

First identification of ganoderma boninense isolated from Sabah based on PCR and sequence homology

Abstract

Basal stem rot (BSR) of oil palm (*Elaeis guineensis*) is caused by *Ganoderma boninense*, and, commercially, is one of the most devastating diseases in South East Asia. Losses of more than 80% of stands by the time they are halfway through their normal economic life have been reported. High incidence of BSR results in economic losses due to zero yields from dead palms and significantly reduced weight and number of fruit bunches in infected but living palms. Due to the importance of oil palm industry to Malaysia's economy, the transfer of any materials that are related to *Ganoderma* is strictly prohibited from Peninsular Malaysia to Sabah and Sarawak. No basic identification method using molecular techniques for the identification of *G. boninense* exist in this study for *G. boninense* isolates from Sabah. The only report on this pathogens isolate in Sabah was based on their morphology and pathogenicity. In conjunction with the morphological similarities among the different isolates, there are numerous opinions on the aggressiveness of the pathogen in Sabah. The isolates of *G. boninense* from Sabah were claimed to be less aggressive compared to those from Peninsular Malaysia. This may be due to lower incidence of BSR in Sabah and Sarawak compared to Peninsular Malaysia. Since the oil palm industry is a fast income-generating tool, data related to it may be highly sensitive. Researchers, plantation managers and entrepreneurs are not forthcoming with the information on oil palm genetic materials or isolates of *G. boninense* with others. The current speculations on the Sabah isolates need further investigation. In this study, we report the identity of isolates *Ganoderma* from Langkon Oil Palm Estate in Sabah, Malaysia. The identity of these isolates was confirmed using DNA sequence analysis after PCR amplification. The latter method shows that the Sabah isolates were very similar to aggressive *G. boninense* strains FA5017 or FA5035 from West Malaysia, with a maximum similarity of 98%.