

**Diversity of *Ralstonia syzygii* subsp. *celebesensis*
and Response of Banana Harboring *Bacillus* sp. Endophyte Against Pathogen Infection**

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Abstract

Blood disease of banana caused by *Ralstonia syzygii* subsp. *celebesensis* (Rsc) in Indonesia was a highly destructive disease. Information on Rsc such as distribution, genetic diversity, genomic profile, and plant-pathogen interaction was not broadly explored recently. This research was conducted to provide information about Rsc distribution, diversity, gene profile, RNA profile, and plant-pathogen interaction. The sample collection, screen house experiment, and laboratory experiment in the Faculty of Agriculture, Universitas Gadjah Mada were conducted from 2018-2022. The study consisted of 5 chapters, literature study, Rsc sample collection, Rsc diversity analysis, whole genome sequence analysis, and transcriptomic analysis of the plant-pathogen. The result revealed the Rsc occurred with various cultivars of banana like Kepok (ABB-genome), cavendish (AAA-genome), Batu (BB-genome), and also Abacca with the common host of the Rsc was Kepok with 90s samples confirmed from various locations. The Rsc differed based on UPGMA analysis with isolate from Kalimantan and Sumatera being the most different compared to another isolate. In the phylogeny analysis, all the isolates were grouped with all Rsc isolates from the genebank. The Rsc UGMSS_Db01 has 5,185,188bp of the genome including 3.568.564bp of Chromosome (92x G. Cov) and 1.614.128bp of Plasmid (102x G. Cov) with 66,5% GC content. The comparison between BDB A2-HR Mardi is close to just 99,98% of chromosome and 99,95% of plasmid based on orthoANI, but the length of the genome was different implicating the number of the genes, coding seq, and tRNA in different numbers also. The transcriptomic analysis provides the list of the genes related to the resistant and plant growth-promoting genes in the banana plant and virulence factor in Rsc. More specifically, Ma01_t19160.1 and Mat14510.1 were up-regulated in the banana plant, and Ma02_t07220.1 and Ma06_t14360.1 were down-regulated. For Rsc the expression of the genes was very varied but in the end addition of ABB and BB host extract induced expression of the virulence-related genes. All the results will provide an understanding of the Rsc and as basic information to develop the next study and disease management to suppress loss caused by this pathogen.

Keywords: blood disease of banana, banana, genomic, *Ralstonia syzygii* subsp. *celebesensis*, transcriptomic

**Keanekaragaman *Ralstonia syzygii* subsp. *celebesensis*
dan Respon terhadap Pisang berbakteri *Bacillus* sp. Endofit Terhadap Infeksi Patogen**

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Abstrak

Penyakit darah pada pisang yang disebabkan oleh *Ralstonia syzygii* subsp. *celebesensis* (Rsc) di Indonesia merupakan penyakit yang sangat merusak. Informasi tentang Rsc seperti distribusi, keragaman genetik, profil genom, dan interaksi patogen tanaman belum dieksplorasi secara luas. Penelitian ini dilakukan untuk memberikan informasi tentang distribusi Rsc , keanekaragaman, profil gen, profil RNA, dan interaksi patogen tanaman. Pengambilan sampel, percobaan rumah kaca, dan percobaan laboratorium di Fakultas Pertanian Universitas Gadjah Mada dilakukan pada tahun 2018-2022. Penelitian terdiri dari 5 bab, yaitu studi literatur, pengumpulan sampel Rsc , analisis keanekaragaman Rsc , analisis sekuens genom utuh, dan analisis transkriptomik patogen tumbuhan. Hasilnya menunjukkan Rsc terdapat pada berbagai kultivar pisang seperti Kepok (genom ABB), cavendish (genom AAA), Batu (genom BB), dan juga Abacca dengan inang umum Rsc adalah Kepok dengan sampel berjumlah 90an yang berasal dari berbagai lokasi. Keragaman Rsc terlihat berdasarkan analisis UPGMA dengan isolat Kalimantan dan Sumatera paling berbeda dibandingkan isolat lainnya. Pada analisis filogeni, seluruh isolat mengelompok dengan seluruh isolat Rsc dari bank gen. Rsc UGMSS_Db01 memiliki 5.185.188bp genom termasuk 3.568.564bp Kromosom (92x G.Cov) dan 1.614.128bp Plasmid (102x G.Cov) dengan konten GC 66,5%. Perbandingan antara BDB A2-HR Mardi adalah 99,98% kromosom dan 99,95% plasmid berdasarkan orthoANI, namun panjang genom berbeda yang berimplikasi pada jumlah gen, urutan pengkodean, dan jumlah tRNA yang berbeda juga. Analisis transkriptomik memberikan daftar gen yang terkait dengan gen tahan dan pemacu pertumbuhan tanaman pada tanaman pisang dan faktor virulensi di Rsc. Lebih khusus lagi, Ma01_t19160.1 dan Mat14510.1 terekspresi lebih pada tanaman pisang, dan Ma02_t07220.1 dan Ma06_t14360.1 terjadi penekanan ekspresi gen. Untuk Rsc, ekspresi gennya sangat bervariasi tetapi pada akhirnya penambahan ekstrak inang ABB dan BB menginduksi ekspresi gen terkait virulensi pada Rsc. Semua hasil tersebut akan memberikan pemahaman tentang Rsc dan sebagai informasi dasar untuk mengembangkan studi selanjutnya dan manajemen penyakit untuk menekan kerugian yang disebabkan oleh patogen ini.

Kata Kunci: penyakit darah pisang, pisang, genomik, *Ralstonia syzygii* subsp. *celebesensis* , transkriptomik