Supporting Information

Lora et al. 10.1073/pnas.1014514108

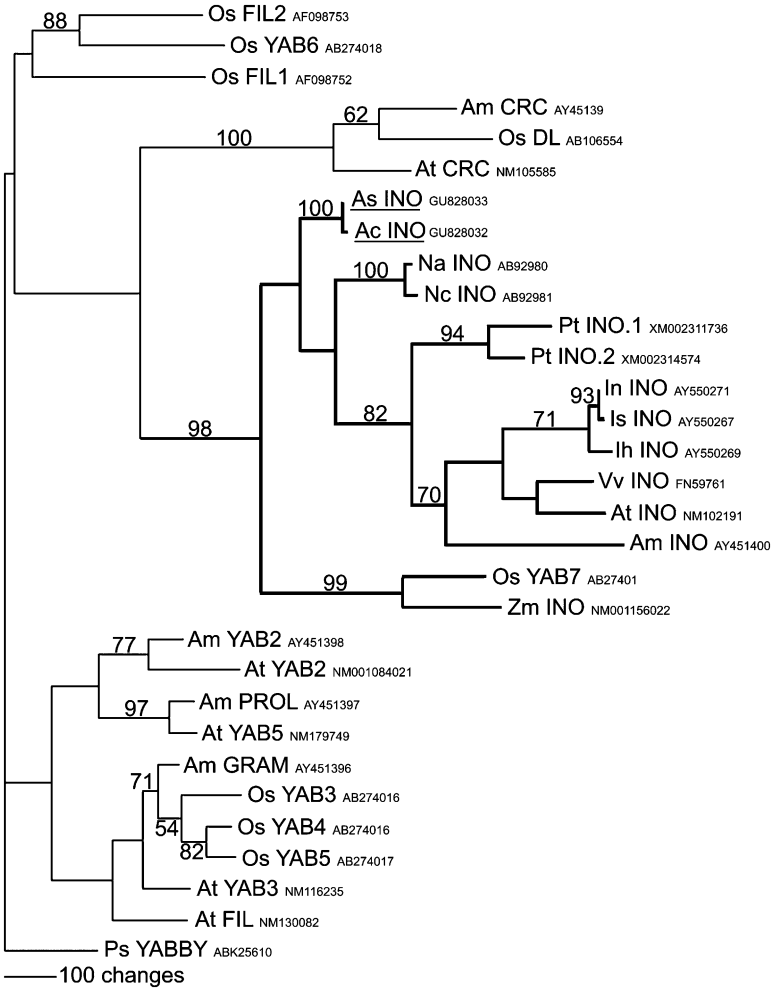

Fig. S1. Phylogenetic relationships of isolated *Annona* genes. The single shortest tree of YABBY protein sequences resulting from 100 replications of a random addition heuristic search under maximum parsimony (recovered in 97/100 replicates, length = 6,647 in arbitrary units; excluding uninformative characters, consistency index = 0.6256, homoplasy index = 0.3744, retention index = 0.6930). Numbers adjacent to nodes indicate support from bootstrap analysis. The clearly resolved clade of INO orthologs is in thicker lines and *Annona* sequences determined in the current study are underlined. Species included in the tree comprise the following: Ac, *Annona cherimola*; Am, *Antirrhinum majus*; As, *Annona squamosa*; At, *Arabidopsis thaliana*; Ih, *Impatiens hookeriana*; In, *Impatiens niamniamensis*; Is, *Impatiens sodenii*; Na, *Nymphaea alba*; Nc, *Nymphaea colorata*; Os, *Oryza sativa*; Ps, *Picea sitchensis*; Pt, *Populus trichocarpa*; Vv, *Vitis vinifera*; Zm, *Zea mays*. GenBank accession numbers are given at the right of each sequence.

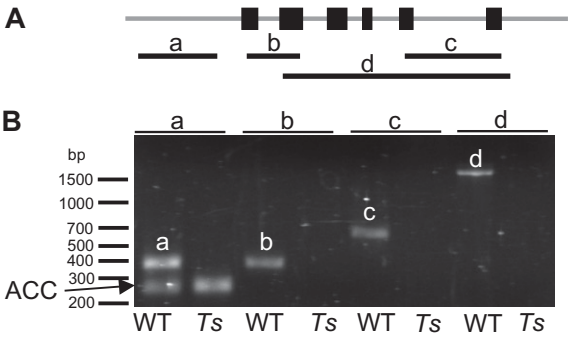

Fig. S2. *INO* gene fragments could not be amplified from *Ts*. (*A*) Primers were designed to the *A. cherimola INO* sequence to enable amplification of the indicated regions. (*B*) All primer pairs amplified the expected fragments from wild-type (WT) *A. squamosa*. These same *INO*-specific primer pairs failed to amplify fragments from *Thai seedless* (*Ts*) DNA, whereas primers specific to an *Annona* 1-aminocyclopropane-1-carboxylate synthase (ACC) gene readily amplified the expected fragment from both wild-type and *Ts* DNA samples even when in a reaction that included primers that failed to amplify an *INO* fragment (lanes "a").

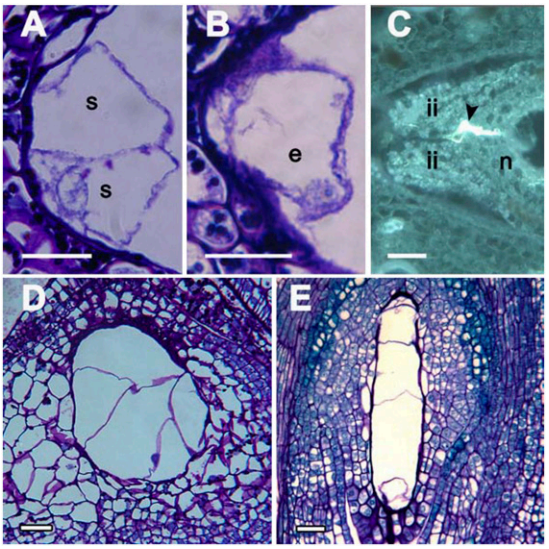

Fig. S3. Embryo sac anatomy and pollen tube growth. (*A*–*D*) Ovule sections of *A. squamosa Ts*. (*A*) Two synergid cells with nuclei and cytoplasms at the base of the embryo sac. (*B*) Egg cell. (*C*) Aniline blue staining of a *Ts* ovule shows a brightly fluorescent pollen tube that has passed through the micropyle and penetrated the nucellus (arrowhead). (*D*) Early-degenerating endosperm 10 d after pollination. (*E*) Cellular endosperm 8 d after pollination in *A. cherimola.* [Scale bar, 10 μm (*A* and *B*); 20 μm (*C*–*E*).] e, egg cell; ii, inner integument; n, nucellus; s, synergid cell.

Table S1. Oligonucleotide primers used in this study

Primer name	Primer sequence (5′-3′)	Temperature (°C)	Fig. 4 band
LMINO1	CCTAAATGAAGGGTTTACATGTGGC	60	a
LMINO2	GCCCACCTTCATTTGCTCCTTGG	60	a
LMINO3	ATGGACATGTCTACATACAACCAC	60	b
LMINO4	CGAGGAACTGCAGTGGAACAAATG	60	b
LMINO5*	AGAAGAGATCCAAAGGCTCAAGG	60	c
LMINO6	GCAGCTCTCTCTATCTCCTTTG	60	c
LMINO7	GCGTGTAAGCAGATTCCCTTTACC	60	d
LMINO8	AGCGTCCCATGCAGCAGCTTGTT	60	d
LMAT1	GATGAGATCTACTCGGGCTCC	60	ACC
LMAT2	GAGGAGATCAAGCTGAAGCTAGAC	60	ACC
LMINOa†	GGTGACGGTCAGATGTGGCCATTGC	60	
LMINOb†	TGTTGGGCTGCTTAGCCTTGAGCC	60	
GW1.3b*	ACGTGCTCCATCAGCATATAACCG	60	
GW1.5a*	CATCACATTAACGGAAAGGAGACC	60	
GW1.5b*	AATGGCCACATCTGACCGTCACC	60	
GW2.3a*	GGTAAAGGGAATCTGCTTACACGC	60	
GW2.3b*	CTTCTCTCTTCCTCCAAAATCACCC	60	
GW2.5a*	GGAGAGGCACAGTAGCCGAATGATT	60	
GW2.5b*	GCTACAGTCATGTAAGTGGTCCAG	60	
GW3.3a*	AGCTATAGTAGCAGAAGATAGCTACA	60	
GW3.3b*	AAATAAAAGGAAGGAGAGGCACAGTA	60	
GW3.5a*	ATAAATTTTCTTATATGAAGGGAAC	60	
GW3.5b*	AAATTTTCTTATATGAAGGGAACAC	60	

*Primers used for the Genome Walker protocol.
†Primers designed from the first isolated fragment of *INO* genomic sequence from *A. cherimola*.