

**[11] Sequencing Analysis of Domestication-Related Genes of Rice Landraces Collected from Taiwan Aboriginal Villages**

**Dr. Yuan-ching TSAI**<sup>1\*</sup>

[botsai@gate.sinica.edu.tw](mailto:botsai@gate.sinica.edu.tw)

**Drs. Yi-fang CHEN<sup>1</sup>, Ming-hsing LAI<sup>2</sup>, Ai-ling HOUR<sup>3</sup>, Yu-chi CHEN<sup>4</sup>, Yu-chien TSENG<sup>4</sup>, Jaw-shu HSIEH<sup>4</sup>, and Yue-ie HSING<sup>1</sup>**

*1. Institute of Plant and Microbial Biology, Academia Sinica, Taipei, 11529, Taiwan*

*2. Crop Science division, Agricultural Research Institute, Taichung, 413, Taiwan*

*3. Department of Life Science, Fu-Jen Catholic University, Taipei, 24205, Taiwan*

*4. Department of Agronomy, National Taiwan University, Taipei, 10617, Taiwan*

Taiwan aboriginal peoples are thought to be the origin of Austronesians. Currently, there are 14 tribes of aboriginal people in Taiwan and they use different languages. The major crops in the aboriginal villages are rice (*Oryza sativa*) and foxtail millet (*Setaria italica*). Sixty rice landraces collected from Taiwan aboriginal villages about 100 years ago were used in this study. These rice landraces show large variation in phenotype, included grain size, plant size and architecture, aboveground biomass, heading habitat and drought tolerance etc. Several rice domestication-related genes have been cloned recently. For instances, *Gs3*, *qSW5*, and *GW2* are responsible for rice grain size, *Rc* (*qSD7-1*) gene controls both seed color and dormancy. In addition, several heading date genes (*Hd1*, *Hd3a*, *Hd6*, *SE5*, *Edh1* and *Edh2*) contribute to heading date. In this study, DNA sequences and Targeting Induced Local Lesions in Genomes (TILLING) analysis illustrate many DNA sequence variations in these domestication-related genes. These variations, including SNP, deletion and insertion, locate at promoters, UTRs, exons or introns. In addition, 52 SSR markers distributed on 12 chromosomes were used to evaluate the genetic diversity and phylogenetic relationship of these landraces. Several loci showed high PIC value and thus indicates that there are significant genetic variations among them. Together with the efforts from archeologists and linguists, we may understand the rice cultivation history of Taiwan and the nearby areas.