

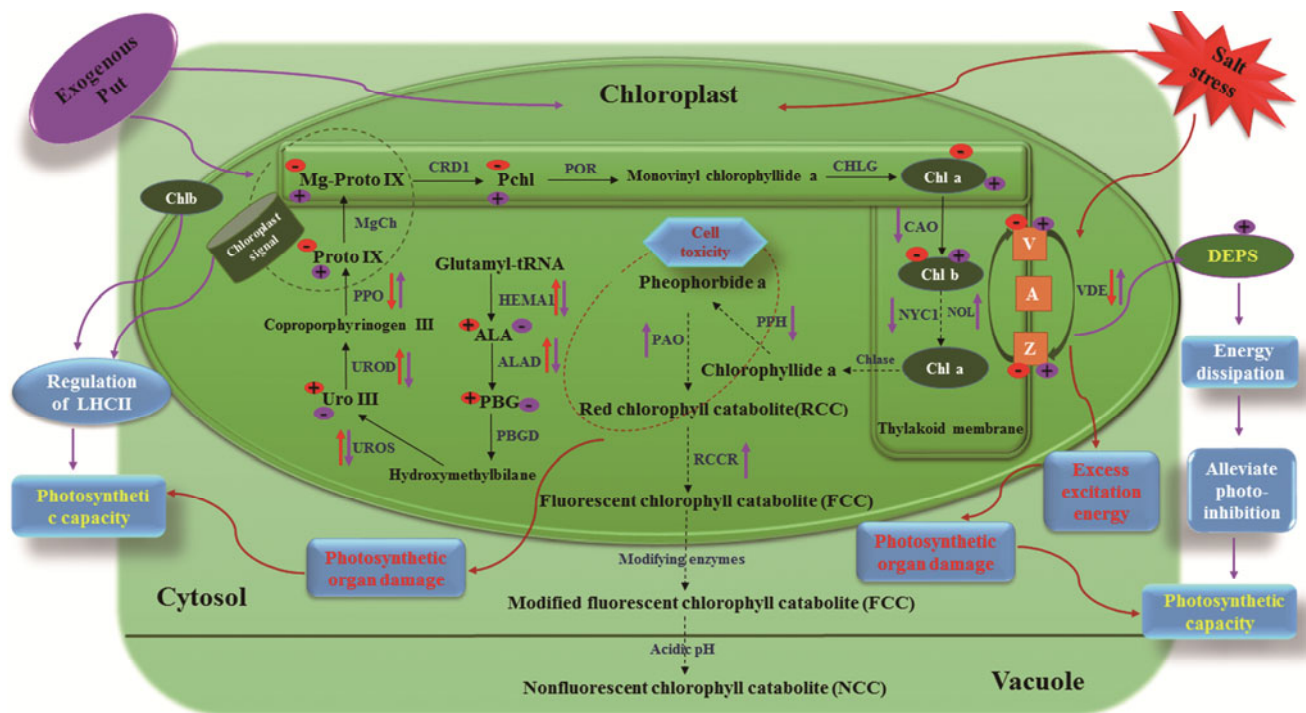


Fig. 1S. A regulating mechanism model of the effects of exogenous Put on chlorophyll metabolism and the xanthophyll cycle in the leaves of salt-stressed cucumber seedlings. The chlorophyll metabolic pathway is classified into three phases: chlorophyll a synthesis from glutamate-tRNA, interconversion of chlorophyll a and chlorophyll b, and the chlorophyll degradation pathway. A – antheraxanthin; ALA – δ -aminolevulinic acid; ALAD – 5-aminolevulinate dehydratase; CAO – chlorophyllide a oxygenase; CBR – chlorophyll b reductase; Chlase – chlorophyllase; CHLG – chlorophyll synthase; CRD1 – Mg-protoporphyrin IX monomethylester cyclase; DEPS – de-epoxidation of the xanthophyll cycle; HEMA1 – glutamyl-tRNA reductase; MgCh – Mg-chelatase; Mg-Proto IX – Mg proporphyrin IX; NOL – NYC1-like; NYC1 – non-yellow coloring 1; PAO – Pheide a oxygenase; PBG – porphobilinogen; PBGD – porphobilinogen deaminase; Pchl – protochlorophyllide; POR – protochlorophyllide oxidoreductase; PPH – pheophytinase; PPO – protoporphyrinogen IX oxidase; Proto IX – protoporphyrin IX; Put – putrescine; RCCR – red chlorophyll catabolite reductase; UroIII – uroporphyrinogen III; UROD – uroporphyrinogen III decarboxylase; UROS – uroporphyrinogen III synthase; V – violaxanthin; VDE – violaxanthin de-epoxidase; Z – zeaxanthin. The model is based on the results presented here. The red arrow and circle indicate the effect of salt stress conditions on cucumber seedlings, and the purple arrow and circle indicate the effect of exogenous Put on cucumber seedlings under salt stress conditions. Up-regulation is indicated by $\uparrow$ and a circle with a + symbol, and down-regulation is indicated by $\downarrow$ and a circle with a – symbol.