

ABSTRAK

Pengendalian penyakit dengan bahan kimia dapat membahayakan kesehatan manusia dan lingkungan, selain itu juga dapat menimbulkan resistensi. Madu manuka memiliki senyawa antimikrobal, berpotensi untuk mengatasi permasalahan antimikrobal resisten. Madu manuka diketahui dapat menurunkan ekspresi gen virulensi dan gen universal stress protein (usp) pada *P. brasiliense*. LysR-type transcriptional regulator (LTTR) merupakan regulator transkripsi terbesar pada prokariot, pengaruh madu manuka terhadap LTTR dari *P. brasiliense* belum diteliti. Penelitian ini bertujuan untuk mengetahui kisaran inang *P. brasiliense*, sequence, dan kekerabatan LTTR pada *P. brasiliense* dan ortolognya dari Enterobacteriales dengan menggunakan analisis filogenetik serta multiple sequence alignment (MSA). Efek madu manuka terhadap ekspresi LTTR diamati menggunakan PCR semi-kuantitatif dan quantitative real time polymerase chain reaction (qRT-PCR). Hasil penelitian menunjukkan isolat *P. brasiliense* yang dinokulasikan menimbulkan gejala pada tanaman tomat, terong, cabai, tembakau, sawi sendok, kubis bunga, kaktus, seledri, dan bawang merah, namun tidak memicu gejala pada padi, jagung, dan pisang. Gen regulator IlvY, KS44_01725, KS44_07475 pada *P. brasiliense* memiliki kekerabatan paling dekat dengan *P. polaris*, BenM berkerabat dekat dengan *P. versatile*, sedangkan gen regulator HdfR dan LrhA berkerabat paling dekat dengan *P. carotovorum*. Analisis ekspresi LTTR yaitu benM, ilvY, KS44_01725, dan KS44_07475 dari *P. brasiliense* menunjukkan penurunan ekspresi 39%, 50%, 85%, dan 97% secara berurutan, sedangkan LrhA dan hdfR menunjukkan peningkatan ekspresi sebesar 26% dan 4% dalam perlakuan madu manuka 5% (w/v).

Kata kunci: LTTR, madu manuka, *Pectobacterium brasiliense*, q-PCR

ABSTRACT

Disease control using chemical substances can pose risks to human health and the environment, and it may also lead to resistance. Manuka honey contains antimicrobial compounds that have the potential to address antimicrobial resistance issues. Manuka honey is known to reduce the expression of virulence genes and universal stress protein (*usp*) genes in *P. brasiliense*. The LysR-type transcriptional regulator (LTTR) is the largest transcriptional regulator in prokaryotes, but the effect of manuka honey on LTTR from *P. brasiliense* has not yet been studied. This research aims to determine the host range of *P. brasiliense*, the sequence, and the relationship of LTTR in *P. brasiliense* and its orthologs from Enterobacteriales using phylogenetic analysis and multiple sequence alignment (MSA). The effects of manuka honey on LTTR expression were observed using semi-quantitative PCR and quantitative real-time polymerase chain reaction (qRT-PCR). The results show that the inoculated *P. brasiliense* isolates caused symptoms in tomato, eggplant, chili, tobacco, mustard, cauliflower, cactus, celery, and shallots, but did not induce symptoms in rice, corn, and bananas. The regulatory genes *IlvY*, *KS44_01725*, and *KS44_07475* in *P. brasiliense* were most closely related to *P. polaris*, while *BenM* was closely related to *P. versatile*, and the regulatory genes *HdfR* and *LrhA* were most closely related to *P. carotovorum*. The expression analysis of LTTRs, namely *benM*, *ilvY*, *KS44_01725*, and *KS44_07475* from *P. brasiliense*, showed a reduction in expression by 39%, 50%, 85%, and 97%, respectively, while *LrhA* and *hdfR* showed an increase in expression of 26% and 4% under the treatment with 5% (w/v) manuka honey.

Keywords: LTTR, manuka honey, *Pectobacterium brasiliense*, q-PCR