

## SUPPLEMENTARY INFORMATION (SI)

**Table 1** List of nuclear microsatellites markers (nSSRs) developed for *Dalbergia monticola* by Favreau et al. (2007) and tested on *Dalbergia melanoxylon* populations\*

*Ta* annealing temperature, *M* monomorphic, *P* polymorphic, *M13* 5'-CACGACGTTGTAAAACGAC-3', *PIG* 5'-GTTTCTT-3'

| Name of Locus | Repeat motif                         | Sequence (5' – 3')                                          | Fluorescent Dye | Allele size range <i>D. monticola</i> (bp) | Allele size range <i>D. melanoxylon</i> (bp) | Ta (°C) | Polymorphism |
|---------------|--------------------------------------|-------------------------------------------------------------|-----------------|--------------------------------------------|----------------------------------------------|---------|--------------|
| MDmCIRA04     | (GT) <sub>7</sub> A(TG) <sub>6</sub> | F: M13-AGTTCTAAACGAGAGGAGG<br>R: PIG-CTTTGGACAATACATCACC    | 6-FAM           | 250 – 276                                  | -                                            | 60      | M            |
| MDmCIRA08     | (CT) <sub>21</sub>                   | F: M13-TCCATTTCCTTCCACAG<br>R: PIG-TCCTCCACTATTATTGCC       | HEX             | 78 - 119                                   | 120 - 195                                    | 60      | P            |
| MDmCIRA12     | (TG) <sub>10</sub>                   | F: M13-ACAACCCACACTCTCAATC<br>R: PIG-CACGACCAACACTTTCAGG    | 6-FAM           | 220 - 250                                  | -                                            | 60      | M            |
| MDmCIRB06     | (GA) <sub>19</sub>                   | F: M13-TAATGTCTTGCTTTGTGGG<br>R: PIG-GTGAATCGGACGGAATAC     | 6-FAM           | 133 - 170                                  | -                                            | 60      | M            |
| MDmCIRC02     | (GT) <sub>18</sub>                   | F: M13-CTCTCTTCTCCAATCCAC<br>R: PIG-CTACCACTCACTCACCCTTC    | HEX             | 227 - 262                                  | 259 - 262                                    | 60      | P            |
| MDmCIRC10     | (CT) <sub>27</sub>                   | F: M13-AGGGGGAATACAGAAAGGC<br>R: PIG-AGAGATGGTGGGTCAAAG     | HEX             | 151 - 204                                  | 202 - 276                                    | 60      | P            |
| MDmCIRD01     | (TC) <sub>17</sub>                   | F: M13-GCACACAAGATATGAGATGGAG<br>R: PIG-AATGAAAAGGGTGAGCAGC | 6-FAM           | 461 - 494                                  | 183 - 263                                    | 64      | P            |
| MDmCIRD02     | (CT) <sub>19</sub>                   | F: M13-CGCACACTCTCCCTTCTTC<br>R: PIG-CGACCACACTCTCCAACAC    | 6-FAM           | 138 - 175                                  | 132 - 144                                    | 60      | P            |

Favreau B, Andrianoelina O, Nunez P, Vaillant A, Ramamonjisoa L, Danthu P, Bouvet J (2007) Characterization of microsatellite markers in the rosewood (*Dalbergia monticola* Bosser & R. Rabev.). *Molecular Ecology Notes* 7. 774e776.

\*For the five polymorphic nSSRs analyzed without the M13 tail and PIG-tail, the observed allele size range was generally greater in *D. melanoxylon* compared to the reference species *D. monticola*. However, exceptions were noted at loci MDmCIRD01 and MDmCIRD02.

**Table 2** List of chloroplast microsatellites markers (cpSSRs) developed for angiosperms from Weising and Gardner (1999) and tested on *Dalbergia melanoxylon*

*Ta* annealing temperature, *M* monomorphic, *P* = polymorphic

| Name of primer | Repeat motif                                                              | Sequence (5' - 3')                                      | Fluorescent Dye | Allele size range in tobacco (bp) | Allele size range <i>D. melanoxylon</i> (bp) | Ta (°C) | Ploymorphism |
|----------------|---------------------------------------------------------------------------|---------------------------------------------------------|-----------------|-----------------------------------|----------------------------------------------|---------|--------------|
| ccmp 1         | (T) <sub>10</sub>                                                         | F : CAGGTAACTTCTCAACGGA<br>R: CCGAAGTCAAAGAGCGATT       | HEX             | 139                               | -                                            | -       | M            |
| ccmp 2         | (A) <sub>11</sub>                                                         | F : GATCCCGGACGTAATCCTG<br>R: ATCGTACCGAGGGTTCGAAT      | 6-FAM           | 189                               | -                                            | -       | M            |
| ccmp 3         | (T) <sub>11</sub>                                                         | F : CAGACCAAAAGCTGACATAG<br>R: GTTTCATTGGGCTCCTTTAT     | HEX             | 112                               | -                                            | -       | M            |
| ccmp 4         | (T) <sub>13</sub>                                                         | F : AATGCTGAATCGAAGACCTA<br>R: CCAAAATATTBGGAGACTCT     | 6-FAM           | 126                               | -                                            | -       | M            |
| ccmp 5         | (C) <sub>7</sub> (T) <sub>10</sub><br>(T) <sub>5</sub> C(A) <sub>11</sub> | F : TGTTCCAATATCTTCTGTGATTT<br>R: AGGTTCCATCGGAACAATTAT | 6-FAM           | 121                               | -                                            | -       | M            |
| ccmp 6         | (T) <sub>5</sub> C(T) <sub>11</sub>                                       | F : CGATGCATATGTAGAAAGCC<br>R: CATTACGTGCGACTATCTCC     | 6-FAM           | 103                               | -                                            | -       | M            |
| ccmp 7         | (A) <sub>13</sub>                                                         | F : CAACATATACCACTGTCAAG<br>R: ACATCATTATTGTATACCTTTC   | HEX             | 133                               | 148- 150                                     | 50      | P            |
| ccmp 8         | (T) <sub>6</sub> C(T) <sub>14</sub>                                       | F : TTGGCTACTCTAACCTTCCC<br>R: TCTTTCTTATTTCGCGAGDGAA   | 6-FAM           | 77                                | -                                            | -       | M            |
| ccmp 9         | (T) <sub>11</sub>                                                         | F : GGATTTGTACATATAGGACA<br>R: CTCAACTCTAAGAAATACTTG    | HEX             | 98                                | -                                            | -       | M            |
| ccmp 10        | (T) <sub>14</sub>                                                         | F : TTTTTTTTAGTGAACGTGTA<br>R: TTCGTCGDCGTAGTAAATAG     | HEX             | 103                               | -                                            | -       | M            |

Weising K, Gardner RC (1999) A set of conserved PCR primers for the analysis of simple sequence repeat polymorphisms in chloroplast genomes of dicotyledonous angiosperms. *Genome*. 42, 9 – 19

**Table 3** MICROCHECKER test for null allele of nSSRs markers

| Markers   | Presence of null alleles | Oosterhout | Chakraborty | Brookfield 1 | Brookfield2 |
|-----------|--------------------------|------------|-------------|--------------|-------------|
| MDmCIRA08 | Oui                      | 0.214      | 0.284       | 0.188        | 0.404       |
| MDmCIRC02 | Non                      | 0          | 0           | 0            | 0.438       |
| MDmCIRC10 | Non                      | -0.108     | -0.086      | -0.079       | 0           |
| MDmCIRD01 | Non                      | -0.104     | -0.077      | -0.070       | 0.603       |
| MDmCIRD02 | Non                      | 0.074      | 0.074       | 0.057        | 0.057       |

**Table 4** Haplotypes frequencies in each population

| Counts | Haplotype | H_Code | Freq_LC | Freq_VC | Freq_YC |
|--------|-----------|--------|---------|---------|---------|
| 32     | 148       | H1     | 0.570   | 0.230   | 0.270   |
| 26     | 149       | H2     | 0.400   | 0.170   | 0.300   |
| 32     | 150       | H3     | 0.030   | 0.600   | 0.430   |

**Freq** = frequencies, **H\_Code** = haplotypes code

K=1



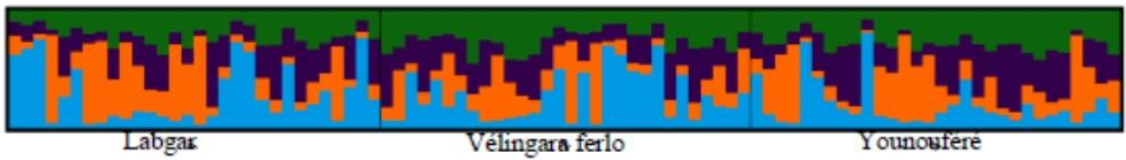
K=2



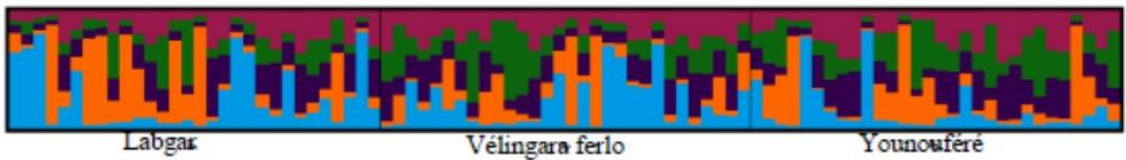
K=3



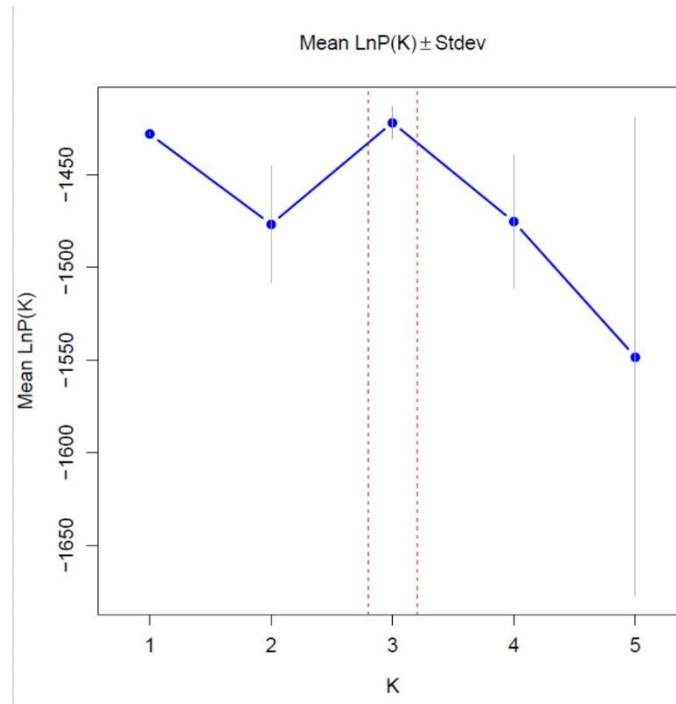
K=4



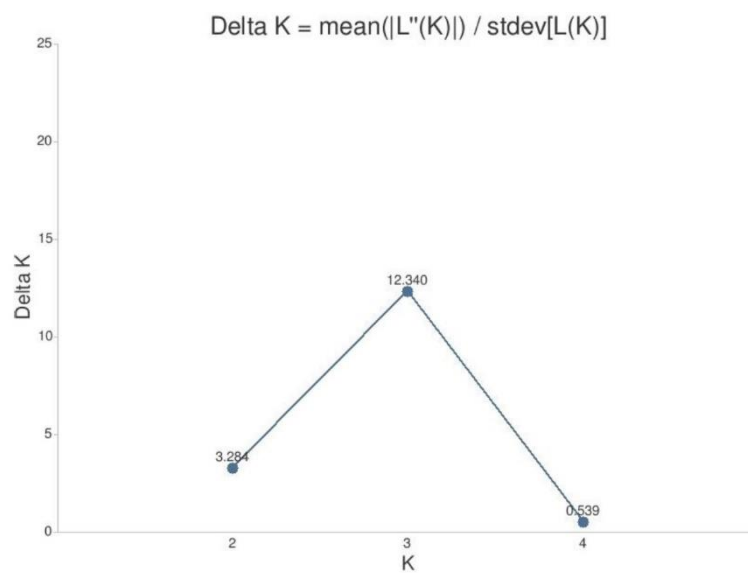
K=5



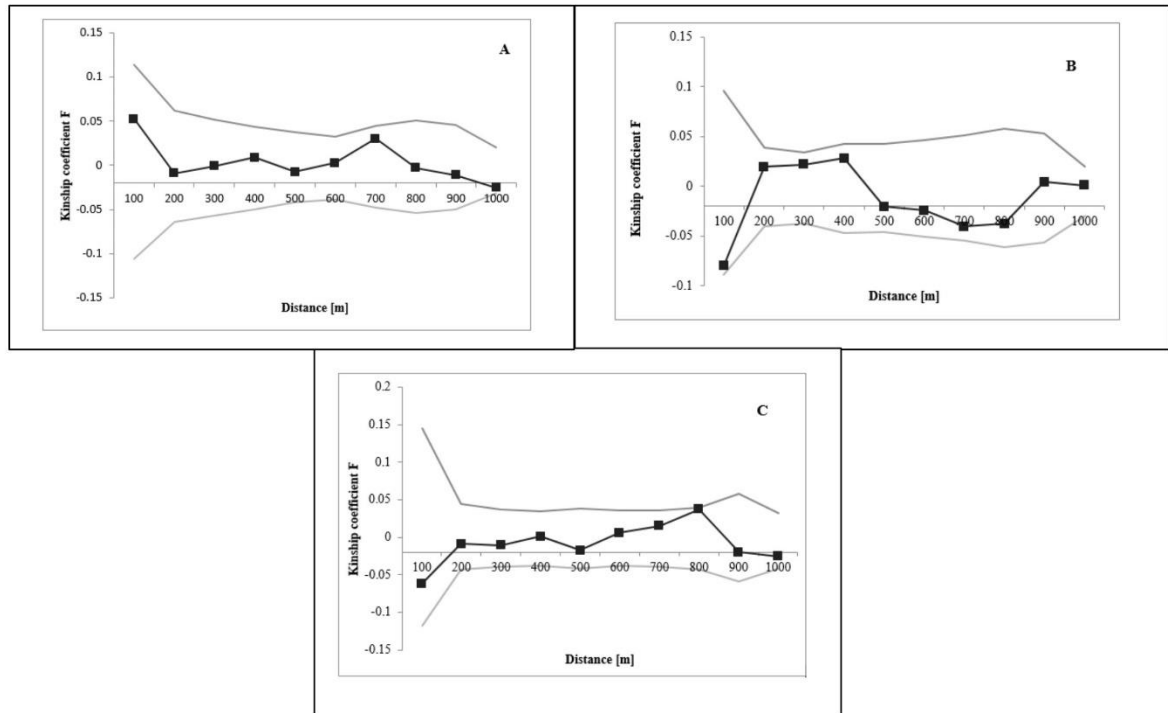
**Fig. 1** Structure plots of 90 samples of *D. melanoxylon* for  $K = 1$  to 5 sorted by population in Ferlo Senegal (1 = LC; 2 = VC and 3 = YC). Structure (Burnin: 10000; MCMC: 10000; Number of Iterations: 5 and  $K = 1 - 5$ )



**Fig. 2** Plot of mean likelihood LnP (K) and variation per K value from Structure using STRUCTURE SELECTOR (online programme) (Li and Liu, 2018)



**Fig. 3** Plot of delta K (Evanno et al. 2005) revealed by STRUCTURE SELECTOR (online programme) (Li and Liu, 2018)



**Fig. 4** Characterization of the fine-scale spatial genetic structure of individuals of each using four nuclear microsatellite markers according to the kinship coefficient of Loiselle et al. (1995) (A = LC ( $S_p = 0.013$ ); B = VC ( $S_p = 0.008$ ) and C = YC ( $S_p = -0.008$ ))