Data Article

Molecular markers dataset to assess the genetic diversity of oriental plane trees from historical sites in Lazio (central Italy)

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A B S T R A C T

The dataset presented in this article is related to the research paper titled “Dimensional and genetic characterization of the last oriental plane trees (Platanus orientalis L.) of historical sites in Lazio (central Italy)” (Ciaffi et al., 2022). Indeed, the molecular analyses reported in that article consisted in a comparison of Italian veteran plane trees with 12 certified accessions of P. orientalis, P. occidentalis and their hybrids P. acerifolia (4 individuals per species). First, LEAFY gene analyses allowed identifying 32 P. orientalis and two P. acerifolia in four sites of the province of Rome, confirming also that the two representative trees from the two gardens of the province of Viterbo belong to P. orientalis. Second, the use of Simple Sequence Repeat (SSR) and Inter Simple Sequence Repeat (ISSR) molecular markers provided useful information regarding the genetic relationships within and among all the historical sites. Owing to the use of SSR and ISSR molecular markers, a dataset of parameters related to the genetic diversity of the same plant material was obtained and presented in this article. For SSR markers, seven loci previously developed for P. occidentalis (Lang, 2010) and two specifically developed for P. orientalis (Rinaldi et al., 2019) were employed. For ISSR markers, DNA samples were amplified with

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eight primers before used for the determination of genetic stability of micro-propagated plantlets of *P. acerifolia* (Huang et al., 2009) and for the genetic characterization of plane trees within the formal gardens of Villa Lante of Bagnaia and Palazzo Farnese (Viterbo, Italy) (Ciaffi et al., 2018). To the best of our knowledge, this is the first report on the genetic diversity data for veteran oriental plane trees within heritage sites, which will offer helpful information for their management and conservation.

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### Specifications Table

| Subject | Genetics |
|---------|----------|
| Specific subject area | Molecular markers analysis |
| Type of data | Table |
| How the data were acquired | For PCR amplification of both SSR and ISSR markers a Mastercycler Gradient Thermal Cycler 5331 was used. The SSR fragments were separated on ABI PRISM 3500 Genetic Analyzer and the amplicon signal peak height and size, from each allele, was quantified using ABI’s Gene Mapper 4.0 software. The ISSR products were separated on 1.5% agarose gels and analyzed using the UVITEC Essential V6 Gel Imaging and Documentation. For both molecular markers the genetic parameters were obtained using the Power Marker 3.25 software. |
| Data format | Raw and analyzed data |
| Description of data collection | - Genomic DNA was extracted from leaves of 36 veteran plane trees from six historical sites of Lazio region and 12 representative accessions of *P. orientalis*, *P. occidentalis* and *P. acerifolia* used as references. - 9 SSR primer pairs were used for the microsatellite amplification (plms29, plms113, plms176, 11FAM, P12A, plms109, plms68, plms130 and plms147). - 8 ISSR primers were used for the amplification (ISSR_12, ISSR_20, ISSR_24, ISSR_25, ISSR_13, ISSR_36, ISSR_14, ISSR_46). |
| Data source location | • City/Region: Grottaferrata, Lazio • Country: Italy • Latitude and longitude: 41° 47' 11.64“ N, 12° 40' 24.93“ E • City/Region: Frascati, Lazio • Country: Italy • Latitude and longitude: 41° 48’ 30.68” N, 12° 40’ 33.98” E • City/Region: Rome, Lazio • Country: Italy • Latitude and longitude: 41° 54’ 10.02” N, 12° 29’ 46.92” E • City/Region: Tivoli, Lazio • Country: Italy • Latitude and longitude: 41° 57’ 35.00” N, 12° 47’ 53.00” E • City/Region: Caprarola, Lazio • Country: Italy • Latitude and longitude: 42°19’44”N 12°14’12”E • City/Region: Viterbo (Bagnaia locality), Lazio • Country: Italy • Latitude and longitude: 42° 25’ 32.99” N, 12° 9’ 16.99” E |
| Data accessibility | Zenodo |
| Related research article | https://doi.org/10.5281/zenodo.6325140 |
| | M. Ciaffi, A.M. Vettraiino, E. Alicandri, A. Tomao, F. Adducci, E. Kuzminsky, M. Agrimi. Dimensional and genetic characterization of the last oriental plane trees (*Platanus orientalis* L.) of historical sites in Lazio (central Italy), Urban For. Urban Green. 69 (2022) 127,506. https://doi.org/10.1016/j.ufug.2022.127506 |
Value of the Data

- This is the first report on the genetic diversity data for veteran oriental plane trees within different historical sites, which will offer helpful information for their management and conservation.
- The data can benefit to any researchers and/or professors working on the veteran plane trees germplasm to provide as much information as possible on the plant material origin as well as for the owners of historical sites, to individuate the better strategies for the tree heritage management.
- The SSR and ISSR markers data reported could be useful tools to provide a dataset for the comparison of the genetic diversity of veteran plane trees belonging to other historical sites of different localities.

1. Data Description

Among the nine selected SSR loci, one (plms147) was monomorphic, thus Table 1 reported the main genetic parameters of the eight remaining polymorphic loci. In the 48 plane specimens analyzed, the identified alleles for the codominant SSR markers were 71 in total, and the number of alleles ranged from 5 (plms130 and plms176) to 15 (PI2A), with an average of 8.88 alleles per locus (Table 1). \( H_e \) ranged from 0.348 (plms109) to 0.771 (11FAM) with a mean of 0.543, while \( H_o \) varied from 0.063 (plms68) to 0.833 (PI2A) with a mean of 0.339 (Table 1). The values of inbreeding coefficients (f) were all significantly different from zero with the exception of 11FAM and PI2A loci, with a mean of 0.450 (Table 1), indicating a relatively high level of inbreeding for the *Platanus* genotypes analyzed. The SSR markers differed in their ability to detect genetic variation among the 48 plane specimens analyzed, as shown by the differences in the number

| Markers | Allele No | MAF  | \( H_o \) | PIC  | \( H_o \) | f   |
|---------|-----------|------|----------|------|----------|-----|
| SSR loci |           |      |          |      |          |     |
| plms29  | 10        | 0.719| 0.471    | 0.458| 0.229    | 0.521|
| plms113 | 11        | 0.760| 0.412    | 0.400| 0.250    | 0.402|
| plms176 | 5         | 0.521| 0.597    | 0.523| 0.229    | 0.622|
| 11FAM   | 11        | 0.333| 0.771    | 0.740| 0.813    | −0.043|
| PI2A    | 15        | 0.344| 0.757    | 0.724| 0.833    | −0.089|
| plms109 | 7         | 0.802| 0.348    | 0.336| 0.146    | 0.587|
| plms68  | 7         | 0.750| 0.417    | 0.394| 0.063    | 0.853|
| plms130 | 5         | 0.531| 0.572    | 0.488| 0.146    | 0.750|
| Mean    | 8.88      | 0.595| 0.543    | 0.508| 0.339    | 0.450|
| St. Dev. |          | 0.189| 0.160    | 0.150| 0.305    | 0.347|

| ISSR   | Total bands | Polymorphic bands (%) | Pol (%) | MAF  | \( H_o \) | PIC  |
|--------|-------------|-----------------------|---------|------|----------|------|
| ISSR_12 | 13          | 12                    | 92%     | 0.832| 0.259    | 0.216|
| ISSR_20 | 10          | 8                     | 80%     | 0.933| 0.117    | 0.104|
| ISSR_24 | 6           | 2                     | 33%     | 0.882| 0.154    | 0.123|
| ISSR_25 | 10          | 8                     | 80%     | 0.929| 0.122    | 0.108|
| ISSR_13 | 18          | 17                    | 94%     | 0.826| 0.257    | 0.213|
| ISSR_36 | 14          | 13                    | 93%     | 0.879| 0.193    | 0.165|
| ISSR_14 | 10          | 8                     | 80%     | 0.921| 0.134    | 0.118|
| ISSR_46 | 11          | 10                    | 91%     | 0.822| 0.263    | 0.217|
| Mean   | 11.5        | 9.75                  | 80%     | 0.878| 0.188    | 0.158|
| St. Dev.|             |                       |         | 0.047| 0.064    | 0.051|

Major Allele Frequency (MAF); Expected Heterozygosity (\( H_e \)); Observed Heterozygosity (\( H_o \)); Polymorphism Information Content (PIC); Inbreeding Coefficient (f); Polymorphism percentage (Pol %).
of alleles, genetic diversity ($H_e$), major allele frequency (MAF) and polymorphism information content (PIC) (Table 1). Overall, the most informative SSR loci were 11FAM and PI2A, which showed the highest PIC (0.740 and 0.724, respectively) and $H_e$ (0.771 and 0.757, respectively) values, and the lowest MAF values (0.333 and 0.344, respectively) (Table 1). On the other hand, the less informative SSR loci with the lowest PIC values were plms109 and plms68, which also were the ones showing the lowest and highest values for $H_e$ and MAF parameters, respectively (Table 1).

It is worth noting that the total number of alleles (71), the average number of alleles per locus (8.88), and the expected heterozygosity (0.543) detected here were higher than the corresponding values reported by Rinaldi et al. (2019) (62, 6.89, 0.406, respectively [3], who analyzed 429 plane tree specimens belonging to 22 P. orientalis populations. In this context, however, it should be noted that, of the 34 private alleles identified, 23 were specific to the four accessions of P. occidentalis used as references (Table 2). Indeed, the same genetic parameters calculated only for the P. orientalis trees indicated that the total number of alleles was 36, with a range from 3 (plms176, plms109 and plms130) to 7 (11FAM, PI2A), and an average of 4.5 alleles per locus (Table 3). $H_e$ ranged from 0.148 (plms109) to 0.651 (11FAM) with a mean of 0.352, while $H_o$ varied from 0.026 (plms29, plms109 and plms130) to 0.868 (PI2A) with a mean of 0.325 (Table 3). Considering only P. orientalis trees, the most informative SSR locus was 11FAM,
which showed the highest PIC (0.609) and $H_e$ (0.651) values, and the lowest MAF values (0.526) (Table 3).

Inbreeding level in plane tree genotypes where higher than in temperate wind pollinated species, which had a low level of inbreeding [6]. Indeed, the values of the observed heterozygosity ($H_o$) were significantly lower than those of the expected ones ($H_e$) for six of the eight SSR loci used (Table 1), indicating deviation from Hardy-Weinberg equilibrium and significant inbreeding, which is somehow unexpected for wind pollinated tree species such as *P. orientalis*, *P. acerifolia* and *P. occidentalis*, but confirming previous data obtained in *P. orientalis* from Rinaldi et al. [3].

Based on the ISSR analysis, 92 bands, ranging from 200bp to 2kb in size, were generated across the 48 plane specimens analyzed, with an average of 11.5 per primer (Table 1). The number of the bands varied from 6 (primer ISSR24) to 18 (primer ISSR13). Moreover, ISSR24 and ISS13 primers produced the lowest (2) and the highest (17) number of polymorphic bands, respectively (Table 1). Overall, 78 polymorphic bands were detected (80% polymorphism). $H_e$ and PIC values for the dominant ISSR markers had relatively low and uniform values, with an average of 0.188 and 0.158, respectively (Table 1). In particular, $H_e$ values ranged from 0.117 (ISSR20) to 0.263 (ISSR46), while PIC values were comprised between 0.104 (ISSR20) and 0.217 (ISSR46).

2. Experimental Design, Materials and Methods

Genomic DNA was extracted from leaves of the analyzed plane tree genotypes as described in [1]. A total of 36 veteran plane trees from historical sites of Lazio region and 12 representative *P. orientalis*, *P. occidentalis* and *P. acerifolia* accessions used as references were genotyped by using SSR and ISSR markers [1].

Nine SSR loci were used, of which seven previously developed for *P. occidentalis* [2] and two specifically for *P. orientalis* [3]. The forward primers of the nine SSR primer pairs were labeled with FAM, TAMRA, or JOE (Eurofins Genomics). PCR amplifications were performed in a 25 µL final volume containing 12.5 µL of 2X Go Taq Hot Start Colorless Master Mix (Promega Corporation, USA), 0.5 µM each of forward and reverse primers and 20 ng of genomic DNA, using the following thermal cycling conditions: 3 min initial denaturation step at 94 °C, followed by 30 cycles of amplification, each 1 min at 94 °C, 30 s at 52–60 °C, 40 s at 72 °C, and a final extension at 72 °C for 5 min. Amplification products were separated on ABI PRISM 3500 Genetic Analyzer (C.I.B.I.A.C.I. www.cibiaci.unifi.it). Allele sizes were determined using the ABI's Gene Mapper 4.0 software (Applied Biosystems) based on the GeneScan 500 LIZ size standard (Applied Biosystems). The raw data were entered in Microsoft EXCEL spreadsheet to create a codominant matrix.

For the ISSR markers, DNA samples were amplified with eight primers previously used for the determination of genetic stability of micro-propagated plantlets of *P. acerifolia* [4] and for the genetic characterization of plane trees within the formal garden of Villa Lante of Bagnaia (Viterbo, Italy) [5]. PCR reactions were carried out in a total volume of 25 µl containing 13 µl of GoTaq® Hot Start Colorless Master Mix (Promega Corporation, USA), 0.5 µM of each primer and 20 ng of genomic DNA. All reactions were performed using the following thermal cycling conditions: 4 min initial denaturation step at 94 °C, followed by 35 cycles of amplification, each 1 min at 94 °C, 1 min at 50–59 °C for 1 min, 2 min at 72 °C, and a final extension at 72 °C for 7 min. Every ISSR PCR reaction was independently conducted twice to verify amplification fidelity. ISSR fragments were separated on 1.5% (w/v) agarose gels, stained with ethidium bromide (0.001%), and visualized under UV light with the UVITEC Essential V6 Gel Imaging and Documentation System (Cleaver Scientific, Rugby, United Kingdom). In the analysis, only distinct, repeatable, and well-resolved fragments spanning from 200 to 2500bp were included. The DNA fragments (bands) in all genotypes were scored as present (1) or absent (0) for each of the ISSR markers, and the raw data were imported into a Microsoft EXCEL spreadsheet to build a binary matrix.
For SSR codominant markers each allele was reported according with its size (pb) and the genetic diversity per locus was evaluated by the following parameters: the number of alleles per locus (Allele No), Major Allele Frequency (MAF), expected (Hₑ) and observed (Hₒ) heterozygosity, Polymorphic Information Content (PIC) and inbreeding coefficient (f), using Power Marker 3.25 software [7].

The genetic diversity for each ISSR locus was evaluated by the following parameters: total number of bands obtained for each ISSR primer, number of polymorphic bands, percentage of polymorphism, MAF, Hₑ and PIC; with these latter three parameters determined using the Power Marker 3.25 software [7].

Ethics Statements

No concern.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data Availability

Tables S1 and S2 (Original data) (Zenodo).

CRediT Author Statement

Enrica Alicandri: Methodology, Software, Investigation, Data curation, Formal analysis, Writing – review & editing; Anna Maria Vettraino: Writing – review & editing; Mariagrazia Agrimi: Funding acquisition, Writing – review & editing; Mario Ciaffi: Conceptualization, Supervision, Writing – original draft, Writing – review & editing; Elena Kuzminsky: Resources, Writing – review & editing.

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