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Genetic structure and isolation by altitude in rice landraces of Yunnan, China revealed by nucleotide and microsatellite marker polymorphisms

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Rice (*Oryza sativa* L.) is one of the earliest domesticated crop species. Its genetic diversity has been declining as a result of natural and artificial selection. Compared with modern cultivars, traditional rice landraces, a genetic reservoir for varietal improvement, are lineages developed by farmers during domestication. To efficiently conserve, manage, and use such germplasm resources, an understanding of genetic structure and differentiation of local rice landraces is required. In this study, we analyzed 188 accessions of rice landraces collected from localities across an altitude gradient from 425 to 2,274 m above sea level in Yunnan Province, China, using the sequences of 10 target genes and 48 SSR markers. Genetic structure revealed the rice landraces from Yunnan clearly differentiated into indica and japonica groups, and the accessions in each group were further separated into two subgroups according to different altitudes, including lower altitude subgroup and higher altitude subgroup. The results of AMOVA showed significant genetic differentiation among altitude zones at SSRs and most gene loci, except the gene *Os1977* and *STS22*. Correlation analysis revealed the relationship between altitudes and distribution of subspecies in landraces: indica rice landraces were better adapted to the lower altitudes, while japonica rice landraces were better adapted to the higher altitudes. Further analyses revealed that landrace populations were differentiated following a model of isolation by altitude, which produced higher gene flow among similar altitude levels than across different altitude levels. Our findings demonstrated that both adaptation to altitude and gene flow limitation among altitude levels played a key role in genetic differentiation of rice landraces in Yunnan Province.

Biography

Di Cui is currently working at Institute of Crop Science, CAAS, mainly engaged in research of rice germplasm resources and genetic breeding, including the investigation, collection, identification, evaluation, reproduction and conservation of the rice germplasm resources; genetic structure and diversity in rice germplasm resources; abiotic stress (cold, draught, salinity, etc.) in rice molecular breeding.

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