



Development of diagnostic methods for detection of basal stem rot disease in oil palm in Colombia

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Abstract

Basal stem rot (BSR) of oil palm is the main constraint of the crop in South East Asia. The disease has been associated with several species of the genera *Ganoderma*. In Malaysia and Indonesia, the largest palm oil producers worldwide, it is responsible of big losses due to death of infected palms. In Colombia, BSR has been reported in 3 of the 4 producer regions, and although no official data are available, plantations reported the death of hundreds of palms in affected areas. Therefore, avoiding the dispersion of BSR in the country is one of the major concerns of oil palm industry. The aim of this work was to develop identification and diagnostic methods that could contribute to the timely management of the disease. Using molecular techniques, the identity of collected basidiocarps was confirmed as *Ganoderma* sp. based on the ITS region sequencing. Phylogenetic analysis of the sequences showed that basidiocarps collected in the Northern region are closely related with a new species of *Ganoderma* associated with BSR in Cameroon, while basidiocarps collected in Central region are related with other species of *Ganoderma* that have not previously been associated with BSR. Two approaches were evaluated for BSR diagnostics, using *Ganoderma* basidiocarps, roots and cross-section tissue samples from affected and healthy palms, collected in two regions. The first approach consisted in the analysis of ergosterol using HPLC, a chemical marker used for detection of these fungi. Basidiocarps showed a high concentration of ergosterol of 2300 $\mu\text{g g}^{-1}$. Roots from infected palms presented higher amounts of ergosterol (128 $\mu\text{g g}^{-1}$) compare to those from healthy palms (3 $\mu\text{g g}^{-1}$). The other approach was based on the Real Time-Polymerase chain reaction. Two sets of primers and hybridization probes were designed based upon the ITS sequences from basidiocarps samples and sequences available in gene database. Both specie-specific sets were tested in real time PCR assays and one of them showed a specific amplification in samples from affected palms. These results showed that both methods could be potentially used as a routinely diagnostic method of detection of BSR disease.