Supplemental Data for

Koodalugodaarachchi, V., Kekulandara, D. S., Gimhani, D. R. (2022). Genetic diversity of Oryza sativa ‘Dahanala’ traditional red rice and molecular markers associated with trichome density on adaxial surfaces. *Genetic Resources* 3 (5), 10–23. doi: 10.46265/genresj.AVEO9374

Supplemental Data 1: Description of seed morphological characters – modified based on IPGRI rice descriptors (IPGRI, 2007)

1. Seed shape (7.5.22)

    Time: At maturity, shape of the grains is classified as:
    1) Round
    2) Semi-round
    3) Half-spindle shaped
    4) Spindle-shaped
    5) Very spindle-shaped

2. Lemma and palea colour are classified into 19 classes (7.5.5) (modified):

    0) Straw
    1) Gold and/or gold furrows on straw background
    2) Brown spots on straw
    3) Brown furrows on straw
    4) Brown
    5) Reddish to light purple
    6) Purple spots on straw background
    7) Purple furrows on straw background
    8) Purple
    9) Black
    10) White
    11) Brownish black
    12) Yellowish gray
    13) Yellowish brown
    14) Brown furrows on gold background
    15) Reddish brown spots on gold background
    16) Black spots on straw background
    17) Brownish black furrows on gold background
    18) Brownish black furrows on straw background
    19) Brown furrows on yellowish background

3. Seed coat (bran) colour (7.5.23) (modified):

    Time: At maturity, brown rice (dehulled grains) is classified into:
    0) Off white
    1) White
    2) Light Brown
    3) Speckled brown
    4) Brown
    5) Red
    6) Variable Purple
    7) Purple
    8) Off white with black apiculus
    9) Off white with brown apiculus

10) Brown seed coat with white strips
11) Red seed coat with white strips
12) Off white seed coat with white strip with black apiculus
13) Off white seed coat with white strips
14) Brown seed coat with black apiculus
15) Light brown seed coat with white strip
16) Brown seed coat with white strip and black apiculus

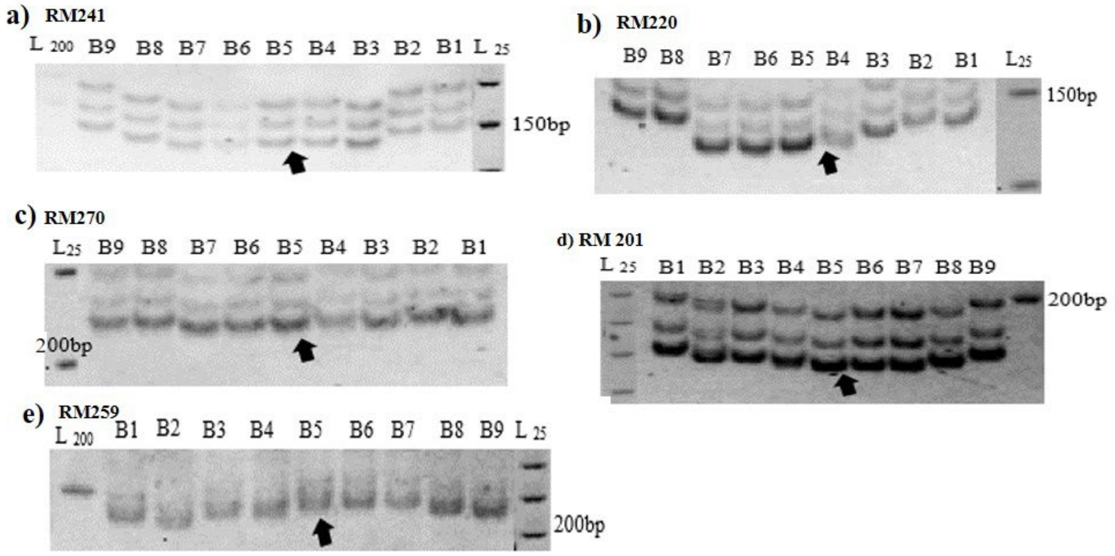
4. Lemma and palea pubescence (7.5.4):
Time: At maturity, pubescence of the hull is classified as:

1) Glabrous
2) Hairs on lemma keel
3) Hairs on upper portion
4) Short hairs
5) Long hairs (velvety)

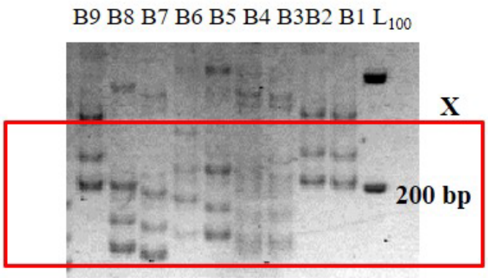
5. Grain length (7. 5. 15):
Time: At maturity, grain length is measured as the distance from the base of the lowermost sterile lemma to the tip (apiculus) of the fertile lemma or palea, whichever is longer. In the case of awned varieties, the grain is measured to a point comparable to the tip of the apiculus

6. Grain width (7. 5. 16):
Time: At maturity, width of grain is measured in millimeters as the distance across the fertile lemma and the palea at the widest point

Supplemental Figure 1: Additional SSR marker profiles amplified from DNA bulks (RM201, RM220, RM241, RM259, RM270). The arrowhead indicates corresponding scored alleles. B1–B8, DNA bulks; B9, Bg360; L25, L100, L200, size markers; bp, basepairs.



Supplemental Figure 2: PCR profile or heterogenic marker RM515 of DNA bulks.

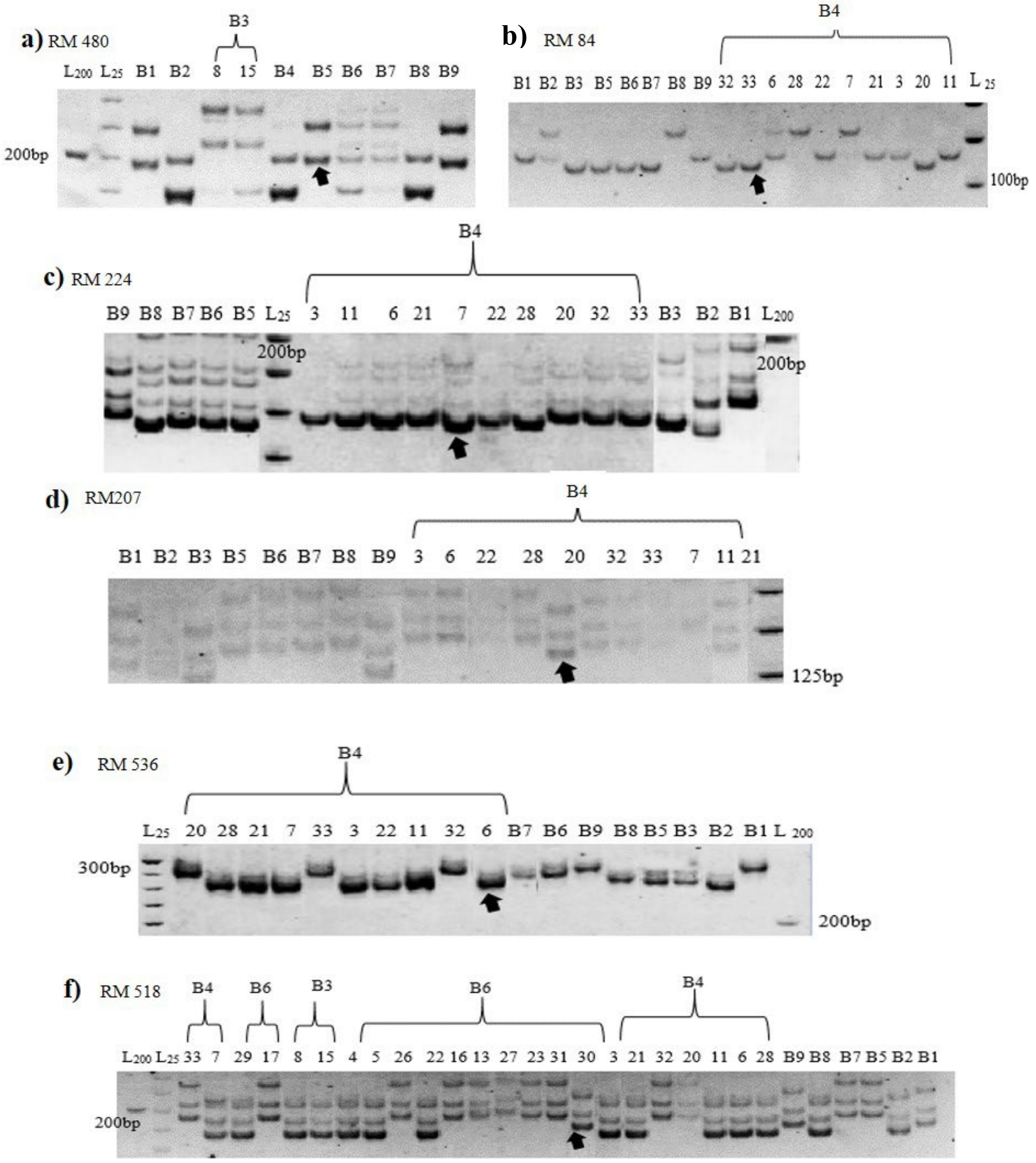


X - Respective allelic region L$_{100}$-100bp Ladder

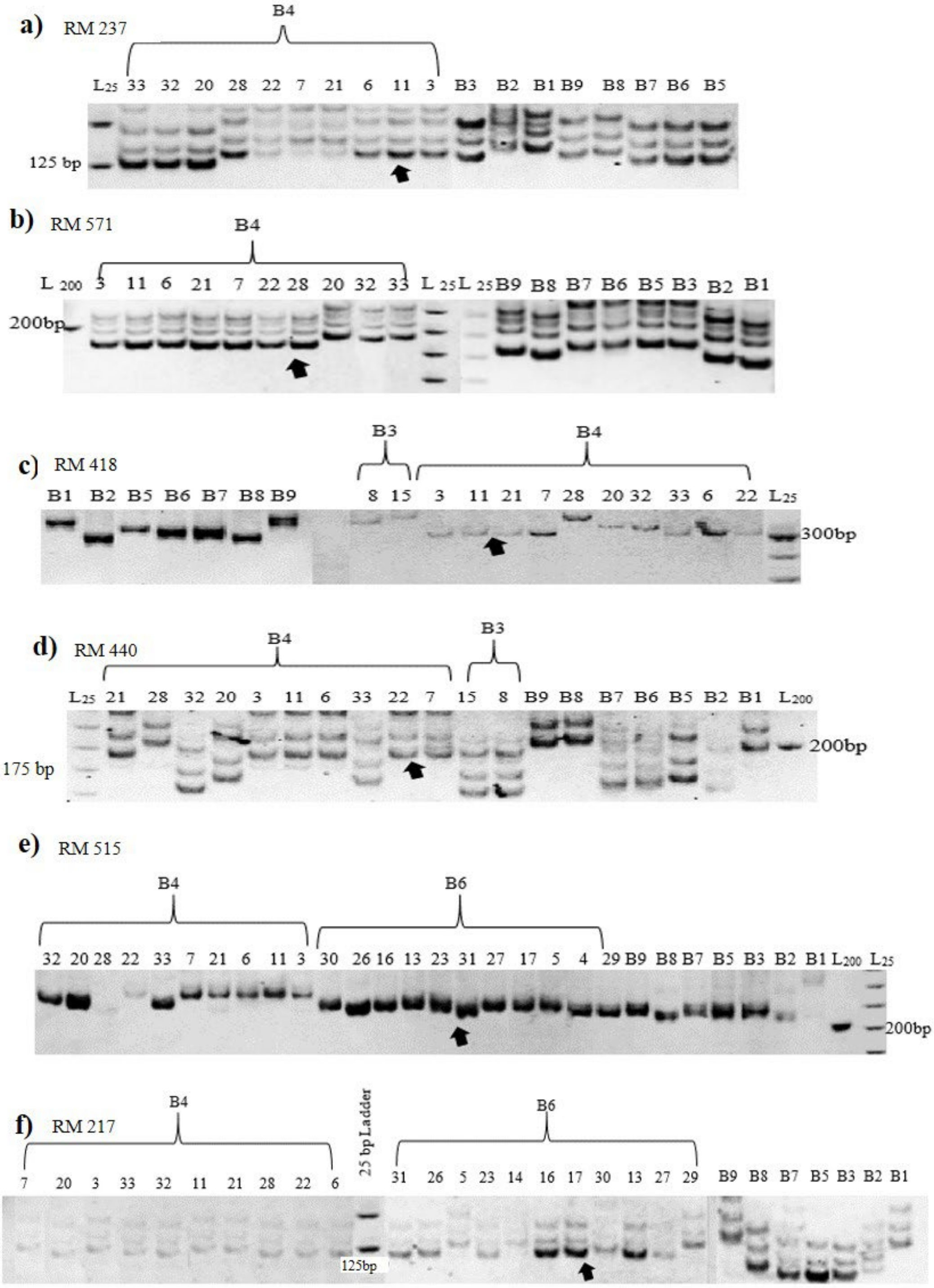
Compared to the B1, B2, B5, B7, B8, B9 bulks B3, B4, and B6 bulks show a heterogeneous pattern in alleles for RM515

Supplemental Figure 3: PCR profiles of expanded DNA bulks for SSR markers (RM84, RM207, RM224, RM480, RM518, RM536)

Amplification of bulked DNA samples and expanded bulks with a) RM480 (Product size: 199–221bp), b) RM84 (Product size: 118–124bp), c) RM224 (Product size: 124–142bp), d) RM207 (Product size: 110–132bp), e) RM536 (Product size: 220–230bp), f) RM518 (Product size: 158–180bp) (resulted with monomorphic alleles) (Product size: 132–154bp). The arrowhead indicates corresponding scored alleles. B1–B8, DNA bulks; B9, Bg360; L25, L100, L200, size markers; bp, basepairs. 8, 15, 3, 11, 6, 21, 7, 22, 28, 20, 32, 33, 19, 4, 5, 17, 31, 27, 23, 13, 16, 26, 30, 29, 9, 24, 12, 18, 14, 9, 24, 12, 18, 14 - Individual accessions included in bulks, numbered as in Table 1.

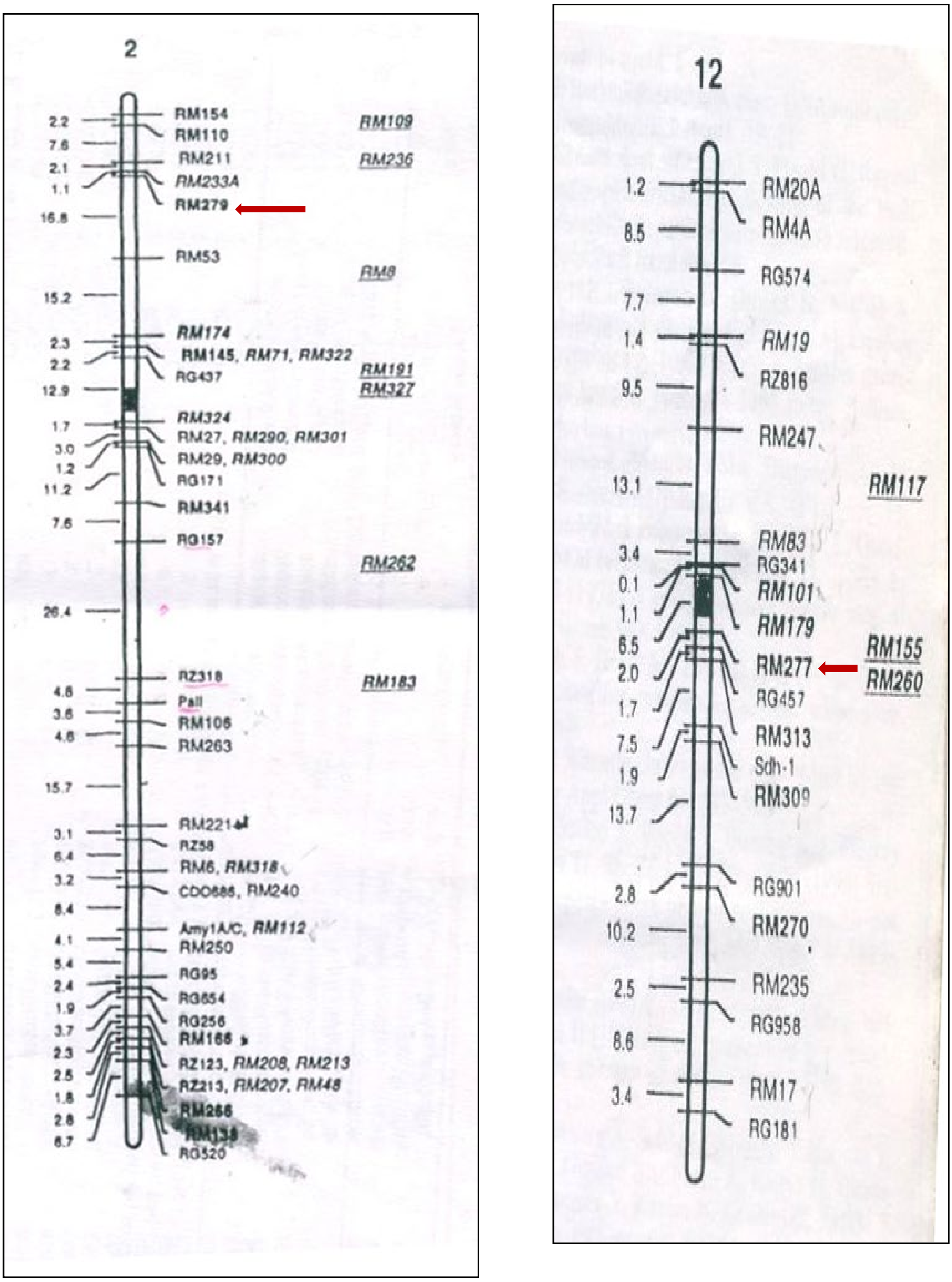


Supplemental Figure 4: PCR profiles of expanded DNA bulks for SSR markers (RM217, RM237, RM418, RM440, RM515, RM571)



Amplification of bulked DNA samples and expanded bulks with a) RM237 (Product size: 124–138bp), b) RM571 (Product size: 182–192bp, c) RM418 (Product size: 245–290bp), d) RM440 (Product size: 161–217bp), e) RM515 (Product size: 211–219bp), f) RM217 (Product size: 114–144bp). The arrowhead indicates corresponding scored alleles. B1–B8, DNA bulks; B9, Bg360; L25, L100, L200, size markers; bp, basepairs. 8, 15, 3, 11, 6, 21, 7, 22, 28, 20, 32, 33, 19, 4, 5, 17, 31, 27, 23, 13, 16, 26, 30, 29, 9, 24, 12, 18, 14, 9, 24, 12, 18, 14 - Individual accessions included in bulks, numbered as in Table 1.

Supplemental Figure 5: Map position of markers RM277 and RM279 on rice chromosomes 12 and 2. (adapted from Temnykh *et al.*, 2000)



References

International Plant Genetic Resources Institute, and West Africa Rice Development Association. Descriptors for Wild and Cultivated Rice (*Oryza* Spp.). Biodiversity International, 2007. https://www.bioversityinternational.org/fileadmin/user_upload/online_library/publications/pdfs/232.pdf

Temnykh, S., Park, W.D., Ayres, N., Cartinhour, S., Hauck, N., Lipovich, L., Cho Y.G., Ishii, T., McCouch, S,R. (2000). Mapping and genome organization of microsatellite sequences in rice (*Oryza sativa* L.). *Theoretical Applied Genetics* **100**, 697–712.