

Genetic Diversity and Population Structure of Yunnan Rice Landraces and Disease Resistance Assessment

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Abstract

Rice landraces are important resources for resistance breeding and sustainability. To clarify the distribution of the genetic diversity of rice landraces and its relationship with rice blast in Yunnan, China. 141 rice landraces from 7 populations in Yunnan were selected to conduct a genetic diversity analysis based on simple sequence repeat (SSR) markers. The results showed that the 7 rice populations in Yunnan have a rich genetic diversity (expected heterozygosity $[H_e] = 0.63$). We also found that the genetic diversity of the 7 rice populations was negatively correlated with geographical longitude in Yunnan ($R^2 = 0.70$, $P < 0.05$). Structural analysis and principal coordinate analysis (PCoA) showed that the genetic structure of the rice populations is complex. Analysis of molecular variance (AMOVA) showed that rice landraces in Yunnan have high genetic variation within populations (94%). In addition, evaluations of blast resistance both in the greenhouse and in the field showed that as the genetic diversity increased, the rice blast occurrence within the rice populations decreased ($R^2 = 0.66$, $P < 0.05$). This study not only implicates excellent materials for rice genetic improvement but also provides a theoretical basis for the protection and utilization of Yunnan rice landraces.

1. Introduction

Genetic diversity is an important part of biological diversity, species diversity and ecosystem diversity [1, 2]. Genetic diversity also plays an important role in agroecosystems [3]. Decreasing genetic diversity could easily lead to fragile agroecosystems and increase the risk of disease epidemics [4]. Host plants and pathogens are in a dynamic equilibrium in nature environment [4]. The gradual narrowing of the genetic background of host plants might disrupt this dynamic balance, resulting in disease outbreaks and reducing crop productivity [5]. Therefore, it is vital to increase the richness of crop genetic diversity.

Some studies have reported that in addition to the variation in genetic material, other factors such as human activities, geography, and climatic conditions also affect the genetic diversity of plant populations [6, 7]. Previous studies have typically reported that the genetic diversity of most species gradually decreases with increasing latitude and altitude [8–10]. However, specific examples have reported genetic diversity is also significantly related to longitude [11]. These results suggest that climate type (due to different longitudes) generated by complex environments might be an important factor affecting genetic diversity.

Yunnan, located in southwestern China, is one of the centers of origin of genetic diversity and Asian cultivated rice worldwide [12]. Yunnan has unique natural environmental conditions and excellent local rice resources [12]. The diverse environments of Yunnan give local rice landraces the capacity to withstand different selection pressures, resulting in genetic variation and rich genetic diversity associated with adaptations to different ecological environments. However, whether these genetic variations would affect the genetic differentiation of rice populations due to climatic factors or geographic distance needs further confirmation [13, 14]. Although studies have pointed out that altitude and temperature have impacts on the genetic diversity of plants growing on Yunnan Hani terraces, there is little detailed proof of

the impact of natural environmental factors on the genetic diversity of rice landrace resources in different regions of Yunnan, especially with respect to longitude [15, 16]. In addition, traditional farming practices (interplanting, mixed planting) and farming activities (seed retention, replacement) in Yunnan, especially the mixed or modified planting of *japonica* and *indica* rice, has resulted in new variations in local rice resources [17–19]. However, it is unclear whether these variations affect the genetic diversity and disease resistance of Yunnan rice landraces.

Therefore, the genetic diversity of 141 rice landraces from 7 rice planting areas in Yunnan was analyzed on the basis of simple sequence repeat (SSR) markers to evaluate genetic differentiation and genetic structure. Identification of blast resistance for all rice landraces was conducted in both the greenhouse and the field to explore the relationship between genetic diversity and rice blast resistance. The results are important in terms of the protection of Yunnan's rice landraces and provide a theoretical basis for food security maintenance and sustainable agricultural development worldwide.

2. Materials And Methods

2.1. Source of rice varieties

Seven rice planting areas in Yunnan (Baoshan, Lincang, Pu'er, Xishuangbanna, Wenshan, Yuxi and Honghe) were selected to collect rice landraces [20]. Two to seven counties were randomly selected in each prefecture. A total of 141 rice varieties belonging to 7 rice populations were collected from the seven planting areas. Five *indica* and *japonica* rice varieties were used as references for the genetic structure analysis (Table S1).

2.2. DNA extraction and PCR amplification

The fresh leaves of rice were collected for genomic DNA extraction according to the cetyltrimethylammonium bromide (CTAB) method [21], and the concentration of genomic DNA was determined by the ethidium bromide fluorescent staining method [22]. Forty-three pairs of fluorescent primers that can effectively distinguish the genetic differentiation of rice varieties were selected (Table S2). An Applied Biosystems 2720 thermal cycler (Applied Biosystems, USA) was used for PCR, and the reaction system volume was 10 μ L, including 1 μ L of DNA template (50 ng), 0.2 μ L of each primer (forward and reverse primer), 0.8 μ L dNTP mix (TAKARA), 0.05 μ L Taq DNA polymerase (Biocolor BioScience, Shanghai), 2 μ L PCR buffer (10 \times , including 2 mmol/L $MgCl_2$) and 6.75 μ L double distilled water. The PCR conditions were as follows: 1 cycle at 94°C for 4 min; 30 cycles at 94°C for 40 s, 55°C for 30 s and 72°C for 30 s; 1 cycle at 72°C for 7 min. PCR products were separated and analyzed by a fluorescent capillary electrophoresis system (ABI 3130xl Genotyper, Applied Biosystems, Genesky, Shanghai). The molecular weights were calculated by the biological software GeneMapper (version 3.7, Applied Biosystems, Inc., USA). SSR data reading was performed according to the size of amplified products, and the products with the same size were regarded as an allele.

2.3. Genetic diversity analysis

Genetic diversity parameters including the percentage of polymorphic loci (P), observed heterozygosity (Ho), number of alleles (Na), effective number of alleles (Ne), Shannon index (I), expected heterozygosity (He) and polymorphic information content (PIC) were calculated using GenALEX 6.502 software [23]. In addition, we also performed analysis of molecular variance (AMOVA) to divide the results of genetic differentiation into within populations and among populations. Based on AMOVA, we also calculated the amount of gene flow (Nm) and paired genetic differentiation coefficient (Fst) to estimate the level of gene flow and differentiation among rice populations. SPSS 26 software was used to estimate the relationships between genetic diversity and longitude and between genetic diversity and rice blast resistance.

2.4. Structure analysis

To infer the genetic structure and genetic relationships between the 7 rice populations, STRUCTURE (version 2.3.4) software [24] was used to analyze the 141 rice landraces. Five typical *indica* rice varieties and five *japonica* rice varieties served as references. The K value was set to 1-7, and 10 replicate calculations were performed. The run parameter burn-in was set to 100000, and the run length was set to 200000. After the operation was complete, the best K value was determined by the Structure Harvester online program (<http://taylor0.biology.ucla.edu/structureHarvester/>) according to previously reported methods [25]. CLUMPP (version 1.1.2) software was used to perform the best comparison for the 10 replicates of the optimal K value [26]. The calibration results were automatically visualized by distruct 1.1 software. Principal coordinate analysis (PCoA) was used to estimate the genetic composition of the rice landraces.

2.5. Resistance evaluation of rice landraces in the greenhouse

Ten rice blast strains donated from Yunnan Academy of Agricultural Sciences (GUY11, 66b, CH1598, CH1139, CH9105a, CH1638, CH1643, CH1633, CH091C, 363) were selected to evaluate their resistance to rice blast. The rice blast strains were cultured at 28°C for 7 days and then sporulated at 28°C under light for 2 days. The spores were washed with distilled water comprising 0.02% Tween 20, and the concentration of the spore suspension was 2×10^5 /mL. Rice seeds were sown in a nursery box after germination. Ten seeds were sown per variety, and 2 replications were included. Rice plantlets at the 3.5-leaf stage were used for inoculation. Investigation of the incidence and disease index of rice leaf blast after seven-days inoculation was followed the Standard Evaluation System for Rice [27].

2.6. Resistance identification of rice landraces in the field

A field trial was conducted in Jianshui, Yunnan in 2019 (longitude 102°46'16", latitude 23°36'2"). The experiment adopted a completely randomized block design. Each plot consisted of 3 rows×20 plants, with a spacing of 5×8 inches, and three replicates were conducted. The highly susceptible variety (Huangkenuo) was used as control variety. Throughout the growth period, water and fertilizer management followed local practices, and pest control instead of disease control measurements was

conducted. Investigation of the incidence and disease index of rice diseases (panicle blast at the maturity stage) was followed the Standard Evaluation System for Rice [27].

2.7. Data analysis

Microsoft Office Excel 2016 software was used for statistics and data maintenance. SPSS 26 software was used for performing analysis of variance, correlation analysis, and least significant difference (LSD) tests. Graphs were constructed via Origin 2019. ArcGIS 10.2 was used to construct a sampling point map.

3. Results

3.1. Genetic diversity among Yunnan rice landraces is rich

The SSR markers selected in this study were highly polymorphic across the populations, and this level of polymorphism could meet the genetic diversity analysis of rice landrace populations. A total of 387 alleles were detected in these rice varieties, with an average of 9 alleles (N_a) at each locus. The average H_e of the SSR markers was 0.63, which varied from 0.30 (RM463) to 0.81 (RM241). The PIC of the SSR markers varied from 0.34 to 0.85, with an average of 0.65. Among them, there were 34 highly polymorphic sites ($PIC > 0.5$), accounting for 79.07%, and there were nine moderately polymorphic sites ($0.25 < PIC < 0.5$), accounting for 20.93% (Table S3). For the genetic diversity of rice populations, seven rice populations collected from seven cities in Yunnan Province also showed high genetic diversity. The H_e of the rice populations was between 0.58 (Wenshan) and 0.68 (Lincang), with a mean value of 0.63. The N_a of the rice populations was 5.01, the Shannon index (I) of the rice populations averaged 1.24, the H_o of the rice populations was 0.09, and the average P of the rice populations reached 99.67% (Table 1). We concluded that rice landraces in Yunnan have a rich basis of genetic diversity.

Table 1
Genetic diversity of seven rice populations in Yunnan.

Populations	P	N	Na	Ne	I	Ho	He
LC ¹	100.00%	32	6.28 (0.37)	3.63 (0.23)	1.40 (0.06)	0.10 (0.01)	0.68 (0.02)
BS	100.00%	22	5.44 (0.33)	3.52 (0.21)	1.34 (0.06)	0.08 (0.01)	0.67 (0.02)
PE	100.00%	38	6.56 (0.40)	3.42 (0.25)	1.36 (0.06)	0.08 (0.01)	0.65 (0.02)
HH	100.00%	13	4.70 (0.27)	3.10 (0.19)	1.21 (0.06)	0.16 (0.02)	0.62 (0.02)
XS	100.00%	19	5.16 (0.29)	3.07 (0.20)	1.23 (0.07)	0.07 (0.01)	0.61 (0.03)
YX	97.67%	7	3.53 (0.16)	2.83 (0.15)	1.08 (0.05)	0.04 (0.01)	0.60 (0.02)
WS	100.00%	10	3.40 (0.16)	2.71 (0.14)	1.03 (0.05)	0.08 (0.01)	0.58 (0.02)
Mean	99.67% (0.33%) ²	20.14 (0.61)	5.01 (0.13)	3.18 (0.08)	1.24 (0.02)	0.09 (0.01)	0.63 (0.01)

¹ The abbreviations of different rice populations. LC, Lincang; BS, Baoshan; PE, Pu'er; HH, Honghe; XS, Xishuangbanna; YX, Yuxi; WS, Wenshan; ² The abbreviations of indicators of genetic diversity. P, percentage of polymorphic loci; N, number of varieties; Na, number of observed alleles; Ne, effective allele number; I, Shannon index; Ho, observed heterozygosity; He, expected heterozygosity. ² The numbers in parentheses indicate the standard errors.

3.2. Genetic diversity in Yunnan rice landraces increases with decreasing longitude

We noticed that the genetic diversity of rice landraces at different locations displays an obvious spatial distribution. The rice landraces in Wenshan with the greatest longitude showed the lowest genetic diversity. As the longitude increases, the genetic diversity gradually decreases. Correlation analysis showed that there was a significant negative correlation between genetic diversity and longitude for all rice landraces ($R=0.70$, $P<0.05$) (Fig. 1a). We concluded that the genetic diversity of the rice landraces gradually decreased from southwestern to southeastern Yunnan (Fig. 1b).

3.3. Relationship between genetic differentiation and gene flow among rice landraces

AMOVA analysis showed that rice landraces in Yunnan have high genetic variation within populations (94%) and 6% genetic variation among populations, indicating that self-pollinated rice has high genetic

diversity within populations (Table 2). In addition, the F statistical calculations of all SSR sites showed that the inbreeding coefficient in the population (F_{is}) and overall inbreeding coefficient (F_{it}) were 0.869 and 0.873, respectively, while the F_{st} was 0.037, indicating that genetic differentiation among populations was limited. Therefore, genetic differentiation among populations could be disregarded.

In addition, paired F_{st} and gene flow (N_m) were calculated to estimate the level of genetic differentiation among populations and gene flow of the various rice populations. We found that high gene flow mainly occurred between adjacent regions. For example, the N_m of the populations between Baoshan and the adjacent region Lincang was 5.39 but was only 1.92 between Baoshan and Wenshan (the most distant region from Baoshan) (Table 3). Similarly, the paired F_{st} also increased with a gradual increase in geographical distance among populations. Genetic differentiation among populations became increasingly obvious, which further confirmed that the genetic diversity of the rice populations in Yunnan was significantly negatively correlated with longitude.

Table 2
Variation of rice landraces of seven rice populations.

Source	df ¹	Sum of squares	Mean squared deviation	Estimated Variance	Percent variation (%)
Among Pops	6	291.278	48.546	0.894	6
Within Pops	275	3902.874	14.192	14.192	94
Total	281	4194.152		15.087	100
F-Statistics	Value	P (rand >= data)			
F_{st} ²	0.037	0.001			
F_{is}	0.869	0.001			
F_{it}	0.873	0.001			
N_m	6.505				
¹ df: degrees of freedom; ² F_{st} : genetic differentiation coefficient; F_{is} : inbreeding coefficient; F_{it} : overall fixation index; N_m : gene flow.					

Table 3
Genetic differentiation coefficient (Fst) values and gene flow (Nm) of 7 rice populations.

Pop code	BS ¹	HH	LC	PE	WS	XS	YX
BS	—	0.05	0.04	0.08	0.12	0.11	0.08
HH	5.09	—	0.04	0.05	0.08	0.06	0.08
LC	5.39	5.51	—	0.03	0.07	0.06	0.05
PE	3.01	5.23	7.01	—	0.07	0.04	0.07
WS	1.92	2.82	3.13	3.53	—	0.07	0.11
XS	2.05	3.63	3.94	6.43	3.46	—	0.05
YX	2.87	3.08	4.79	3.25	2.12	4.54	—

¹ The abbreviations of different rice populations. BS, Baoshan; HH, Honghe; LC, Lincang; PE, Pu'er; WS, Wenshan; XS, Xishuangbanna; YX, Yuxi. The data in the upper-right corner indicates the genetic differentiation coefficient, and the data in the lower-left corner indicates the gene flow coefficient.

3.4. Genetic structure analysis of rice landrace populations

STRUCTURE software was used to analyze the genetic structure of the populations of the collected rice landraces, and five *japonica* and five *indica* typical rice varieties were used as references. The results showed that the genetic structure of the rice populations in the 7 localities was complex and that there was no single genetic component. Nonetheless, the genetic structure could be divided into two main genetic components (those associated with *indica* (yellow) and *japonica* (blue)) when the K value was determined to be 2 (Fig. 2a). Moreover, both the *indica* and the *japonica* rice genetic components were present in all seven rice populations (Fig. S1). There was a subpeak representing a further substructure when K value was 3, indicating that the genetic structure could be divided into three subgenetic components, which are represented by blue, yellow and red colors. The abovementioned three genetic components were found in all 7 rice populations (Fig. 2b). PCoA confirmed that there were three subgenetic components in the genetic structure analysis, which were labeled SP1, SP2, and SP3 (Fig. 3). Notably, typical *indica* and *japonica* rice varieties clustered only in SP1 and SP2. In addition, the rice populations of all localities were present in the three components except for the rice population of Yuxi (which was not present in SP3). We could conclude that the rice landraces in the populations were randomly mixed and included each component, indicating that there was large genetic differentiation in the population and thus confirming the high gene flow among the populations.

3.5. Genetic diversity is positively correlated with rice blast resistance

To verify the relationship between the genetic diversity and rice blast resistance of the seven rice populations, the 141 rice landraces were used to evaluate rice blast resistance both in the greenhouse

and in paddy fields. The results showed that the rice landraces have good blast resistance, the resistance frequency of rice landraces in the greenhouse was 75.62% (Table S4). Moreover, correlation analysis showed that there was a significant positive correlation between genetic diversity (N_a) and resistance ($R^2=0.66$, $P<0.05$) (Fig. 4a). Further field experiments showed that seven rice populations had low disease incidence (6.97%) and a low disease index (3.50). However, the disease incidence and disease index of the susceptible variety Huangkenuo (CK) were 53.19% and 14.18%, respectively. Notably, the rice population in Lincang with the highest genetic diversity ($H_e=0.68$) had the lowest disease incidence (1.86%) and disease index (0.44), while the local rice population with the lowest genetic diversity (Wenshan) ($H_e=0.58$) had the lowest incidence (19.96%) and disease index (12.89). Thus, we concluded that genetic diversity and field resistance are correlated (Fig. 4b, c).

4. Discussion

Genetic diversity is an important part of rice germplasm resource utilization. A total of 141 local rice landraces from seven cities in Yunnan were analyzed for their genetic diversity in our experiment, and the results showed that the rice landraces have rich genetic diversity, which are the same as the previous studies [28, 29]. Although the genetic diversity of rice populations in the seven localities was high ($H_e = 0.63$), the population diversity level was not evenly distributed, showing a clear spatial distribution and a significantly negative correlation with geographical longitude. This shows that the longitude gradient has an impact on the genetic diversity of Yunnan rice populations. There was study reported that when populations were divided according to latitude and longitude, the variance of the genetic diversity within populations was small, indicating that latitude and longitude are important factors affecting the genetic diversity of populations [30]. In addition, some people found that the biological genetic diversity throughout the Mediterranean basin is significantly correlated with longitude [11]. They also declared that it is difficult to use a single factor to explain the genetic diversity across Mediterranean areas, which have complex environments with specific climate types, nonetheless, longitude was an important factor [11]. Some studies have shown that factors such as temperature and altitude have varying degrees of influence on genetic diversity because of the complex terrain of Yunnan, but no specific analysis has been made from the perspective of longitude [31]. This study found that there is a significant correlation between rice genetic diversity and longitude in Yunnan. Thus, we provide a new way to study rice genetic diversity and new ideas for rice germplasm innovation and genetic diversity protection.

Genetic differentiation indicates the degree of variation within a population [32]. This study showed that the genetic variation of the rice population in Yunnan is driven mostly by variation within populations (94%). The F_{st} was low (0.037), which is consistent with the findings of previous studies. William [33] used SSR markers to assess the genetic diversity of rice genotypes and found that 70% of the genetic variation originates from variation within populations. Tu [34] also used SSR markers to analyze the genetic diversity of 60 rice germplasms in Yunnan and reported similar results. Wright [32] reported that self-pollinated rice has high genetic differentiation within populations, while genetic differentiation among populations is limited. We found that Yunnan rice populations experienced a high degree of gene

flow (Nm) (6.505) and showed obvious distance isolation. In addition, geographically close populations showed a high degree of gene flow, which was limited to geographically separated populations, which are similar to the results of rice populations in Sri Lanka [35]. Some studies have reported that the frequency of landrace seed exchange is more than ten times that of foreign exchanges among farmers in Yunnan, these frequent exchange of seeds between neighboring regions may affect gene flow [36, 37]. Thus, we speculated that seed exchange between farmers and regions may be the reason for the formation of high gene flow in geographically close regions.

As one of the basic characteristics of species and populations, genetic structure is the result of multiple factors such as selection, mutation, genetic drift, migration, and gene flow [38]. Structural analysis in this study showed that the genetic structure of rice populations includes components associated with two main groups: *japonica* and *indica* rice (Fig. 3a, $K=2$). Using SSR markers, Chen [39] analyzed the population structure of rice germplasm resources from 16 cities in Yunnan, and the results showed that 908 rice germplasms could be divided into two major groups (*japonica* and *indica*), which was consistent with our results. However, Yunnan is divided into three types of rice planting areas, i.e., an *indica* area, an *indica-japonica* overlapping area and a *japonica* area, due to the unique geography and climatic [40]. When the K value in the structure analysis was 3, we found that two genetic components were typical *japonica* rice and typical *indica* but that a third component was not typical *indica* or *japonica* rice (Fig. 3b, $K=3$). PCoA also showed that there were three subgroups, two of which included typical *japonica* or *indica*, and the third subgroup was an intermediate type (Fig. 4). In addition, we found that most rice populations (except Yuxi) included all three components (Figure 3b), indicating that there was large genetic differentiation within populations and further confirming that there was high gene exchange within populations.

Rice blast control is an important part of improving the yield and quality of rice [41]. The results of this study showed that rice populations have a rich genetic diversity and that there is a positive correlation between genetic diversity and rice blast resistance (Fig. 5a). Zhu [42] found that genetic diversity was a significant factor in the control of rice blast. Tu [34] and He [43] also reported that the higher the genetic diversity of rice varieties was, the higher the resistance of the varieties to rice blast. Therefore, it is highly important to determine the relationship between the genetic diversity of rice landraces and the rice blast resistance of genotypes. Applying these important germplasm resources to rice production is a future endeavor.

5. Conclusions

In this study, we found that seven rice populations in Yunnan showed an abundance of genetic diversity and that the genetic diversity decreased with increasing longitude. Structural analysis and PCoA showed that the genetic structure of the seven rice populations in Yunnan is complex. When the K value was 2, the rice populations were divided into two genetic components: *japonica* and *indica* ones. When the K values was 3, in addition to the two components of *indica* and *japonica*, there was a third, unknown genetic component. AMOVA showed that rice landraces in Yunnan have high genetic variation within

populations (94%). In addition, evaluation of blast resistance both in the greenhouse and in the field showed that there was a correlation between genetic diversity and rice blast occurrence: as the genetic diversity increased, the rice blast occurrence throughout the rice populations decreased.

Declarations

Supplementary Materials: The online version contains supplementary material available at <https://doi.org/xxx>. Fig.S1: The distribution of K-values with ΔK . Table S1: Information of tested rice materials. Table S2: Primer sequences of the 43 simple sequence repeat (SSR) markers used in this study. Table S3: Genetic diversity of 43 pairs of SSR markers. Table S4. Resistance identification of 7 populations in the greenhouse.

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Declarations

Conflicts of Interest: The authors declare that they have no conflict of interest.

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References

1. Vellend M (2005) Species Diversity and Genetic Diversity: Parallel Processes and Correlated Patterns. *Am Nat* 166:199–215. <https://doi.org/10.1086/431318>
2. Hughes A, Inouye B, Johnson M, Underwood N, Vellend M (2008) Ecological consequences of genetic diversity. *Ecol Lett* 11(6):609–623. <https://doi.org/10.1111/j.1461-0248.2008.01179.x>
3. Yang J, Shi Z, Gao D et al (2012) Mechanism on biodiversity managing crop diseases. *Hereditas* 34(11):1390–1398. <https://doi.org/10.3724/sp.j.1005.2012.01390>
4. Wernberg T, Coleman MA, Bennett S et al (2018) Genetic diversity and kelp forest vulnerability to climatic stress. *Scientific reports*. 8(1)
5. Lang J, Han G, Xu J et al (2015) Impact of genetic divergence between intercropped rice varieties on their efficiency of resistance to rice blast disease. *Journal of Yunnan Agricultural University (Natural*

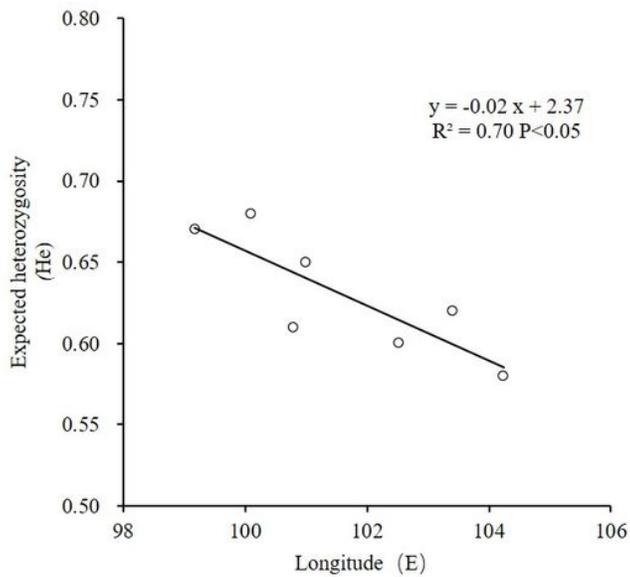
- Science) 30(3):338–345. [https://doi.org/10.16211/j.issn.1004-390X\(n\).2015.03.003](https://doi.org/10.16211/j.issn.1004-390X(n).2015.03.003)
6. Brown JL, Weber JJ, Alvarado-Serrano DF et al (2016) Predicting the genetic consequences of future climate change: The power of coupling spatial demography, the coalescent, and historical landscape changes. *Am J Bot* 103(1):153–163. <https://doi.org/10.3732/ajb.1500117>
 7. Kremer A, Le Corre V (2012) Decoupling of differentiation between traits and their underlying genes in response to divergent selection. *Heredity (Edinb)* 108(4):375–385. <https://doi.org/10.1038/hdy.2011.81>
 8. Gaston KJ (2000) Global patterns in biodiversity. *Nature* 405(6783):220–227. <https://doi.org/10.1038/35012228>
 9. Wang Z, Fu MJ, Zhu HG et al (2019) Enhanced genetic diversity of weedy rice populations associated with latitude decreases revealed by simple sequence repeat fingerprints. *Journal of Systematics and Evolution* 57(1):66–74. <https://doi.org/10.1111/jse.12428>
 10. Nara TK (2010) General Latitudinal Gradient of Biodiversity Is Reversed in Ectomycorrhizal Fungi. *New Phytologist* 185(2):351–354. <https://doi.org/10.1111/j.1469-8137.2009.03134.x>
 11. Conord C, Gurevitch J, Fady B (2012) Large-scale longitudinal gradients of genetic diversity: a meta-analysis across six phyla in the Mediterranean basin. *Ecol Evol* 2(10):2600–2614. <https://doi.org/10.1002/ece3.350>
 12. Zeng Y, Zhang H, Li Z et al (2007) Evaluation of Genetic Diversity of Rice Landraces (*Oryza sativa* L.) in Yunnan, China. *Breeding Science* 57:91–99. <https://doi.org/10.1270/jsbbs.57.91>
 13. Xu FR, Yang YY, Zhang EL, Xin Xiang A, Dai LY (2012) On-farm conservation and utilization of paddy rice, wheat and maize landrace varieties in 15 unique ethnic groups in Yunnan, China. *Hereditas (Bjing)*. 34:1465–1474. <https://doi.org/10.3724/SP.J.1005.2012.01465>. 11
 14. Cui D, Tang C, Li J, Xinxiang A, Koh HJ (2017) Genetic structure and isolation by altitude in rice landraces of Yunnan, China revealed by nucleotide and microsatellite marker polymorphisms. *Plos One* 12(4):e0175731. <https://doi.org/10.1371/journal.pone.0175731>
 15. Yan HM, Dong C, Zhang EL et al (2012) Analysis of genetic variation in rice paddy landraces across 30 years as revealed by microsatellite DNA markers. *Hereditas* 34(1):87–94. <https://doi.org/10.3724/sp.j.1005.2012.00087>
 16. Liu H, Yingjie S, Chunlin L (2020) Genetic diversity of rice landraces in Yuanyang Hani terraced rice fields under In-situ conservation: research progress. *Chin Agric Sci Bull* 36(10):87–94
 17. Yu T, Guilan C, Longzhi H et al (2016) Diachronic analysis of genetic diversity in rice landraces under on-farm conservation in Yunnan, China. *Theoretical & Applied Genetics International Journal of Breeding Research & Cell Genetics*
 18. Wang Y, Wang Y, Sun X (2016) Influence of ethnic traditional cultures on genetic diversity of rice landraces under on-farm conservation in southwest China. *Journal of Ethnobiology and Ethnomedicine* 12(1):51. <https://doi.org/10.1186/s13002-016-0120-0>
 19. Wang H, Wang Y, Yang Y et al (2019) Farmer's seed system and agricultural cultural landscape pattern in the Yuanyang Hani Terraced fields. *Ecology and Environmental Sciences* 28(1):16–28

20. Dall LY, Xrong JH, Wen GS et al (1995) Further Information on the Genetic Variation of Indigenous Rice Varieties in Yunnan Province, China. *Japanese Journal of Breeding* 45(3).
<https://doi.org/10.1270/jsbbs1951.45.397>
21. Milligan BG, Hoelzel AR (1992) Plant DNA isolation. *Plant DNA isolation*
22. Creste S, Neto AT, Figueira A (2001) Detection of single sequence repeat polymorphisms in denaturing polyacrylamide sequencing gels by silver staining. *Plant Molecular Biology Reporter* 19(4):299–306. <https://doi.org/10.1007/BF02772828>
23. Peakall R, Smouse PE (2012) GenAEx 6.5: genetic analysis in Excel. Population genetic software for teaching and researchan update. *Bioinformatics*. 28(19). [https://doi.org/GenAEx 6.5: genetic analysis in Excel. Population genetic software for teaching and researchan update](https://doi.org/GenAEx%206.5%3A%20genetic%20analysis%20in%20Excel.%20Population%20genetic%20software%20for%20teaching%20and%20researchan%20update)
24. Pritchard J, Stephens M, Donnelly P (2000) Inference of population structure using multilocus genotype data. *Genetics* 155(2). <https://doi.org/10.1093/genetics/155.2.945>
25. Evanno G, Regnaut S, Goudet J (2005) Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. *Molecular ecology* 14(8). <https://doi.org/10.1111/j.1365-294X.2005.02553.x>
26. Jakobsson M, Rosenberg NA (2007) CLUMPP: a cluster matching and permutation program for dealing with label switching and multimodality in analysis of population structure. *Bioinformatics* 23(14). <https://doi.org/10.1093/bioinformatics/btm233>
27. IRRI, ed. Standard evaluation system for rice. ed. t. edition, Box PO (2013) : Manila: International Rice Research Institute
28. Sun J, Yu T, Tang C et al (2013) Analysis of genetic diversity within populations of rice landraces from Yunnan using microsatellite markers. *Chinese Journal of Rice Science* 27(1):41–48.
<https://doi.org/10.3969/j.issn.1001-7216.2013.01.006>
29. Mengli M, Yun Z, Xiaomei Z et al (2018) Genetic diversity analysis of red rice from Hani's terraced fields in Yunnan province. *Crops*. (5):21-26. <https://doi.org/10.16035/j.issn.1001-7283.2018.05.004>
30. Zhang Y, Cao G, Han L (2007) Analysis of relationships for Indica local rice from different places of China. *Acta Agronomica Sinica* 33(5):757–762
31. He X, Sun Y, Gao D et al (2011) Comparison of agronomic traits between rice landraces and modern varieties at different altitudes in the paddy fields of Yuanyang terrace, Yunnan Province. *Journal of Resources and Ecology* 2(1):46–50. <https://doi.org/10.3969/j.issn.1674-764x.2011.01.007>
32. Wright S (1978) *Evolution and Genetics of Populations: Variability within and among Natural Populations*. <https://doi.org/10.1017/S0021932000008543>
33. Suvi WT, Shimelis H, Laing M, Mathew I, Shayanowako A I T (2019) Assessment of the genetic diversity and population structure of rice genotypes using SSR markers. *Acta Agriculturae Scandinavica, Section B – Soil & Plant Science* 70(1):76–86.
<https://doi.org/10.1080/09064710.2019.1670859>
34. Tu M, Wang Y, Lu B, Yang X (2011) A study on correlation between blast resistance and genetic diversity of rice varieties in Yunnan province. *Hubei Agricultural Sciences* 50(6):1149–1152.

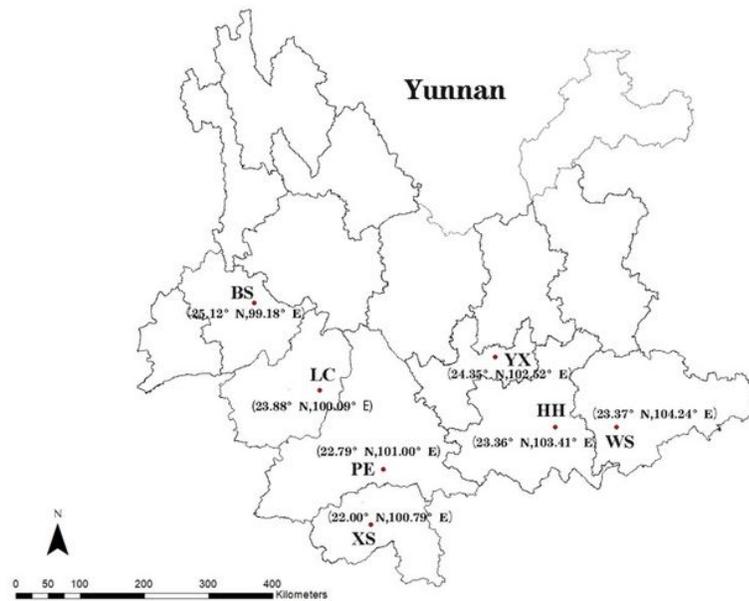
<https://doi.org/10.14088/j.cnki.issn0439-8114.2011.06.042>

35. He Z, Jiang X, Ratnasekera D et al (2014) Seed-mediated gene flow promotes genetic diversity of weedy rice within populations: implications for weed management. *PloS one* 9(12).
<https://doi.org/10.1371/journal.pone.0112778>
36. Song ZJ, Wang Z, Feng Y et al (2015) Genetic divergence of weedy rice populations associated with their geographic location and coexisting conspecific crop: Implications on adaptive evolution of agricultural weeds. *Journal of Systematics & Evolution* 53(4):330–338.
<https://doi.org/10.1111/jse.12152>
37. Wang Z, Fu M, Zhu H et al (2019) Enhanced genetic diversity of weedy rice populations associated with latitude decreases revealed by simple sequence repeat fingerprints. *Journal of Systematics and Evolution* 57(1):9. <https://doi.org/10.1111/jse.12428>
38. Ellstrand NC (2014) Is gene flow the most important evolutionary force in plants? *Am J Bot* 101(5):737–753. <https://doi.org/10.3732/ajb.1400024>
39. Chen Y, Chen L, Zhang D et al (2019) Genetic diversity and population structure analysis of rice germplasm resources in Yunnan province. *Acta Agriculturae Boreali-occidentalis Sinica* 28(11):1778–1789. <https://doi.org/10.7606/j.issn.1004-1389.2019.11.006>
40. Yang ZY, Yan SU, Cao YS et al (2008) Studies on Geographical Distribution of Rice Germplasm Diversity in Yunnan Province. *Journal of Plant Genetic Resources*.
<https://doi.org/10.3724/SP.J.1005.2008.01083>
41. Wang X, Jia MH, Ghai P, Lee FN, Jia Y (2015) Genome-Wide Association of Rice Blast Disease Resistance and Yield-Related Components of Rice. *Molecular Plant Microbe Interactions* 28(12):1383–1392. <https://doi.org/10.1094/MPMI-06-15-0131-R>
42. Zhu Y, Chen H, Fan J et al (2000) Genetic diversity and disease control in rice. *Nature* 406(6797):718.
<https://doi.org/10.1038/35021046>
43. He P, Wang C, Zhang N et al (2021) Multi-genotype varieties reduce rice diseases through enhanced genetic diversity and show stability and adaptability in the field. *Phytopathology Research* 3(1).
<https://doi.org/10.1186/s42483-021-00105-x>

Figures



(a)



(b)

Figure 1

Genetic diversity among Yunnan rice landraces increases with decreasing longitude. (a) Correlation between genetic diversity (He) and longitude of Yunnan province. (b) Distribution of the collection areas of rice landraces in Yunnan.

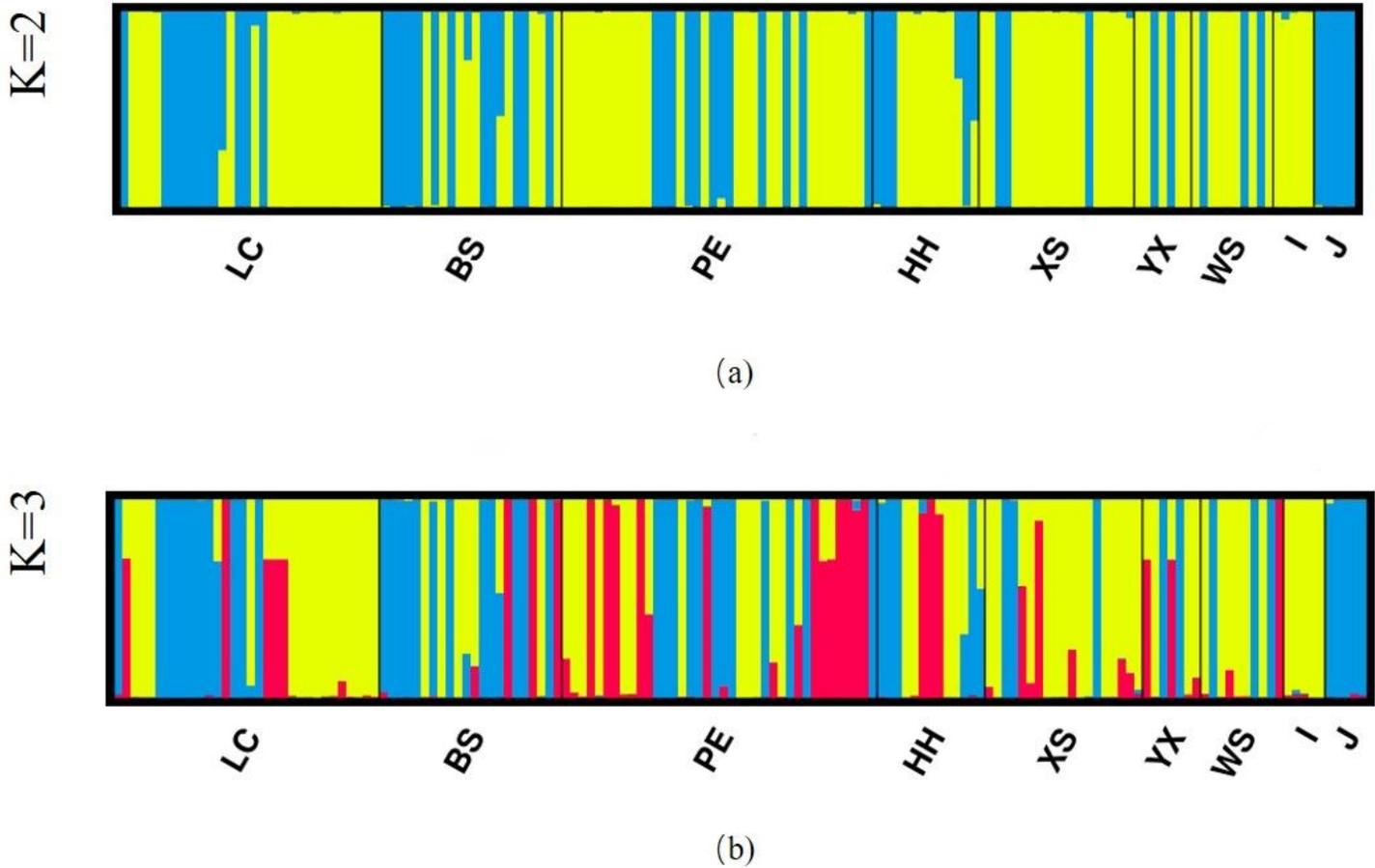


Figure 2

Genetic structure analysis of seven rice populations in Yunnan. (a) Genetic structure analysis of seven rice populations in Yunnan when $K = 2$. (b) Genetic structure analysis of seven rice populations in Yunnan when $K = 3$. K represents the number of the main genetic populations inferred by the model: $K = 2$ is the most suitable K value, and $K = 3$ is the second most suitable K value. The different colors indicate different genetic components, and each local rice population is separated by a black vertical line. Individual varieties are represented by a vertical bar whose length is proportional to the inferred genetic component. I and J represent control populations: I represents the genetic component of *indica* rice, which is shown in yellow, and J represents the genetic component of *japonica* rice, which is shown in blue. The rice populations include Lincang (LC), Baoshan (BS), Pu'er (PE), Honghe (HH), Xishuangbanna (XS), Yuxi (YX), and Wenshan (WS).

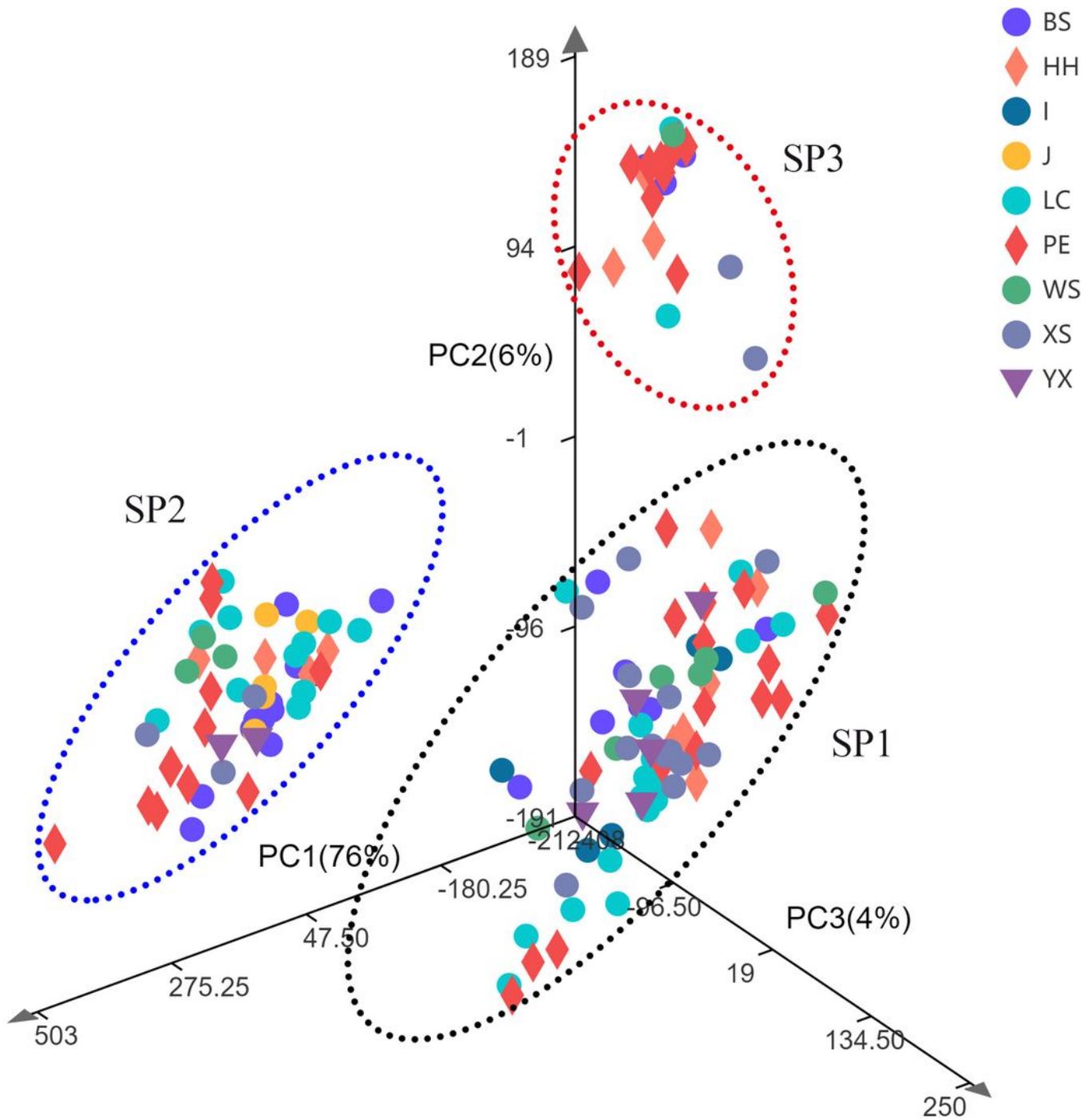
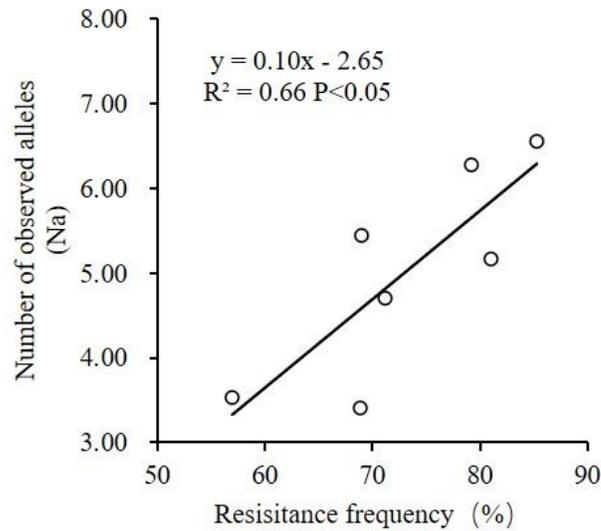
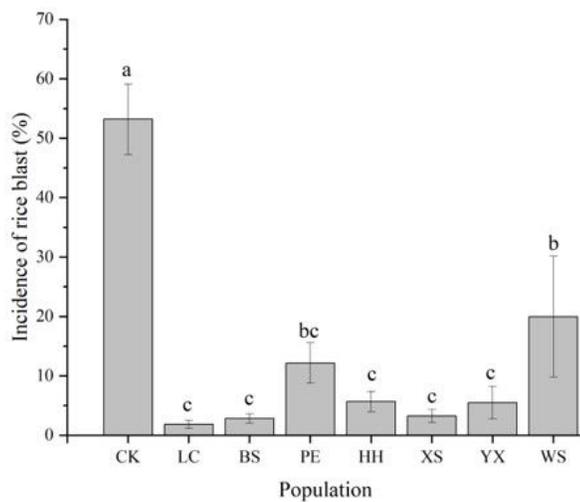


Figure 3

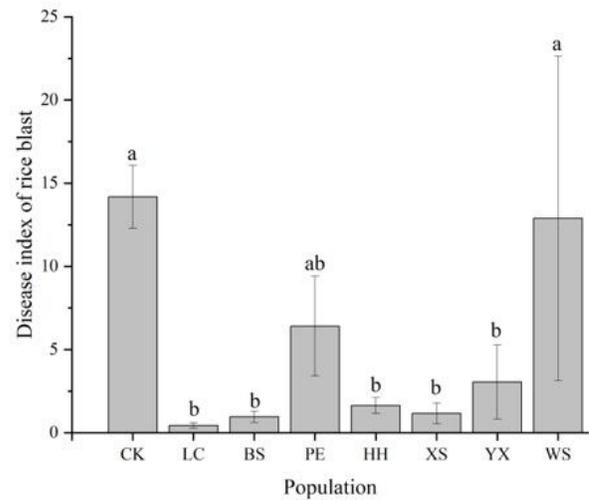
Principal coordinate analysis of the genetic structure of seven rice populations in Yunnan. The seven rice populations were divided into three main populations: SP1, SP2 and SP3. I and J represent control populations, which are *indica* and *japonica* populations, respectively. The rice populations include Lincang (LC), Baoshan (BS), Pu'er (PE), Honghe (HH), Xishuangbanna (XS), Yuxi (YX), and Wenshan (WS).



(a)



(b)



(c)

Figure 4

Relationship of genetic diversity and rice blast occurrence of rice landraces. (a) Positive correlation of the number of alleles (Na) and blast resistance in the greenhouse. (b) Rice blast disease incidence of seven rice populations in the field. (c) Blast disease index of seven rice populations in the field. The different lowercase letters in the columns indicate significant differences ($P < 0.05$). LC, Lincang; BS, Baoshan; PE, Pu'er; HH, Honghe; XS, Xishuangbanna; YX, Yuxi; WS, Wenshan.

Supplementary Files

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