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# ISOLATION AND CHARACTERIZATION OF 12 MICROSATELLITE LOCI IN SOAPBARK, *QUILLAJA SAPONARIA* (QUILLAJACEAE)<sup>1</sup>

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- **Premise of the study:** Microsatellite primers were developed for the endemic Chilean tree *Quillaja saponaria* (Quillajaceae), a common member of the sclerophyllous Mediterranean forest, to investigate intraspecific patterns of genetic diversity and structure.
- **Methods and Results:** Using an enriched library, 12 polymorphic microsatellite loci were developed in *Q. saponaria*. All loci consisted of dinucleotide repeats. The average number of alleles per locus was 5.3 (2–13), with a total of 64 alleles recorded in 39 individuals from three populations.
- **Conclusions:** The microsatellite markers described here are the first characterized for *Q. saponaria*. The polymorphic loci will be useful in studies of genetic diversity and genetic population differentiation in natural populations of this species.

**Key words:** Chile; microsatellites; *Quillaja saponaria*; Quillajaceae; soapbark.

*Quillaja saponaria* Molina is an endemic Chilean tree, known as soapbark, soap bark tree, or quillay (as it is known in Chile). It is an evergreen tree of the family Quillajaceae (Kubitzki, 2007), found from the Coquimbo Region to Arauco Province in the Bío-Bío Region, approximately between 31° and 38° south (García and Ormazabal, 2008). It grows from sea level to 1600 m a.s.l., preferably in dry areas that are poor in nutrients. The family is monotypic with a single genus and two species from warm-temperate South America (Chile, Brazil, and northern Argentina). *Quillaja saponaria* is considered one of the most important and representative species of the sclerophyllous forest from central Chile, and these communities are part of a biodiversity hotspot called the Chilean Winter Rainfall–Valdivian Forest (Mittermeier et al., 1998; Myers et al., 2000). Moreover, *Q. saponaria* is a timber species (García and Ormazabal, 2008), its flowers are melliferous (Montenegro et al., 2009), and the bark is rich in saponins and medicinal adjuvants (Kensil et al., 1991; San Martín and Briones, 1999).

Our purpose is to evaluate the effects of anthropogenic fragmentation on the patterns of genetic variation and connectivity in populations of *Q. saponaria*. For this reason, we isolated and characterized 12 nuclear microsatellite loci that are being successfully applied to describe spatial patterns of genetic structure. These are the first microsatellite markers developed for a *Quillaja* Molina species.

## METHODS AND RESULTS

Microsatellite isolation was performed by the simple sequence repeat (SSR) development company Genetic Marker Services (Brighton, United Kingdom; [www.geneticmarkerservices.com](http://www.geneticmarkerservices.com)). Genomic DNA was extracted from a single *Q. saponaria* (Qsa) individual collected in the locality of Coya, near the city of Rancagua, O'Higgins Region, Chile (locality 5 in Appendix 1), using a modified cetyltrimethylammonium bromide (CTAB) protocol described by Doyle and Doyle (1990), and used to develop an enriched library to isolate microsatellite (SSR)-containing loci. Enrichment involved incubating adapter-ligated restricted DNA with filter-bonded synthetic repeat motifs: (AG)<sub>17</sub>, (AC)<sub>17</sub>, (AAC)<sub>10</sub>, (CCG)<sub>10</sub>, (CTG)<sub>10</sub>, and (AAT)<sub>10</sub>. Thirty-two motif-positive *Escherichia coli* JM109 clones were detected and sequenced, of which 23 contained exploitable repeat motifs with sufficient flanking regions to design forward/reverse primer pairs. The online primer design software Primer3 (Rozen and Skaletsky, 1999) was used to develop primer pairs amplifying fragments ranging in size from 100 to 250 bp, to help minimize later multiloading overlap ambiguities during sequencer genotyping. The primers were then tested for successful amplification on one individual from each of seven populations, chosen to represent the whole latitudinal range of the species' distribution (Cuesta el Espino, Cuesta Los Cristales, Santa Marta, Fundo La Rosa, La Gatera, San Fabián de Alico, and Santa Bárbara; Appendix 1), using a touchdown PCR protocol. PCR amplifications were performed in a 25-μL final volume containing 7 pmol of each primer, 1.5 mM of MgCl<sub>2</sub>,

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0.2 mM of each dNTP, 1× PCR buffer, 0.8 µg/µL bovine serum albumin (BSA), 0.5 units *Taq* polymerase (Promega Corporation, Madison, Wisconsin, USA), and 1.5 µL of DNA diluted 20-fold. For all loci, the same touchdown PCR program was used, consisting of 32 cycles with denaturation at 95°C for 60 s; annealing for 60 s with temperature decreasing 1°C every two cycles from 64°C to 59°C (12 cycles), then 10 cycles at 58°C, and 10 cycles at 57°C; elongation at 72°C for 60 s; and a final extension at 72°C for 5 min. Products were checked for specificity and polymorphism on a cooled high-resolution agarose gel, consisting of 4% MetaPhor (Lonza, Basel, Switzerland) agarose in TAE, run in a cold room at 10°C. Sixteen loci showed clear and specific bands with size variation among the seven individuals assayed (Table 1). Of these, the 12 with the highest degree of apparent polymorphism were chosen for fluorescent labeling (Table 1).

To determine the number of alleles, expected and observed heterozygosity, and to test for deviations from Hardy–Weinberg equilibrium (HWE) and linkage disequilibrium, we tested the 12 fluorescent-labeled primer pairs on 39 individuals from three different populations, situated in the northern and southern parts of the species' range (i.e., Angostura, Astillero, and Cuesta Batuco; localities 1, 8, and 9 in Appendix 1). The PCR amplifications were performed with the Platinum Multiplex PCR Master Mix (Applied Biosystems, Carlsbad, California, USA) using three mixes, each with four fluorescent-labeled primers (Applied Biosystems, Warrington, United Kingdom; Table 1): Mix 1 (Qsa7, Qsa11, Qsa13, Qsa24), Mix 2 (Qsa16, Qsa17, Qsa18, Qsa70), and Mix 3 (Qsa19, Qsa26, Qsa28, Qsa66). The PCR amplifications were performed in a 5-µL final volume containing final concentrations of 1× Platinum Multiplex PCR Master Mix, 2 mM of additional MgCl<sub>2</sub>, 0.10 µM of primer mix, and 20 ng of template DNA, with the following cycling conditions in all cases: an initial heat activation at 94°C for 5 min; followed by a touchdown PCR consisting of 32 cycles with denaturation at 95°C for 60 s; annealing for 60 s with temperature decreasing 1°C every two cycles from 64°C to 59°C (12 cycles), then 10 cycles at 58°C

and 10 cycles at 57°C; elongation at 72°C for 60 s; and a final extension at 72°C for 5 min. The PCR products (2 µL) were mixed with 10 µL of Hi-Di formamide and 0.3 µL of GeneScan 600 LIZ Size Standard before analysis on an automatic ABI-PRISM 3100-Avant sequencer (Applied Biosystems, Carlsbad, California, USA). Fragment analysis and final sizing were performed using Peak Scanner software (version 1.0; Applied Biosystems, Carlsbad, California, USA).

The number of alleles, expected and observed heterozygosity, and the significance of the deviations from HWE and linkage equilibrium were estimated with Arlequin 3.5.1.2 (Excoffier et al., 2005). The average of the total number of alleles per locus was 5.3, with a range between two (Qsa24) and 13 (Qsa19). Significant deviations from expectations under HWE after a Bonferroni correction for multiple comparisons were found in three loci from population Astillero, and in two loci from Cuesta Batuco, probably due to the small sample sizes or to the presence of null alleles, particularly in the case of the heterozygote deficits observed at loci Qsa26 and Qsa66 in population Astillero and at Qsa66 in Cuesta Batuco (Table 2). No instances of significant linkage disequilibrium were found among pairs of loci after Bonferroni correction.

## CONCLUSIONS

The 12 microsatellite loci characterized here for *Q. saponaria* are the first developed for this species and genus. These markers will be useful in studies of the population genetic diversity and structure of the species for the purpose of conservation under a scenario of land use and climate change.

TABLE 1. Characteristics of 16 microsatellite loci developed in *Quillaja saponaria*.

| Locus  | Primer sequences (5'–3')                             | Repeat motif       | Allele size range (bp) | Fluorescent dye | GenBank accession no. |
|--------|------------------------------------------------------|--------------------|------------------------|-----------------|-----------------------|
| Qsa7   | F: TGAAGAACGCTGTGTGTGAGAA<br>R: AATTCCAAATGCCAGCAGA  | (AG) <sub>10</sub> | 116–124                | 6-FAM           | KP775627              |
| Qsa11  | F: TCTCTACCAGGTCTTGCTCA<br>R: AAACACTTATGCCTTCGCAGA  | (TG) <sub>8</sub>  | 148–154                | NED             | KP775628              |
| Qsa13  | F: CGCAGACATGCTTCTAGTTC<br>R: CAAAAGCTTAGCGACAAAC    | (GA) <sub>14</sub> | 158–166                | VIC             | KP775629              |
| Qsa16  | F: AACCGTCTCAACCACATACA<br>R: GGAAGAGGGTGAAAATGAAA   | (CT) <sub>15</sub> | 205–221                | NED             | KP775630              |
| Qsa17  | F: TTGGGGTATGAAAACATTGA<br>R: AAAGGCATTCACATATAAG    | (AG) <sub>12</sub> | 136–144                | 6-FAM           | KP775631              |
| Qsa18  | F: TGGAGCTAGGTTTACTCGTTGG<br>R: AAGCCACGATTACATATTCA | (TG) <sub>6</sub>  | 112–122                | PET             | KP775632              |
| Qsa19  | F: AGAATTGGGGTGTGAGGACT<br>R: TAGGAAAATCCCAGCAAGCA   | (AG) <sub>15</sub> | 120–150                | VIC             | KP775633              |
| Qsa24  | F: TTCTTTGGTTTTTGTGCTC<br>R: GCAAAGGTCGCTACAGTTTT    | (TG) <sub>9</sub>  | 133–135                | PET             | KP775634              |
| Qsa26  | F: AACTCACAGTGACGACTTCTCA<br>R: GGAGTCTGTGCTGGTAGTGG | (TC) <sub>9</sub>  | 93–97                  | NED             | KP775635              |
| Qsa28  | F: GTACTACTAGCTAGAACTCCCC<br>R: GACCTAGTCCTTCTTTGTGT | (TC) <sub>10</sub> | 160–174                | NED             | KP775636              |
| Qsa66  | F: TTGGGGATATGTCGGGTAGA<br>R: CACCAACGCAATCAAACATT   | (AG) <sub>11</sub> | 151–163                | PET             | KP775637              |
| Qsa70  | F: TTTGGAGCTGGTGTGTGAA<br>R: AATACCGGACAACCATGAGG    | (TTC) <sub>8</sub> | 126–130                | NED             | KP775638              |
| *Qsa29 | F: CAAGTGCGACAGTCAATCTG<br>R: TGCTGCCAGAAATTCCTAGAT  | (AG) <sub>16</sub> | 200                    |                 | KP775639              |
| *Qsa30 | F: GATTGCCAGAACAAAGTGAA<br>R: AATTCATTTCACATTCACAAAA | (TC) <sub>13</sub> | 199                    |                 | KP775640              |
| *Qsa31 | F: GATTTTGGGCGATTGAAAAA<br>R: TGTCAACGTCATTCGCTAAA   | (AG) <sub>9</sub>  | 122                    |                 | KP775641              |
| *Qsa32 | F: ATTGATCAGATGTGCGGTTG<br>R: TCTCCTCTCCTCACTTGGA    | (AG) <sub>11</sub> | 160                    |                 | KP775642              |

\* Untested for polymorphism.

TABLE 2. Genetic properties of 12 newly developed microsatellites of *Quillaja saponaria*.<sup>a</sup>

| Locus | Angostura (n = 11) |                |                |       | Astillero (n = 14) |                |                |         | Cuesta Batuco (n = 14) |                |                |         |
|-------|--------------------|----------------|----------------|-------|--------------------|----------------|----------------|---------|------------------------|----------------|----------------|---------|
|       | A                  | H <sub>o</sub> | H <sub>e</sub> | HWE   | A                  | H <sub>o</sub> | H <sub>e</sub> | HWE     | A                      | H <sub>o</sub> | H <sub>e</sub> | HWE     |
| Qsa7  | 3                  | 0.778          | 0.582          | 0.712 | 5                  | 0.385          | 0.729          | 0.003   | 3                      | 0.545          | 0.537          | 1.000   |
| Qsa11 | 3                  | 0.545          | 0.437          | 1.000 | 3                  | 0.500          | 0.489          | 0.141   | 3                      | 0.917          | 0.620          | 0.035   |
| Qsa13 | 3                  | 0.909          | 0.589          | 0.043 | 4                  | 0.929          | 0.664          | 0.092   | 3                      | 0.667          | 0.627          | 1.000   |
| Qsa16 | 3                  | 0.750          | 0.633          | 0.703 | 7                  | 0.857          | 0.746          | 0.328   | 6                      | 0.917          | 0.728          | 0.559   |
| Qsa17 | 3                  | 0.300          | 0.689          | 0.028 | 4                  | 0.286          | 0.704          | 0.002   | 4                      | 0.214          | 0.680          | 0.004   |
| Qsa18 | 3                  | 0.818          | 0.541          | 0.115 | 3                  | 0.429          | 0.421          | 0.632   | 3                      | 0.714          | 0.540          | 0.420   |
| Qsa19 | 8                  | 0.818          | 0.861          | 0.200 | 9                  | 0.692          | 0.846          | 0.018   | 8                      | 0.786          | 0.786          | 0.470   |
| Qsa24 | 2                  | 0.545          | 0.416          | 0.506 | 2                  | 0.429          | 0.349          | 1.000   | 2                      | 0.583          | 0.489          | 0.593   |
| Qsa26 | 3                  | 0.182          | 0.450          | 0.009 | 2                  | 0.000          | 0.492          | 0.0003* | 3                      | 0.286          | 0.579          | 0.005   |
| Qsa28 | 4                  | 0.636          | 0.567          | 0.322 | 4                  | 0.923          | 0.591          | 0.0009* | 5                      | 0.786          | 0.659          | 0.0013* |
| Qsa66 | 3                  | 0.100          | 0.279          | 0.052 | 3                  | 0.000          | 0.283          | 0.002*  | 4                      | 0.214          | 0.431          | 0.000*  |
| Qsa70 | 3                  | 0.364          | 0.450          | 0.085 | 2                  | 0.357          | 0.304          | 1.000   | 2                      | 0.571          | 0.423          | 0.506   |

Note: A = number of alleles sampled; H<sub>e</sub> = expected heterozygosity; H<sub>o</sub> = observed heterozygosity; HWE = P values of the exact test of Hardy–Weinberg equilibrium; n = number of individuals sampled.

<sup>a</sup> See Appendix 1 for geographic coordinates and voucher information. All three populations are located in Chile.

\* Locus showed significant deviations from Hardy–Weinberg equilibrium, after Bonferroni correction (P < 0.001).

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APPENDIX 1. Voucher information for *Quillaja saponaria* samples used in this study. Vouchers are deposited at Herbarium CONC., Departamento de Botánica, Facultad de Ciencias Naturales y Oceanográficas, Universidad de Concepción, Chile.

| ID | Locality <sup>a</sup>                 | Geographic coordinates <sup>b</sup> | Altitude (m a.s.l.) | Collector                   | Collection date | Accession no. | n  | Use                            |
|----|---------------------------------------|-------------------------------------|---------------------|-----------------------------|-----------------|---------------|----|--------------------------------|
| 1  | Coquimbo Region, Angostura            | 31°27'00"S, 71°31'32"W              | 341                 | Letelier L. & A. Valderrama | 10/29/2011      | 201105        | 11 | Determining genetic properties |
| 2  | Coquimbo Region, Cuesta El Espino     | 31°21'28"S, 71°05'26"W              | 1413                | Letelier L. & A. Valderrama | 11/01/2011      | 201106        | 1  | Initial testing                |
| 3  | Coquimbo Region, Cuesta Los Cristales | 31°40'43"S, 71°08'41"W              | 669                 | Letelier L. & A. Valderrama | 11/01/2011      | 201107        | 1  | Initial testing                |
| 4  | Valparaíso Region, Santa Marta        | 32°19'07"S, 71°11'35"W              | 200                 | Letelier L. & A. Valderrama | 11/02/2011      | 201108        | 1  | Initial testing                |
| 5  | O'Higgins Region, Coya                | 34°12'19"S, 70°36'33"W              | 904                 | Letelier L. & A. Valderrama | 03/25/2012      | 201203        | 1  | Development of SSR library     |
| 6  | O'Higgins Region, Fundo La Rosa       | 34°19'10"S, 71°14'28"W              | 390                 | Letelier L. & A. Valderrama | 10/10/2011      | 201103        | 1  | Initial testing                |
| 7  | O'Higgins Region, La Gatera           | 34°49'12"S, 70°56'03"W              | 449                 | Letelier L. & A. Valderrama | 10/17/2011      | 201104        | 1  | Initial testing                |
| 8  | Maule Region, Astillero               | 35°21'48"S, 71°15'48"W              | 303                 | Letelier L. & A. Valderrama | 08/25/2011      | 201102        | 14 | Determining genetic properties |
| 9  | Maule Region, Cuesta Batuco           | 35°17'46"S, 71°58'14"W              | 267                 | Letelier L. & A. Valderrama | 08/11/2011      | 201101        | 14 | Determining genetic properties |
| 10 | Bío-Bío Region, San Fabián de Alico   | 36°30'52"S, 71°37'37"W              | 450                 | Letelier L. & A. Valderrama | 03/20/2012      | 201202        | 1  | Initial testing                |
| 11 | Bío-Bío Region, Santa Bárbara         | 37°36'37"S, 72°07'42"W              | 200                 | Letelier L. & A. Valderrama | 03/18/2012      | 201201        | 1  | Initial testing                |

Note: n = number of individuals.  
<sup>a</sup> State (region) and locality in Chile, the order of localities follows the north–south orientation of the states and within each state the sites are listed in alphabetical order.  
<sup>b</sup> Datums: World Geodetic System 1984 (WGS84).