RINGKASAN

Kelapa sawit merupakan salah satu komoditas perkebunan yang strategis di Indonesia. Tahun 2016, produksi minyak sawit menurun sebesar 0,16% dari tahun sebelumnya. Salah satu faktor penting yang menyebabkan penurunan hasil adalah penyakit busuk pangkal batang (BPB) yang mengakibatkan kerugian besar pada produksi tandan buah segar yang dikarenakan berkurangnya jumlah tanaman kelapa sawit di perkebunan. Penyakit ini disebabkan oleh *Ganoderma boninense* yang menginfeksi akar tanaman kelapa sawit. Saat ini, cendawan tersebut tidak hanya menyerang pertanaman kelapa sawit yang tua tetapi juga yang muda, sehingga semakin berbahaya untuk perkebunan kelapa sawit.

Pendekatan bioteknologi modern seperti analisis ekspresi gen yang terkait *G. boninense* digunakan untuk mempelajari mekanisme molekuler dari respon tanaman terhadap infeksi patogen, pengaruh biologis dan biosintesis hormon. Gen yang terkait dengan mekanisme molekuler tersebut, yaitu *MDIS1-interacting receptor like kinase 1-like* (*MIK1*), *Wall-associated receptor kinase 5-like* (*WAKL5*), *Cytosolic sulfotransferase 12-like isoform XI* (*SOT12*), *1-aminocycloporane-1-carboxylate oxidase* (*ACO1*), dan *Glutathione S-transferase U19-like* (*GSTU19*). Metode *Real-Time quantitative Polymerase Chain Reaction* (RT-qPCR) digunakan untuk studi ekspresi gen karena memiliki kepekaan yang tinggi, efisien dan *reliable*. Metode ini digunakan untuk memperkirakan tingkat transkrip gen (mRNA). Penelitian ini bertujuan untuk mengetahui tingkat ekspresi gen putatif spesifik pada tanaman kelapa sawit hasil persilangan yang diduga rentan dan moderat tahan terhadap *G. boninense.*

Dua genotipe tanaman kelapa sawit rentan dan satu genotipe tanaman kelapa sawit moderat tahan terhadap *G. boninense* dari hasil persilangan dilakukan pengujian kuantitatif menggunakan lima primer yang mengkode gen putatif yang diduga berhubungan dengan penyakit busuk pangkal batang. Gen putatif tersebut, yaitu *EgMIK1*, *EgWAKL5*, *EgSOT12*, *EgACO1*, dan *EgGSTU19*. Gen *housekeeping EgActin* digunakan sebagai gen referensi pada kontrol internal proses *real-time* qPCR. Variabel yang diamati terdiri atas *amplification plot*, *melting curve*, ekspresi basal dan nilai rasio ekspresi. Hasil penelitian menunjukkan bahwa lima gen putatif diregulasi secara berbeda antara genotipe tanaman kelapa sawit A09, 23 dan 27. Ekspresi gen putatif dibandingkan antara genotipe tanaman kelapa sawit yang rentan (A09 dan 23) dan moderat tahan (27). Tiga gen putatif *up-regulated EgACO1*, *EgSOT12* dan *EgWAKL5* pada akar dapat dipertimbangkan sebagai biomarker positif yang potensial untuk tanaman kelapa sawit yang rentan. Hasil menunjukkan perbedaan regulasi molekuler antara tanaman kelapa sawit yang rentan dan moderat tahan terhadap *G. boninense.*

Kata kunci: Kelapa sawit, *Ganoderma boninense*, *real-time* qPCR, ekspresi gen

SUMMARY

Oil palm is one of the most strategic plantation commodity in Indonesia. In 2016, oil palm production decreased around 0,16% from the previous year. One of the critical factor that induced the declining of the yield is basal stem rot (BSR) disease that caused high loss of the production of the fresh fruit bunch caused by decreasing of a number of the oil palm trees in the plantation. The disease was affected by Ganderma boninense that infected on root oil palm plants. Now, this fungus not particularly attacked mature oil palm trees but also the juvenile in the nursery, it makes them an extremely serious problem in the oil palm plantation.

Modern biotechnology approach such as genes expression that related to G. boninense is used to study molecular mechanism of plants responses to pathogen, biological influence and hormone biosynthesis. The genes associated with molecular mechanism were MDIS1-interacting receptor like kinase 1-like (*MIK1*), *Wall-associated receptor kinase 5-like* (*WAKL5*), *Cytosolic sulfotransferase 12-like isoform XI* (*SOT12*), *1-aminocycloporane-1-carboxylate oxidase* (*ACO1*), dan *Glutathione S-transferase U19-like* (*GSTU19*). *Real-Time quantitaive Polymerase Chain Reaction (RT-qPCR) method was used to study genes expression because this method has a higher sensitivity, efficient and reliable. This method was used to estimate of transcript gene level (mRNA). This research aimed to determine the expression level of specific putative genes in oil palms from crosses that are susceptible and moderate resistance while attacked by G. boninense.*

Two susceptible and one moderate resistance oil palm genotype to G. boninense from crosses were by quantitative assays using five primers allegedly encoded putative genes related to basal stem rot disease. The putative genes were EgMIK1, EgWAKL5, EgSOT12, EgACO1, and EgGSTU19. A housekeeping gene like EgActin used as a reference gene in internal control of a real-time qPCR process. The observed parameters consisted of the amplification plot, melting curve, basal expression and expression ratio value. The result showed that five putative genes were differentially regulated between A09, 23 and 27 oil palm genotype. The expression of these putative genes was compared between susceptible (A09 and 23) and moderate resistance (27) oil palm genotype. Three up-regulated putative genes EgACO1, EgSOT12 and EgWAKL5 in root can be considered as potential positive biomarkers for susceptible oil palm. The results suggested distinct molecular regulation between susceptible and moderate resistance oil palm to G. boninense.

Keywords: Oil palm, Ganoderma boninense, real-time qPCR, gene expression