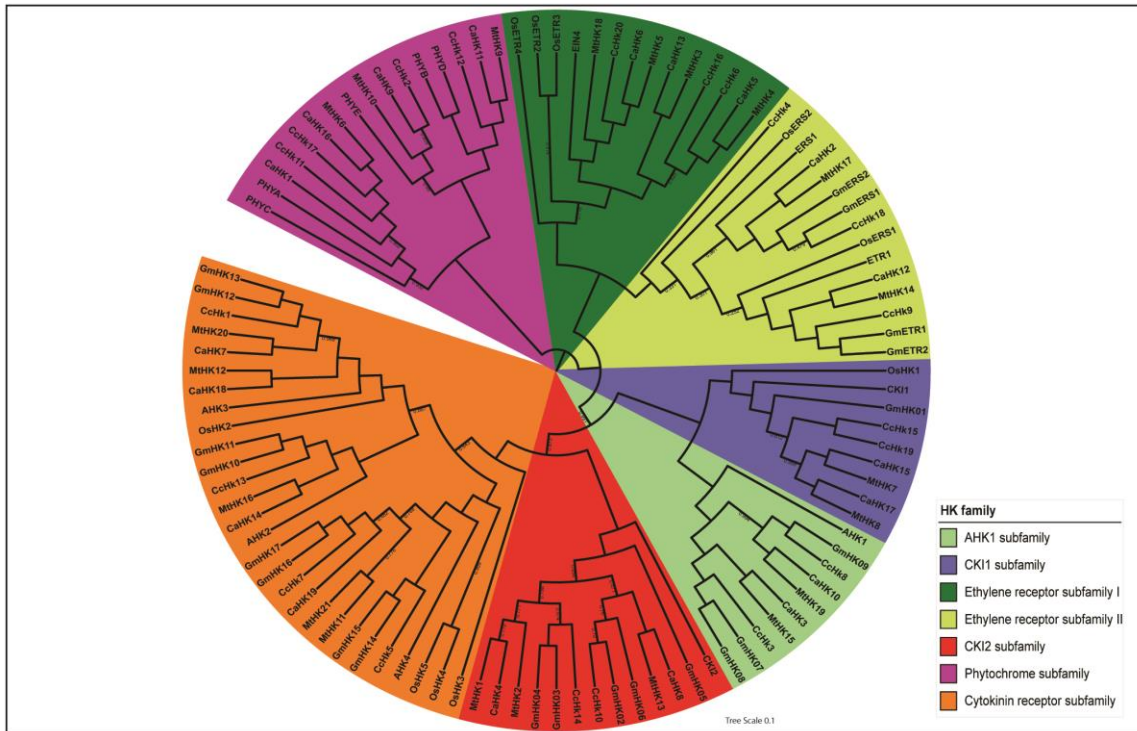
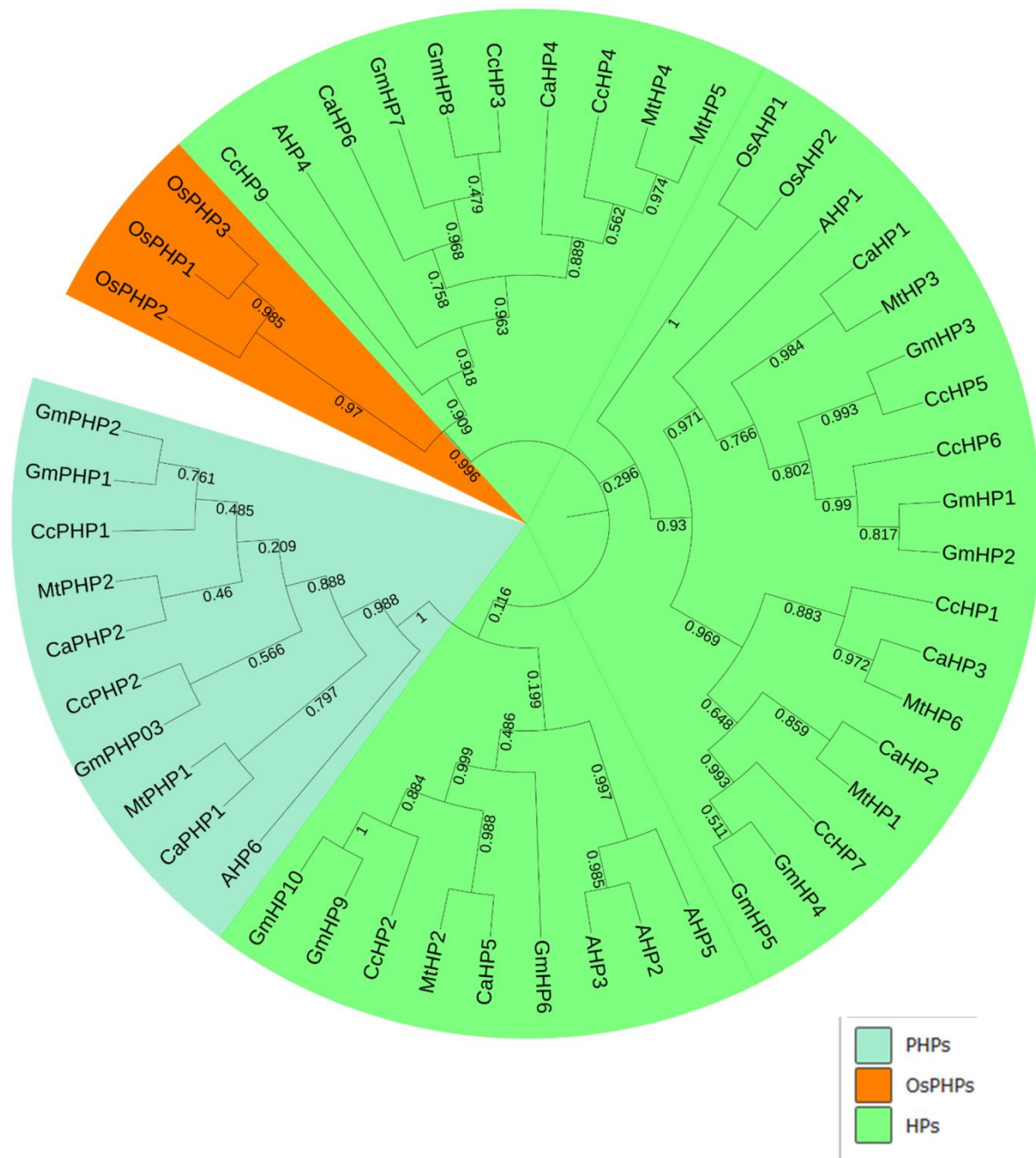


**Supplemental Fig. 1.** Phylogenetic classification of various crop species and distribution of TCS members

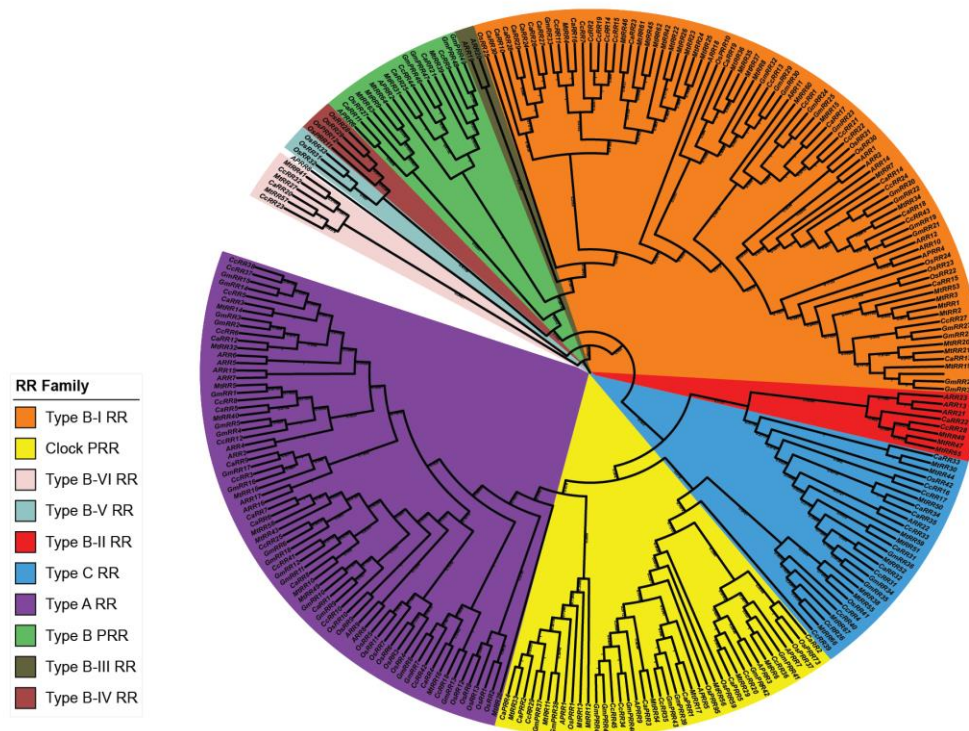




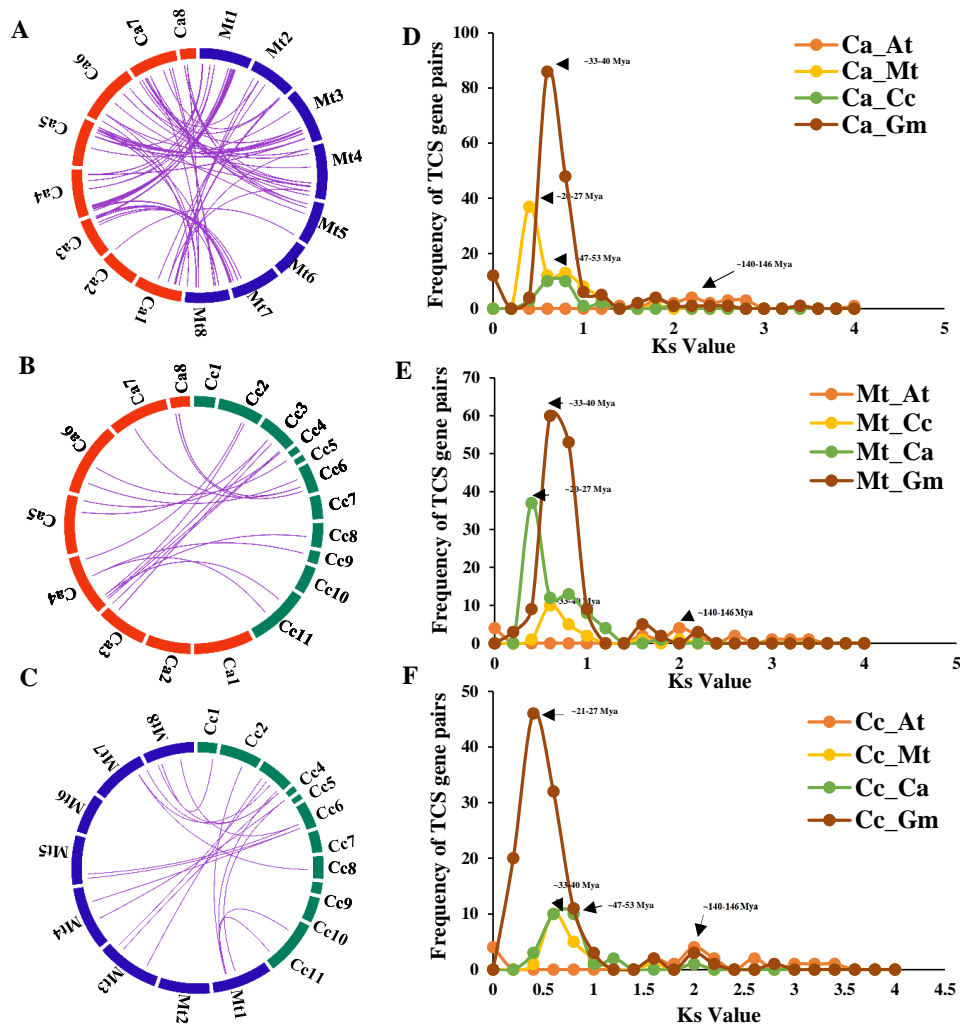
**Supplemental Fig. 3. Phylogenetic analysis of HKs.** Phylogenetic relationships of histidine kinase family proteins from chickpea, *Medicago*, *C. cajan*, soybean, rice and Arabidopsis. The bootstrap values are depicted as numerical values.



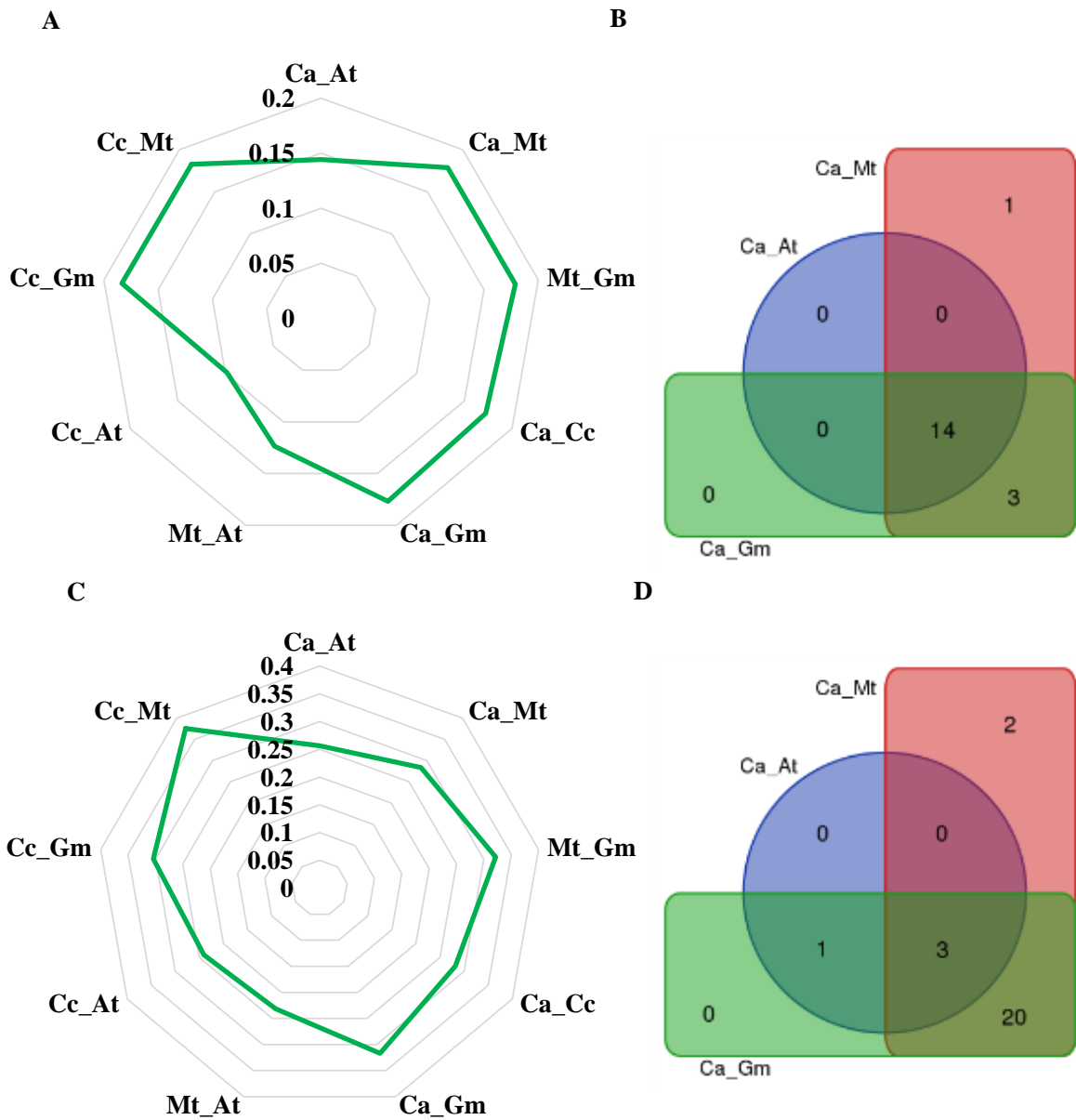
**Supplemental Fig. 4. Phylogenetic analysis of HPs.** The phylogenetic tree of histidine phosphotransferase and pseudo histidine phosphotransferase in different crops. The bootstrap values are depicted as values.



**Supplemental Fig. 5. Phylogenetic analysis of RRs.** The phylogenetic tree classified the response regulator family into TypeA RR, TypeB RR, TypeC RR and PseudoRR subfamily. The bootstrap values are depicted as numerical values.



**Supplemental Fig. 6. Synteny and collinearity analysis of TCS members among legumes.** (A-C). Segmentally duplicated pairs in (A) chickpea-*Medicago* (Ca-Mt), (B) chickpea-pigeonpea (Ca-Cc) and (C) *Medicago*-pigeonpea (Mt-Cc) visualized by Circos (D-F). Graphs represent Ks values plotted against number of segmentally duplicated pairs for estimating time of divergence between the legumes and non-legumes (*Arabidopsis*), (D) chickpea, (E) *Medicago* and (F) *Cajanus cajan*. The Y-axis indicates the frequency of TCS gene pairs and the horizontal axis indicates the Ks values. Arrows are indicating the time of divergence in million year ago (Mya).



**Supplemental Fig. 7. Evolutionary analysis of TCS members. (A-B).** Spider web indicates pair-wise comparison of median values of Ka/Ks ratio of (A) HKs and (B) RRs (C-D). Venn diagram denotes the pair-wise comparison of number of (C) HKs and (D) RRs in chickpea with Arabidopsis (Ca-At), chickpea with *M. truncatula* (Ca-Mt), chickpea with *Glycine max* (Ca-Gm), chickpea with Pigeonpea (Ca-Cc), *M. truncatula* with Arabidopsis (Mt-At), *M. truncatula* with *Glycine max* (Mt-Gm), Pigeonpea with *M. truncatula* (Cc-Mt), Pigeonpea with *Glycine max* (Cc-Gm) and Pigeonpea with Arabidopsis (Cc-At).





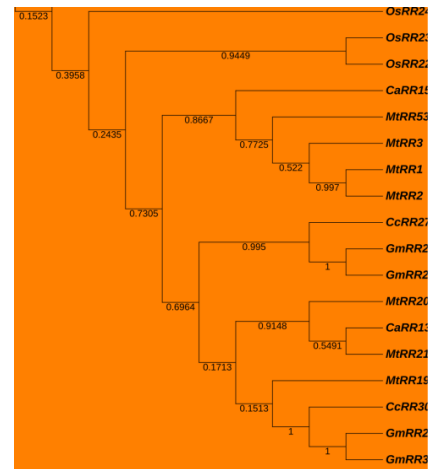
**A**

CaRR13 --- 616 AA (protein)  
1852 nt (CDS)

**C**

>CaRR13(Ca\_01726,Ca\_14780.1)-PEP  
MDDPSDRFPIGMRVLA<sup>VDDDDPTCLFVLETLLRRCQYHVTTTSQA</sup>IKALAMLRENKD  
KFDLVISDVHMPDMDGFKLELVGLEMDLPVIMLSAYGDTKLV<sup>MKGISHGACD</sup>YLL  
KPVRIEELKNIWQHVI<sup>RRKKS</sup>DPKEKNKTSNRDKTTS<sup>D</sup>SGEENGKLNK<sup>RRK</sup>DQDED  
EDEDKENDHDNEDPSAQ<sup>KKPRVVVSV</sup>ELHRKFVDAV<sup>NRLGIDKAVPK</sup>KILDMMMN  
VENITRENKYRLYLKRISCVANQQASMVA<sup>AFGSADQSYLRMAGSGH</sup>FHNNAFRSF  
SSSGFISSLNTPAGLNGHGFPPSGILQLGQSQNLN<sup>SSNDQLKFQSAITPVNQ</sup>NVLH  
GTPMSIGFDHSQNSKGVLSVQNLTTDDVKTTFPIPDQRLRLATSSSYPPSLGITNNAS  
SSSGASRHSFPPFSMIDQSRHSDNWSSAVQLSGIQ<sup>TNSFP</sup>SECFRQTAIPPSDNMA  
SLPLQGAYLSGQSIASLCSQSHGSLADMHSQGAFF<sup>TNPPEYGN</sup>SNLPPFQGWEDHN  
QDAIYHSNVTCGSTNSPFGAVVPSGLTTTNSALHRNLDTR<sup>FCDDPIQMKHAG</sup>FGE  
LVECSSRQPRANVVSQQKFSNNLGSLEYLVSS<sup>TMEQEQDKMKLLNGDLIC</sup>DNYSL

■ Rec Domain    ■ Myb Domain    ■ Nuclear localization signal

**B****D**

Sequences producing significant alignments							Download	Manage Columns	Show
							100		
							Graphics	Distance tree of results	Multiple alignment
Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession			
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<input checked="" type="checkbox"/> <a href="#">DNA binding site</a>	87.0	106	12%	3e-25	67.80%	Query_10008			

**Supplemental Fig. 9. CaRR13 sequence, domain and homology.** (A) The nucleotide and the amino acid length of the *CaRR13* gene and protein. (B) The Type-B RR clade representing clustering of *CaRR13* in a legume specific clade. (C) Marked functional domains and DNA binding segment of *CaRR13* protein. (D) Percent identity of *CaRR13* protein with *Medicago* homologs *MtRR20* and *21*.