

CHAPTER 1

INTRODUCTION

Snow pea, *Pisum sativum* var. *saccharatum*, is one of the most important fresh pod food legumes worldwide. The increasing demand in this crop is due to a good source of protein for human nutrition. The amount of fresh frozen pea pod exported to Japan is as much as the amount of fresh consumption in Thailand (Export-Import Bank of Thailand, 2004). Snow pea is a major winter annual pulse crop which needs cool conditions, the optimum temperature is between 13-18°C, for good growth and seed development, so that the greatest yield and quality have been found in winter crop production in Thailand. In contrast, poor yield and quality are shown in the other production seasons, summer and rainy season (Khumpai *et al.*, 2001). The major areas of snow pea production are in the northern part of Thailand, especially in Chiang Mai, Chiang Rai and on the highland of Petchaboon and Tak Provinces. (Pongphal *et al.*, 2003)

The commercial snow pea cultivar which widely used by farmer, give high yield but is very susceptible to powdery mildew disease. Thus, the produce has been absent from the market even though the consumption demand is high. In order to meet the needs, snow pea pods including sugar snap pea, the second most imported vegetable, have been imported from China, from October 2010 to September 2011 the amount was 2,402.14 tons, valued of 25,211,700.56 Baht (Anonymous, 2011). In Thailand, generally, peas are not favorable to Thai farmers, due to intensive management and high investment. Snow pea is a determinate plant and the trellises are required to be supported. In addition, snow pea is very susceptible to disease,

starting from seedling stage until harvesting stage. All stages of snow pea are subjected to an array of serious fungal, bacterial and viral diseases that can devastate the crop. For the disease, powdery mildew which is caused by the obligate parasite *Erysiphe pisi*, an air-borne disease, is a serious disease of snow pea, reducing both yield and quality. The disease can cause 25-50% yield losses (Munjaj *et al.*, 1963), reducing the total biomass yield, number of pods per plant, number of seeds per pod, plant height and number of nodes (Gritton and Ebert, 1975)

In Thailand, powdery mildew is a common disease of snow pea, and it causes by the *Oidium sp.* (Wanasiri, 2007). It can cause severe damage in areas where pea is cultivated in every seasons. Thus, chemical control of the disease is needed, that extends to high cost of production. In addition, most Thai farmers do not have enough education for a safe application of pesticides. Today, breeders want to develop new snow pea lines that are resistant to the disease to reduce chemical use and costs (Keller *et al.*, 2000; Slusarenko *et al.*, 2002). The use of resistant varieties is the most efficient, economical and ecological strategies for controlling disease (Fondevilla *et al.*, 2007). To establish the resistant line, source of resistant germplasm is very important.

Conventional plant breeding differs considerably from natural selection. Over the centuries, this process has become more scientific, bringing major improvement in the yield, quality and diversity of agricultural and horticultural crops. It can generate a breeding population that is highly variable for traits that are agriculturally interesting. Selected parents are crossed to initiate gene recombination which combination of certain desired characteristics can occur, such as high yield and resistance to pests and diseases (Manshardt, 2004).

Backcross breeding has been an important tool for plant breeders for more than 80 years. The goal of most backcrossing programs is to improve a particular strain (recurrent parent) for specific characteristics, usually a single gene, obtained from a donor parent. In most backcrossing programs the objective is to recover the recurrent parent essentially unchanged except for the introgression of the new characteristics.

Genetic control of powdery mildew resistant trait is a single recessive gene, *erer*, on a specific locus (Sharma and Yadav, 2003). Thus, selfing generations from hybridization have to be created for gene segregation that causes breeding program to be delayed. To make the conventional breeding process more efficient and shorter, it is desirable to find genetic markers to be used as marker-assisted selection (MAS) strategy (Barone, 2007). Generally genetic marker can provide information on genotypes related to phenotype trait, *e.g.* height, color, response to pathogens. There are two types of genetic markers, phenotypic and genotypic markers. Expression of phenotypic markers depend at a particular time or under particular developmental or environmental conditions, whereas genotypic marker provide an almost unlimited supply of markers that identify specific sequences across the genome. The advantages are:

- 1) Single base changes in DNA can be identified, providing many potential marker sites across a genome,
- 2) Independent of developmental stage, environment or expression,
- 3) Markers can be found in non-coding or repetitive sequences.
- 4) Additional to that, molecular marker allows greater precision and more rapid incorporation of alleles into cultivars (Tracy, 2004).

5) Most DNA marker sequences are selectively neutral.

Using the molecular approaches to identify molecular markers, in combination with an appropriate mapping population of plants plus or minus the trait of interest, many markers have been identified which are closely linked to genes for agronomic traits of interest. These markers can be used for MAS (The British Society of Plant Breeders, 2010). They have been widely used to speed up the processes of crop improvement. Many types of molecular marker were used to identify the powdery mildew resistant gene (*er-1* and *er-2*), such as Janila and Sharma (2004) reported that three primers, OPU17, OPO02, and ScOPD10, could detect *er* gene linkage markers which discovered in Indian pea resistance. Tiwari *et al.* (1998) used AFLP marker for identified powdery mildew resistance gene *er-2* in pea.

In this study, three SCAR markers, namely OPU17, OPO02, and ScOPD10, which linked to powdery mildew (Janila and Sharma, 2004), was screened and used to identify resistant parent and backcrossed hybrid snow pea plants. To date, many published research were still not popular to use MAS to identify resistance of snow pea in Thailand. Therefore, in this study, MAS was used to find markers linked to powdery mildew resistance by using SCAR primer in PCR technique. Furthermore, MAS was used to confirm powdery mildew resistance in hybrids, which could support selection process of hybrids in snow pea breeding program.