

CHAPTER I

GENERAL INTRODUCTION

1.1 Rationale

Rice is the staple for about half of the world's population, and in almost every rice-growing country, aromatic rice features strongly. Most people recognise two major types of aromatic rice: basmati from India and Pakistan; and jasmine from Thailand because these are the most highly exported. However, the Genetic Resources Centre (GRC) at IRRI has both glutinous and non-glutinous accessions of traditional varieties of aromatic rice from almost every rice-growing country in the world.

The staple food in the Lao PDR is glutinous rice, and the favoured of these are the aromatic rices, in particular, Hom Nang Nouane (HNN) and Kai Noy Leuang (KNL). In the Lao PDR, the aromatic rices are traditional, and this is often characterised by low-yields. The rice improvement programs of Lao need to understand the quality traits of these traditional varieties to develop higher yielding glutinous varieties with the excellent quality of the traditional aromatic varieties. Development of such varieties could lead to export opportunities and have significant economic and social impact, especially for Lao rice farmers.

Fragrance, an important quality trait in Lao, is due to the presence of the volatile compound 2-acetyl 1-pyrroline (2AP) (Buttery et al., 1982). In most varieties, 2AP accumulates because of mutations in the betaine aldehyde dehydrogenase (BADH2) gene on exon 7 (Bradbury et al., 2005a). So far, ten mutations have been found, all leading to the production of 2AP, but no mutation was found in two highly fragrant Lao varieties KNL and Khau Tan Luong (KTL) (Fitzgerald et al., 2008; Kovach et al., 2009). One of the objectives of this study is to identify and characterise the genetic basis of aroma in KNL by developing several mapping populations to find the gene and to test the quality of the aroma.

KNL and HNN are popular varieties in Lao PDR, and consumers can readily tell the difference in aroma and taste between the two. Studies show that different varieties of rice differ in taste and flavour (Champagne et al., 2010), but data from

sensory panels has not been developed for quality evaluation programs, perhaps because the compounds conferring the taste have not been identified. Taste and flavour involves compounds detected by the nose and by the mouth. Metabolomic profiling is a new science that is able to detect small compounds of different chemical nature. Many of these compounds have not been detected and databases of compounds are being newly populated (Hall, 2006; Hall et al., 2002; Hall et al., 2008). A new project, bringing together different capabilities in metabolomic profiling of plants (Hall, 2007) will collaborate with the present study to analyse the primary and secondary polar metabolites and volatile metabolites in the two aromatic varieties from the Lao PDR, and a high-yielding non-aromatic variety that will be selected in the first experiment. The non-aromatic high-yielding variety will be chosen to be the parent in mapping populations that will be developed. The compounds will be analysed to find those that are unique to each variety and those which could contribute to the flavour profiles of each.

Developing mapping populations to appropriate levels of genetic purity takes many generations of backcrossing with the recurrent parent. The previous decade has witnessed an exponential development in characterising the rice genome (Garris et al., 2005; Kovach et al., 2009; McCouch and CGSNL, 2008; Xu et al., 2005; Zhao et al., 2010) and developing that knowledge into genotyping tools for rice improvement (Thomson et al., In preparation; Wright et al., 2010). In this project, single nucleotide polymorphisms will be determined at 384 loci to select the lines from the mapping populations with the donor allele of interest (the fragrance locus) and backgrounds with the highest proportion of recurrent parent genome.

1.2 The specific objectives of this study

- 1) Determine the best improved variety to be the agronomically adapted background for mapping populations.
- 2) Develop mapping populations to find the compounds in the pathway of aroma.
- 3) Determine the compounds in the grains of each that distinguish the varieties and that contribute to unique metabolomic profiles and taste/flavour profiles.
- 4) Attempt to identify the biochemical pathway leading to 2AP.

5) Identify the genetic basis of aroma in KNL and characterise the properties of aroma in this variety.

1.3 Scope of the study

1) Study on the effect of N on yield and grain aroma; and metabolites in the grains of HNN, KNN and TSN1 that lead to unique flavours for each.

2) Using metabolomic profiling to investigate the compounds involved in the pathways to 2AP from developed population.

3) Using genome-wide SNP genotyping to select the purest Near Isogenic Lines (NILs) at BC₄F₂, and use these to identify the biochemical and genetic basis of aroma in KNL.

1.4 Expected outputs

1) Knowledge of N effects on yield components, fragrance, and metabolites in aromatic and non-aromatic and improved varieties.

2) Knowledge of compounds involved in the pathways to 2AP.

3) Candidate genes that are responsible for aroma.

4) Markers for genes of aroma.

5) Publications in international journals.