As keystone species, fig trees (*Ficus* L., Moraceae) play a significant role in both tropical and subtropical ecosystems by providing food for many vertebrates (Shanahan et al., 2001). Some *Ficus* species are widely cultivated outside their natural distribution range, providing a valuable opportunity to explore the mechanism of range limits of *Ficus* species. However, little is known about its genetic background.

*Methods and Results:* Fifteen polymorphic microsatellite markers were developed using the biotin-streptavidin capture method. Polymorphism was tested in 85 *F. virens* individuals sampled from three populations. The number of alleles ranged from three to 17. The observed and expected heterozygosity of each population varied from 0.0667 to 0.9286 and 0.0650 to 0.8890, respectively. Cross-species amplification was also carried out in eight other *Ficus* species.

*Conclusions:* These 15 markers will be valuable for studying the genetic variation and population structure of *F. virens* and related *Ficus* species.

**Key words:** cross-amplification; *Ficus virens*; genetic diversity; microsatellite; Moraceae; southwest China.

**METHODS AND RESULTS**

Plant material and DNA extraction—Young and healthy leaves of *F. virens* were collected in Chengdu (30.68271°N, 104.10363°E), Mianyang (31.47661°N, 104.78943°E), and Chongqing (29.8217°N, 106.42913°E) in southwestern China (Appendix 1). The sampled leaves were kept in alochroic silica gel for drying. Genomic DNA was extracted from 0.03 g dry leaves using a Plant Genomic DNA Kit (Tiangen Biotech, Beijing, China).

Development of microsatellite primers—Microsatellite primers were developed using the biotin-streptavidin capture method following the procedure of Kijas et al. (1994) and Zhang et al. (2016). *MsoI* (New England Biolabs, Beverly, Massachusetts, USA) was applied to digest the genomic DNA in a 25-μL reaction volume overnight at 37°C. Then the fragments were ligated to *MsoI* adapters (F: 5′-TACTCAGAGTCAT-3′, R: 5′-GAGGATGCTGCTGAAG-3′) and amplified with *MsoI*-N primer (5′-GATGAGTCTGCTGAAT-3′) with the following conditions: 3 min denaturation at 95°C, followed by 20 cycles of 30 s denaturation at 94°C, 1 min annealing at 53°C, and 1 min extension at 72°C; with a final extension of 72°C for 8 min. The PCR products were mixed with 5-biotinylated probe (AC)15 followed by 5 min denaturation at 95°C, and 2 h hybridization at 48°C. Hybridization products were captured with streptavidin-coated magnetic beads (Promega Corporation, Madison, Wisconsin, USA). The enriched product was amplified with *MsoI*-N as primers for an additional 30 cycles according to the conditions described above. Purification was then performed with a multifunctional DNA Extraction Kit (Sangon Biotech, Shanghai, China), the products were ligated into pGM-T vector (Tiangen Biotech), and then transformed into *Escherichia coli* strain DH5α (Tiangen Biotech). In total, 108 positive clones were selected and sequenced. These were tested by PCR using (AG)15 and M13′/M13″ as primers. The selected positive clones were sequenced with primer M13′/M13″ on an ABI 3730 DNA Sequence Analyzer (Applied Biosystems, Foster City, California, USA) at Sangon Biotech. Eighty-two clones contained simple sequence repeats, 47 of which were discarded because their sequences were too short for primer design. The remaining clones were used to design primers with Primer Premier version 5.0 (PREMIER Biosoft International, Palo Alto, California, USA). The criteria for primer design were as follows: (1) product size from 100 to 300 bp; (2) primer size from 16 to 23 bp with an optimum size of 20 bp; (3) primer melting temperature from 45°C to 65°C with an optimum temperature of 55°C; and (4) GC content of primers from 40% to 60%.

Thirty-five pairs of microsatellite primers were designed and successfully amplified. The polymorphism of each designed primer was tested using 23 randomly selected individuals. PCRs were performed in a 15-μL volume containing 1.5 μL of 10× PCR buffer (with Mg2+), 0.3 μL dNTPs (2 mM each), 0.1 μL each primer (1 of 3)
Mianyang was measured using selected polymorphic primers to further test the amplification and visualized by silver staining with pUC19 DNA/HindII (Fermentas Osaka, Japan), and 12.6 μM of L Blend Taq (2.5 units; Toyobo Co. Ltd., Osaka, Japan), and 12.6 μl of DNase-free water. PCR cycling was performed using the program described by Zhang et al. (2016). The products were first checked on 1% agarose gels, then settled on 8% denaturing polyacrylamide gels, and visualized by silver staining with pUC19 DNA/HindII (Fermentas International, Burlington, Ontario, Canada) as the ladder. Of the 35 microsatellite primers, 20 were monomorphic and 15 were polymorphic.

Genetic variation of three populations (Chengdu, Mianyang, and Chongqing) was measured using selected polymorphic primers to further test the amplification stability of each primer. The forward primers of each polymorphic locus were labeled with fluorescent dyes (5’ TAMRA, 5’ ROX, 5’ FAM [FITC]; Sangon Biotech) for scoring fragment length on an ABI 3130 automated sequencer (Applied Biosystems), using GeneScan 500 LIZ (Applied Biosystems) as an internal lane standard. The fragment lengths were calculated by GeneMapper 4.0 (Applied Biosystems) software.

**Data analysis**—Linkage disequilibrium and Hardy–Weinberg equilibrium (HWE) were calculated using GENEPOP 4.0 (Rousset, 2008), and occurrence

| Locus | Primer sequences (5'→3') | Repeat motif | Allele size (bp) | T<sub>c</sub> (°C) | A | GenBank accession no. |
|-------|--------------------------|--------------|-----------------|-----------------|---|----------------------|
| V33   | F: TGGTGAAAGCCACGACGACCACAGGT | (CT)<sub>12</sub> | 112 | 58 | 3 | KU795125 |
| V42   | R: CCAAGAAAGCAACGCAAGAT | (AG)<sub>10</sub>(AG)<sub>12</sub> | 154 | 58 | 4 | KU795126 |
| V70   | F: CCACTCGCAGCCAGAAGTA | (AC)<sub>11</sub> | 190 | 58 | 12 | KU795127 |
| V98   | R: GGTTATTTGTGCGAAGAG | (CT)<sub>9</sub> | 156 | 58 | 9 | KU795128 |
| V99   | F: GTAGGCTTAACTTTGAGGACC | (AG)<sub>6</sub> | 111 | 58 | 9 | KU795129 |
| V131  | F: TCAAGCAAAAGACGACGACT | (AG)<sub>6</sub> | 149 | 58 | 10 | KU795130 |
| V149  | F: ATGTAGGACTTTGGGACC | (TC)<sub>10</sub> | 202 | 58 | 8 | KU795131 |
| V159  | R: AGCACGACGAGCACAGTG | (AG)<sub>12</sub> | 131 | 58 | 6 | KU795133 |
| V171  | F: GAGATGCGGAGCAACACA | (AG)<sub>12</sub> | 234 | 58 | 17 | KU795134 |
| V183  | R: CCTGATGCTGGCGTGGT | (GA)<sub>17</sub> | 263 | 58 | 15 | KU795135 |
| V212  | F: CTCGGCGGTCAGTCAGTACA | (TC)<sub>6</sub>(CT)<sub>6</sub>(AT)<sub>3</sub> | 132 | 58 | 5 | KU795136 |
| V217  | R: GGTGTCATCATCATATGTCCC | (AG)<sub>4</sub> | 175 | 58 | 6 | KU795137 |
| V230  | F: CCCACCAGGAGGAGGTTAG | (AG)<sub>9</sub> | 119 | 56 | 10 | KU795138 |
| V254  | R: GCGCCAGGACATGCT | (TC)<sub>3</sub> | 190 | 58 | 11 | KU795139 |

Note: A = number of alleles sampled; T<sub>c</sub> = annealing temperature.

| Locus | Primer sequences (5'→3') | Repeat motif | Allele size (bp) | T<sub>c</sub> (°C) | A | GenBank accession no. |
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| V70   | F: CCACTCGCAGCCAGAAGTA | (AC)<sub>11</sub> | 190 | 58 | 12 | KU795127 |
| V98   | R: GGTTATTTGTGCGAAGAG | (CT)<sub>9</sub> | 156 | 58 | 9 | KU795128 |
| V99   | F: GTAGGCTTAACTTTGAGGACC | (AG)<sub>6</sub> | 111 | 58 | 9 | KU795129 |
| V131  | F: TCAAGCAAAAGACGACGACT | (AG)<sub>6</sub> | 149 | 58 | 10 | KU795130 |
| V149  | F: ATGTAGGACTTTGGGACC | (TC)<sub>10</sub> | 202 | 58 | 8 | KU795131 |
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| V230  | F: CCCACCAGGAGGAGGTTAG | (AG)<sub>9</sub> | 119 | 56 | 10 | KU795138 |
| V254  | R: GCGCCAGGACATGCT | (TC)<sub>3</sub> | 190 | 58 | 11 | KU795139 |

Note: A = number of alleles sampled; H<sub>e</sub> = observed heterozygosity; A<sub>1</sub> = number of alleles sampled; H = observed heterozygosity; HWE = Hardy–Weinberg equilibrium; n = number of individuals sampled.

*Voucher and locality information are provided in Appendix 1.
* Significant deviation from HWE (P < 0.05).

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of null allele frequences was tested with MICRO-CHECKER 2.2.3 (van Oosterhout et al., 2004). The genetic variations were estimated for two sampled populations by FSTAT 2.9.3.2 (Goudet, 2001), using the parameters of the number of alleles at each locus, observed heterozygosity, and expected heterozygosity.

Linkage disequilibrium was not detected in any loci. The number of alleles per locus ranged from three to 17, with an average of 9.333 (Table 1). The observed heterozygosity and expected heterozygosity of each population ranged from 0.0667 to 0.9286 and 0.0650 to 0.8890, respectively (Table 2). The observed heterozygosity and expected heterozygosity of each population ranged from 0.0667 to 0.9286 and 0.0650 to 0.8890, respectively (Table 2). Five loci (V70, V159, V183, V212, V254) in Chengdu, four loci (V98, V159, V212, V254) in Mianyang, and three loci (V42, V212, V254) in Chongqing showed significant departure from HWE. Two loci (V212, V254) showed consistent deviation from HWE. This could be caused by the presence of null alleles (present in six loci: V70, V98, V159, V183, V212, and V254) or by homozygote excess.

Cross-amplification in additional species — Cross-amplification of polymorphic microsatellite primers was performed on eight related species (n = 5 for each species), including F. altissima Blume, F. benjamina L., F. deltoidea Jack, F. hispida L., F. microcarpa L., F. montana Burm., F. rumphii Blume, and F. sarmentosa Buch.-Ham. ex Sm.

All 15 polymorphic primers amplified successfully (amplified a distinct band when the PCR products were checked on 1% agarose gel) in at least one of the eight additional Ficus species tested (Table 3). Two of the markers (V188, V254) were successfully amplified in all eight species, while one locus (V212) was only successfully amplified in F. altissima. Successful amplification across species did not appear to be correlated with the closeness of the genetic relationship of the species tested with F. virens. However, the cross-species sample size was limited and it is still likely that these markers will be most useful for closely related species.

CONCLUSIONS

In this study, 15 microsatellite markers were developed specifically for F. virens and showed considerable polymorphism in all three studied populations. These markers can be used in further studies to explore the mating system, population genetic structure, and gene flow of F. virens.

APPENDIX 1. Voucher and locality information for Ficus virens specimens used in this study.a

| Voucher accession no. | Collection locality | Geographic coordinates |
|-----------------------|---------------------|------------------------|
| HWNU-FV20160805001-XqY, XYD | Chengdu, Sichuan | 30.68271°N, 104.10363°E |
| HWNU-FV20160801002-LT, Rhf | Mianyang, Sichuan | 31.47661°N, 104.78943°E |
| HWNU-FV20160818003-LT, Rhf | Chongqing | 29.8217°N, 106.42913°E |

a Vouchers are deposited in the Herbarium of China West Normal University, Nanchong, Sichuan, China.

b Collectors: XqY = Xiqian Yang; XYD = Xiangyue Ding; LT = Lu Tan; Rhf = Ronghua Fu.