10.1071/FP12093_AC

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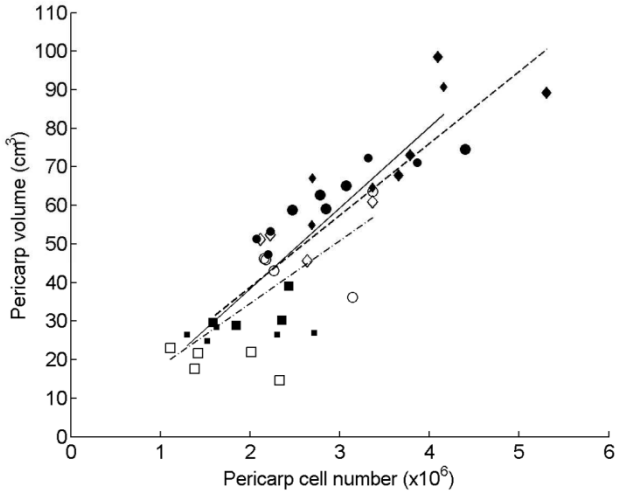
Supplementary material

Table S1. Primer sequences used to amplify gene-specific regions

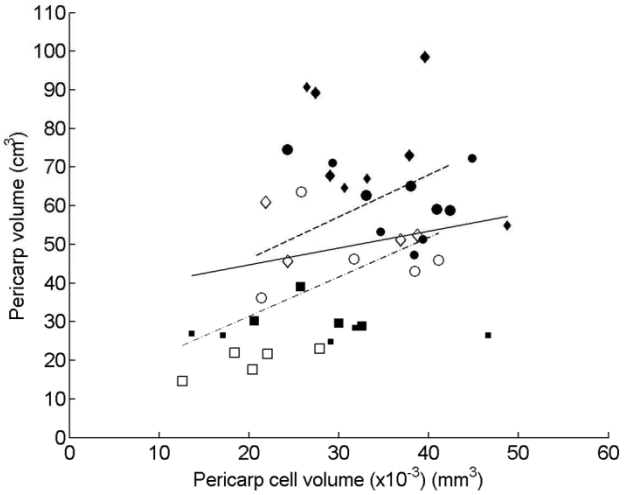
For each gene the accession number and reference are given

cDNA	Primer sequence	Accession number	References
CycB2	Forward ATTCAATCTTGGAGAGGATTAAAG Reverse GTAGCCATTTCAGCCCTATC	AJ243455	Joubès *et al*. 2000
CycD3	Forward CAAGGAGAAGGTGGAGAGGATG Reverse GGTGATGAAGTAACTGATGTAGC	AJ002590	Kvarnheden *et al*. 2000
CDKB1	Forward ATGGAGAAATACGAGAAATTGGAG Reverse ACGATGTAGAGAGAATGAGATAGC	AJ297916	Joubès *et al*. 2001
TIP41	Forward GCTGCGTTTCTGGCTTAGG Reverse ATGGAGTTTTTGAGTCTTCTGC	SGN-U321250	Exposito-Rodriguez *et al*. 2008

(*a*)


Pericarp volume (cm3)
Pericarp cell number (x10^6)

(*b*)


Pericarp volume (cm3)
Pericarp cell volume (x10^-3) (mm3)

(*c*)

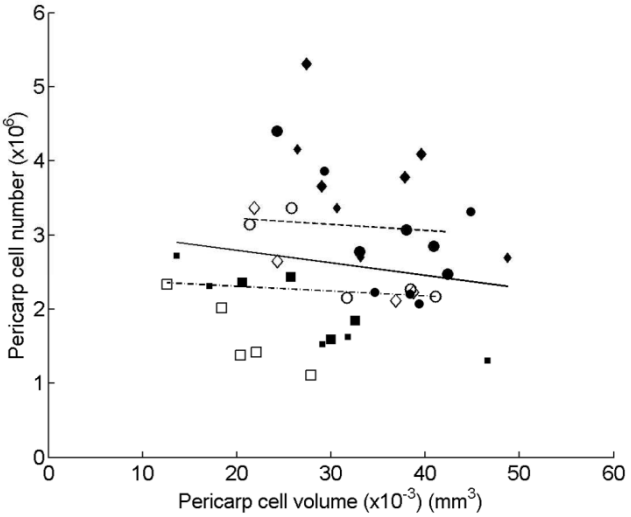

Pericarp cell number (x10^6)
Pericarp cell volume (x10^-3) (mm3)

Fig. S1. Relationships between (*a*) pericarp volume and cell number, (*b*) pericarp volume and cell volume, and (*c*) cell number and cell volume. Each point is an individual fruit at the breaker stage of genotypes g36 (square), Moneyberg (circle) and g49 (diamond) measured in 5&5F (opened symbols and dash-dot lines), 5&2F (small symbols and continuous lines) and 2&2F (filled symbols and dashed lines) fruit load treatments. Slope (α) of regression is (*a*) α = 15.8, R^2 = 0.48, *P* = 0.006 (5&5F); α = 20.0; R^2 = 0.71, *P* < 0.001 (5&2F) and α = 18.2, R^2 = 0.79, *P* < 0.001 (2&2F); (*b*) α = 1.08; R^2 = 0.31, *P* = 0.04 (5&5F); α = 0.50; R^2 = 0.05, *P* = 0.43 (5&2F), and α = 1.19; R^2 = 0.12, *P* = 0.23 (2&2F), (*c*) α = –0.006; R^2 = 0.006, *P* = 0.80 (5&5F), α = –0.017; R^2 = 0.04, *P* = 0.50 (5&2F), α = –0.007; R^2 = 0.002, *P* = 0.89 (2&2F).