

# Identification of Grimelysin-Like Metalloprotease Gene in the Genome of Bacterium *Providencia stuartii*

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## Abstract

© 2016, Springer Science+Business Media New York. *Providencia stuartii* is an opportunistic pathogen often seen in patients with severe burns or long-term indwelling urinary catheters. Nowadays, the clinical significance of opportunistic microorganisms is growing and the study of their pathogenesis mechanisms is necessary. Microbial proteases are recognized as important virulence factors of diverse bacterial pathogens. We have shown that *P. stuartii*'s bacterial extracts have the ability to cleave actin. It is well known that metalloprotease grimelysin from *Serratia grimesii* is characterized by high specificity towards actin. Using the BLAST program, we identified a gene of hypothetical metalloprotease in the genome of the annotated strain *P. stuartii* MRSN 2154. We have constructed gene-specific primers and sequenced a homologous metalloprotease gene from clinical isolate *P. stuartii* NK. The amino acid sequence of this gene has the 42 % identity with grimelysin metalloprotease. In this study, we have done a comparative analysis of this novel protease from the clinical isolate of *P. stuartii* NK with the grimelysin from *S. grimesii* A2.

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## Keywords

Actinase activity, BLAST alignment, Enterobacteriaceae, Grimelysin, Metalloprotease gene, *Providencia stuartii*, Sequence

## References

- [1] Lüthje, P., & Brauner, A. (2014). Virulence factors of uropathogenic *E. coli* and their interaction with the host. *Advances in Microbial Physiology*, 65, 337-372.
- [2] Manageiro, V., Sampaio, D. A., Pereira, P., Rodrigues, P., Vieira, L., Palos, C., et al. (2015). Draft genome sequence of the first NDM-1-producing *Providencia stuartii* strain isolated in Portugal. *Genome Announcements*, 10, 01077-15.
- [3] Lantz, M. S. (1997). Are bacterial proteases important virulence factors? *Journal of Periodontal Research*, 32, 126-132.
- [4] Miyoshi, S., & Shinoda, S. (2000). Microbial metalloproteases and pathogenesis. *Microbes and Infection*, 2, 91-98.
- [5] Delston, R. B., Kothary, M. H., Shangraw, K. A., Tall, B. D. (2003). Isolation and characterization of a zinc-containing metalloprotease expressed by *Vibrio tubiashii*. *Canadian Journal of Microbiology*, 49, 525-529.
- [6] Abreu, A. G., et al. (2015). The serine protease pic from enteroaggregative *Escherichia coli* mediates immune evasion by the direct cleavage of complement proteins. *Journal of Infectious Diseases*, 212(1), 106-115.

- [7] Adekoya, O. A., & Sylte, I. (2009). The thermolysin family (M4) of enzymes: therapeutic and biotechnological potential. *Chemical Biology and Drug Design*, 73, 7–16.
- [8] Bozhokina, E. S. (2008). Grimelysin, a novel metalloprotease from *Serratia grimesii*, is similar to ECP32. *Biochemical and Biophysical Research Communications*, 4, 888–892.
- [9] Kothary, M. H., et al. (2007). Characterization of the zinc-containing metalloprotease encoded by *zpx* and development of a species-specific detection method for *enterobacter sakazakii*. *Applied and Environmental Microbiology*, 73, 4142–4151.
- [10] Harrington, D. J. (1996). Bacterial collagenases and collagen-degrading enzymes and their potential role in human disease. *Infection and Immunity*, 64, 1885–1891.
- [11] Xiang, G., et al. (2010). Structural basis for the autoprocessing of zinc metalloproteases in the thermolysin family. *Proceedings of the National Academy of Sciences of the United States of America*, 41, 17569–17574.
- [12] Spudich, J. A., & Watt, S. (1971). The regulation of rabbit skeletal muscle contraction. I. Biochemical studies of the interaction of the tropomyosin-troponin complex with actin and the proteolytic fragments of myosin. *Journal of Biological Chemistry*, 246, 4866–4871.
- [13] Laemmli, U. K. (1970). Cleavage of structural proteins during the assembly of the head of bacteriophage T4. *Nature*, 227, 680–685.
- [14] Mullis, K. B., & Faloona, F. A. (1987). *Methods in Enzymology*, 155, 335–350.
- [15] Sambrook J, Russell DW. (2001). Cold Spring Harbor Laboratory Press, Cold.
- [16] Clifford, R. J. (2012). Complete genome sequence of 0020Providencia stuartii clinical isolate MRSN 2154. *Journal of Bacteriology*, 14, 3736–3737.