

Bioinformatic Analysis of Strawberry PGR5 Gene

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Abstract. PGR5 has always been known as a key factor of Heat response in plant testa. Recent studies show that PGR5 (proton gradient regulation 5) is a proton gradient regulatory protein, which transfers cycle electronic I encoding thylakoid membrane proteins and optical systems, and helps to induce pH heat dissipation. In this research we chosen PGR5 gene of 9 kinds species, downloaded their nucleotide and protein sequence from NCBI as the research object, found strawberry PGR5 gene via bioinformation analyses, constructed phylogenetic tree. At the same time, we analyzed the strawberry PGR5 gene of physical and chemical properties and its protein structure and so on. The phylogenetic tree showed that strawberry and *Morus notabilis* were closest relative. By the protein prediction, we found that the protein owed one proper signal peptide without obvious transmembrane regions.

1. Introduction

PGR5 (proton gradient regulation 5) is a proton gradient regulatory protein, which transfers cycle electronic I encoding thylakoid membrane proteins and optical systems, and helps to induce pH heat dissipation [1]. Recent studies show that In photosynthesis, PSI ring electron transfer consists of two pathways, one requiring a complex compound protein known as NADH or NDH dehydrogenase complex [2] and the other one of at least two proteins: PGR5 complex [3] proton gradient regulated protein 5 (proton gradient regulation 5, PGR5 1 (PGR5-like) and protein protein 1 (A, PGRL1) located in the thylakoid membrane protein), like protein 1 and PGR5 interaction in structure and function. PGR5 and PGRL1 interact with PSI and form a complex, causing PsbS to control qE (quantum electronics) [4]. The qE mechanism of light protection is stimulated under the low pH cavity, and the PGR5 protein is used to acidification the cavities of the cavities of [5]. The PGRL1-PGR5 complex participates in the transformation of residual electron flow to CEF, accepts electron from Fd (feroxin) and restores PQ (plastid quinone) library. Therefore, it acts as a Fd-PQ reductase [6] to promote the cyclic electron flow cycle. Light is the root cause of PSI photoperiod, and the ring type electron transfer can be up-regulated at the time of drought stimulation. Linear electron transfer 3 times more than; in the long term under high light stress, Arabidopsis Fd2-KO plant plastoquinone pool by cyclic electron transfer to PGR5 improvement depends on the relative balance of reduction oxidation recovery level, fd2 and pgr5 in high light photosynthesis severely damaged, Fd2-KO plants showed that PGR5, [29] play a role in adaptation light on the high strength of the. The cyclic electron transfer dependent on proton gradient regulatory protein (proton gradient regulation 5, PGR5) contributes to the redox balance of chloroplasts. When plants are destroyed, such as rice chloroplasts, PGR5 is the [7] necessary to maintain the ability of redox protein quinone reduction.

2. Result and Analysis

2.1 Strawberry PGR5 Find and Phylogenetic Tree Construction of PGR5

Run BLAST in the *Fragaria × ananassa* database of GDR and Strawberry GARDEN respectively using Arabidopsis thaliana PGR5 as a sample. Select the sequence with ideal S and C value, we find strawberry PGR5.

We have chosen PGR5-like gene of 9 kinds species (Table 1), downloaded their nucleotide and protein sequence from NCBI as the research object, analyzed sequences via MEGA6.0, constructed

phylogenetic tree on the genetic distance base (Figure 1). The relationship between strawberry and petunia is closer than others, due to they all contain a lot of anthocyanins probably.

Table 1. Basic information of pgr5 gene in different species

Species	mRNA Accession Number	Protein Accession Number	Amino Acid Number
<i>Fragaria vesca</i>	XM_004296356.2	764568155	880
<i>Morus notabilis</i>	XM_010111443.1	703149999	372
<i>Cucumis sativus</i>	XM_004133996.2	778678100	855
<i>Cucumis melo</i>	XM_008440250.2	1035393427	942
<i>Gossypium arboreum</i>	XM_017759347.1	1050587011	550
<i>Gossypium hirsutum</i>	XM_016821285.1	1029025831	606
<i>Citrus clementina</i>	XM_006420254.1	567854394	930
<i>Citrus sinensis</i>	XM_006489596.1	568873020	758
<i>Cucumis melo genomic chromosome</i>	LN713260	DHL92	35939859

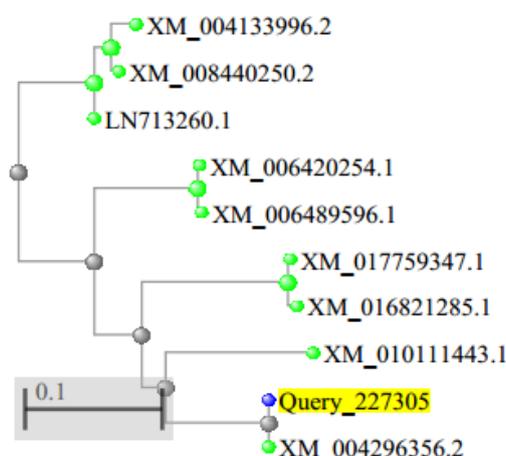


Figure 1. Phylogenetic Tree of Strawberry PGR5.

2.2 Strawberry PGR5 Protein Physical Analysis

Analyze strawberry PGR5 protein physical feature using ProtPrm. Result shows as following: the protein is composed by 381bp, molecular weight is 30558.94, theoretical pI is 5.26, electric neutrality, molecular formula is C₁₁₂₇H₁₈₇₅N₃₈₁O₄₆₆S₇₃. Because the N-terminal of the sequence considered is A (Ala), the estimated half-life is 30 hours in mammalian reticulocytes (in vitro), 20 hours in yeast (in vitro) and 10 hours in Escherichia coli (in vitro). The instability index (II) is computed to be 34.88, so the protein is unstable. The aliphatic index of the protein is 32.55. Grand average of hydropathicity (GRAVY): 0.806.

Amino acid composition result is settings as following (Table 2): the peptide chain consists many Ala as 32.5%.

Table 2. Strawberry pgr5 gene amino acid composition

Amino Acid	Count	Percentage
Ala (A)	124	32.5%
Cys (C)	73	19.2%
Gly (G)	100	26.2%
Thr (T)	84	22.0%

2.3 Strawberry PGR5 Protein Signal Peptide Forecast

Forecast strawberry PGR5 protein signal peptide using SignalP 4.1. Result shows as following (Figure 2). There is one signal peptide in the PGR5 between 19th base and 20th base.

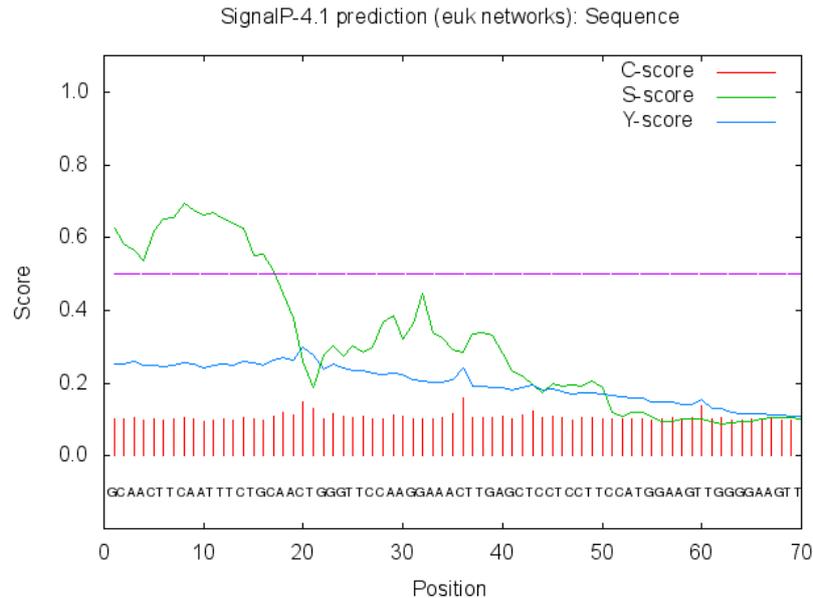


Figure 2. Signal peptide forecast of strawberry PGR5.

2.4 Strawberry PGR5 Protein Transmembrane Domain Forecast

Forecast strawberry PGR5 protein transmembrane domain using TMHMM Server. Result shows as following (Figure 2). There isn't transmembrane domain in the strawberry PGR5, thus the protein is not cytomembrane receptor or located on cytomembrane.

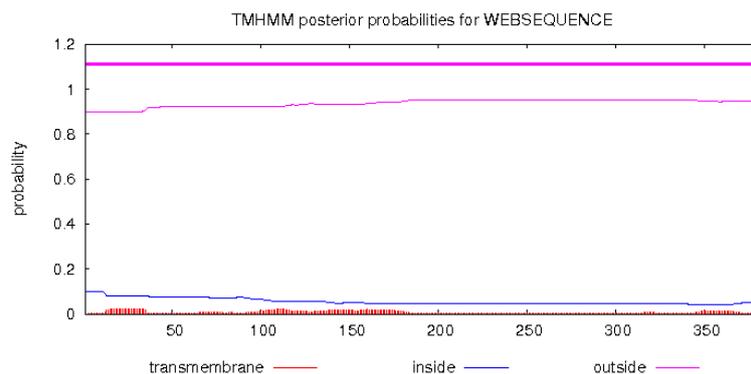


Figure 3. Transmembrane domain forecast of strawberry PGR5.

3. Materials and Methods

Sequences access from NCBI (<https://www.ncbi.nlm.nih.gov/>). BLAST run in GDR (<https://www.rosaceae.org/>), and Strawberry GARDEN(<http://strawberry-garden.kazusa.or.jp/>). Phylogenetic tree is constructed via MEGA6.0, forecast strawberry PGR5 protein signal peptide using SignalP 4.1 (<http://www.cbs.dtu.dk/services/SignalP/>), forecast strawberry PGR5 protein transmembrane domain using TMHMM Server (<http://www.cbs.dtu.dk/services/TMHMM/>).

4. Conclusion

Enhanced hydrogen production rates in the *pgr11*, *pgr5*, and the *pgr5 pgr11* double mutant under S deplete conditions lead to the highest continuous photobiological produced hydrogen amounts of eukaryotic cells reported so far. These rates are achieved by a prolonged residual PSII activity providing an increased electron supply toward the hydrogenase. PSII activity can be maintained in the mutants without inhibiting the oxygen sensitive hydrogenase, because the oxygen consumption capacity is increased. Our results suggest that respiration and light-dependent O₂-uptake rates are higher in the *pgr* mutants, and that this is responsible for the faster transition to anaerobiosis,

especially when the greater residual PSII activity of the mutants is taken into account [8]. The exploration on strawberry TT12, which is forward gene to strawberry PGR5, have been attempt in our lab, we would focus on the interaction between strawberry TT12 and PGR5 so as to provide reference for further study and utilization.

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