

Kajian Ketahanan Tanaman Padi Berpigmen (*Oryza sativa* L.) terhadap Penyakit Blas melalui Pendekatan Transkriptomik dan Metabolomik

Eggie Febrianto Ginanjar

13/356605/PMU/7965

INTISARI

Tujuan penelitian adalah mengetahui ekspresi gen *PBZI* dan *PRI* terkait ketahanan terhadap blas dan membandingkan profil metabolomik kultivar tanaman padi berpigmen tahan dengan rentan terhadap penyakit blas.

Penelitian diawali *non-choice bioassay* pada enam kultivar padi: Ireng Tinggi (CI), Ireng INDMIRA (IM), Abang Wangi (AW), Abang Tinggi (AT), Asahan (AS) dan Kencana Bali (KB) terhadap penyakit blas. Koleksi sampel daun dilakukan pada hari setelah inokulasi (HSI) ke-0, 3 dan 7 untuk analisis ekspresi gen *PBZI* dan *PRI* dengan RT-PCR. Analisis *PRI*, marker Systemic Acquired Resistance (SAR), dilanjutkan dengan qPCR untuk mengetahui level ekspresi gen. Analisis metabolomik dilakukan dengan NMR pada tanaman *mock* terpilih mewakili padi tahan, moderat tahan dan rentan. Data NMR diolah dengan M-NOVA dan dianalisis PCA untuk mengetahui perbedaan profil metabolitnya.

Hasil kultivar yang tahan: CI, AW, AT, AS, moderat tahan: IM, dan rentan: KB. Ekspresi gen *PBZI* dan *PRI* ditemukan pada semua kultivar padi perlakuan. Gen *PBZI* mulai terdeteksi pada HSI-0 untuk kultivar tahan, sedangkan kultivar rentan HSI-3. Ekspresi *PRI* terdeteksi pada semua hari perlakuan. Hasil qPCR menunjukkan level ekspresi gen *PRI* tertinggi dimulai pada HSI-3 pada kultivar CI dan AW. Hasil analisis metabolomik, kultivar rentan berada di kuadran positif, terpisah dari kultivar lainnya dengan variansi 53,46%, kultivar moderat tahan mengelompok ditengah, dan kultivar tahan pada kuadran negatif dari komponen utama 1. Metabolit kultivar tahan didominasi oleh senyawa fumarat, tirosin, dan fenilalanin.

Ekspresi gen *PBZI* dan *PRI* pada kultivar tahan tereksresi lebih cepat dibandingkan kultivar rentan. Profil metabolomik kultivar tahan memiliki hubungan erat dengan SAR melalui jalur sikimat.

Kata kunci: Padi berpigmen, blas, SAR, transkriptomik, metabolomik

Transcriptomics and Metabolomics Study of Pigmented Rice (*Oryza sativa* L.) Resistant to Blast Disease

Eggie Febrianto Ginanjar
13/356605/PMU/7965

Abstract

This research aimed to reveal the expression of *PBZI* and *PRI*, and compare metabolomic profile between pigmented rice resistant to blast disease with susceptible one.

Firstly, non-choice bioassay of six cultivars was performed on Ireng Tinggi (CI), Ireng INDMIRA (IM), Abang Wangi (AW), Abang Tinggi (AT), Asahan (AS) and Kencana Bali (KB) against blast disease. The leaves were collected at 0, 3, and 7 days post-inoculation. Samples were subjected for RT-PCR to evaluate the expression gen of *PBZI* and *PRI*. The *PRI* analysis was continued by qPCR. Metabolomics analysis was conducted by NMR on selected *mock* cultivars. NMR data was processed by M-NOVA and PCA to determine metabolites responsible to the resistant character.

The resistant cultivars were CI, AW, AT and AS, and moderate resistance cultivars IM, while susceptible cultivar KB. The *PBZI* and *PRI* were expressed on all cultivars and *PBZI* was induced faster in resistant cultivar than susceptible. *PRI* was detected in all samples. qPCR analysis showed the highest level of gene expression for *PRI* started on 3rd day in CI and AW. Metabolomics analysis indicated that susceptible cultivar placed separated from others cultivars with 53.46% variance. The moderate resistant cultivar clustered in the middle, and resistant cultivars were in negative quadrant of the PC 1.

It can be concluded that *PBZI* and *PRI* were expressed in both resistant and susceptible cultivars, but the resistants were induced earlier than susceptible rice in pathogenesis situation. Metabolomic profile of resistant-pigmented rice showed a closely related metabolite for SAR mechanism.

Keywords: pigmented rice, blas, SAR, transcriptomics, metabolomics