1.0 INTRODUCTION

Rice is one of the most important staple foods in the world as over half of the world's population depends on rice in their diet. However, rice production in Malaysia is only able to generate about 73 % of the total rice consumed locally (MARDI, 2010). According to the International Rice Research Institution (2008), total world rice production is about 661 million tonnes while total rice production in Malaysia is only 2 million tonnes. However, an estimated 700 million tonnes are needed to feed an additional 650 million rice eaters by the year 2025 (Dawe *et al.*, 2000). Therefore, research is needed to improve and to increase rice yields in order to supply enough food for the growing world population.

Oryza sativa ssp. *indica* cv. MR219 and *Oryza rufipogon* (IRGC105491) have been crossed towards producing varieties with improved yield and yield-related traits in a current local rice breeding program. *Oryza sativa* ssp. *indica* cv. MR219 a Malaysian elite rice variety was selected as the recurrent parent. Its characteristics are high grain yield, short maturation period, major pest resistance and good eating quality (MARDI, 2002). *Oryza rufipogon* is a wild type rice species, indigenous to Malaysia. The choice of *Oryza rufipogon* as donor parent for the current breeding program was based on the fact that this species has a large proportion of the existing genetic variation for *Oryza* genus although it's phenotype is agronomically undesirable (Xiao *et al.*, 1998; Sabu *et al.*, 2006; McCouch *et al.*, 2007). This species has been used in other breeding programs to solve the problem of the narrowing of the gene pool of modern rice cultivars (Xiao *et al*., 1998; Sabu *et al*., 2006; McCouch *et al*., 2007). Therefore, *Oryza sativa* ssp. *indica* cv. MR219 and *Oryza rufipogon* are being used in order to develop a new rice variety with high yield production in the current Malaysian Breeding program (Sabu *et al*., 2006).

The leucine-rich repeat (LRR)-like type Receptor-Like Kinase (RLK) family was identified experimentally as a potential candidate contributing to yield increase in rice (He *et al*., 2006). Therefore, in this current study putative *Receptor-like Protein Kinase 1* (putative *RPK1*) and putative *CLAVATA1 Receptor-like Kinase* (putative *CLV1*) genes were selected for molecular characterization and expression analysis. It is possible to obtain further molecular insight through comparison gene expression profiling between different organs at different developmental stages in rice.

RNA interference (RNAi) is a phenomenon where small double-stranded RNA or small interference RNA (siRNA) can induce efficient sequence-specific silencing of gene expression (Vaucheret, 2006; Fire *et al*., 1998). In this study it was specifically aimed to decrease the expression of two candidate yield-related genes by RNAi knockdown in rice lines used in a local breeding program, to determine their impact on yield.

The objectives of this study were:

i. To isolate and identify full length complementary deoxyribonucleic acid (cDNA) of putative *RPK1* of *Oryza sativa* ssp. *indica* cv. MR219 and *Oryza rufipogon* (IRGC105491).

ii. To study expression of putative *RPK1* and putative *CLV1* between vegetative organs and rice panicles at different stages of donor parent *Oryza rufipogon* (IRGC105491), recurrent parent *Oryza sativa* ssp. *indica* cv. MR219, backcross progeny BC_2F_7 line 7 and backcross progeny BC_2F_7 line 23.

iii. To determine the gene copy numbers of putative *RPK1* and putative *CLV1* in parental plant *Oryza sativa* ssp. *indica* cv. MR219 and *Oryza rufipogon* *(*IRGC105491).

iv. To generate RNAi vectors in order to study knockdown of gene expression of putative *RPK1* and putative *CLV1* in rice.