

## Supplementary material

**Table S1** Twenty three polymorphic nuclear loci used for exploring population genetic structure of three *Ficus* species (a,b and c represent *F. bizanae*, *F. craterostoma* and *F. sur* respectively)

| Locus                | Primer sequence (5' - 3')   | Tm (°C) | Repeats  | Species |
|----------------------|-----------------------------|---------|--|---------|
| MFC1 <sup>1</sup>    | F: ACTAGACTGAAAAACATTGC     | 58      | (CT) <sub>13</sub>   | a b     |
|                      | R: TGAGATTGAAAGGAAACGAG     |         |  |         |
| MFC8 <sup>1</sup>    | F: GTGGCGTCGTCTCTAATAAT     | 58      | (CA) <sub>9</sub> TA<br>(CA) <sub>14</sub> (TA) <sub>6</sub>                       | c       |
|                      | R: TATTCTATGCTGTCTTATGTCA   |         |  |         |
| Frac202 <sup>2</sup> | F: AGAGATATGATGTTCTAGTGCA   | 59      | (TG) <sub>13</sub>   | b c     |
|                      | R: CTCGCTCCCACTTAAATACAAG   |         |  |         |
| Frub29 <sup>2</sup>  | F: CCACTTTGGAATGTCACCTGGA   | 59      | (AG) <sub>24</sub>   | b c     |
|                      | R: TGAACACGCCAACTGAGAATG    |         |  |         |
| Frub38 <sup>2</sup>  | F: ACACGTGCAGTGCTGCTGA      | 59      | (AG) <sub>8</sub> AAC<br>(GA) <sub>13</sub>  | c       |
|                      | R: ACAGCTGCCCAATTCCTTGA     |         |  |         |
| Frub61 <sup>2</sup>  | F: GTACACTCTTTAGCTGCC       | 59      | (TC) <sub>24</sub>   | a b c   |
|                      | R: TACCTTTCTCTGGACATTC      |         |  |         |
| Frub391 <sup>2</sup> | F: AGATGTCAAATAAGGTCAGCT    | 59      | (TG) <sub>19</sub>   | a       |
|                      | R: AGATGCAGTTCATACAATTC     |         |  |         |
| Frub415 <sup>2</sup> | F: GCACGTAGTCGGTGTTAAGC     | 59      | (AC) <sub>10</sub>   | b       |
|                      | R: CTGTGCGGAATAAAAGCTAGC    |         |  |         |
| FinsI12 <sup>3</sup> | F: GAACCTTCAACCTCAATCAA     | 58      | (TC) <sub>5</sub> (CT) <sub>11</sub>   | c       |
|                      | R: CTCCCCTTTCCTAGTCCTTA     |         |  |         |
| FinsJ10 <sup>3</sup> | F: AGGTGGAATGAGGAGAGAGT     | 58      | (TC) <sub>11</sub>   | c       |
|                      | R: AAACATCCTTTCTGGACTTG     |         |  |         |
| FinsM5 <sup>3</sup>  | F: ATGAATGGTGAAATCCTGAA     | 58      | (TC) <sub>13</sub>   | c       |
|                      | R: CATGGCCTCAACTTAGAAAC     |         |  |         |
| FinsN1 <sup>3</sup>  | F: AGGGCTGAGATAGGTTGATT     | 58      | (TA) <sub>2</sub> (CA) <sub>10</sub><br>(TA) <sub>7</sub><br>CATA(TG) <sub>2</sub> | b       |
|                      | R: TAAGTTGGTGTGTGGCATC      |         |  |         |
| FinsQ6 <sup>3</sup>  | F: TTCTCCAATTAAACCTCCAA     | 58      | (TG) <sub>7</sub><br>AG(TG) <sub>5</sub>   | a       |
|                      | R: CATGAAATCACCTTCCTCAT     |         |  |         |
| FinsA1 <sup>3</sup>  | F: AATCCCCGTACTIONACTTG     | 58      | (CT) <sub>12</sub>   | b c     |
|                      | R: AGAACTTATTGCACGGACAG     |         |  |         |
| FM3-64 <sup>4</sup>  | F: GATGGTGTGTTGTCTGATGGTCAT | 59      | (CAA) <sub>8</sub>   | b       |
|                      | R: GCGGCTCGGTGGAACCTTGAG    |         |  |         |
| FM4-70 <sup>4</sup>  | F: CAGATGAGGTTGACGATGTTATTG | 59      | (GAA) <sub>20-1</sub>  | b       |
|                      | R: TAAACCCTCTTCAAATTCACCTC  |         |  |         |
| FS4-11 <sup>4</sup>  | F: AAGGCAACGGGGATAAAGTATTCA | 59      | (CGA) <sub>6</sub>   | c       |

|                      |                                |    |                                      |     |
|----------------------|--------------------------------|----|--------------------------------------|-----|
|                      | R: CTCCGAGAGCAACTCCATCACG      |    |                                      |     |
| LMFC20 <sup>5</sup>  | F: ATGGAGGCTTAGATAGAAAT        | 54 | (AAG) <sub>9</sub>                   | a b |
|                      | R: ACAACACAAAAAGAAATATCA       |    | (AG) <sub>18</sub>                   |     |
| LMFC32 <sup>5</sup>  | F: GAAAGAAAGTCGAATAATGTA       | 54 | (GA) <sub>23</sub>                   | b   |
|                      | R: TATAAAGAGGGTGGTCTTAGT       |    |                                      |     |
| Fsync13 <sup>6</sup> | F: TGGAGATGTGAATATCATTGGACGTG  | 59 | (GAAA) <sub>8</sub>                  | b   |
|                      | R: CGACGAACAGTTAGTATCGGTAACAGC |    |                                      |     |
| FT02 <sup>7</sup>    | F: CAAAATCGGAATAATGACAGC       | 58 | (CT) <sub>13</sub>                   | a   |
|                      | R: AAAGACAACGAAACTAAGAGG       |    |                                      |     |
| FT07 <sup>7</sup>    | F: CCACAAC TACCCAACCAAG        | 58 | (TG) <sub>7</sub> A(GA) <sub>8</sub> | a   |
|                      | R: GCTGGAGCCAAATCATCTA         |    |                                      |     |
| FT14 <sup>7</sup>    | F: GAAGAGGCCCTGAGATAA          | 58 | (GA) <sub>12</sub>                   | a   |
|                      | R: GATCAAGCGATGACAACC          |    |                                      |     |

<sup>1</sup> Khadari et al., 2001

<sup>2</sup> Giraldo et al., 2005

<sup>3</sup> Zavodna et al., 2005

<sup>4</sup> Vignes et al., 2006

<sup>5</sup> Ahmed et al., 2007

<sup>6</sup> Crozier et al., 2007

<sup>7</sup> Tan et al., 2016

**Table S2** Null allele frequencies for each locus at each population for each species. (no indicates no null allele)

| Species        | CODE |       |         |         |        |         |         |         |        |        |        |        |         |
|----------------|------|-------|---------|---------|--------|---------|---------|---------|--------|--------|--------|--------|---------|
|                |      | MFC1  | Frub61  | Frub391 | FinsQ6 | LMFC20  | FT-02   | FT-07   | FT-14  |        |        |        |         |
| F.bizane       | MKA  | no    | no      | no      | no     | 0.142   | no      | no      | no     |        |        |        |         |
|                | MBO  | no    | no      | no      | 0.225  | no      | no      | 0.152   | no     |        |        |        |         |
|                | DEW  | no    | no      | no      | 0.151  | 0.290   | no      | no      | 0.211  |        |        |        |         |
|                |      | MFC1  | Frac202 | Frub29  | Frub61 | Frub415 | FinsN1  | FinsA1  | FM3-64 | FM4-70 | LMFC20 | LMFC32 | Fsync13 |
|                | NGO  | no    | no      | no      | no     | no      | no      | no      | no     | no     | no     | no     | no      |
|                | ING  | 0.194 | 0.027   | 0.055   | no     | no      | no      | no      | no     | no     | no     | 0.062  | 0.047   |
| F.craterostoma | MBO  | 0.114 | 0.179   | 0.247   | 0.09   | 0.215   | 0.097   | no      | no     | no     | no     | 0.202  | no      |
|                | DWE  | 0.17  | 0.096   | 0.129   | 0.173  | 0.272   | 0.204   | 0.165   | 0.123  | no     | 0.186  | 0.094  | 0.085   |
|                | MAN  | 0.149 | no      | 0.177   | 0.177  | 0.188   | 0.176   | 0.102   | no     | no     | 0.16   | 0.188  | no      |
|                |      | MFC8  | Frac202 | Frub29  | Frub38 | Frub61  | FinsI12 | FinsJ10 | FinsM5 | FinsA1 | FM4-11 |        |         |
|                | NGO  | no    | no      | 0.163   | no     | no      | no      | no      | no     | no     | no     |        |         |
|                | MKA  | no    | 0.117   | no      | no     | no      | no      | no      | no     | no     | 0.287  |        |         |
| F.sur          | MBO  | 0.080 | 0.180   | no      | no     | no      | 0.076   | no      | no     | 0.116  | 0.111  |        |         |
|                | DWE  | no    | 0.151   | no      | no     | no      | no      | 0.163   | no     | no     | no     |        |         |
|                | MAN  | no    | 0.130   | no      | no     | no      | no      | 0.113   | 0.080  | 0.027  | 0.064  |        |         |
|                | PIR  | no    | no      | no      | no     | 0.112   | no      | no      | no     | no     | 0.235  |        |         |

**Table S3** Pairwise  $F'_{ST}$  for each species (a *F. bizanae*, b *F. craterostoma*, c *F. sur*)

a

|     | MKA   | MBO   | DWE |
|-----|-------|-------|-----|
| MKA | 0     |       |     |
| MBO | 0.209 | 0     |     |
| DWE | 0.224 | 0.283 | 0   |

b

|     | NGO   | ING   | MBO   | DWE   | MAN |
|-----|-------|-------|-------|-------|-----|
| NGO | 0     |       |       |       |     |
| ING | 0.076 | 0     |       |       |     |
| MBO | 0.175 | 0.082 | 0     |       |     |
| DWE | 0.286 | 0.231 | 0.152 | 0     |     |
| MAN | 0.276 | 0.203 | 0.142 | 0.033 | 0   |

c

|     | NGO   | MKA   | MBO   | DWE   | MAN   | PIR |
|-----|-------|-------|-------|-------|-------|-----|
| NGO | 0     |       |       |       |       |     |
| MKA | 0.138 | 0     |       |       |       |     |
| MBO | 0.199 | 0.101 | 0     |       |       |     |
| DWE | 0.267 | 0.179 | 0.129 | 0     |       |     |
| MAN | 0.167 | 0.100 | 0.101 | 0.101 | 0     |     |
| PIR | 0.180 | 0.129 | 0.039 | 0.043 | 0.054 |     |