

INTISARI

Universal stress protein (usp) mendukung kelangsungan hidup suatu organisme dengan meningkatkan ekspresinya dalam kondisi cekaman, meliputi kekurangan nutrisi, *heat shock*, dan antibiotik. Namun, ekspresi gen *uspA* pada *meticilin-resistant Staphylococcus aureus* (MRSA) dilaporkan menurun setelah terpapar madu Manuka. Madu manuka juga diketahui menghambat pertumbuhan *Pectobacterium brasiliense*, meskipun pengaruhnya terhadap ekspresi gen *usp* dari patogen busuk lunak ini belum diteliti. Penelitian ini bertujuan untuk mengetahui kekerabatan Usp *P. brasiliense* dan ortolognya dari Enterobacteriales dengan menggunakan analisis filogenetik serta *Multiple Sequence Alignment* (MSA) dan pengaruh madu Manuka terhadap ekspresi gen *usp* diamati menggunakan *quantitative reverse transcription polymerase chain reaction* (qRT-PCR) dan uji patogenisitas *P. brasiliense* pada sawi putih. Hasil penelitian menunjukkan bahwa UspA, UspB, dan UspE dari *P. brasiliense* memiliki kekerabatan paling dekat dengan *P. carotovorum*, sedangkan UspG memiliki kekerabatan paling dekat dengan *P. polaris*. Ekspresi keempat *usp* tersebut menurun masing-masing sebesar 0,05 kali, 0,16 kali, 0,1 kali, dan 0,62 kali dalam perlakuan madu Manuka 5% (w/v). *P. brasiliense* dengan perlakuan madu Manuka menimbulkan lesi yang lebih kecil dibandingkan dengan kontrol saat diuji pada sawi putih. Penurunan virulensi *P. brasiliense* ini mungkin berhubungan dengan penurunan ekspresi gen *usp* yang dipicu oleh madu Manuka.

Kata kunci: madu manuka, *Pectobacterium brasiliense*, qRT-PCR, busuk lunak, *universal stress protein*

ABSTRACT

Universal stress protein (*usp*) supports the survival of an organism by increasing its expression under stress conditions. These stress conditions include nutritional deficiencies, heat shock, and antibiotics. However, *uspA* gene expression in methicillin-resistant *Staphylococcus aureus* was reported to decrease after Manuka honey exposure. Manuka honey is also known to inhibit the growth of *Pectobacterium brasiliense*, although its effect on the *usp* gene of this soft rot pathogen has never been studied. This study aimed to determine the diversity of the Usp of *P. brasiliense* and its ortholog from *Enterobacteriales* using phylogenetic analysis and multiple sequence alignment (MSA) and the effect of Manuka honey on *usp* gene expression was investigated using quantitative reverse transcription polymerase chain reaction (qRT-PCR) and pathogenicity assay of *P. brasiliense* on Chinese cabbage. The results revealed that the UspA, UspB, and UspE of *P. brasiliense* had the closest similarity to those of *P. carotovorum*, while the UspG had the closest similarity to that of *P. polaris*. Their expressions were down-regulated by 0.05 fold, 0.16 fold, 0.1 fold, and 0.62 fold, respectively, in 5% (w/v) Manuka honey treatment. *P. brasiliense* treated with Manuka honey caused smaller lesion symptoms compared to that control treatment when tested on Chinese cabbage. This reduced virulence of *P. brasiliense* might be related to reduced expression of the *usp* genes triggered by Manuka honey.

Keywords: Manuka honey, *Pectobacterium brasiliense*, qRT-PCR, soft rot, universal stress protein