Recommended design of figures:

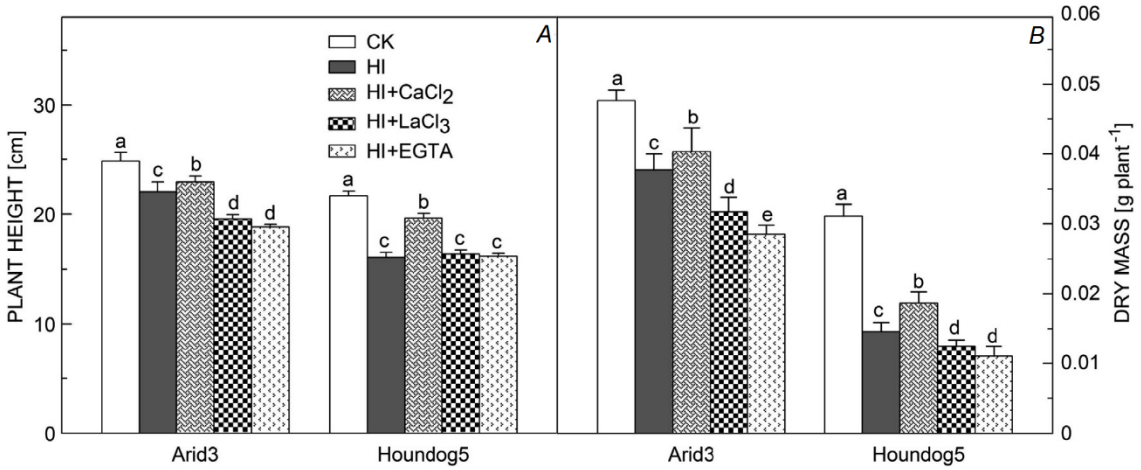

Fig. 1. The effects of calcium on plant height (*A*) and dry mass (*B*) in Arid3 and Houndog5 under a high irradiance (500 μmol m^{-2} s^{-1}) stress. The plants were grown under PPFD of 100 μmol m^{-2} s^{-1} (LI; CK) or 500 μmol m^{-2} s^{-1} (HI) and with the addition of 20 mM $CaCl_2$, 1 mM $LaCl_3$, or 2 mM EGTA. Means ± SDs, n = 3; bars with different letters are significantly different at 5 % level. (From Xu *et al*. 2016)

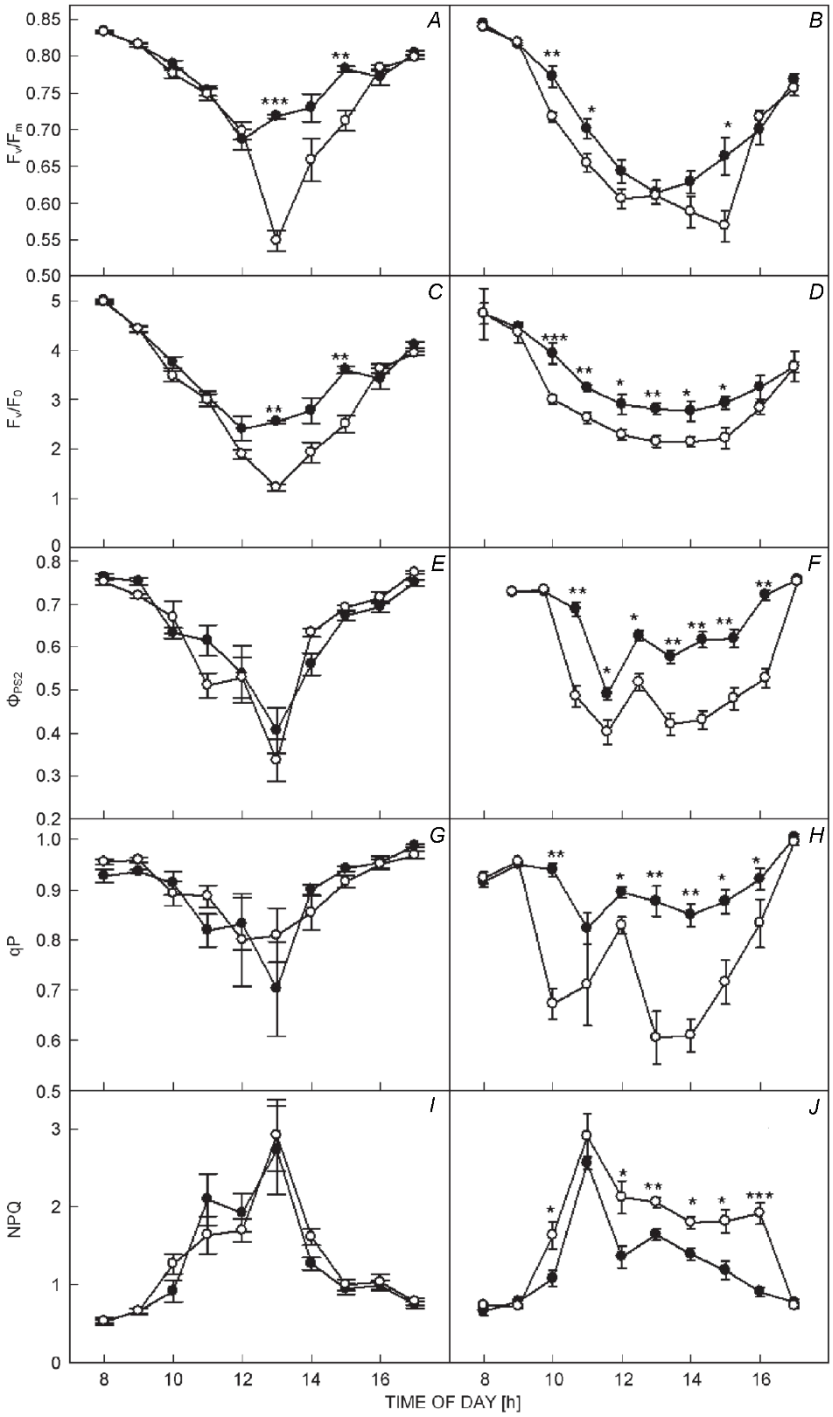

Fig. 2. Diurnal variations in the maximum efficiency of PS 2 photochemistry (F_v/F_m), the maximum ratio of quantum yields of photochemical and concurrent non-photochemical processes in PS 2 (F_v/F_o), actual efficiency of photochemical energy conversion in PS 2 under steady-state conditions (Φ_{PS2}), photochemical quenching coefficient (qP) and non-photochemical Chl fluorescence quenching (NPQ) in source leaves under low sink demand ('girdling' treatment, *open circles*) on days 2 (*A*, *C*, *E*, *G*, *I*) and 4 (*B*, *D*, *F*, *H*, *J*) after the treatment, compared with the control ('no girdling', *closed circles*). Means ± SE (n = 5). ** and * indicate significant difference at $P < 0.01$ and $P < 0.05$ between the treated and control plants, respectively. (From Yan *et al*. 2011)

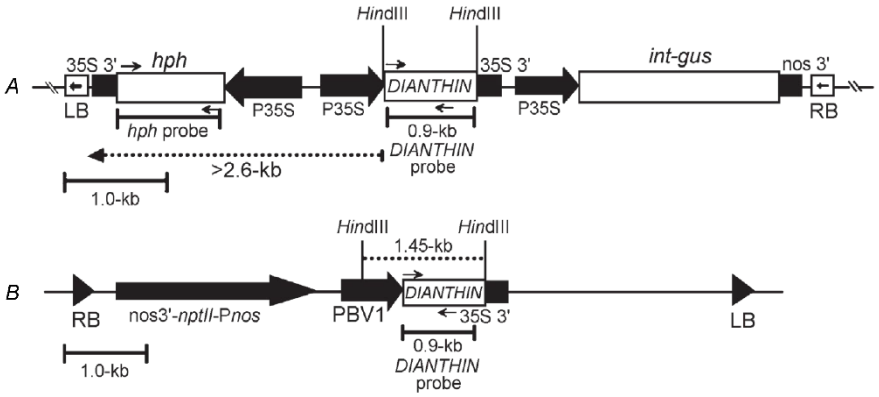

Fig. 3. The T-DNA regions of binary plasmids. The T-DNA of pJAS1 (*A*), which harbors P35S-*DIANTHIN*, P35S-*hph* and P35S-*int-gus* genes. The left border junction fragment (>2.6 kb, the distance between the *Hin*dIII site and LB), marked with a *dotted arrow*, will hybridize to the *hph* probe (marked with a *full line*). The 0.9-kb *DIANTHIN* gene (marked with a *full line*), flanked by *Hin*dIII sites on either side, will hybridize to a 0.9-kb *Hin*dIII fragment. P35S, *Cauliflower mosaic virus* 35S promoter; 35S3', *Cauliflower mosaic virus* 3' region; LB, left T-DNA border; RB, right T-DNA border; *hph*, hygromycin phosphotransferase gene; *int-gus*, β-glucuronidase gene with an intron; nos3', nopaline synthase gene 3' region. The T-DNA of pRAJ18 (*B*), which harbors the PBV1-*DIANTHIN* and P*nos*-*npt*II genes. The 1.45-kb internal T-DNA fragment, flanked by two *Hin*dIII sites (marked with a dotted line) will hybridize to the *DIANTHIN* probe (marked with a *full line*). P*nos*, nopaline synthase gene promoter; *nptII*, neomycin phosphotransferaseII. Scale (1.0 kb) is marked. *Arrows* mark the locations of forward and reverse primers of *hph* and *DIANTHIN* genes. (From Shah and Veluthambi 2010)

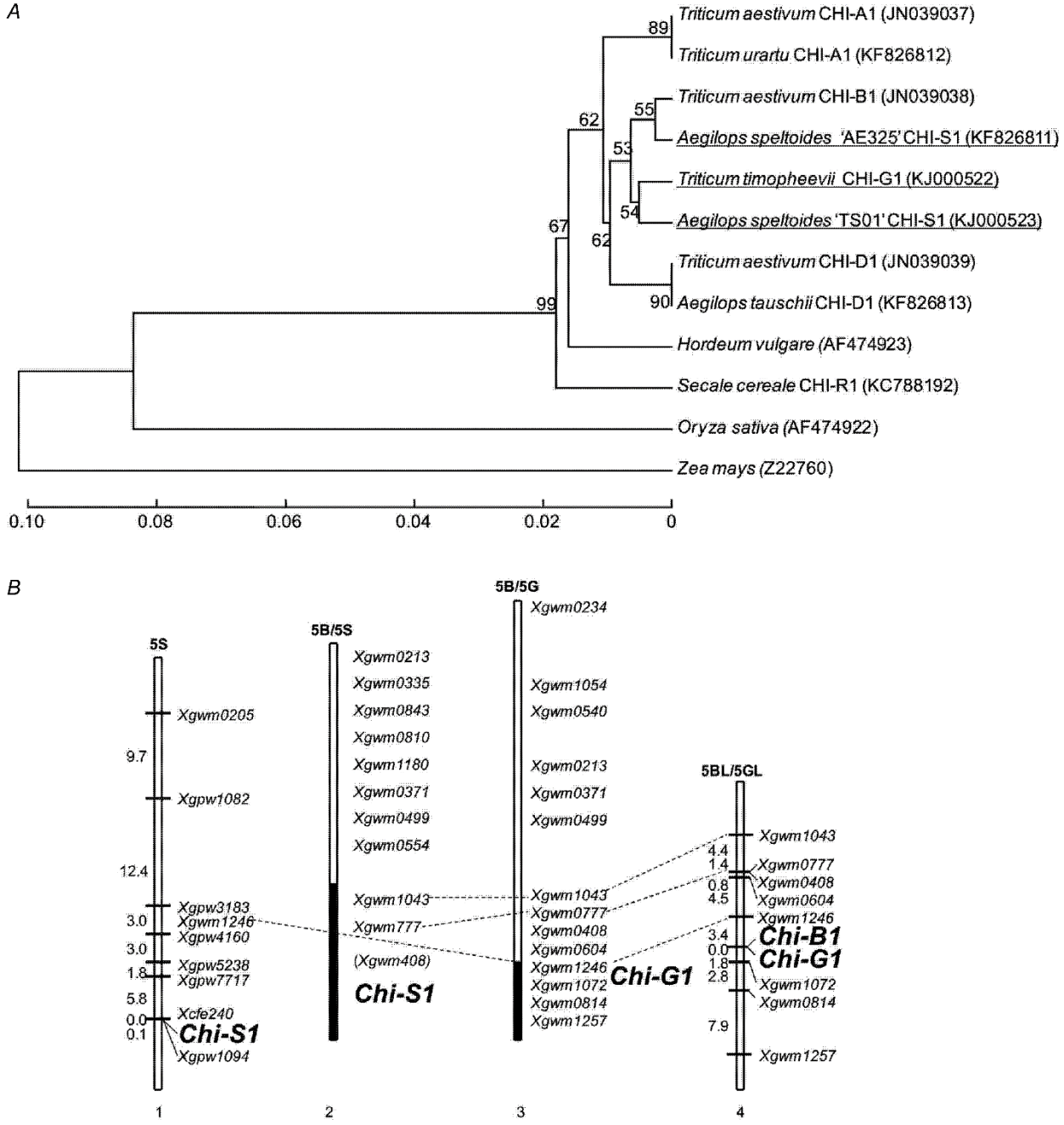

Fig. 1. *A* - Phylogeny of chalcone-flavanone isomerase (CHI) polypeptides. Those determined in the current study are *underlined*. Relevant GenBank accession numbers are given to the right. The numbers at each node represent a bootstrap value as percentage of 1 000 replicates. The genetic distance is displayed under the tree. *B* - Genetic (schemes 1 and 4) and physical (schemes 2 and 3) mapping *Chi-1* genes. Intrachromosomal positions of *Chi-S1*, *Chi-G1*, and *Chi-B1* were obtained from genotypic data acquired in the current study. The microsatellite loci *Xgwm*, *Xgpw*, and *Xcfe* were placed according to Dobrovolskaya *et al.* (2011), Adonina *et al.* (2012), Leonova *et al.* (2002 and unpublished), and Timonova *et al.* (2013). Introgression fragments of alien genetic material in bread wheat chromosome 5B are shown in *black* (schemes 2 and 3). The genetic distances are given in centimorgans to the left of each linkage group. (From Shoeva *et al*. 2016)

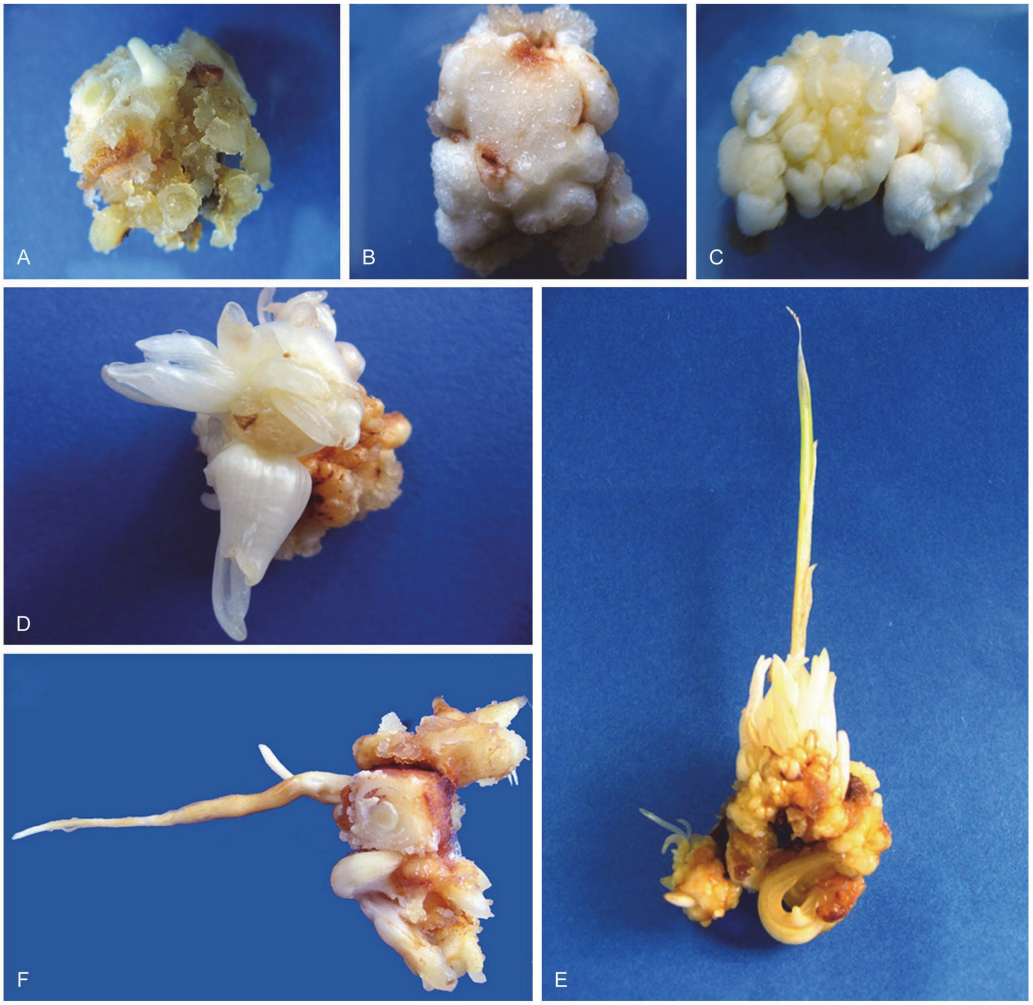

Fig. 4. Shoot and root regeneration from callus of *C. sativus* on MS medium. Three types of meristem-derived callus on MS medium containing different combinations of growth regulators: *A* - 1.0 mg dm^{-3} NAA + 2.0 mg dm^{-3} KIN (type I); *B* - 1.0 mg dm^{-3} NAA + 2.0 mg dm^{-3} TDZ (type II); *C* - 10 mg dm^{-3} PIC + 4.0 mg dm^{-3} KIN (type III). *D* - shoot regeneration through callus on medium with 1.0 mg dm^{-3} TDZ + 1.0 mg dm^{-3} NAA; *E* - sprouted shoot after transfer of regenerated shoot to medium with 1.0 mg dm^{-3} BAP + 1.0 mg dm^{-3} NAA under 16-h photoperiod; *F* - root regeneration through callus on medium with 2.0 mg dm^{-3} KIN + 1.0 mg dm^{-3} NAA. (From Vatankhah *et al.* 2010)

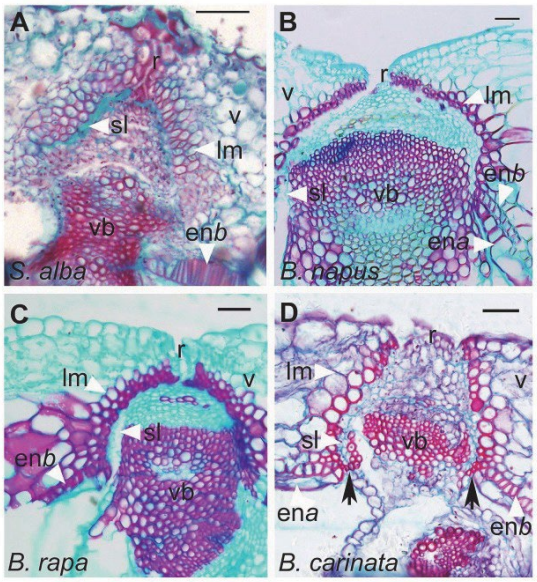

Fig. 3. Transverse sections showing a stage 19 fruit in *S. alba* (*A*), *B. napus* (*B*), *B. rapa* (*C*), and *B. carinata* (*D*). The valve on the left side has already separated from the replum at the separation layer (*B* and *C*). A lignified bridge is present between the lignified valve margin cells and the lignified replum vasculature as indicated by the *black arrow* (*D*). The *white arrows* point to v - valve, r - replum, vm - valve margin, separation layer, lm - lignified layer at the valve margin, en*b* - endocarp *b* layer, en*a* - endocarp *a* layer, and vb - vascular bundle. *Scale bars* = 50 μm. (From Zhang *et al*. 2016)

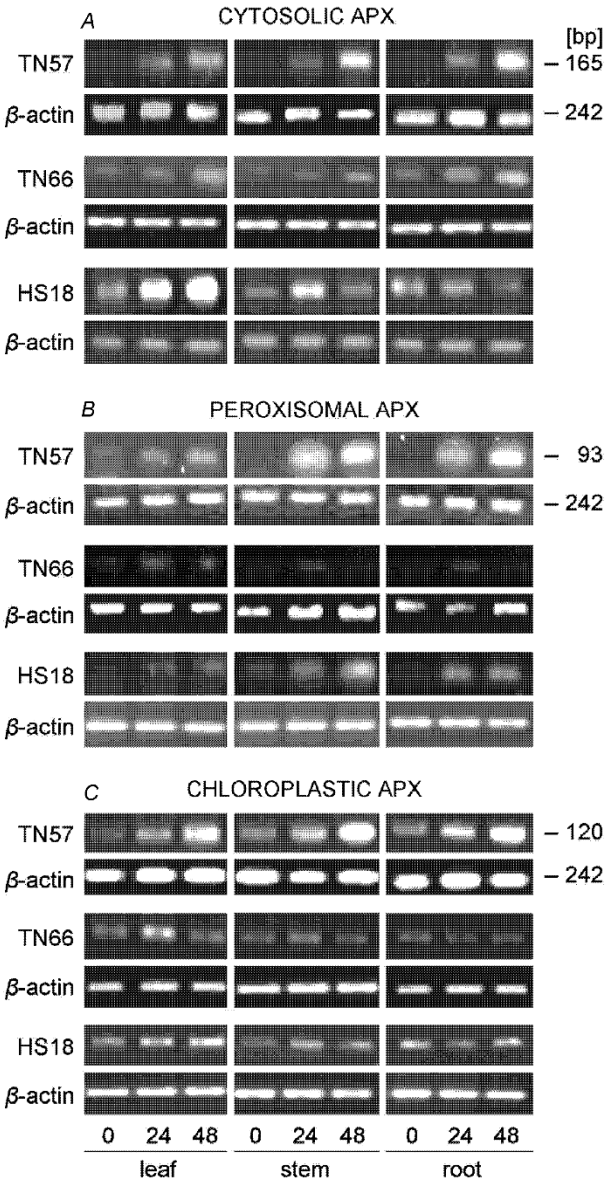

Fig. 5. Semiquantitative RT-PCR of cytosolic (*A*), peroxisomal (*B*) and chloroplastic (*C*) ascorbate peroxidase (*APX*) transcript responses in leaves, stems, and roots of the TN57, TN66 and HS18 genotypes exposed to 450 mM NaCl stress for 0, 24 and 48 h (β-actin was used as the positive control). (From Lin and Pu 2010)

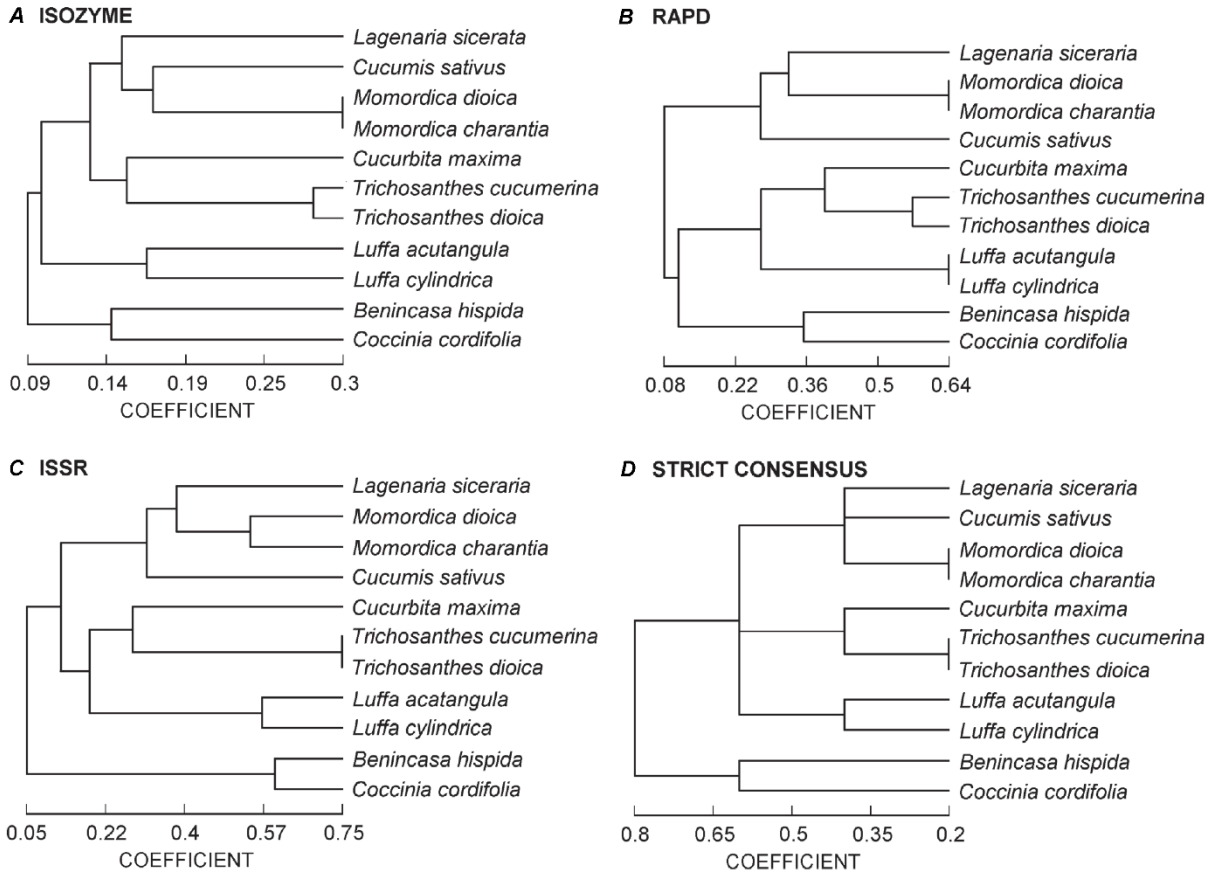

Fig. 6. Dendrograms generated using unweighted pair group method with arithmetic average (UPGMA) analysis, showing relationships between different members of *Cucurbitaceae*, using isozyme (*A*), RAPD (*B*), ISSR (*C*) data and a strict consensus tree based on both RAPD and ISSR data (*D*). (From Sikdar *et al*. 2010)