

The Conservation and Utilization of Rice Germplasm Resources in China

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1. The conservation, evaluation, and utilization of rice germplasm resources in China

1) The conservation of rice germplasm resources

By 2017, a total of 84,935 rice accessions have been catalogued, regenerated and conserved in Chinese National Gene Bank. 92.35% of all are cultivated rice resources. Among them, *indica* and *japonica* rice are account for 63.25% and 36.75%; lowland and upland rice are account for 93.42% and 6.58%; non-glutinous and glutinous rice are account for 83.37% and 16.63%. The number of *indica*, lowland and non-glutinous rice is remarkably larger than that of *japonica*, upland and glutinous rice, respectively.

2) The evaluation of rice germplasm resources

The phenotypic traits are identified and evaluated, including morphoscopic features, biological characteristics, quality characteristics, stress, disease and insect resistance, etc. So far, more than 95% of rice accessions in gene bank have been identified and evaluated for morphoscopic and biological characteristics. Around 78 % of accessions have been identified and evaluated for resistance to rice blast and bacterial blight. Around 72 % of accessions have been identified and evaluated for resistance to rice BPH (brown plant hopper), and 56 % of accessions have been identified and evaluated for resistance to rice WBPH (white back plant hopper), respectively. 35 % of accessions have been identified and evaluated for drought, salt and cold tolerance. Around 43 % of accessions have been identified and evaluated for quality characteristics.

3) Sharing and utilization of rice germplasm resources

We have selected a number of elite rice accessions including which are insensitivity to temperature and light, disease resistant (rice blast, bacterial blight, sheath blight and false smut), and abiotic stress resistant (drought, salt, cold and heat), etc., by accurate and repeat identification. To provide these elite rice accessions to breeding, we conduct the exhibition of elite rice germplasm resources at regular intervals and provide more than 3000 accessions of rice germplasm resources to 40 to 50 breeding institutes, which make important contribution to effective utilization of rice germplasm resources and facilitate rice breeding and the development of seed industry.

2. The conservation of genetic diversity in rice landraces

1) Comparative genetic diversity within single-origin pairs of rice landraces

The genetic diversity of eight pairs of Yunnan rice landraces collected in 1980, and 2007, and 24 pairs of rice landraces (including fourteen pairs of Yunnan rice landraces, four pairs of Guizhou rice landraces and six pairs of Guangxi rice landraces) collected in 1980 and 2014 were studied using microsatellite markers. Each pair of rice landraces shares a name and origin and has similar seed and plant traits. For all pairs of rice landraces, compared to the population collected in 1980, the number of alleles, the number of rare alleles showed a significant increase in the populations collected in 2007 and 2014. For most pairs of rice landraces, compared to the population collected in 1980, Nei's genetic diversity index were higher in the populations collected in 2007 and 2014. AMOVA showed that except two pairs of rice landraces, the within-landrace genetic structure differed significantly between the two periods.

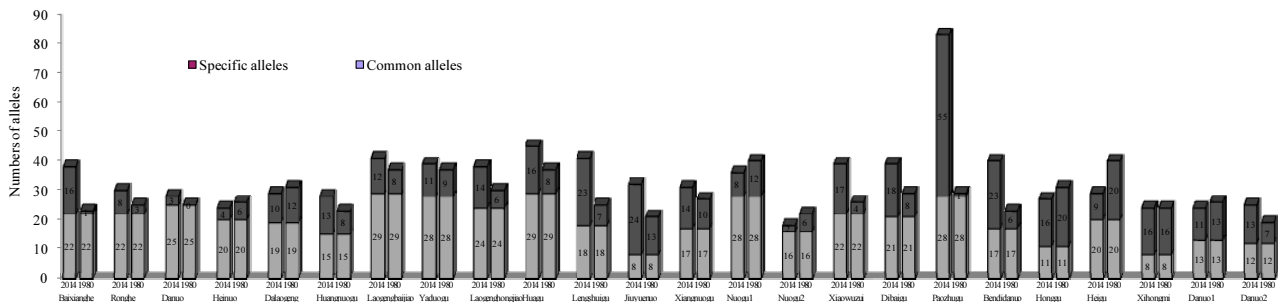


Fig. 1. Change in numbers of alleles between the same name rice landraces populations collected in different periods

2) Diachronic analysis of genetic diversity in rice landraces

We performed large-scale sampling of 600 rice accessions with high diversity, which were collected in 1980 and 2007, using 48 SSRs to study. Population structure revealed that the rice landraces both collected in 1980 and 2007 were clearly divided into *indica* and *japonica* group, and further divided into upland and lowland, non-glutinous and glutinous rice. The number of alleles, the number of effective alleles and PIC between rice landraces collected in 1980 and 2007 showed no significant difference, which indicated genetic diversity was successfully maintained under on-farm conservation.

We further analyzed using ten unlinked nuclear loci and found that the number of haplotypes and nucleotide diversity between rice landraces collected in 1980 and 2007 showed no significant difference for most of the gene loci, which also indicated genetic diversity was successfully maintained under on-farm conservation. We found rice landraces from EZIII (ecological zone III) had the richest diversity in both 1980 and 2007, and lost less haplotype richness than those grown in the other ecological zones, which could better maintain the genetic diversity.

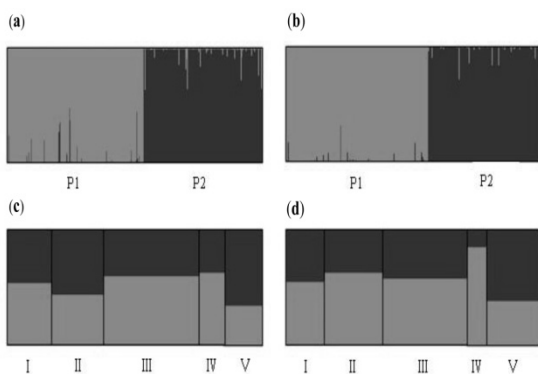


Fig. 2. Model-based ancestries and their distribution in ecological zones.

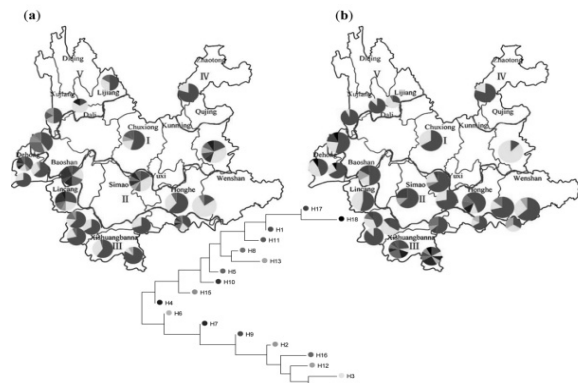


Fig. 3. A map showing the sampled populations of rice landraces and the distribution of haplotypes.

3. Selection imprints in on-farm conserved rice landraces during short-term domestication

We performed sequencing of 108 core on-farm conserved rice landraces (including 56 accessions collected in 1980 and 52 accessions collected in 2007) from the base collection (600 accessions), which can represent more than 97% of the primal genetic diversity in accordance with DNA information. Our findings showed most genetic diversity was retained during 27 years of domestication; however, large changes in allele frequency were found in some genome regions. We further found that SNPs with marked allele frequency differences between rice landraces collected in 1980 and 2007 were enriched for genic regions, which suggested changes in genic regions may have played a much more prominent role in short-term domestication than changes in intergenic regions. We identified 186 and 183 potential selective-sweep regions in *indica* and *japonica* genome, respectively and the regions relevant to agronomic important traits and biotic or abiotic stress were particularly targeted which showed signatures of parallel selection in both subspecies during short-term domestication. Our integrative analyses demonstrate that the rice landraces under on-farm conservation have the potential to be a dynamic, evolving genetic system that can undergo genetic changes in response to evolutionary pressures, both natural and those imposed by farmers. On-farm, in situ conservation is an essential strategy for future crop breeding efforts.

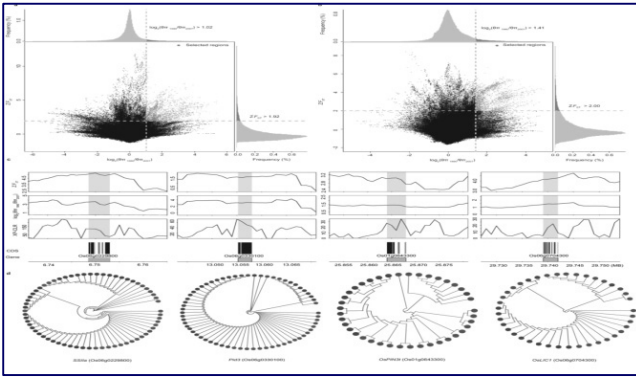


Fig.4. Genomic regions with strong selective-sweep signals in rice landraces during short-term domestication.

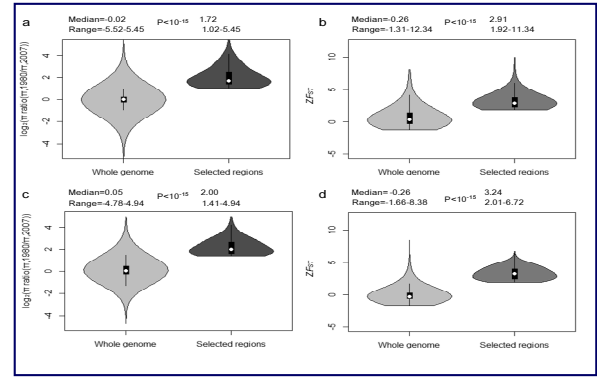


Fig. 5. Violin plot of $\log_2(\theta_{\pi}$ ratio) and ZF_{ST} values for regions of indica (a, b) and japonica (c, d) rice landraces.

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