

CHAPTER I

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important cereal crops and edible medicinal plants (Lim 2012). Rice can be grouped into colored and white rice according to the pericarp color. Colored rice grains possess colored pericarps ranging from red to dark purple whereas the pericarp of white rice is pale (Deng et al. 2013). Rice grains have been consumed as a major food of more than half of the populations in the world. Most rice grains are mainly produced in Southeast Asia for the domestic consumption and worldwide exports. Rice grains and the other rice by-products such as brans, husks, and straws are important raw materials used in a diverse array of industries including foods, medicines, cosmetics, beverages, livestock and poultry (Lim 2012). Furthermore, rice grains and brans have also been consumed as functional foods or have been used as major ingredients for food supplement production.

Chemical compositions such as antioxidants, nutrients, and bioactive compounds have been investigated in both edible and inedible plant parts of rice. Unpolished rice or whole grains are nutritious diets and rich in natural antioxidants more than polished rice (Huang and Ng 2011). Rice bran is a mixture of germs and seed coats obtained from the milling process. This rice by-product has been found to be a rich source of bioactive phytochemicals such as vitamin E, γ -oryzanol, and γ -aminobutyric acid or GABA (Islam et al. 2011). Interestingly, phenolic acids including *p*-coumaric and ferulic acids have been found abundantly in seed husk (Butsat et al. 2009). The presence of phytochemicals in different parts of rice suggests that the

other parts of rice plants could be used as ingredients or phytochemical resources for the development of food supplements and functional foods.

The production of phytochemicals and nutrients in rice are controlled by gene functions. Additionally, special agronomic traits of the rice plants such as stress tolerance, disease resistance, and high yielding varieties are also regulated by genes involving different pathways (Pérez-Torres et al. 2009). The comprehension in the regulation and function of these genes is necessary for crop improvement. Promoter is a regulatory region that plays a crucial role in gene function and regulation. Constitutive, tissue-specific, and chemical-inducible promoters have been used for gene expression analysis in plants. Among them, chemical-inducible promoters can spatially and temporally regulate the expression of target genes. However, most of this promoters are derived from non-plant organisms (Padidam 2003). For example, an ethanol-inducible system is derived from fungus *Aspergillus nidulans* (Felenbok et al. 1988) which has a substantial genetic distance from plants. Therefore, the use of chemical-inducible promoters derived from plants to regulate target genes in model plants, including rice, is of interest. Moreover, rice is the most important model plant for functional genomic analysis of monocotyledons, especially cereal crops (Ohnishi et al. 2011). The genomes of cereals including rice, wheat, sorghum, maize, barley, and millet are highly conserved (Eckardt 2001), therefore knowledge of gene functions in rice could be widely applied for crop improvement programs of other cereals.

Thailand is one of the world leading rice producers and exporters (Lim 2012). Various rice cultivars have been distributed and cultivated throughout Thailand. A lot of value-added products are produced and developed from Thai rice including food

supplements and functional foods. However, only the famous colored rice cultivars, for examples, red rice Sang Yod Phatthalung or สิ้นข์หยดพัทลุง and black rice Kum Luem Pua or กำลิมบัว; have been used as ingredients in food supplement production. The chemical composition and bioactive compounds of rice differ among different cultivars (Fasahat et al. 2012; Kang et al. 2011), therefore the other Thai rice cultivars including colored and white rice may similarly possess a high content of nutrients, natural antioxidants, and bioactive compounds as those famous rice cultivars. Moreover, various Thai rice cultivars that have special agronomic traits could be used for the production of new hybrid rice lines. Functional genomic analysis of these specialty rice cultivars could provide more useful information for crop improvement programs. The use of chemical-inducible promoters including an ethanol-inducible promoter derived from rice itself may be suitable for gene expression studies rather than that derived from different organisms.

Thai rice germplasm could be used as genetic resources for functional genomic analysis. Thus, this study aimed to determine the effects of ethanol on the growth of rice plants and identify ethanol-inducible genes in young rice panicles from ethanol-treated rice plants. The 5' upstream region (UTR) of a highly conserved ethanol-inducible gene was isolated and analyzed for *cis*-acting regulatory elements. The information gained from this study provides an alternative way to regulate gene expression. In addition, this information could be useful for generating of transgenic cereal crop plants with desirable traits. Furthermore, the germplasm of Thai rice is an interesting resource for the screening and selection of antioxidant-rich rice cultivars. Therefore, this study also aimed to evaluate the antioxidant activity of juices squeezed from grasses harvested at the jointing stage for fourteen colored and white

Thai rice cultivars and wheat (*Triticum aestivum* L.). The total phenolic content and total monomeric anthocyanins that may be responsible for the antioxidant activity of rice grass juice were determined. The obtained information could be used for the development of new food supplement or functional food from various Thai rice cultivars. Moreover, the use of rice ethanol-inducible promoter accompanying with knowledge of antioxidant-rich Thai rice cultivar would be aid the development and production of new hybrid rice cultivars.

