

分子生物学科・環境科学研究センター・ SUPER FORUM 共催セミナーのご案内

7月24日(金) 16:20～17:30 理学部3号館二階11番教室

Genetic diversity of foxtail millet (*Setaria italica*
(L.) Beauv.) germplasm and its relationship with
the indigenous groups in Taiwan

時間：16:20-17:30 (講演50分、質疑応答20分)

演者：Dr. Song-Bin Chang (台湾 国立成功大学)

問い合わせ先：
分子生物学科 西田 生郎





Dr. Song-Bin Chang

Assistant Professor,
Department of Life Sciences,
National Cheng Kung University, Tainan, Taiwan

Research interests:

Molecular cytogenetics
Genomics

Abstract

Foxtail millet (*Setaria italica*) can thrive in harsh conditions and is one of the important traditional crops for the indigenous people in Taiwan. However, the shift of diet to rice and less millet culture had led to species origins declined recently. To preserve this crop, the genetic diversity must be revealed, which is useful for germplasm conservation. Traditionally, species diversity was investigated by phenotypic traits. As the development of molecular markers, inspection of genotypic traits is widely used for this purpose. Microsatellite markers are considered to be one of the most powerful tools because of their abundance in the genome, co-dominant inheritance, high reproducibility, ease of manipulation, low requirement for genome DNA, and the speed of their use. Therefore, the objective of this study is to investigate the genetic diversity of foxtail millet by phenotypic and genotypic traits and to canvass the dispersal and distribution of the foxtail millets in Taiwan by microsatellite markers. Additionally, the correlation of the indigenous migration, cultural exchange and the genetic diversity of foxtail millets is also discussed.

Three hundred and twenty-four foxtail millet landraces collected from Taiwan and two out-group landraces came from mainland of China were used in this research. Thirty-three agronomic traits were examined and the data was operated using UPGMA analysis. All foxtail millets are divided into three clusters, which were mainly identified by some qualitative traits. As for the genotypic traits investigation, five hundred random primers were operated by RAPD-PCR to construct a small DNA fragments library. Then, short dinucleotide repeat sequence fragments were manipulated as primers by PCR. Among 3095 clones, 570 clones had shown positive results. After sequencing, 134 microsatellites were obtained and 86 primer pairs had showed polymorphic pattern by PCR testing. The most common dinucleotide and trinucleotide repeat motifs are AC/TG (72.09%) and ATG (19.77%), respectively. Genetic diversity and relationships in 324 foxtail millet landraces was then analyzed by 40 randomly selected primer pairs, which showed high level of average alleles per microsatellite locus, 2.4. The sum of the PIC value of these SSR loci were total 15.24, with an average of 0.381 per locus. The average observed heterozygosity (HObs) and average expected heterozygosity (HExp) were 0.190 and 0.354, respectively. By the result of deviation from Hardy-Weinberg equilibrium test, 87.5% microsatellite loci exhibit significant genetic diversity ($p < 0.05$). The results of UPGMA clustering analysis and principal component analysis (PCA) using microsatellites showed 324 foxtail millet landraces divided into three groups, which coincided with the geographic regions in Taiwan. Referring to the historical records, we demonstrated that the genetic diversity of foxtail millets in Taiwan had close relationships with the indigenous migration and cultural exchange.