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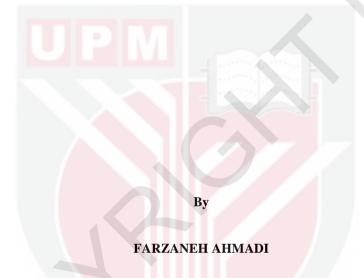
ISOLATION AND FUNCTIONAL CHARACTERIZATION OF THE HIGH-AFFINITY PHOSPHATE TRANSPORTER, PHT1, GENE PROMOTER OF OIL PALM (Elaeis guineensis Jacq.)

FARZANEH AHMADI

IPTSM 2017 2



ISOLATION AND FUNCTIONAL CHARACTERIZATION OF THE HIGH-AFFINITY PHOSPHATE TRANSPORTER, *PHT1*, GENE PROMOTER OF OIL PALM (*Elaeis guineensis* Jacq.)



Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia, in Fulfillment of the Requirement for the Degree of Doctor of Philosophy

March 2017

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DEDICATION

To my dearest MOTHER and FATHER and my lovely husband, for their close cooperation and continuous moral and financial support in this long journey.



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Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfillment of the requirement for the degree of Doctor of Philosophy

ISOLATION AND FUNCTIONAL CHARACTERIZATION OF THE HIGH-AFFINITY PHOSPHATE TRANSPORTER, *PHT1*, *GENE* PROMOTER OF OIL PALM (*Elaeis guineensis* Jacq.)

By

FARZANEH AHMADI

March 2017

Chairman: Professor Datin Siti Nor Akmar Abdullah, PhD Institute: Tropical Agriculture and Food security

Phosphorus is one of the least available elements for plant growth especially in tropical soils. The high-affinity Pi transporters are assumed to be the main system responsible for Pi uptake by plant roots. The objectives of the study were to isolate the promoter of the high-affinity phosphate transporter gene from oil palm (EgPHT1) and to perform functional characterization using transgenic Arabidopsis and transient expression assay in oil palm tissues. The third objective was to study the effects of some exogenous signals and abiotic factors on the *EgPHT1* promoter activity. Analysis of the isolated full-length *EgPHT1* promoter region (1467 bp) using PLACE and PlantCARE databases revealed the presence of a number of putative *cis*-regulatory elements associated with response to Pi and various environmental and biotic-stress signals. Under Pi deprivation, excessive quartenary roots formation was observed and the GUS activity was induced to 5.5-fold higher compared to under Pi-sufficient condition in the transiently transformed oil palm roots but no activity was observed in the leaves. In transgenic Arabidopsis, 29-fold greater induction of GUS expression was observed in the Pi-starved roots with no activity in other tissues. Increasing the Pi concentration from 0 to 1250 µM resulted in reduction of the GUS activity from 9109 to 315.3 pmol/min/mg protein in the transgenic plants. As the duration of Pi starvation increased from 1 to 6 days, the GUS activity increased from 660 to 9091 pmol/min/mg protein. Increasing exogenous sucrose concentration from 0.1% to 3% elevated the GUS expression from 296 to 9151.3 pmol/min/mg protein under Pi deprivation. Glucose and fructose as metabolizable sugars could induce the promoter activity, but at low level. Pi deficient inducibility of the promoter was maintained even under high salinity up to 100 mM. Application of IAA led to strong GUS expression, but BAP suppressed the expression under Pi deprivation. Finally, progressive 5'-deletion analyses of the E_gPHT1 promoter demonstrated that the region from - 690to -1 bp as the minimal promoter is sufficient to drive root- and Pi deprivationspecific expression in transgenic Arabidopsis. Deletion of the promoter region containing the P1BS element significantly reduced the promoter activity in the roots. The results also suggest the probable influenced of other positive/enhancer motifs such as Wbox, G-box and E-box for maximal promoter activity. While the root-specific motifs ROOTMOTIFTAPOX1 and RAV1AAT BOX are critical for its root-specific activity.

This is the first report on the high-affinity Pi transporter gene promoter of oil palm whose activity is induced exclusively in the root under low Pi. It contains the conserved elements for driving expression in both monocots and dicots and would be a potentially valuable candidate as a genetic engineering tool.



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Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk ijazah Doktor Falsafah

PENGASINGAN DAN PENCIRIAN KEFUNGSIAN PROMOTER GEN PENGANGKUT FOSFAT AFFINITI TINGGI, *PHT1* KELAPA SAWIT (*Elaeis guineensis* Jacq.)

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Fosforus adalah salah satu daripada makronutrien yang paling sukar diserapi untuk pertumbuhan pokok di dalam tanah tropika. Pengangkut Pi berafiniti tinggi dianggap sebagai sistem utama bertanggungjawab ke atas penyerapan Pi oleh akar tumbuhan. Objektif kajian ini adalah untuk memencilkan promoter gen pengangkut fosfat berafiniti tinggi dari kelapa sawit (EgPHT1) dan untuk membuat pencirian kefungsian menggunakan Arabidopsis transgenik dan esei pengekspresan transien dalam tisu kelapa sawit. Objektif ketiga adalah untuk mengkaji kesan isyarat eksogenus dan faktor abiotik ke atas aktiviti promoter *EgPHT1*. Analisis urutan lengkap promoter *EgPHT1* (1467 bp) yang dipencilkan menggunakan pangkalan data PLACE dan PlantCARE mendedahkan kewujudan sejumlah elemen yang dianggap *cis*-pengawalatur yang berkaitan dengan respons terhadap Pi dan pelbagai isyarat alam sekitar dan tekanan biotik dan pengekspresan khusus akar. Di bawah deprivasi Pi, pembentukan akar halus yang berlebihan dan aktiviti teraruh GUS yang 5.5-kali ganda lebih tinggi berbanding keadaan Pi yang mencukupi didapati di dalam akar tetapi tiada aktiviti dikesan dalam daun. Dalam Arabidopsis transgenik didapati 29-kali ganda lebih tinggi induksi ekspresi GUS di dalam akar yang kebuluran Pi dengan tiada pengesanan aktiviti dalam tisu yang lain. Apabila kepekatan Pi ditingkatkan dari 0 ke 1250 µM, aktiviti GUS menurun dari 9109 ke 315.3 pmol/min/mg protein dalam tumbuhan transgenik tersebut. Apabila tempoh kebuluran Pi dipanjangkan dari 1 ke 6 hari, aktiviti GUS meningkat dari 660 to 9091 pmol/min/mg protein. Peningkatan sukrosa eksogenus dari 0.1% ke 3% meningkatkan ekspresi GUS dari 296 ke 9151.3 pmol/min/mg protein dalam keadaan kebuluran Pi. Glukosa dan fruktosa sebagai gula yang boleh dimetabolisme boleh mengaruh aktiviti promoter, tetapi pada kadar rendah. Pengaruhan semasa kebuluran Pi bagi promoter ini kekal dalam kehadiran garam yang tinggi sehingga 100 mM. Aplikasi IAA membawa kepada ekspresi tinggi GUS, namun BAP menindas ekspresi semasa kebuluran Pi. Akhirnya, analisis penghapusan progresif huluan 5' promoter EgPHT1 menunjukkan kawasan dari -690 kepada -1 bp sebagai promoter minima yang mencukupi untuk mengarah ekspresi khusus akar dan kebuluran Pi di dalam Arabidopsis transgenik. Penghapusan kawasan promoter mengandungi unsur P1BS mengurangkan secara luar biasa aktiviti promoter *EgPHT1* di dalam akar. Hasil kajian juga mencadangkan aktiviti maksima promoter ini berkemungkinan dipengaruhi oleh motif positif/penggalak seperti W-box, G-box dan E-box. Manakala motif khusus akar ROOTMOTIFTAPOX1 and RAV1AAT BOX adalah penting untuk aktiviti khusus akar. Promoter E_gPHT1 adalah promoter pertama yang dilaporkan untuk gen pengangkut Pi afiniti tinggi daripada kelapa sawit yang mana aktivitinya diaruhkan secara eksklusif dalam akar di bawah Pi rendah. Ia mengandungi unsur terpelihara untuk mengarah ekspresi dalam kedua monokot dan dikot dan berpotensi sebagai calon untuk kegunaan dalam kejuruteraan genetik.



ACKNOWLEDGEMENTS

I wish to express my deepest endless thanks to God who made it possible to complete another step of my life and best regards from God to the last Prophet, Mohammad and his family.

I would like my deepest gratitude to the numerous people who have walked with me along the journey of this thesis. First and foremost, I would like to express my deep gratefulness to my supervisor Prof. Datin Dr. Siti Nor Akmar Abdullah for her kind support, critical advice, encouragement, suggestionsand direction throughout my research and preparation of this thesis.

I also wish to extend my sincere gratitude and appreciation to my supervisory committee, Assoc. Prof. Dr. Maheran Abdul Azizand Prof. Dr. Zaharah A. Rahman for her guidance, understanding, encouragement and supervision throughout the preparation and completion of this thesis. I would also like to express my gratitude towards Assoc. Prof. Dr. Halimi Mohd Saud and Mr Azmi Abdul Rashid for their kind support, cooperation and permission to work in their laboratory.

My sincere appreciation goes to all of my lab mates, staff and friends, who helped and supported me in the laboratory. Last but not the least, my heart-full gratitude and love to my parents and my loving husband Amin whose unconditional support, patience and understanding made this dream come true for me. I certify that a thesis Examination Committee has met on ------ to conduct the final examination of Farzaneh Ahmadi on her thesis entitled "Isolation and Functional Characterization of Phosphate-Starvation-Inducible *PHT1* Promoter from Oil Palm in a Transient Assay System and Transgenic *Arabidopsis Thaliana*" in accordance with the Universities and College Act 1971 and the constitution of the University Putra Malaysia [P.U.(A)106] 15 March 1998. The committee recommends that the student be awarded the doctor of philosophy.

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- 3.9 Transient expression of the full-length *EgPHT1* (FL) and CaMV35S (35S) promoter constructs in oil palm root (A) and leaf (B) tissues. The activity of each construct reported as the ratio of GUS (pmole/min/mg) to GFP (μ g/mg). Data are expressed as mean of three separate bombardments (each replicated five times) with the standard deviation.
- 3.10 Analysis of the T₃ homozygous transgenic *Arabidopsis* plants by PCR using leaf tissues and transgene-specific primers. Lanes 1–5 are PCR products obtained using FL-specific primers (F1 and R1) and DNA from leaves of plants from independent transgenic lines transformed with *EgPHT1-GUS*. B: Lanes 1–5 are PCR products obtained using CaMV 35S promoter-specific primers (CaMV35S-F and CaMV35S-R) and DNA from leaves of plants from independent transgenic lines transformed with *CaMV35S-GUS*. In both panels M: GeneRuler DNA Ladder Mix (Thermo Fisher Scientific Inc.), C+: Positive control; C-1: negative control (untransformed wild type *Arabidopsis* gDNA); C-2: negative control (with *virG* gene primers).
- 3.11 Histochemical localization of GUS expression in T_3 transgenic 55 Arabidopsis after growing in Pi-deficient medium. A: transgenic seedling carrying EgPHT1-GUS gene construct after six days of Pi starvation; B and C: mature transgenic seedlings carrying EgPHT1-GUS gene construct after 10-12 days of Pi starvation; D: transgenic seedling carrying CaMV35S-GUS gene construct after six days of Pi starvation; E: wild type Arabidopsis seedling plant after six days of Pi starvation.
- 3.12 GUS activities of the T_3 homozygous transgenic *Arabidopsis* 56 seedlings grown in the MS medium supplemented with various concentrations of Pi. A: GUS activity of the transgenic *Arabidopsis* roots carrying the full-length *EgPHT1* promoter (FL), CaMV35S (positive control) and wild type seedlings (negative control). B: GUS activity of the transgenic *Arabidopsis* shoots carrying the full-length *EgPHT1* promoter (FL), CaMV35S (positive control) and wild type seedlings (negative control). B: GUS activity of the transgenic *Arabidopsis* shoots carrying the full-length *EgPHT1* promoter (FL), CaMV35S (positive control) and wild type seedlings (negative control). Values were as the means \pm SE of three replicates.
- 3.13 GUS activities of the T_3 homozygous transgenic *Arabidopsis* roots 57 carrying the *EgPHT1*-GUS construct grown in the MS medium without Pi under various duration of Pi deprivation. Values were as the means \pm SE of three replicates.
- 3.14 GUS activities of the T_3 homozygous transgenic *Arabidopsis* roots 58 carrying the *EgPHT1*-GUS construct under various Pi replenishment time (Re). Twelve day-old seedlings were deprived of Pi for 5 days and then transferred to medium with Pi for 0, 1, 2, 3, 4 and 5 days. The GUS activity was reported as pmol/mg/min. Values were the means \pm SE of three replicates.

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- 4.1 Schematic representations of *EgPHT1* full-length promoter and 5' deletion derivatives. Numbers inside the bars demonstrate the nucleotide position of each truncation. Negative one (-1) indicates the first nucleotide on the left of the start codon (ATG). The symbols on the promoter region indicate the putative regulatory motifs involved in Pi-stress response that are annotated below the diagram.
- 42 Double digestion of 5' deletion series constructs of EgPHT1 promoter isolated from A. tumefaciens LBA4404 after transformation. M1: GeneRuler 1 kb DNA Ladder (Thermo Fisher Scientific Inc.), M2: GeneRuler 100 bp DNA Ladder (Thermo Fisher Scientific Inc.).
- 4.3 Confirmation of putative transformed *Arabidopsis* lines (T_3) via PCR. Amplification was carried out using specific pair of primers for the 5' deletion series of the *EgPHT1* promoter as indicated. M1: GeneRuler DNA Ladder Mix (Thermo Fisher Scientific Inc.). M2: GeneRuler 1 kb DNA Ladder (Thermo Fisher Scientific Inc.), C+: Positive control: C-1: negative control (untransformed wild type Arabidopsis gDNA); C-2: negative control (with virG gene primers). Lanes labled 1, 2, 3, 4 and 5 are independent lines of putative transformed Arabidopsis.
- Histochemical localization of GUS staining driven by the full-4.4 length and different 5'-deletion fragments of the EgPHT1 gene promoter in T₃ homozygous transgenic Arabidopsis plants. The wild type and 12-day-old T3 transgenic Arabidopsis lines of FL and 5' deletion series constructs were treated for six days in Pideprived MS media and used for histochemical GUS analysis. A represent the full-length promoter (FL) and B-G were various truncated constructs including C (D1279), D (D1045), E (D891), F (690), G (D457) and H (D250). H shows the wild type plant.
- 4.5 GUS activities of the transgenic Arabidopsis root lines carrying 73 the full-length of the *EgPHT1* promoter and its 5' deletion derivatives under +Pi and -Pi conditions. Values were the means \pm SE of three replicates.
- 4.6 GUS activities of the T₃ homozygous transgenic Arabidopsis root 74 lines carrying the full-length of the *EgPHT1* promoter under various nutrient stresses. Values were the means \pm SE of three replicates.
- 4.7Quantification of GUS activities of the T₃ homozygous transgenic Arabidopsis roots harboring the full-length EgPHT1-GUS construct grown under different concentration of sucrose in the presence or absence of Pi on the MS medium. An increase in the sucrose level higher than 0.01 % induced GUS expression under Pi deficiency. Values were the means \pm SE of three replicates.
- 4.8 Histochemical localization of GUS staining driven by the fulllength of the EgPHT1 gene promoter in T_3 homozygous transgenic Arabidopsis plants under control of sucrose. A

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represents the T3 transgenic *Arabidopsis* lines carrying full-length promoter (FL) grown on Pi-deprived MS medium without sucrose (3%) and B with sucrose (3%). C represents the T₃ homozygous transgenic *Arabidopsis* lines carrying full-length promoter (FL) grown on Pi-sufficient MS medium without sucrose (3%) and D with sucrose (3%).

- 4.9 Quantification of GUS activities of the T_3 homozygous transgenic *Arabidopsis* roots harboring the full-length *EgPHT1* fragment grown in the presence or absence of Pi in the MS medium supplemented with different sugars. The strongest GUS expression was observed in Pi-deprived plants in the presence of sucrose and followed by glucose and fructose. The other treatments had no significant Gus activity. Values were as the means \pm SE of three replicates.
- 4.10 GUS activities of the T_3 homozygous transgenic *Arabidopsis* roots 76 harboring the full-length *EgPHT1* fragment grown in the presence or absence of Pi in the MS medium supplemented with different metabolizable and non-metabolizable sugars. Supply of sucrose and glucose as metabolizable sugars induced the promoter under low Pi. Values were as the means \pm SE of three replicates.
- 4.11 Reversibility of induction of the full-length *EgPHT1* promoter 77 upon resupply of sucrose to P-limited T_3 homozygous *Arabidopsis* roots. The transgenic plants grown on +Pi and –Pi MS media without sucrose for six days and then resupplied with sucrose and harvested at different replenishment times of 0, 8, 12, 24, 48 and 72 hours. Suppression of the promoter was reversed after 8 hours of resupplying of Pi-deprived plants with sucrose. Values were as the means \pm SE of three replicates.
- 4.12 Effect of phytohormones on the *EgPHT1* promoter activity. The T₃ homozygous transgenic *Arabidopsis* grown in MS medium with or without Pi containing 1 μ M of either 6-Benzylaminopurine (BAP) or indole-3-acetic acid (IAA) for seven days. A and B represent P-deprived transgenic plants treated with the same concentration of IAA and BAP, respectively. C and D show Pi-sufficient transgenic plants treated with the same concentration of IAA and BAP, respectively.
- 4.13 Light-dependent induction of the *EgPHT1* promoter. The T₃ 79 homozygous transgenic *Arabidopsis* grown in +Pi or –Pi were treated with 16 h light/8 h dark (L/D) or continuous dark conditions (D) for two days. Values were as the means ± SE of three replicates.
- 4.14 Effect of salinity on the induction of the *EgPHT1* promoter. The T₃ homozygous transgenic *Arabidopsis* grown in +Pi or –Pi were treated with or without high salt (100 mM NaCl) for five days. Values were as the means \pm SE of three replicates.

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LIST OF ABBREVIATIONS

bp CaMV35S CDNA DNA dNTP *E.coli* EDTA GSP Kb PCR g

 \mathbf{G}

Base pair 35S promoter from cauliflower mosaic virus Complementary DNA Deoxyribonucleic acid Deoxyribonucleoside triphosphate *Escherichia coli* Ethylenediaminether tetra-acetic acid Gene-specific primer Kilobase pair Polymerase chain reaction Gravity

CHAPTER 1

INTRODUCTION

Oil palm (*Elaeis guineensis* Jacq.) is a tropical plant belonging to the *Aracaceae* family with its origin in West Africa. It is now grown in more than 20 countries in South Asia, Africa and South America (Dransfield *et al.*, 2005). It is the second most important oil crop next to soybean and is poised to become the dominant oil crop early in the new decade (Sheil *et al.*, 2009). Producing 17.32 million tonnes of crude palm oil on about 5.74 million hectares of land in 2016, Malaysia is now the second greatest producer after Indonesia and the largest exporter of palm oil in the world (MPOB, 2014). Palm oil is mainly used for edible and industrial purposes such as for deep fat frying, margarine, biofuels, cosmetics, soap, detergents and surfactants (Murphy, 2007).

With the rapid expansion of the world's population, per-capita oil and fat consumption is likely to increase tremendously and the oil palm being the most productive and profitable oil crop will continue to expand in its cultivation in tropical and subtropical regions to meet this demand. Oil palm is recognized as having a high requirement for nutrients due to its high dry matter production (Goh *et al.*, 2009). However, the low fertility of highly weathered tropical soils needs to be paid greater attention for sustainable oil palm cultivation.

Phosphorus (P) is an essential macronutrient for plant growth and development. Although it is an abundant nutrient in the rhizosphere, it is largely immobile and inaccessible for assimilation by plants. This is due to its tendency to associate strongly with positively charged cations such as Fe and Al, which are plentiful in acidic tropical and subtropical soils and consequently, limits plant growth and crop yield (Sanchez *et al.*, 1997; Sanchez and Uehara, 1980). A common agricultural solution to this problem is to enrich the soil with Pi-containing fertilizers. Generally, phosphate is applied in the form of phosphate rocks at the rate of 1.0-1.25 kg per palm per year (Mutert *et al.*, 1999). However, the use of Pi fertilizers is unsustainable and may cause pollution. Hence, there is a need to develop crops that either acquire Pi or use Pi more efficiently, so that agriculture will be more sustainable with less required Pi fertilizers.

To cope with growth under low Pi availability, plants have developed a number of morphological, physiological, biochemical and molecular adaptive strategies aimed at conservation of use or enhancement of acquisition of Pi (Jain *et al.*, 2007; Raghothama, 1999; Vance *et al.*, 2003). One of the best-conserved adaptations of plants to low Pi supply is the induced expression of high-affinity Pi transporter genes. These are known as *PHT1* transporters to distinguish them from the low-affinity Pi transporters which are in the *PHT2* family. Structurally, the *PHT1* transporters are integral membrane-spanning segments linked by a hydrophilic region (Schachtman *et al.*, 1998; Smith *et al.*, 2000). Several high-affinity Pi transporters have been identified in some important crops such as rice, barley, wheat, maize, tomato and potato (Gordon-Weeks *et al.*, 2003; Nagy *et al.*, 2006; Paszkowski *et al.*, 2002; Rae *et al.*, 2003). Among the *PHT1* genes examined

so far, many are either exclusively or predominantly expressed in root tissues under Pi deficiency, consistent with the role in the uptake of Pi from the soil solution (Raghothama and Karthikeyan, 2005; Schünmann *et al.*, 2004a; Xiao *et al.*, 2006). However, expression of some of the *PHT1* genes in other organs such as stem, leaves, flowers and pollen grains indicate that *PHT1* proteins are involved not only in Pi acquisition from soil but also in distribution between different organs and remobilization within the plant (Liu *et al.*, 1998; Mudge *et al.*, 2002; Rae *et al.*, 2003).

Transcriptional activation of Pi transporters in response to Pi starvation seems to be a major regulatory mechanism for Pi uptake (Jain *et al.*, 2012; Raghothama, 2000). An effective approach to study transcriptional regulation is to monitor the activity of reporter genes driven by the specific gene promoters (Karthikeyan *et al.*, 2002). Previous studies have demonstrated that the isolated phosphate transporter genes contain *cis*-acting elements within their promoter sequences for the binding of specific transcription factors to enable them to be regulated in a tissue-specific and Pi-dependent fashion (Miao *et al.*, 2009; Schünmann *et al.*, 2004a; Tittarelli *et al.*, 2007).

Although some high-affinity phosphate transporter (*PHT1*) promoters have been isolated from different dicot and monocot plant species, especially model plants, and their regulatory functions well characterized (Miao *et al.*, 2009; Mudge *et al.*, 2002; Tittarelli *et al.*, 2007), they have not been studied in oil palm yet. Additionally, there is no report on the functional characterization of the promoter of the high-affinity phosphate transporter (*EgPHT1*) gene isolated from oil palm. Studies on the molecular mechanism for phosphate uptake is important for oil palm as it is usually grown in acidic tropical soils with low bioavailability of Pi which is a major problem limiting crop productivity.

Hence, the main aims of this study were:

- 1) To isolate the promoter of the high-affinity phosphate transporter gene (*EgPHT1*) from oil palm and identify the putative *cis*-regulatory elements involved in inducible activity of the promoter under phosphate deficiency.
- To evaluate the root-specific activity of the *EgPHT1* promoter activity using a transient biolistic-based reporter assay in transformed oil palm tissues and transgenic *Arabidopsis*.
- 3) To analyse the functionality of the *EgPHT1* promoter in response to Pi signals including different concentrations of Pi, duration of Pi deficiency and Pi replenishment.
- 4) To analyse the induction of the *EgPHT1* promoter in response to some exogenous signals including sucrose, other nutrients (iron, potassium and nitrogen), phytohormones (auxin and cytokinin), light conditions and salinity.
- 5) To determine the promoter sequences necessary for *EgPHT1* expression in transgenic *Arabidopsis thaliana* using 5' deletion analysis.

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