ABSTRACT

In this research, the effects of low temperature (LT) on 5 varieties of Thai rice, namely Supanburee1, KDML105, SPTC80182, SMGC02002 and Numroo, were determined on physiological changes, metabolite accumulation and gene expression.

Comparing with the controls, LT-treated seedlings of 3 rice varieties (SPTC80182, SMGC02002 and Numroo) exhibited the fewer extents of reduced relative growth rates and depleted chlorophyll contents than seedlings of Supanburee1 and KDML105 varieties. Moreover, the significant increase in the contents of malonaldehyde, a product of lipid peroxidation, was observed in seedlings of Supanburee1 and KDML105. The presence of malonaldehyde content implied the accumulation of reactive oxygen species that caused damages to membrane lipids. Thus, these rice varieties could be separated into LT-tolerant group (SPTC80182, SMGC02002 and Numroo) and LT-sensitive group (Supanburee1 and KDML105).

The changes in contents of some stress-related metabolites as well as antioxidative ability of plant extracts from both rice groups were investigated. It was found that LT significantly induced the accumulation of detected compatible solutes, i.e. soluble sugars and proline, in LT-sensitive group. These rice groups exhibited differential responses in polyamine accumulation when exposed to LT. While the most increased polyamine in LT-tolerant varieties was putrescine, that in LT-sensitive varieties was spermidine. The study of free radical-scavenging activities demonstrated that the significant increase in antioxidative ability in LT-tolerant varieties, but not in LT-sensitive rice plants. However, the correlation between LT tolerance and changes in flavonoid contents was unclear. In the presence of LT, the decrease in anthocyanin and the increase in flavonol and flavone levels were observed in only 2 LT-tolerant varieties,
namely SPTC80182 and SMGC02002. By contrast, the opposite responsive pattern was presented in all sensitive varieties as well as Numroo, the other LT-tolerant rice.

The expression of genes from polyamine biosynthetic pathway encoding spermidine synthase (SPDS) and S-adenosyl methionine decarboxylase (OsSAMDC and SAMDC) was analyzed using RT-PCR. The results showed that correlation between spermidine contents and the overall transcript levels of the detected genes was observed in LT-sensitive rice but not in LT-tolerant rice.