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Effects of human activities on the genetic characteristics of Phaius flavus populations

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Abstract

Human activity often has profound effects on plant growth and evolution. Orchids are the most diverse group of flowering plants and are threatened by habitat fragmentation, over-harvesting, and urbanization. A population of *Phaius flavus* from Beikengding Mount (BM) in Fujian Province was divided into two patches by road construction, and its genetic characteristics were evaluated using restriction site-associated DNA sequencing (RAD-seq) data. The purpose of this study is to explore the impact of road construction on the evolution of different patches within a population. Analysis revealed that the genetic diversity of patch B was slightly higher than that of patch A in the BM population of *P. flavus*. Principal component and phylogenetic analyses, genetic structure, genetic differentiation, and bottleneck detection indicated phase-independent genetic differentiation between the two patches. Thus, the construction of the Y013 village road may have influenced different patches of this population on a genetic level. This study provides a rational basis for research on the impact of human activities on biodiversity conservation.

Background

Population genetic diversity is the genetic information carried by different individuals within a population and the core element of biodiversity, which is susceptible to factors such as gene flow, genetic drift, life history, reproductive patterns, and human interference [1–3]. As societies and civilizations progress, increasing ecological imbalances caused by human activities threaten and reduce biodiversity [4]. Over-exploitation of natural resources by humans has led to varying degrees of habitat destruction in plants and animals, accelerating the rate of habitat fragmentation [5, 6]. Habitat fragmentation divides the original habitat into multiple patches [7] and disrupts biological processes, directly affecting population size and spatial isolation between populations. It primarily diminishes genetic diversity and enhances genetic differentiation through genetic drift, inbreeding, and restricted gene flow between populations [8].

Roads have played a crucial role in human activities throughout the agricultural development and urbanization process, negatively impacting the genetic diversity and differentiation of wild plant populations [9], by reducing plant diversity and limiting certain species [10]. Orchids, one of the most sensitive plants in nature, suffer from habitat fragmentation due to indiscriminate mining and overexploitation [11–13], resulting in changes in their genetic structure and reduced genetic diversity. An evaluation of 653 orchid species in China revealed that 65% of these species face challenges related to habitat fragmentation [14].

With the development of triple sequencing technology, single nucleotide polymorphisms (SNPs) have emerged as a more suitable tool for evaluating the genetic diversity and structure of populations, providing a more accurate estimate of population-level diversity and a better ability to identify populations in clustering analyses [15]. Furthermore, SNPs exhibit a range of variations at the genomic level, offering comprehensive insights into the genetic basis of populations [16]. Within the orchid family, SNPs have been used to elucidate phylogenetic relationships [17], evaluate genetic diversity [18], and

detect genetic variations [19]. Scientists have developed microsatellite markers to examine the level of genetic diversity and gene flow in three species of *Phaius* [20]. However, these studies were unable to elucidate the genetic relationships among the three species.

Phaius flavus is a terrestrial evergreen perennial orchid belonging to the family *Phaius* Collabiinae (Orchidaceae), which grows on humid mountain slopes at an altitude of 300–2,500 m. It is widely distributed in China, India, Japan, and other Southeast Asian countries [21]. *Phaius flavus* is an important genetic breeding resource, contributing to 11 registered *Phaius* graxes registered with the Royal Horticultural Society (RHS) as a parentage. The loss of adult individuals from the three populations of *P. flavus* in the Fujian Province was caused by anthropogenic disturbances [22]. Because of habitat fragmentation and illegal harvesting, the congener *P. australis* is listed as endangered in Australia [20]. In our study, the *P. flavus* Beikengding Mount (BM) population was divided into two patches due to the construction of the Y013 village road from 2010 to 2012, which provided good material for examining the impact of human activities on the genetic characteristics of the population. To evaluate the impact of human activities on this population, the genetic variation, genetic structure, and gene flow within the BM population of *P. flavus* were investigated. The following questions were investigated: (1) Does the construction of the Y013 village road affect the genetic characteristics of the two patches in the BM population? (2) In addition to road construction, which factors affect the population genetic characteristics of the two patches?

Methods

Geographic distribution and sample collection

The materials for this study were obtained from the BM population located at the forestry station in Zhangji Village, Beikengding Mount, Youxi County, Sanming City, Fujian Province, China. This area exhibits the typical characteristics of a subtropical monsoon climate, including high summer temperatures, more rain, and mild winters with less rain and sunshine duration. The frost-free period throughout the year was slightly shorter than that in the southern subtropical areas.

The BM population was comprised of two patches (patches A and B), which was divided by Y013, a village road in Youxi County (Fig. 1a) located along the border of Yuanhu Creek, where habitat fragmentation occurred due to human disturbances. No other aggregated distributions were found within the pollination distance range of this population. Patch A is located on large boulders deep in the creek valley, with a gentler slope and higher levels of depression and moisture. It is located near the Yuanhu Creek and village, and has been affected by grazing and farming. (Fig. 1b). In contrast, patch B was located on steep slopes along the roadside, with a gradient approaching 80°, lower moisture but higher light levels, and was untraversed (Fig. 1c). The soil types and major climatic factors of the study area are listed in Table 1.

A total of 38 individuals from the BM population were collected, 23 from patch A and 15 from patch B (Table S1). Based on a previous population biology survey of *P. flavus* [22], fresh and disease-free leaves

at the base of each plant were selected as leaf molecular samples. The leaves were cut using sterilized scissors, cleaned with sterile water, and parts that were insect-infested and broken were removed, leaving intact leaf tissues. Subsequently, the processed leaves were quick-frozen with liquid nitrogen and transferred to − 80°C for storage.

Table 1
Overview of study area.

Study area	Beikengding Mount
Climate zone	Central Subtropical region
Soil type	Red Earth, Yellow-red Soli
Dimensionality (N)	26°21'49"~26°20'21"
Longitudes (E)	118°6'14 ~ 118°25'22"
Altitudes /m	198 ~ 1220
Average temperature /℃	19.6
Average annual precipitation /mm	1700
Annual sunshine hours /h	1864.8

DNA extraction and sequencing

Total DNA was extracted using a modified CTAB method [23]. DNA integrity was assessed by 1% agarose gel electrophoresis. The DNA concentration and quality were determined using a Thermo Nanodrop 2000 micro UV-split tube photometer. Subsequently, qualified DNA samples were digested with EcoR1. The fragments were ligated to P1 junctions with individually specific indices, mixed, and randomly cut. The ends were then repaired and dA ligation was added to junction 2. After purification, the resulting joint-containing products were enriched by PCR amplification, conducted by BGI Genomics (Wuhan), for subsequent sequencing.

Data QC and SNP calling

To ensure the quality of subsequent analyses, the raw data were subjected to an initial quality assessment using fastp (v0.20.0). Subsequently, Trimmomatic (v2.1.0) was used to filter the data to obtain clean data by removing bases with a quality of less than five at both ends, and bases with an average quality below 20 were removed.

The *Phaius* genome is currently unavailable; therefore, the *Dendrobium catenatum* genome was used as the reference for this study. The clean data were aligned to the reference genome using BWA software (v0.1.17) to generate SAM files [24]. Subsequently, the resulting SAM file was sorted by chromosome size

using the Picard tool [25], while concurrently marking duplicate fragments. Samtools software (v1.11) was used to remove duplicates and categorize the comparison results for subsequent SNP detection [24]. Initially, GATK software (4.1.4.1) was employed to eliminate false-positive SNPs and minimize comparison errors through local realignment, thereby enhancing data accuracy. Next, the Unified Genotyper tool was used for SNP screening, and raw SNPs obtained from the preliminary screening were stored in a VCF file. Finally, the raw SNP datasets were filtered and evaluated using filters with *FS* = 15, *QD* = 30, and a deletion rate of 20%, resulting in a higher-quality SNP dataset.

Genetic diversity analysis

Statistical analyses of genetic diversity included indicators such as nucleotide diversity (*Pi*), observed heterozygosity (*Ho*), expected heterozygosity (*He*), and the inbreeding coefficient (*Fi*). Nucleotide diversity (*Pi*) primarily characterizes polymorphisms in a population [26] and provides an overall indicator of population genetic diversity [27]. Heterozygosity reflects the uniformity of individuals within a population and is used to measure the degree of genetic variation within a population. Lower values indicated a lower degree of variation within the population, generally encompassing both *Ho* and *He*. To calculate nucleotide diversity at individual points, the CFTools software (v0.1.13) was employed with a uniform parameter setting of a 10-kb sliding window.

Phylogenetic and principal components analysis

The relationship between the two patches and population stratification was assessed by principal component analysis (PCA) using a high-quality SNP dataset. Initially, the map and ped files were obtained by converting the VCF files using Vcftools (v0.1.13) and Plink software (v1.07). Subsequently, the tmp pca.eigenval and tmp pca.eigenvec files were obtained as outputs from GCTA software (v0.1.0). Finally, the first line in the tmp pca.eigenvec file was labeled pc1, pc2, and pc3. After saving the data, plotting was performed using R package.

A maximum likelihood tree was constructed based on the genetic distances computed at the SNP loci with RAxML-HPC2 on XSEDE from the evolutionary analysis website CIPRES. Finally, it was viewed and edited using the Figtree software.

Genetic structure and genetic differentiation analysis, bottleneck effect detection

The cryptic genetic outcomes between patches within the BM population must be determined using genetic structural analysis. The first step involved converting the filtered VCF file into a Plink file. Subsequently, the number of clusters (*K*) was set from 1 to 6 with 1,000 iterations. The Admixture software was utilized for detailed validation, which led to the determination of the optimal number of clusters as *K* = 2. Finally, the R language was used for drawing.

To understand the gene flow between the two patches of the BM population and test whether DNA sequences adhere to a neutral evolutionary model. The genetic divergence index (*Fst*) and bottleneck effect test (expressed as Tajima's *D*) for the two patches were calculated using the Vcftool software (v0.1.13). Tajima's $D = 0$ indicates no selection, Tajima's $D > 0$ suggests population expansion, and Tajima's $D < 0$ indicates a bottleneck effect in the population.

Results

Total DNA extraction, quality testing and SNP detection

A total of 38 samples from two patches of the BM population were split and filtered, resulting in 282.93 Gb of valid data (clean data), with an average sequencing volume of 8.32 Gb per sample. The statistical analysis of the output data obtained from the 38 samples is presented in Table S1. The percentage of bases with quality values (Q) exceeding 20 accounted for 96.02% of the total read length. Therefore, the sequencing data were of high quality, making them suitable for subsequent analyses. Following SNP calling and screening, 325,954 high-quality SNP loci were identified, that could be used for genetic diversity and other analyses.

Genetic diversity

The genetic diversity indices of *P. flavus* and the two patches in the BM population are listed in Table 2. At the species level, the genetic diversity statistics of *Pi*, *Ho*, and *He* were moderate ($Pi = 1.439 \times 10^{-4}$, $Ho = 0.788$, $He = 0.707$). At the patch level, *Ho* values exceeded *He* values in both patches, with patch A exhibiting a lower *Pi* (1.429×10^{-4}) than that of patch B ($Pi = 2.794 \times 10^{-4}$). Patch A exhibited a slightly higher *Ho* (0.824) than that of patch B ($Ho = 0.754$), while patch A's *He* (0.714) was comparable to patch B's ($He = 0.700$). The *He* value of patch A was slightly higher than that of patch B, whereas the *He*-to-*Ho* ratio of patch B approached zero.

At the species level, the *Fi* for *P. flavus* from the BM population was 0.224. Notably, both patched in BM population exhibited positive *Fi* values, suggesting the absence of heterozygotes within these two patches and the occurrence of inbreeding mating events. Specifically, the *Fi* value of patch A ($Fi = 0.373$) was slightly lower than that of patch B ($Fi = 0.477$).

Table 2
Genetic diversity parameter of *P. flavus*

Population numbers	*N*	*Pi*	*Ho*	*He*	*Fi*
Beikengding Mount	34	1.439×10^{-4}	0.788	0.707	0.224
Patch A	20	1.429×10^{-4}	0.824	0.714	0.373
Patch B	14	2.794×10^{-4}	0.754	0.700	0.477

Note: *N* = Sample size; *Pi* = Nucleotide polymorphism; *Ho* = Observed heterozygosity, *He* = Expected heterozygosity; *Fi* = Inbreeding coefficient.

Principal component and phylogenetic analysis

Phaius flavus BM population was distributed across all four quadrants, mainly in Quadrants 1, 2, and 4. Individuals from patch A were mainly concentrated in Quadrant 2, with a few individuals distributed across the other three Quadrants. In contrast, patch B was distributed in Quadrants 1 and 4 (Fig. 2). The distribution of the patches was relatively independent, with only minimal overlap, indicating that individuals within the two patches occupied distinct genetic positions.

Genetic distances were computed based on 325,954 SNP loci, and a phylogenetic tree was constructed using the Figtree software (Fig. 3). The higher support rate demonstrated a clear differentiation and clustering of the two patches within the BM population into a single unit. However, support for distinguishing individuals within the two patches post-branching was generally low, indicating close genetic relatedness which makes differentiate difficult (Fig. 4).

Genetic structure, genetic differentiation and gene flow analysis

The results of the genetic structure analysis revealed that 14 individuals, including A13A, A18A, B10A, and B11A, were fully distinguishable (Fig. 5); therefore, our results suggested that patches A and B were from two gene pools. However, 59% of the individuals could not be clearly distinguished because of the more frequent exchanges between the two gene pools. This result is consistent with those of previous analyses.

Genetic differentiation among populations potentially affects species viability. The genetic differentiation index ($Fst = 0.055$) between the two patches indicated a certain degree of genetic differentiation. The gene flow analysis results ($Nm = 13.733$, $Nm > 1$) suggested frequent gene flow between the two patches.

Bottleneck effect detection

In the BM population, Tajima's *D (D)* value was − 0.570 and 0.379 for patches A and B, respectively. The nonzero *D* values in both patches suggested the occurrence of a natural selection event rather than a neutral mutation. Specifically, *D* values below zero in patch A indicated a lower heterozygous locus than expected, leading to an increased frequency of rare alleles. Conversely, *D* values above zero in patch B indicated a higher observed heterozygosity than expected, leading to a decreased frequency of rare alleles.

Discussion

Overall genetic diversity of the P. flavus BM population

Population genetic diversity is an important component of biodiversity, and the level of genetic diversity represents the magnitude of environmental adaptability of a species. In general, populations with high genetic diversity are more likely to survive in variable environments [28], and the genetic diversity of the *P. flavus* BM population may explain its wide distribution. *Phaius flavus* (*Pi* = 1.439×10^{-4}, *Ho* = 0.788, *He* = 0.707) from the BM population exhibited a higher level of genetic diversity. This is in contrast to other orchids such as *Cypripedium macranthos* (*Pi* = 0.154, *Ho* = 0.134, *He* = 0.153) [13], *Geodorum eulophioides* (*Pi* = 0.158, *Ho* = 0.012, *He* = 0.025) [18], and *D. catenatum* (*Pi* = 0.158, *Ho* = 0.099, *He* = 0.158) [29]. Similarly, *P. flavus* from the BM population showed significant genetic diversity compared to congeneric *Phaius* such as *P. australis* and *P. bernaysii* [20]. Although *G. eulophioides* has a similar clonal growth pattern, a population with a high clone proportion (66.7%) results in lower genetic diversity [28]. In contrast, *P. flavus* maintained substantial sexual reproduction, perhaps because of its longer lifespan, meeting the requirements for individual growth and development, and symbiotic fungi during germination and growth of *P. flavus*.

Genetic diversity among patches were affected by habitat fragmentation

Habitat fragmentation transforms the natural environment into multiple relatively isolated patches, which is crucial for the sustenance of organisms. Anthropogenic disturbances are the primary drivers of this phenomenon and significantly reduce the habitat quality of plant populations via edge effects [30]. Habitat fragmentation significantly affects population size and species distribution patterns [4], leading to a reduction in genetic diversity and enhancement of genetic differentiation in small populations [31]. In our study, patch B had fewer individuals than patch A. However, genetic diversity analysis results indicated a higher level of genetic diversity in patch B (*Pi* = 2.794×10^{-4}, *Ho* = 0.754, *He* = 0.700) than in patch A (*Pi* = 1.429×10^{-4}, *Ho* = 0.824, *He* = 0.714). Generally, populations with a large number of individuals have longer survival times, and reductions in the number of individual plants can lead to decreased or lost population genetic diversity [32]. This phenomenon is prevalent in populations exposed to long-term habitat fragmentation, primarily due to a combination of rapid genetic drift [33], reduced gene flow [34], and inbreeding [35].

To ensure population survival, young *P. flavus* populations prioritize asexual reproduction [22]. We suggest that the population size of patch A was larger than that of patch B, which may lead to smaller genetic diversity in patch A. This may have been caused by the following three conditions: (1) upon fragmentation of the BM population, the population size of patch A exceeded that of patch B; (2) following the bottleneck effect, the population of patch A entered a phase of expansion, mainly relying on asexual reproduction for survival; and (3) under the influence of (2), the genetic diversity level in the two patches was subjected to the environment. The expected influence of reproductive modes on genetic diversity has been acknowledged, although existing dataset do not clarify the specific mechanisms through which reproductive strategies influence population variation within patches.

Genetic differentiation is undergoing between patches

Habitat fragmentation is a strong determinant of the genetic structure of populations and can influence their genetic structure by affecting the population size, reproductive mode, and environmental factors. In the BM population, two patches were divided owing to the construction of the Y013 village road (cement road) in Youxi County, which was primarily affected by intermittent flow disturbance. Genetic structure analysis suggested that the construction of the village road might have limited genetic exchange between the two patches in the BM population, leading to ongoing genetic differentiation in this population (*Fst* = 0.055). Genetic variation and drift can lead to genetic differentiation between individuals, which is exacerbated by an increase in isolation by distance (IBD), leading to a new genetic structure [36, 37]. Our study shows that habitat fragmentation diminishes the connectivity of populations between patches. Short-distance isolation between the two patches allowed for independent differentiation of the BM population, which was consistent with the results of the principal component and phylogenetic analyses.

Moreover, the ability of the population to adapt to the environment and reproductive methods may change because of increased environments differences, which can increase the genetic differentiation of populations and change their genetic structure [38]. Orchidaceae are more sensitive to environment changes. Studies have shown that genetic differentiation in orchids is affected by the combination of IBD and isolation by environment (IBE) [39]. The environments of the two patches in the BM population were significantly different, therefore, individuals in the two patches had to adapt to the effects of environmental differences. Environmental changes directly affect population reproduction [40]. For example, pollinator behavior is affected by light [41], temperature [41] and humidity [42]. In the BM population, patch A was located in an environment with lower temperature and light than patch B and had higher humidity. Thus, the abiotic environment of patch A was unfavorable for pollinator visits, which may have had a negative impact on sexual reproduction. In summary, our results indicate that the BM population may differentiate because of distance and environmental isolation caused by human activities. Furthermore, the lower level of genetic differentiation suggests that genetic differentiation occurred between the patches. Despite the absence of pre-construction data, it is imperative to monitor the genetic levels and environmental conditions of the population over the next 8–10 years. This will facilitate a precise evaluation of the influence of human activities on the BM population.

Gene flow between patches may be maintained by sexual reproduction

Habitat fragmentation disrupts the gene flow between populations [43], and is mainly manifested in sexual reproduction, often through seeds and pollen between populations [44]. The sexual reproduction of flowering plants in any life-history trait or habitat type is susceptible to the negative effects of habitat fragmentation [45], where isolation between patches tends to influence pollinator multiplicity and abundance. However, the effects depend on the degree of habitat fragmentation [46]. The role of seed dispersal in shaping small-scale spatial genetic structures cannot be ignored [47], especially for small seeds that are resistant to fragmentation. Orchidaceae seeds are small and light, enabling them to disperse over long distances from the wind, which is a typical feature of anemophily [48]. In our study, nearly a decade had passed since the completion of the Y013 village road, yet a high-frequency gene flow (*Nm* = 13.733) existed in the two patches. Our findings indicate that the seed dispersal of *P. flavus* is insensitive to geographical isolation.

Additionally, habitat fragmentation can directly or indirectly change the pollination structure of pollinators, thereby affecting the gene flow among populations [46, 49], with profound implications for the genetic characteristics of populations. *Phaius* reproduces primarily through both sexual and asexual means. The sticky pollinia of *Phaius* are incapable of wind dispersal, and rely on pollinators for long-distance transmission [50]. Similar to its congener *Phaius*, *P. flavus* employs deceptive pollination strategies. Although the division of the BM population into two patches was due to the construction of the Y013 village road, there were two patches with a relatively short distance between them (approximately 1km), which account for the recognized pollination distance (2 km). Therefore, gene flow (*Nm* = 13.733) persisted between patches. In contrast, *P. flavus* sustains its lifespan, stabilizes population size, and accumulates nutrients mainly through clonal reproduction, whereas the production of new individuals primarily depends on sexual reproduction [22]. Therefore, our findings suggest that gene flow between the two patches of the BM population is primarily maintained through sexual reproduction, whereas asexual reproduction restricts the exchange of genes between the two patches due to dispersal constraints [51, 52]. Furthermore, *P. flavus*, a long-lived plant, exhibits hysteresis and specificity for habitat fragmentation [53, 54]. These factors may have contributed to the observed high-frequency gene flow within the population.

Conclusions

In the present study, the genetic characteristics of the *P. flavus* BM population were altered. At the species level, our findings revealed that the BM population of *P. flavus* had a high level of genetic diversity compared to that of other orchid species. The population genetic diversity revealed that the genetic diversity of patch A was lower than that of patch B. The bottleneck effect detection results showed that patch A was in the stage of population expansion after the bottleneck effect, indicating that it was caused by priority development of asexual reproduction in patch A. Principal component and phylogenetic analyses indicated that the individuals in two patches occupied different genetic positions,

but 59% of the individuals were still indistinguishable. Moderately low genetic differentiation (*Fst* = 0.055) was observed between the two patches, suggesting that the BM population may have been affected by construction of the Y013 village road. Furthermore, our results suggest that sexual reproduction may have maintained a high gene flow (*Nm* = 13.733) between the two patches. This study illustrate how human activities affect the genetic traits of natural Orchidaceae populations, and serves as a valuable reference for biodiversity conservation.

Abbreviations

BM Beikengding Mount

RAD-Seq Restriction site-associated DNA sequencing

He Expected heterozygosity

Ho Observed heterozygosity

Fst Genetic differentiation index

Pi Nucleotide diversity

Fi Inbreeding coefficient

D Tajima's *D*

SNP Single nucleotide polymorphisms

IBD Isolation by distance.

IBE Isolation by environment

Nm Number of Migrants

Declarations

Ethics approval and consent to participate

The materials in this study were collected from state-owned land, and not in the natural reserve. Sample collection in this study is conducted by the Regulations of the People's Republic of China on the Protection of Wild Plants and China's List of Wild Plants under State Priority Conservation.

Consent for publication

Not applicable.

Competing interests

There are no competing financial interest to declare.

Availability of data and materials

All the plant materials were collected from the natural population in Beikengding Mount, Fujian Province. The raw RAD-seq data are available at NCBI with the SRA accession number PRJNA1082066. The voucher specimen for this study was only stored in Herbarium, College of Forestry, Fujian Agriculture and Forestry University(FJFC), deposition number: FJFC19091801, Specimen Identifier: Junwen Zhai.

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Authors` contributions

JZ managed the project and acquired the funding. CL wrote and reviewed the manuscript, and made the distribution map. JL designed the study, investigated, and collected samples. CL, SL, and HZ disposal data. CL and JL analyzed the data. JZ and JM were responsible for the software. CL, SL, HZ, and JZ improved the manuscript. SW, CL, SL, HZ, JZ, and SH modified the manuscript format. JZ and ZL supervised the research project. SW, ZL, and JZ reviewed the manuscript content.

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Figures

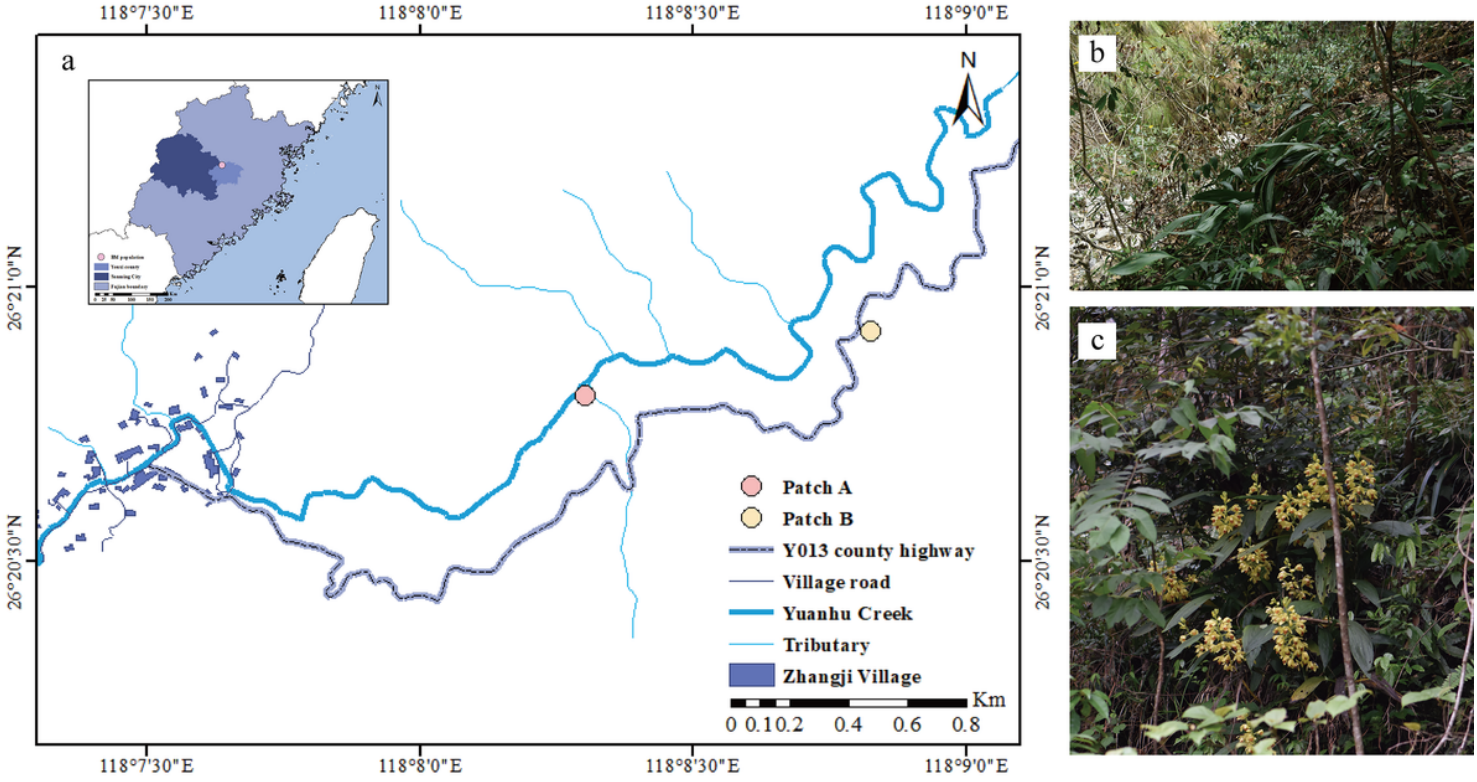


Figure 1

Geographical location maps of the study area: a. distributional position of the BM population of the P. flavus in Fujian Province and the location of patches A and B in the BM population; b. habitat of Patch A (photo was taken by Jun Li in December 2018); c. habitat of Patch B (photo was taken by Jun Li in March 2019). Map from http://lbs.tianditu.gov.cn/home.html and http://www.arcgis.com/index.html.

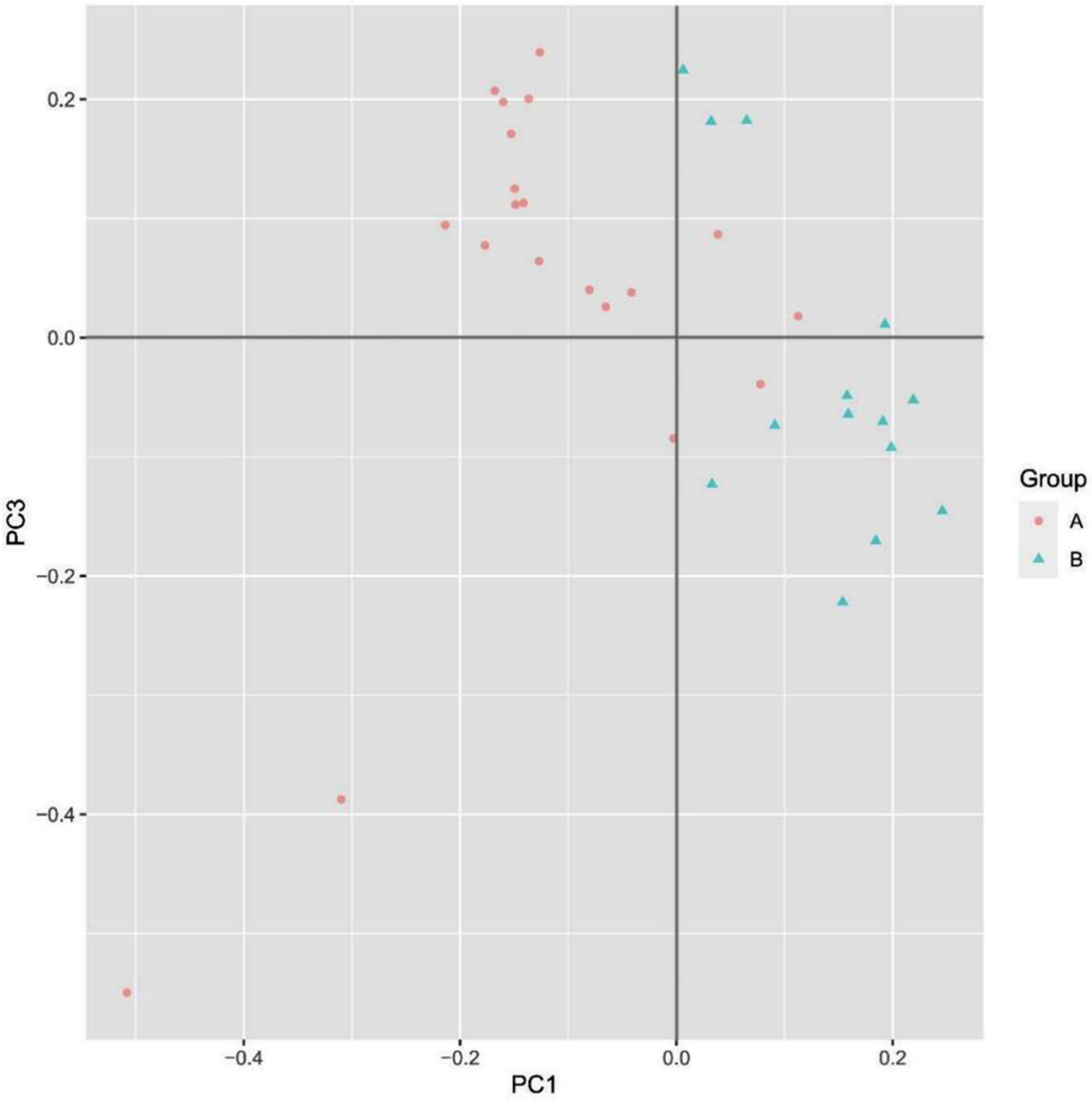


Figure 2

Principal component analysis of patch A & B *P. flavus* populations. Patch A is clustered in the second Quadrant, while patch B is distributed in the first and fourth Quadrants.

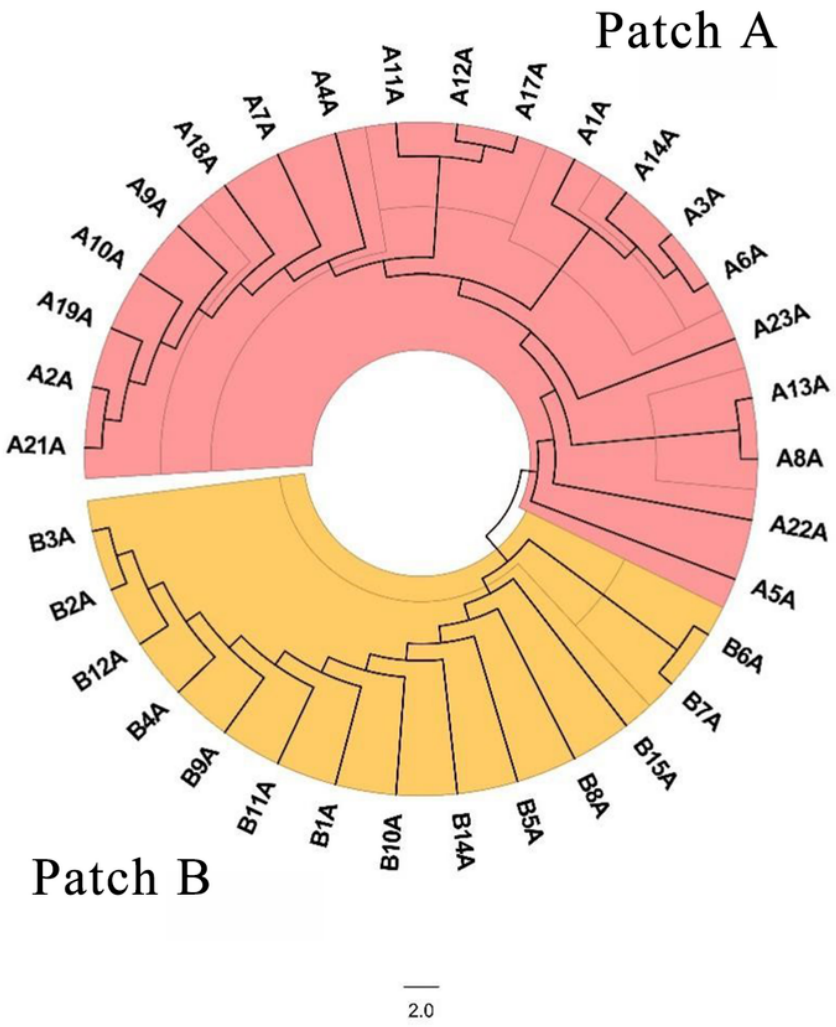


Figure 3

The phylogenetic analysis of *P. flavus*populations. Patch A and patch B can be clearly distinguished. The red color marks the branch of patch A and the yellow color marks the branch of patch B.

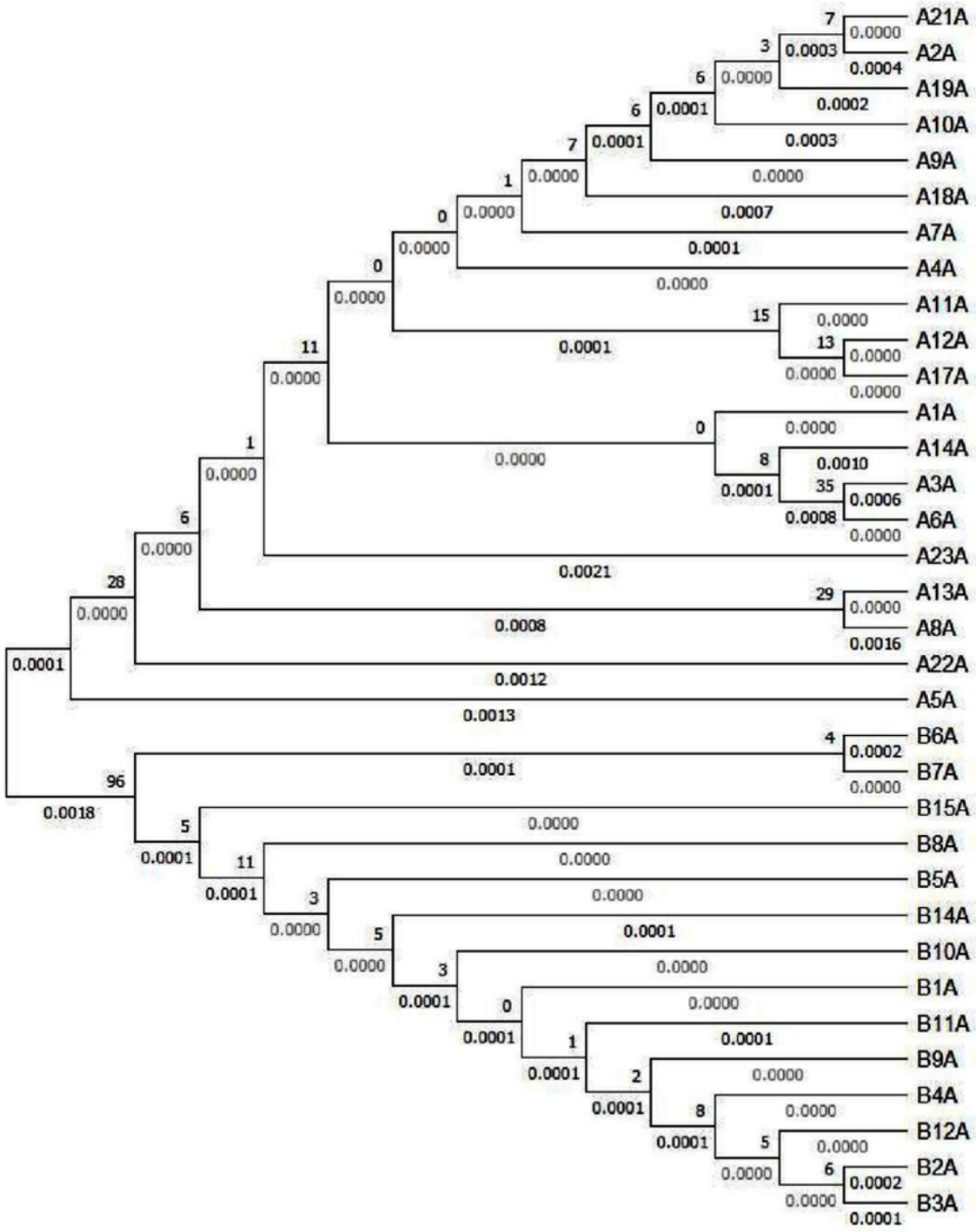


Figure 4

The original phylogenetic analysis of *P. flavus* populations. The individuals of patches A and B differentiates independently.

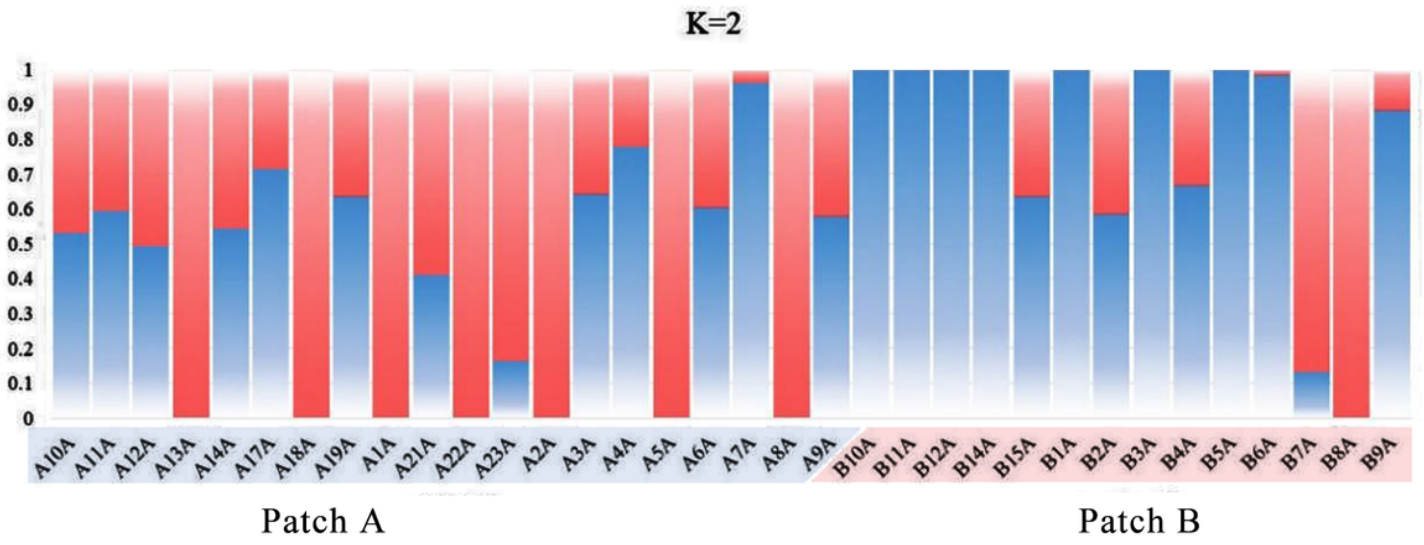


Figure 5

Population structure between patches A & B of the *P. flavus* population. It shows ancestry coefficients for *K*=2. The x-axis shows the different individuals from patch A and patch B; the y-axis quantifies the proportion of an individual's variation from inferred ancestral populations.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- TableS1Allsamplesequencingdatastatistics.xlsx