalloprotease Gene from *Morganella morganii* Strain ZM

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Abstract *Morganella morganii* is an opportunistic pathogen which causes a wide range of clinical infections. It is well known that metalloproteases synthesized by pathogenic microorganisms play an important role as virulence factors. In this work, we have conducted bioinformatic analysis, sequencing, and cloning of the gene encoding a putative metalloprotease from *M. morganii* (AN CP004345.1, MU9_1718). We detected that the amino acid sequence of putative metalloprotease from *M. morganii* strain KT has 37% identity to actin-specific metalloproteases grimelysin and protealysin from *Serratia grimesii* and *Serratia proteamaculans*, respectively. Based on ORF MU9_1718 sequence, we have identified a metalloprotease gene in the genome of clinical isolate *M. morganii* ZM. The gene was cloned under the control of arabinose promoter into pBAD/Myc-His expression vector, and *Escherichia coli* DH5α cells were subsequently transformed by this vector. We also provide data indicating that the metalloprotease was overexpressed in *E. coli* DH5α cells as a 35 kDa protein.

Keywords *Morganella morganii* · Metalloprotease · Cloning · Expression

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1 Introduction

Morganella morganii is a gram-negative bacterium which belongs to the *Enterobacteriaceae* family. These bacteria are naturally found in the environment and in the intestinal tracts of humans and other mammals as normal microflore [1]. However, *M. morganii* is also an important opportunistic pathogen which causes a wide range of clinical infections such as urinary tract infections, wound infections, and septicemia [2].

It is known that bacterial metalloproteases play an important role in the development of infections. These enzymes can destroy components of extracellular protein matrix, cleave some plasma membrane proteins that allow bacteria to invade host cells, and enhance vascular permeability leading to tissue necrosis. Furthermore, degradation of extracellular matrix may cause destruction of plasmalemma of endothelial cells and leakage of blood components into surrounding tissues facilitating the passage of pathogens through blood-brain barrier [3]. Majority of such metalloproteases are extracellular enzymes. However, there are also some reports about potential virulent activity of intracellular metalloproteases. For example, thermolysin-like proteases grimelysin from *Serratia grimesii* and protealysin from *Serratia proteamaculans* can promote bacterial invasion into host cells by hydrolysis of actin [4]. In this light, the analysis of *M. morganii* metalloproteases has a particular interest due to the notion that these enzymes can be potential virulence factors. Accordingly, we have decided to detect a homolog of a thermolysin-like protease in the genome of *M. morganii*. For this purpose, the clinical isolates of *M. morganii* ZM have been used.