Chapter 1

Introduction

1.1 Background

Rice is the most important food crop for the world's population. The world annual rice production has to be increased in order to meet a requirement of 764 million tonnes by 2025. At the current rate of population growth and per capita consumption in India alone, the rice requirement by 2020 would be about 135–140 million tonnes (Krishnaiah *et al.*, 2001). Rice is synonymous with food security in most parts of Asia which produces more than 91 percent of the global harvest. In Thailand, 2006, rice is planted annually about 67 million rai and produces average grain yield of 465 kilograms per rai (Office of Agriculture Economy, 2008) while neighboring countries produce higher. Successful development and utilization of hybrid rice in China has demonstrated that rice yield potential can be increased by commercial exploitation of heterosis. Hybrids have shown 15–20 percent higher yields than the best semi-dwarf inbred varieties, not only in China (Yuan, 1994; Yuan *et al.*, 1994) but also in some other countries (Virmani, 1994). Considering the potential of hybrid rice technology, there is an immediate need to employ newer and innovative techniques involving cytological, cytogenetical and biotechnological approaches to strengthen and reorientate the breeding approaches appropriately.

Recent progress in plant breeding researches indicated that significant shifts in the yield frontiers could be possible through hybrid rice. Many years of practice and experience have proved that three-line breeding, utilizing a cytoplasmic genic male sterility system (CMS), is an effective way to develop rice hybrids and will continue to play an important role in heterosis breeding. But this system has some constraints such as a yield plateau in rice hybrids, dependence on a CMS source, restriction on choice of male parents due to problems associated with fertility restoration and complex seed production procedures and high seed cost (Yuan, 1997). So that, a two-line system of hybrid breeding utilizing environment-sensitive genic male sterility (EGMS) is considered as an alternative to overcome the problems associated with three-line breeding and to exceed the yield plateau. For breeding of two-line hybrids under tropical conditions where day length differences are so marginal, thus, a temperature-sensitive genic male sterile (TGMS) system is considered more useful than the photoperiod-sensitive genic male sterile (PGMS) system (Virmani, 1996). After the identification of the TGMS mutant Annong S-1 (Tan *et al*. 1990), several TGMS lines have been developed in China, IRRI and elsewhere. For the successful exploitation of this novel male sterility system in heterosis breeding, more TGMS lines need to be developed and characterized for their sterile and fertile phases, critical stage and temperatures for fertility alteration. As well, studying the inheritance of TGMS will help breed the new TGMS lines with diverse genetic backgrounds.

The present investigation attempts to understand the genetic mechanisms of the expression of sterility/fertility through cytological evidence, especially while adopting the most promising two-line system to exploit heterosis in rice.

For breeding TGMS lines program, there are problems in selection TGMS lines since the TGMS trait is controlled by one recessive gene. This trait will not express in F_1 or BC_nF_1 but it will express in F_2 or BC_nF_2 generation. If using the traditional backcross method, two successive generations are needed to be grown. In addition, TGMS lines become fertile during the winter growing season. To overcome these problems, marker-assisted selection (MAS) is an useful procedure for short cut in selecting TGMS lines, since molecular markers are able to detect TGMS lines in F_1 or BC_nF_1 progenies.

1.2 Objectives

The study on the selection of thermo-sensitive genic male sterile line in rice using molecular marker has the following objectives:

1. To study inheritance of TGMS characteristic.
2. To study molecular marker for assisting selection of TGMS lines in backcross's progeny.
3. To transfer TGMS gene to Thai rice cultivars.