Table 1 Suppl. Sequences of the adaptors and primers used in fluorescence-labeled methylation-sensitive amplified polymorphism .

	*Eco*RI (5’-3’)	*Hpa*II/*Msp*I (5’-3’)
Adapter 1	CTCGTAGACTGCGTACC	GACGATGAGTCCTGAG
Adapter 2	AATTGGTACGCAGTCTAC	CGCTCAGGACTCAT
Preselective-amplification primers	GACTGCGTACCAATTC (E00)	GATGAGTCCTGAGCGG (H/M00)
Selective-amplification primers	E00-AAC (E1)	H/M00-AGC (H/M1)
	E00-ACC (E2)	H/M00-AGT (H/M2)
	E00-AGC (E3)	H/M00-CAC (H/M3)
	E00-GTT (E4)	H/M00-ATC (H/M4)
	E00-TCG (E5)	
	E00-TCT (E6)	
Primer sets	E1-H/M1, E2-H/M3, E3-H/M1, E3-H/M3	
	E4-H/M3, E5- H/M2, E5-H/M3, E6-H/M4	

Table 2 Suppl. Transformation of the raw 1/0 matrix obtained from MSAP (methylation-sensitive amplified polymorphism) into the four types of new matrix corresponding to unmethylation, hemi-methylation, full methylation, and hypermethylation.

Raw matrix for *Hpa*II/*Msp*I	1/1 (type I)	1/0 (type II)	0/1 (type III)	0/0 (type IV)
Unmethylation	1	0	0	0
Hemi-methylation	0	1	0	0
Full methylation	0	0	1	0
Hypermethylation	0	0	0	1

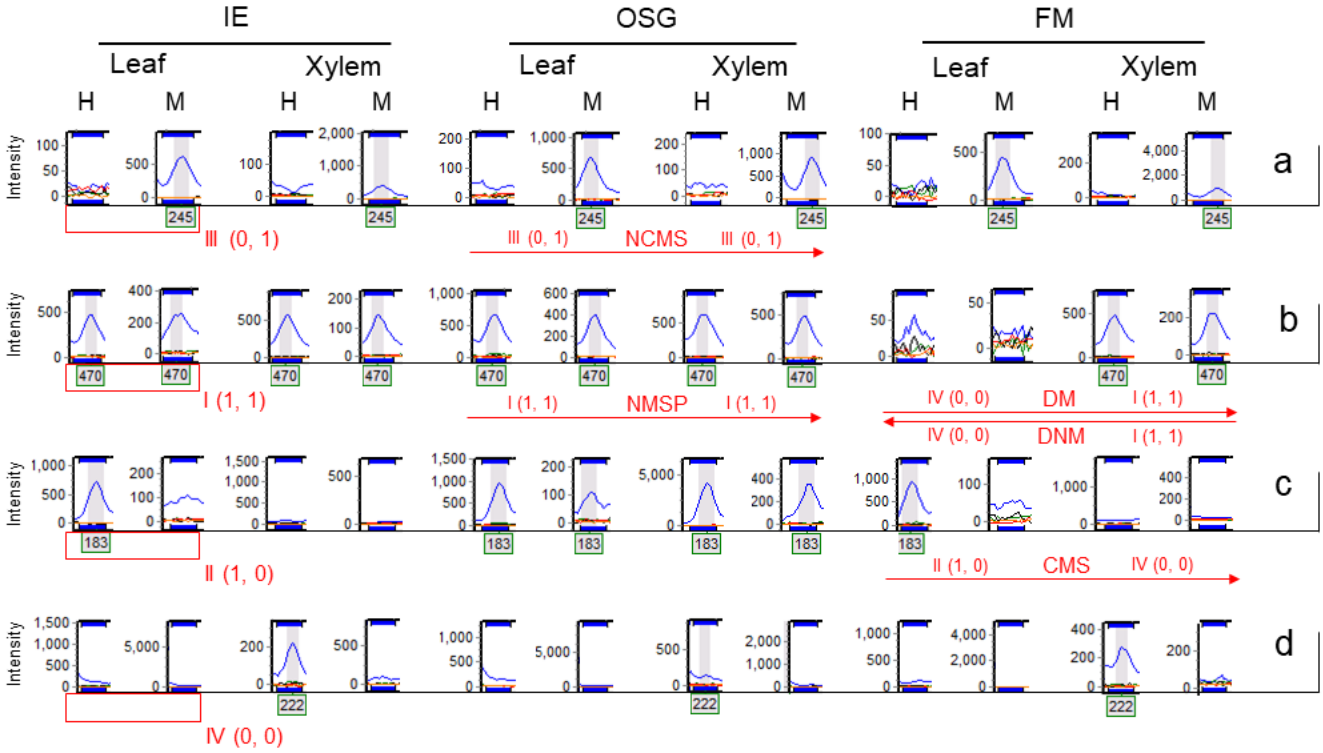

Fig. 1 Suppl. Examples of methylation patterns detected in pecan cv. Pawnee leaves and xylem at the inflorescence emergence (IE), ovaries start growth (OSG), and fruit maturity (FM) stages using primer combinations E1-H/M1 (*a*, *b*, *c*) and E2-H/M3 (*d*). The amplified bands from the fluorescence-labeled methylation-sensitive amplified polymorphism procedures were detected by capillary electrophoresis, and the electrophoresis data were analyzed using *GeneMarker 2.2.0*. The values at the *bottom* of the peak figures represent the existence of the bands amplified from the digested product of *Eco*RI/*Hpa*II (H) or *Eco*RI/*Msp*I (M); otherwise, no bands were produced in the corresponding lanes. Type I (1, 1), II (1, 0), and III (0, 1) refer to unmethylation, hemi-methylation, and full methylation, respectively; type IV (0, 0) indicates the existence of hypermethylation when other samples with the same genotype present anyone of the other three types at the same site. In this figure, examples of the methylation events between the leaves and xylem at one stage and over three stages are shown. Five methylation events were present between the two tissues at one stage, including nonmethylation state preservation (NMSP), no change in pattern of methylation state (NCMS), demethylation (DM), *de novo* methylation (DNM), and changes in pattern of methylation state (CMS). *a*, *b*, *c*, *d* - different methylation events in the sites of leaves and xylem over three stages including the same patterns present between the leaf and the xylem at any stage (*a*), polymorphic patterns present between leaf and xylem at one stage (*b*), two stages (*c*), and any stage (*d*).

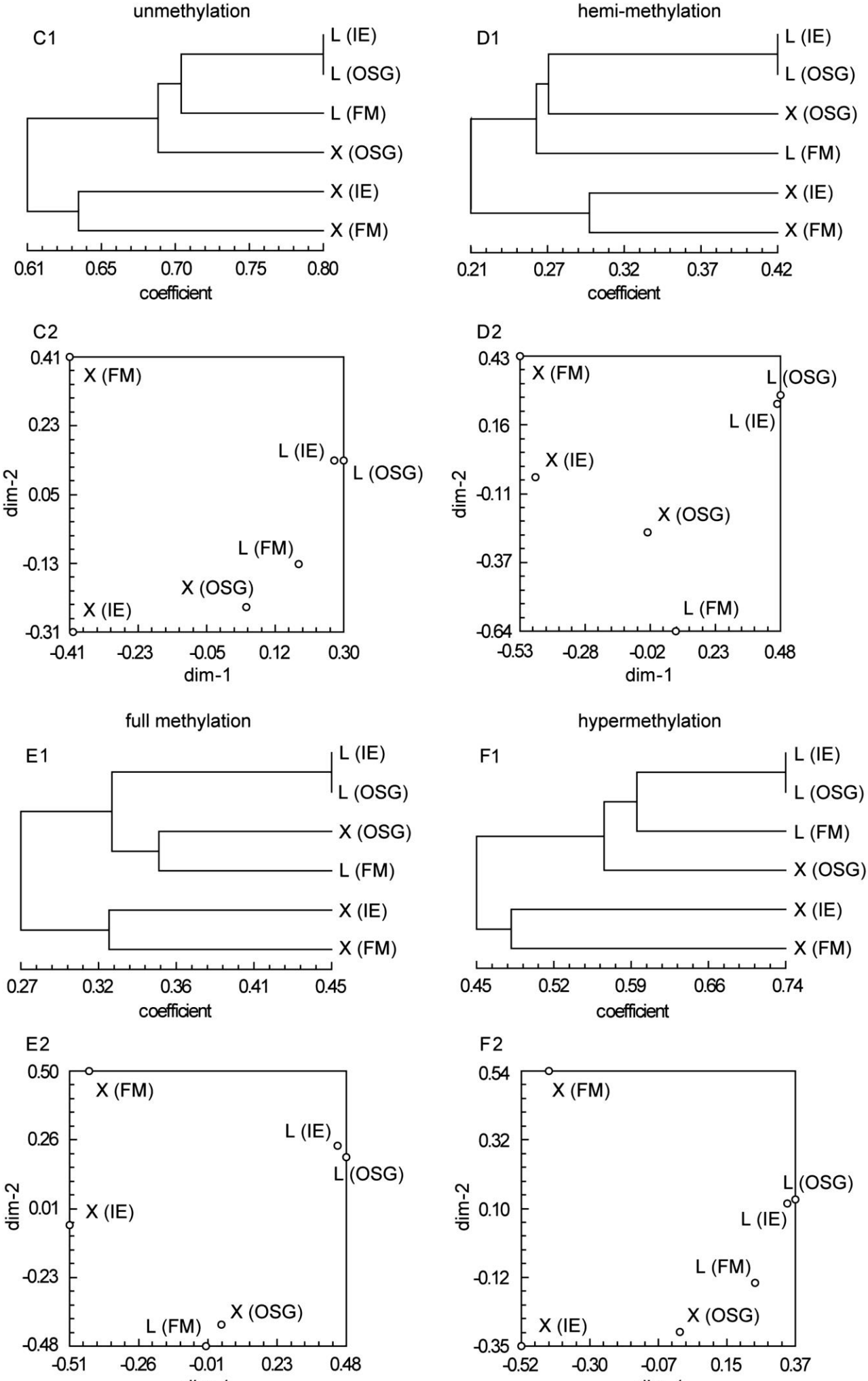
unmethylation
C1
L (IE)
L (OSG)
L (FM)
X (OSG)
X (IE)
X (FM)
0.61 0.65 0.70 0.75 0.80
coefficient
hemi-methylation
D1
L (IE)
L (OSG)
X (OSG)
L (FM)
X (IE)
X (FM)
0.21 0.27 0.32 0.37 0.42
coefficient
C2
0.41 0.23 0.05 -0.13 -0.31
dim-2
X (FM)
L (IE)
L (OSG)
L (FM)
X (OSG)
X (IE)
-0.41 -0.23 -0.05 0.12 0.30
dim-1
D2
0.43 0.16 -0.11 -0.37 -0.64
dim-2
X (FM)
L (OSG)
L (IE)
X (IE)
X (OSG)
L (FM)
-0.53 -0.28 -0.02 0.23 0.48
dim-1
full methylation
E1
L (IE)
L (OSG)
X (OSG)
L (FM)
X (IE)
X (FM)
0.27 0.32 0.36 0.41 0.45
coefficient
hypermethylation
F1
L (IE)
L (OSG)
L (FM)
X (OSG)
X (IE)
X (FM)
0.45 0.52 0.59 0.66 0.74
coefficient
E2
0.50 0.26 0.01 -0.23 -0.48
dim-2
X (FM)
L (IE)
L (OSG)
X (IE)
L (FM)
X (OSG)
-0.51 -0.26 -0.01 0.23 0.48
F2
0.54 0.32 0.10 -0.12 -0.35
dim-2
X (FM)
L (OSG)
L (IE)
L (FM)
X (IE)
X (OSG)
-0.52 -0.30 -0.07 0.15 0.37

Fig. 2 Suppl. Cluster analysis (*C1*, *D1*, *E1*, *F1*) and principal coordinate analysis (*C2*, *D2*, *E2*, *F2*) of leaf (L) and xylem (X) samples at inflorescence emergence (IE), ovary start growth (OSG), and fruit maturity (FM) stages. The "mixed-scoring 2" method was referenced to generate four types of new 1/0 matrix, including the matrix for unmethylation (unmethylated fragments recorded as 1; other fragments recorded as 0), hemi-methylation (hemi-methylated fragments - 1; other fragments - 0), full methylation (fully methylated fragments - 1; other fragments - 0), and hypermethylation (hypermethylated fragments - 1; other fragments - 0). *C1* and *C2*, *D1* and *D2*, *E1* and *E2*, *F1* and *F2* were obtained according to the cluster analysis and the principal coordinate analysis of the corresponding four types of data matrix.