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Nucleotide sequence of a full length cDNA clone of ribulose bisphosphate carboxylase small subunit gene from green dark-grown pine (*Pinus tunbergii*) seedling

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Light has been shown to induce the expression of gene encoding ribulose bisphosphate carboxylase small subunit(RuBisCO SSU)(1). Since dark-grown seedling of coniferous plant is green, we have constructed cDNA library and cloned full length cDNA (pPDSSU4) for RuBisCO SSU from dark-grown pine (Pinus thunbergii) seedlings in pUC8, which was identified by immunoscreening and hybrid release translation. The cDNA included 516 bp of the open reading frame, and 96 and 303 nucleotides of 5'- and 3'-untranslated sequences, respectively. From the putative cleavage site(arrow head), the transit and mature polypeptides have been estimated to be composed of 51 and 120 amino acids, respectively. This result also shows the expression of the gene in the dark-grown seedling.

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                                    -96 TGATCTGGCTTGGCTTCAGAGCTCAAAAATAC
-64 ATGGCCTCTGCGATCATGTCCTCCACACTGTAGTGCAGCAGTACTGCGCCCCTCAAGACCAGCA
  1 ATG.GCA.ACG.GGA.GCG.GGA.GCG.GGA.GCA.GCA.ACC.GTG.GTG.TCG.GCG.TTC.
    Met-Ala-Thr-Gly-Ala-Gly-Ala-Gly-Ala-Ala-Thr-Val-Val-Ser-Ala-Phe-
 49 ACG.GGG.CTC.AAG.TCC.ACG.GCG.CAA.TTC.CCC.TCC.AGC.TTC.AAG.ATG.AGC.
    Thr-Gly-Leu-Lys-Ser-Thr-Ala-Gln-Phe-Pro-Ser-Ser-Phe-Lys-Met-Ser-
 97 AAC.GCC.GCA.GCG.GAA.TGG.GAG.CAG.AAG.ACA.ACG.AGC.AAC.GGT.GGG.CGA.
    Asn-Ala-Ala-Ala-Glu-Trp-Glu-Gln-Lys-Thr-Thr-Ser-Asn-Gly-Gly-Arg-
145 GTG.CGA.TGC.ATG.CAG.GTG.TGG.CCT.CCA.TTC.GGA.AAC.CCC.AAG.TTT.GAG.
    Val-Arg-Cys-Met-Gln-Val-Trp-Pro-Pro-Phe-Gly-Asn-Pro-Lys-Phe-Glu-
193 ACT.CTG.TCC.TAC.CTC.CCT.ACG.CTA.ACC.GAG.GAG.CAG.CTG.GTG.AAG.GAG.
    Thr-Leu-Ser-Tyr-Leu-Pro-Thr-Leu-Thr-Glu-Glu-Gln-Leu-Val-Lys-Glu-
241 GTT.GAG.TAC.TTG.TTG.AGG.AAC.AAG.TGG.GTG.CCT.TGT.CTA.GAG.TTT.GAT.
    Val-Glu-Tyr-Leu-Leu-Arg-Asn-Lys-Trp-Val-Pro-Cys-Leu-Glu-Phe-Asp-
289 CTG.GAA.GGA.TCC.ATC.TCG.AGG.AAG.TAT.AAT.AGG.AGC.CCG.GGG.TAC.TAC.
    Leu-Glu-Gly-Ser-Ile-Ser-Arg-Lys-Tyr-Asn-Arg-Ser-Pro-Gly-Tyr-Tyr-
337 GAT.GGG.AGA.TAC.TGG.GTG.ATG.TGG.AAG.TTG.CCG.ATG.TTT.GGG.TGC.ACA.
    Asp-Gly-Arg-Tyr-Trp-Val-Met-Trp-Lys-Leu-Pro-Met-Phe-Gly-Cys-Thr-
385 GAG.GCA.TCT.CAG.GTG.ATA.AAC.GAG.GTG.AGA.GAG.TGT.GCC.AAG.GCA.TAC.
    Glu-Ala-Ser-Gln-Val-Ile-Asn-Glu-Val-Arg-Glu-Cys-Ala-Lys-Ala-Tyr-
433 CCC.AAA.GCC.TTC.ATC.CGT.GTC.ATT.GGC.TTT.GAC.AAC.GTC.CGC.CAA.GTG.
    Pro-Lys-Ala-Phe-Ile-Arg-Val-Ile-Gly-Phe-Asp-Asn-Val-Arg-Gln-Val-
481 CAG.TGC.ATC.TCC.TTC.ATC.GTC.CAC.AAG.CCC.GAA.TAA.TCAATTTGTGTGCGTC
    Gln-Cys-Ile-Ser-Phe-Ile-Val-His-Lys.Pro.Glu.---
533 TCCTTTTCTTCTCGTTCATGTCACCTCCATGATTTGGGTAGGTGCACCTGAGCGTTGAGCCGTG
597 AGTAAGTTTGAGGAGAAGCTGCTGTGTTACTAGTAGATTAATTAATTATTAGTGGTGAGCTAAT
661 GACTCTTCAAATAATTTGAAGTCATGTGGAACACTTGTTTCTGCATGTGGAAGCCACATTTTGA
725 GGATCAATCGTTTTGTGATTCTAGTGGGCAATTGATGTTTATGGATGTGGCTCGTTTAATAATA
789 AGGTAACACCCATTGGTGGGGTTAACT
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