

CHAPTER VIII

CONCLUSION AND RECOMMENDATIONS

8.1 Selecting the parents

In this study, TSN 1 is selected to be the agronomically adapted parent because of its high response to N treatment. However, TDK 1 also showed a similar response to N treatment, but TDK 1 gave reproducibly lower milling percentage than TSN 1. To combine the quality of KNL or HNN with the yield of TSN 1, it is necessary to understand important quality traits and be able to select for them in a breeding program.

8.2 Characterising parents

In the past, all rice improvement programs select on the basis of quality, but the present study shows that classic quality evaluation data, obtained previously, does not discriminate between the genotypes. The tools of quality evaluation, developed for non-waxy rice, cannot discriminate between waxy types. However, KNL and HNN, using a large panel of Lao farmers, were investigated, and significant differences were found between the two varieties, indicating a need to understand the differences, in order to develop ways to screen for them in a quality evaluation program. Tools to measure taste and flavour are not routinely used in any rice quality program, but the science of metabolomic profiling is developing rapidly and offers new opportunities to begin to collect and test such data. In the present study, volatile and polar primary metabolites were targeted since these compounds are the ones most likely to be detected in the mouths and noses of rice consumers.

In this study, all platforms of metabolomic profiling indicate that compounds and minerals that discriminated between varieties, forming the unique metabolomic signatures, are compounds with nutritional value or are compounds that are likely to contribute to taste, flavour and aroma.

8.3 Population development using new generation tools

To develop introgression lines, as close to isogenic lines as possible, requires at least 6 generations of back-crossing to minimise background impurity. Genome wide SNP profiling enables the selection of relatively genetically pure introgression lines after only 4 generations of back-crossing. The major conclusions found by carrying out this SNP genotyping in the two BC₄F₂ populations are i) that introgression from the recurrent parent ranges significantly from very little to a significant amount across the progeny, and ii) much higher background introgression is seen in progeny derived from two indica parents than from one indica and one japonica parent. By utilising the genotyping, as well as phenotyping for the correct introgression, lines could be selected with minimal background introgression and the gene of interest. The lines, in order of genetic purity from 0.9% - 4.7% with the donor parent KNL, are 626, 557, 609, 664, 558, 631 and 629. For the HNN set, 5 introgression lines were selected for multiplication and further work based on genetic purity. These are line 116, 142, 266, 269 and 280. The selected lines, the first of their type in Laos, will provide a valuable resource for identifying variability at important loci governing farmer and consumer adoption. The selected BC₄F₂ lines from each of the HNN and the KNL set are to be multiplied and used to understand the genetics of fragrance in KNL, and complete the understanding of the genetic pathway of fragrance involving the *BADH2* gene.

8.4 Fragrance pathway Hom Nang Nouane lines

It is possible the pathways of 2AP in rice grains occurs as a fortuitous side-effect of polyamine catabolism, and the acetylation step occurs to enable the plant to maintain its ability to regulate polyamine concentration in the grains.

8.5 Identification of a novel allele of *Badh 2* in Lao traditional variety Kai Noy

Leuang

KNL contains high amount of 2AP compared to other Lao varieties, and the 2AP content does not decrease significantly upon storage.

Most aromatic varieties carry a 7 bp deletion in the *BADH2*, but in KNL and KTL, we found that there are 806bp deletion in the *BADH2* gene spanning across

exons 4 to 5, which induces a premature stop codon rendering the BADH2 enzyme non-functional. This is by far, the largest alteration of *BADH2* reported. It could also be considered as one of the rarest alleles of *BADH2* since among the 300 and 100 aromatic accessions previously, only 2 varieties have been found, KNL and KTL, that carry this allele. We will refer to the new allele as badh2.11. The quality of 2AP from badh2.11 has been shown to be higher than that of other alleles. It does not change over storage and the amount is greater. Therefore, the discovery of this allele could be very important for rice improvement programs, and the development of indica and japonica germplasm carrying this allele, as well as primers, is a valuable output of this study.