INTISARI

ISOLASI DAN IDENTIFIKASI BAKTERI PENGHASIL ACC DEAMINASE DARI PERTANAMAN JAGUNG DAN KACANG-KACANGAN YANG TERCEKAM SALINITAS

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Bakteri penghasil ACC deaminase dapat mengurangi produksi etilen berlebih yang dihasilkan oleh tanaman tercekam karena ACC deaminase dapat memotong substrat ACC menjadi amonium dan α-ketobutirat. Penelitian ini bertujuan untuk mendapatkan bakteri endofitik dan rhizosferik penghasil ACC deaminase dari pertanaman jagung, kacang tolo dan kacang tanah yang tercekam salinitas, serta mengidentifikasi isolat terpilih. Isolasi dilakukan menggunakan metode *surface plating* pada medium NA. Seleksi isolat dilakukan secara kualitatif menggunakan medium DF+AIB, dan secara kuantitatif dengan pengukuran aktivitas enzim ACC deaminase. Identifikasi dilakukan melalui pengamatan morfologi dan sekuen gen 16S rRNA. Pada penelitian ini diperoleh isolat AJG3, RJG6, ATL5, dan RTN10 yang berturut-turut memiliki aktivitas spesifik enzim ACC deaminase sebesar 693, 617, 504, dan 185 nmol α-ketobutirat/mg/jam. Isolat AJG3, RJG6, dan ATL5 merupakan bakteri gram negatif, sedangkan RTN10 merupakan bakteri gram positif. Isolat AJG3, RJG6, ATL5, dan RTN10 berturut-turut teridentifikasi memiliki kemiripan tertinggi dengan spesies *Klebsiella variicola, Rhizobium pusense*, *Agrobacterium tumefaciens*, dan *Bacillus stratosphericus.*

Kata kunci : ACC deaminase, bakteri, gen 16S rRNA, identifikasi, salinitas

ABSTRACT

ISOLATION AND IDENTIFICATION OF ACC DEAMINASE PRODUCING BACTERIA FROM RHIZOSFER AND PLANT ROOTS OF MAIZE, COWPEA, AND GROUNDNUT GROWING UNDER SALINE STRESS

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ACC deaminase producing bacteria reduces the excess ethylene produced by stressed plant because ACC deaminase catalyzes the cleavage of ACC into ammonium and α-ketobutyrate. ACC deaminase is produced by several rhizospheric and endophytic bacteria. This study was aimed to obtain ACC deaminase producing bacteria isolated from rhizosfer and plant roots of maize, cowpea, and groundnut growing under saline stress. Isolation was conducted by surface plating on NA medium. Qualitative selection was based on the growth of isolate on DF + AIB medium, quantitative selection based on ACC deaminase activity assay. Identification of the isolates was carried out by morphologycally and sequencing of 16S rRNA gene. Isolation and selection resulted 4 bacterial isolates (AJG3, RJG6, ATL5, and RTN10). Those bacterial isolates have the ACC deaminase activity beetwen 184,65 to 692,54 nmol α-ketobutyrate. mg^{-1}. h^{-1}. AJG3, RJG6, and ATL5 isolates were gram negative bacteria, only one isolate was gram positive bacteria (RTN10). Based on 16S rRNA gene sequence, AJG3, RJG6, ATL5, and RTN10 isolates have a high similarity with *Klebsiella variicola, Rhizobium pusense, Agrobacterium tumefaciens*, and *Bacillus stratosphericus* respectively.

Keyword : ACC deaminase, bacteria, 16S rRNA gene, identification, and salinity