

## Fine-mapping and identification of a candidate gene underlying the *d2* dwarfing phenotype in pearl millet, *Cenchrus americanus* (L.) Morrone.

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**File S1**

**Sequence of DNA fragment obtained with primer set Ca\_Sb07g023730F1/R5 in the tall inbred line ICMP 451.**

ICMP 451\_Ca\_Sb07g023730F1R5

TACGCCTTCTACTTCCTCGTCGTCGGGGCAGCCATCTGGGCATCCTCCTGGGCCGAGATCTCCTGCTGGAT  
GTGGACCGGCGAGCGCCAGTCCACCCGGATGCGCATCCGCTACCTCGACGCCGCCCTCCGCCAGGACGTCT  
CCTTCTTCGACACCGACGTCCGCGCCTCCGACGTCATCTACGCCATCAACGCCGACGCCGTCTCGTCCAG  
GACGCCATCAGCGAGAAGCTCGGCAACCTCATCCACTACATGGCCACCTTCGTCGCCGGATTTCGTCGTCGG  
CTTACCCGCCGCCTGGCAGCTCGCGCTCGTACGCTCGCCGTCGTACCGCTCATCGCCGTCATCGGGGGGC  
TCAGCGCCGCCGCGCTCTCCAAGCTCTCCGCCAGGAGCCAGGACGCGCTCTCCGGCGCCAGCGCCATCGCC  
GAGCAGGCGCTGGCGCAGATACGGATCGTGCAGGCCTTCGTCGGCGAGGAGCGCGCCATGCGGGCGTACTC  
GGCGGCGCTGGCCGTCGCGCAGAAGATCGGCTACCGGAGCGGCGTCGCCAAGGGGCTCGGGCTCGGCGGCA  
CCTACTTCACCGTCTTCTGCTGCT

File S2

Sequence of DNA fragments obtained with primer set Ca\_Sb07g023730F10/R10 in the tall inbred line ICMP 451 (A) and in the dwarf inbred line Tift 23DB (B). The synonymous SNP that differentiates the ICMP 451 and Tift 23DB sequences is shown in red.

A. ICMP 451\_Ca\_Sb07g023730F10/R10

GCAGGTTCTCCTTGATGCTCGTCGCGAACAGCGTCGGCTCCTGACTCACCAGGCCCATCTGCTGCCGGAGC  
CACCGGAGCTTCAGGCTCTTGAGGTCATGCCCGTCCAGCAGGATCTCACCTGTTGCAATTGCAATTCCCAT  
CGCTCATCAGAATAGTAGTTTGTCTTAGTAGTAGACTTTTCTGCCTATTACTAGAGGATGCCTATGAAT  
GACTGTGACTGGACAAGAGGATGATGCAGCGCAAAGGAAGCAGCCCATGAGGCCGGCAAGCTCTGCTCCAA  
TCCAAGCACTACTTGCTTGCTTGCTTGCAACCACCCACCCAGCAATGGCGGGCAATGCTGATTACTGATG  
GCTCCAATCCAACAAGAGAATGTAACCAACAACGGGTATACCTGCGCTGGGGTCGTAGAACCCTCTCGATGA  
GCGACACGACGGTGCTCTTCCCGGAGCCGGAGCTGCCGACCAGCGCGATGGTCTTCCCGGCGGGCACGGTG  
AGGGAGAAGGCGCGCAGGATGGGCACGTCCGGCCGCGTCGGGTACGCGAAGTCGACGCCCCGCATCTCTAC  
CCGCCCCGTGACGGACTCCAGCTCCACCTGGCCGTCCCGCGAGATCCCCGGCTTGTGTCGATGATGCGGA  
AGATCTTGGCCGCCGCGACGCGGCCTTGGCGAAGGCGGCCATGCTCGGCGCCGACTGCCCCAGCGCGATG  
CCCCCGATCATGACGGAGAACATGGTGGCGATGGCGAGCCCCCGTTGGTGCGGTGGCCGCGCACCAGGTG  
GCCCCCGTACCAGAGCAGCAGCCCGTAGCAGCAGAAGACGGTGAAGTAGGTGCCTCCGAG

B. Tift 23DB\_Ca\_Sb07g023730F10/R10

GCAGGTTCTCCTTGATGCTCGTCGCGAACAGCGTCGGCTCCTGACTCACCAGGCCCATCTGCTGCCGGAGC  
CACCGGAGCTTCAGGCTCTTGAGGTCATGCCCGTCCAGCAGGATCTCACCTGTTGCAATTGCAATTCCCAT  
CGCTCATCAGAATAGTAGTTTGTCTTAGTAGTAGACTTTTCTGCCTATTACTAGAGGATGCCTATGAAT  
GACTGTGACTGGACAAGAGGATGATGCAGCGCAAAGGAAGCAGCCCATGAGGCCGGCAAGCTCTGCTCCAA  
TCCAAGCACTACTTGCTTGCTTGCTTGCAACCACCCACCCAGCAATGGCGGGCAATGCTGATTACTGATG  
GCTCCAATCCAACAAGAGAATGTAACCAACAACGGGTATACCTGCGCTGGGGTCGTAGAACCCTCTCGATGA  
GCGACACGACGGTGCTCTTCCCGGAGCCGGAGCTGCCGACCAGCGCGATGGTCTTCCCGGCGGGCACGGTG  
AGGGAGAAGGCGCGCAGGATGGGCACGTCCGGCCGCGTCGGGTACGCGAAGTCGACGCCCCGCATCTCTAC  
CCGCCCCGTGACGGACTCCAGCTCCACCTGGCCGTCCCGCGAGATCCCCGGCTTGTGATCGATGATGCGGA  
AGATCTTGGCCGCCGCGACGCGGCCTTGGCGAAGGCGGCCATGCTCGGCGCCGACTGCCCCAGCGCGATG  
CCCCCGATCATGACGGAGAACATGGTGGCGATGGCGAGCCCCCGTTGGTGCGGTGGCCGCGCACCAGGTG  
GCCCCCGTACCAGAGCAGCAGCCCGTAGCAGCAGAAGACGGTGAAGTAGGTGCCTCCGAG

**Table S1 Primer sequences, their melting temperature and location in the sorghum, rice and foxtail millet genomes of markers mapped in the *d2* region**

| Marker         |    | Primer sequences      | Tm<br>( <sup>o</sup> C) | Corresponding sorghum gene | Location in sorghum genome (Mb) <sup>1</sup> | Corresponding rice gene | Location in rice genome (Mb) <sup>1</sup> | Corresponding foxtail millet gene | Location in foxtail millet genome (Mb) <sup>1</sup> |
|----------------|----|-----------------------|-------------------------|----------------------------|--|-------------------------|---|-----------------------------------|---|
| B224C4P2       | F2 | TTCCTGGGATCAAAAGGTTC  | 59-52                   | -                          | -  | -                       | -   | -                                 | -   |
|                | R1 | CCATATCTCCAAGCTGCATAG |                         |                            |  |                         |   |                                   |   |
| Ca_Sb07g024020 | F  | CCACGCCTTCTTCTCC      | 61                      | Sb07g024020                | 7: 59.04                                     | Os08g0560300            | 8: 28.15                                  | Si015992m                         | VI: 35.69   |
|                | R  | TCCTCCACCTCGGACACG    |                         |                            |  |                         |   |                                   |   |
| Ca_Sb07g023910 | F  | CATGCACTGACGAGTTGG    | 53                      | Sb07g023910                | 7: 58.93                                     | Os080562100             | 8: 28.23                                  | Si013632m                         | VI: 35.76   |
|                | R  | TGCCCCATTTTGGATGAGC   |                         |                            |  |                         |   |                                   |   |
| RGR1963        | 2F | GTACGCCTACAGTCAAGGTG  | 59-52                   | Sb07g023850                | 7: 58.82                                     | Os08g0562700            | 8: 28.27                                  | Si013315m                         | VI: 35.80   |
|                | 2R | CCAAGCTCGTGTGCGCAG    |                         |                            |  |                         |   |                                   |   |
| Ca_Sb07g023840 | F  | ACATCCTCCCCTCCGATTC   | 53                      | Sb07g023840                | 7: 58.81                                     | Os08g0562800            | 8: 28.27                                  | Si013571m                         | VI: 35.81   |
|                | R  | ATGGAGAAGCTGCCCTGAAG  |                         |                            |  |                         |   |                                   |   |
| Ca_Sb07g023810 | F  | CTTGGCTCACCATGTGGTG   | 61                      | Sb07g023810                | 7: 58.78                                     | Os08g0563400            | 8: 28.30                                  | Si015156m                         | VI: 35.83   |
|                | R  | GACTCTAGTTCTGCTTGACG  |                         |                            |  |                         |   |                                   |   |

|                |    |                         |           |             |          |              |           |           |           |
|----------------|----|-------------------------|-----------|-------------|----------|--------------|-----------|-----------|-----------|
| Ca_Sb07g023730 | F1 | TACGCCTTCTACTTCCTCGTC   | 61        | Sb07g023730 | 7: 58.61 | Os080564300  | 8: 28.36  | Si013123m | VI: 35.86 |
|                | R5 | AGCAGCAGAAGACGGTGAAGTAG |           |             |          |              |           |           |           |
| Ca_Sb07g023630 | F  | GCTCTTTTCAGCAACCCCTTC   | 53        | Sb07g023630 | 7: 58.53 | Os08g0564800 | 8: 28.39  | Si013125m | VI: 35.88 |
|                | R  | CGCTAACTGCAGCAGCAAGG    |           |             |          |              |           |           |           |
| Ca_Sb07g023520 | F  | GCCATTTTGGCGGAGATTGC    | 53        | Sb07g023520 | 7: 58.42 | Os080566000  | 8: 28.44  | Si013435m | VI: 35.92 |
|                | R  | CTGCGCACCAGCAATAGG      |           |             |          |              |           |           |           |
| Ca_Sb07g023500 | F  | GCTTTAGACGGTGCAGAC      | 59-<br>52 | Sb07g023500 | 7: 58.40 | Os08g0566400 | 8: 28.46  | Si015293m | VI: 35.94 |
|                | R  | GAAGCTCATCCAATCCCTC     |           |             |          |              |           |           |           |
| Ca_Sb07g023470 | F  | AGCTTCAGCTCCGTGCTTC     | 59-<br>52 | Sb07g023470 | 7: 58.39 | Os080566600  | 8: 28.47  | Si015371m | VI: 35.95 |
|                | R  | GGAATCCGAGCTTCTCTCC     |           |             |          |              |           |           |           |
| Ca_Sb07g023460 | F2 | GCATCTGTCCAACTGACAGC    | 59-<br>52 | Sb07g023460 | 7: 58.38 | Os080566900  | 8: 28.48  | Si014505m | VI: 35.95 |
|                | R2 | ATCTTGCTGCCTTGAGGTTT    |           |             |          |              |           |           |           |
| Ca_Sb07g023440 | F  | CGCCTTCGACATGGACGAC     | 53        | Sb07g023440 | 7: 58.37 | Os080567100  | 8: 28.49  | Si015189m | VI: 35.96 |
|                | R  | CTTGTCGTGGCGGTAGTCG     |           |             |          |              |           |           |           |
| Ca_Sb07g023430 | F  | TGATAAACCCAGCAACCTTGG   | 53        | Sb07g023430 | 7: 58.37 | Os12g0641500 | 12: 27.75 | Si013129m | VI: 35.97 |
|                | R  | GAATCAAGTACACAGCTATGC   |           |             |          |              |           |           |           |

|         |    |                           |     |             |           |   |   |          |          |
|---------|----|---------------------------|-----|-------------|-----------|---|---|----------|----------|
| PSMP344 | F  | CGTCCTGTACCTCAGCCTTG      | 59- | Sb07g007800 | 7: 12.59- | - | - | Si015622 | VI: 9.10 |
|         | R  | ATGCTACACCTGTCAGAACTAAGAG | 52  |             | 12.61     |   |   |          |          |
| PSMP344 | F2 | GGCTTGTCACGTCCTGTACC      | 53  | Sb07g007800 | 7: 12.59  | - | - | Si015622 | VI: 9.10 |
|         | R2 | TCAATCATGCAGCAGCAATC      |     |             |           |   |   |          |          |
| PSMP305 | F  | TGCAATAGTTTCCAGTTGTC      | 53  | -           | -         | - | - | -        | VI: 1.36 |
|         | R  | TCAACAATTTGGTACAGACG      |     |             |           |   |   |          |          |

<sup>1</sup>The number before the colon indicates the chromosome number; the number following the colon is the chromosomal location in Mb.

**Tables S2-S6**

**Table S2: Height of individual plants within F<sub>3</sub> families derived from informative F<sub>2</sub> plants.**

**Table S3: Genotypic scores for *d2* and 12 markers in 23 informative F<sub>2</sub> plants from the cross Tift 23DB x ICMP 451**

**Table S4: Genotypic scores for *d2* and 11 markers in 16 informative F<sub>2</sub> plants from the cross PT 732B x P1449-2**

**Table S5: Annotated genes in the distal 10 Mb of sorghum chromosome 7 and their orthologs in *Setaria italica*, *Oryza sativa* and *Brachypodium distachyon*. For each gene, the start and end positions are given.**

**Table S6: Genes annotated in the sorghum genome in the region flanked by Sb07g023430 and Sb07g023810**

Tables S2-S6 are available for download at <http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.113.005587/-/DC1>.