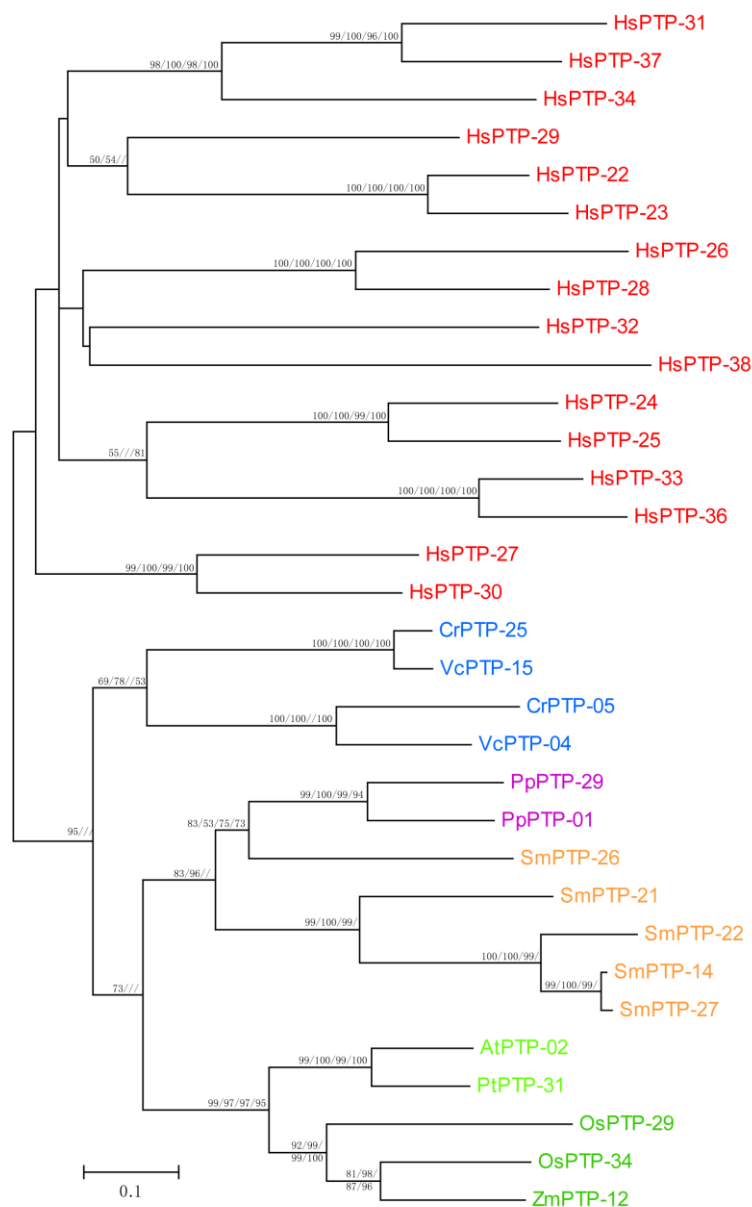


Comprehensive and evolutionary analysis of protein tyrosine phosphatases (PTP) in the green plants

Lujun Yu[†], Dongru Feng[†], Wenyan Li, Hongbin Wang, Jinfa Wang and Bing Liu***Fig S1.** Sub. I-A (classic PTP) GPPTP phylogramPhylogram of I-A (classic PTP) PTPc domain (PF00102) includes GPPTP I-A and *Hs* homologs (Table S3) as comparative genes.

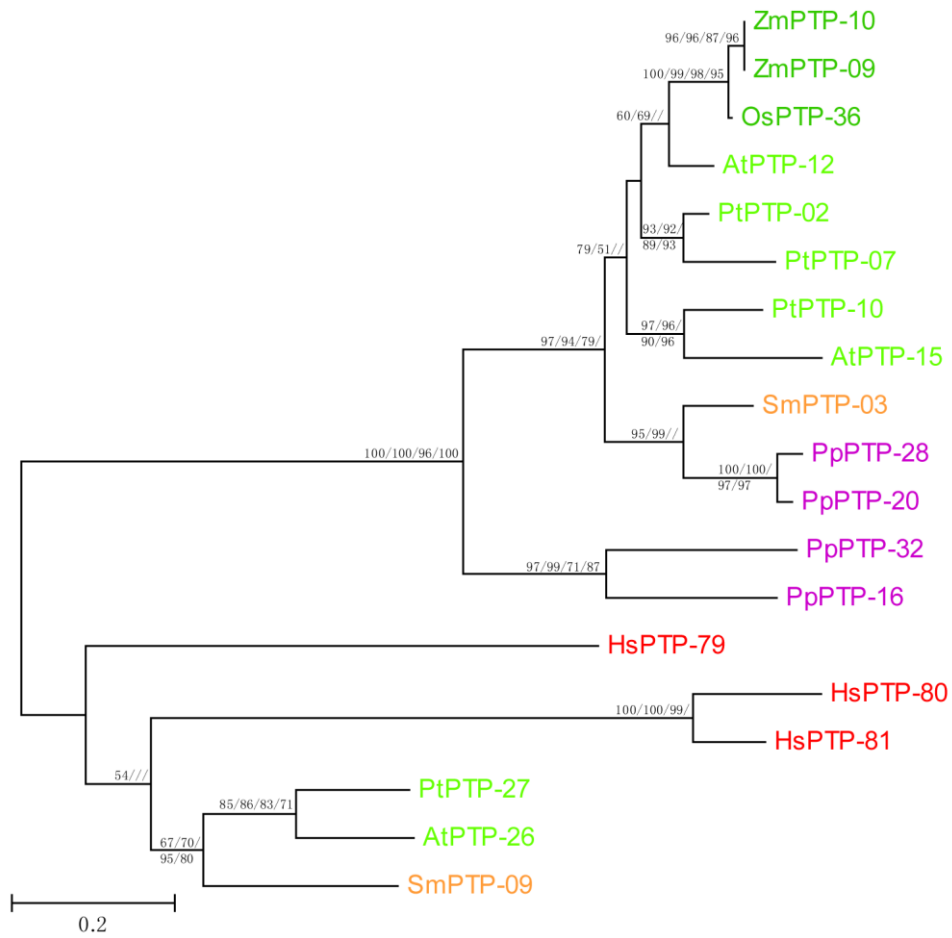


Fig S2. PTEN-C2 domain phylogram of the Sub. I-B (PTEN) GPPTPs

The phylograms of the PTEN-C2 domain (PF10409) includes GPPTP I-B (PTEN) and *Hs* homologs (Table S3) as comparative genes.

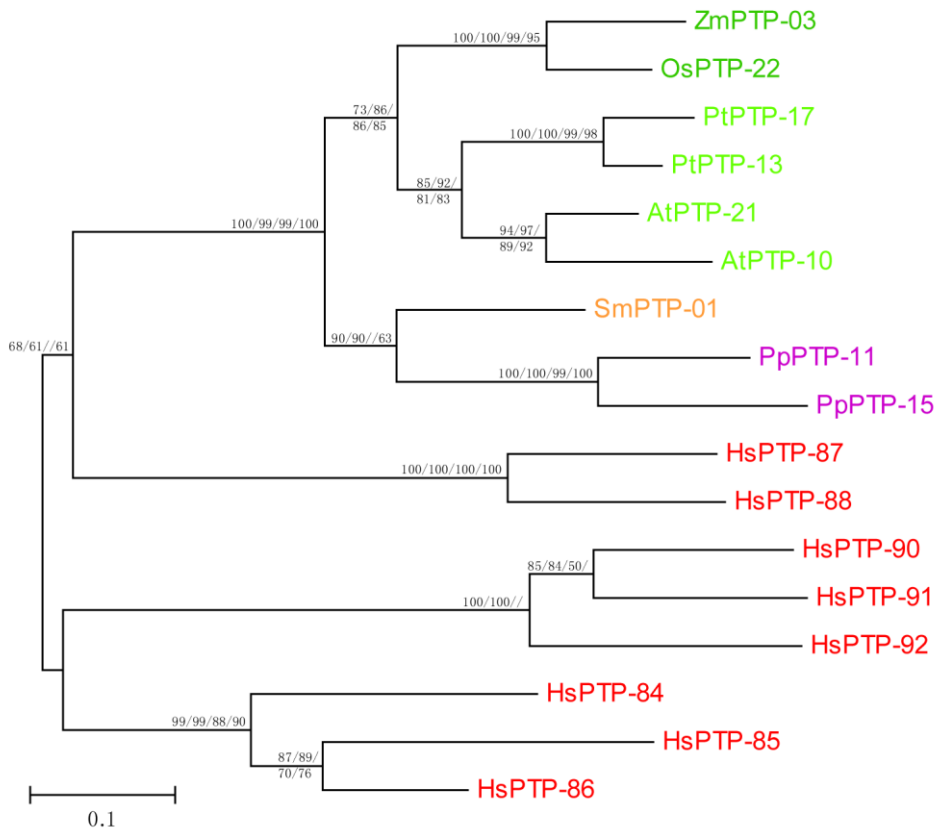


Fig S3. MTMR domain phylogram of the Sub. I-C (MTMR) GPPTPs

MTMR domain (PF06602) phylograms include GPPTP I-C (MTMR) and *Hs* homologs (Table S3) as comparative genes.

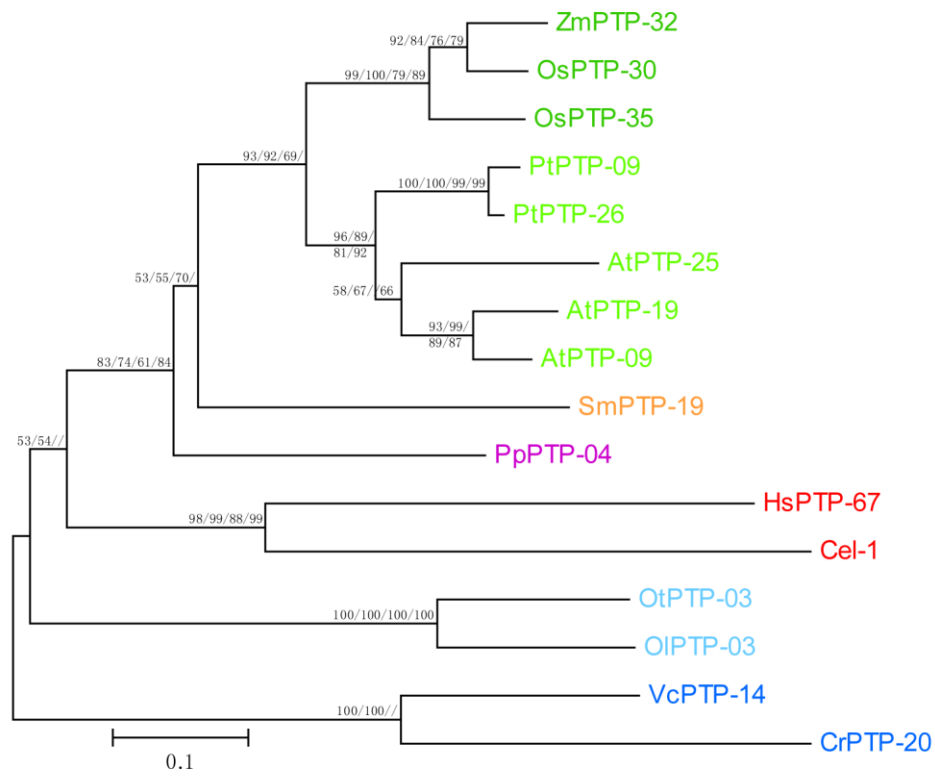


Fig S4. Sub. I-E (mRNA) GPPTP phylogram

The phylograms of Sub. I-E (mRNA) DSP domain (PF00782) includes GPPTP Sub. I-E, *Hs* homologs and *Cel-1* genes (Table S3) as comparative genes.

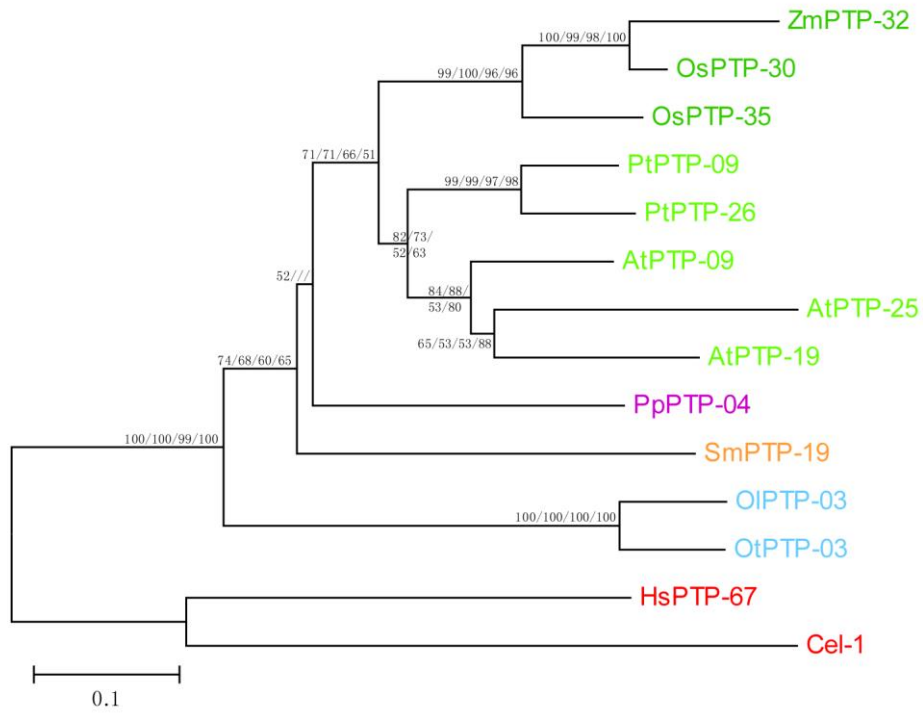


Fig S5. Sub. I-E (mRNA) GPPTP phylogram

The phylograms of Sub. I-E (mRNA) mRNA_capping domain (PF01331) includes GPPTP Sub. I-E, *Hs* homologs and *Cel-1* genes (Table S3) as comparative genes.

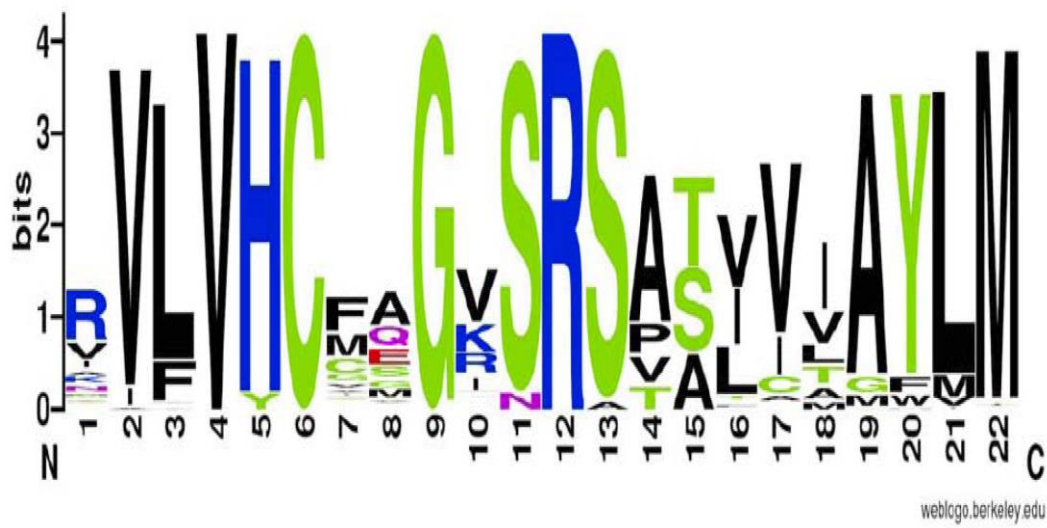


Fig S6. Sequence Weblogo analysis of PTP loop sequence and its flanking sequence of I-F-4 GPPTP (GPMKPs).

The overall stack height indicates the sequence conservation at that position, while the symbol height within the stack indicates the relative frequency of each amino acid at that position. All GPMKP PTP loop have the AYLM amino acid sequence standing on the right of the C××G××R signature sequence.

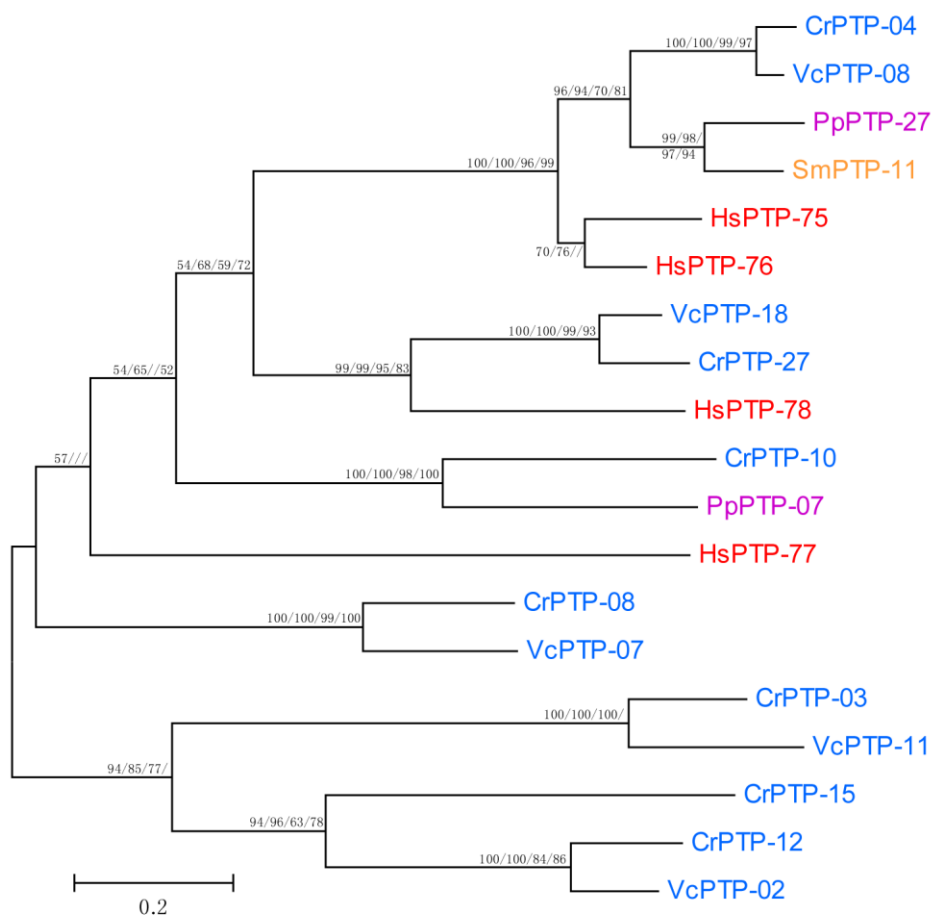


Fig S7. Sub. I-G (CDC14-like) GPPTP phylogram.

I-G (CDC14-like) DSP domain (PF00782) phylogram includes GPPTP I-G genes and *Hs* homologs (Table S3) as comparative genes.