Table S1. The key P*i* transporters of terrestrial plants.

|  |  |  |  |
| --- | --- | --- | --- |
| **Transporter** | **Organism** | **Remarks**  | **Refs.** |
| \*PTx family of high-affinity P*i* transporters (e.g. AtPT1 from *A. thaliana*) | *A. thaliana*, *Licopersicon esculentum*, *Medicago sativa*, *Nicotiana tabacum* etc. | Membrane proteins from MFC family. | [1-3] |
| Phtx family of low-affinity P*i* transporters | *A. thaliana*, *Oryza sativa* etc. | Pi:H+ symporters; apparent Km for P*i* — 0.4 mM |
| PHR1, homolog of Psr1 | *A. thaliana*, *Brassica* spp. etc. | P*i* starvation-inducible, homologous to β-glucosidase, may induce deglycosylation and regulation of acid phosphatasesduring Pi starvation |

Table S2. Key genes involved in P acquisition and polyP metabolism in eukaryotic microalgae with C*. reinhardtii* as reference. Most of the genes involved are under control of the transcription factor psr1 (see further detail in [4-6] )

| **Gene or enzyme** | **Annotation 1** | **Annotation 2** | **Remarks**  | **Refs.** |
| --- | --- | --- | --- | --- |
| *Psr1* (phosphorus starvation regulator 1)  | (Cre12.g495100) | Q9S807 | Putative transcriptional activator, crucial for acclimation of the alga to P*i* starvation | [5,7] |
| *Lpb1* (low-P bleaching) | (Cre12.g554250) | Q4VGM5 |  | [8] |
| *Pta1-4*  | (Cre02.g075050;Cre16.g686800;Cre16.g686750;Cre16.g686850) | Q8LP71Q8LP70Q8LP69A8ISD7 | P*i* transporter (H+/P*i* family) |  |
| *Ptb1–5,6a,7–9,12* | Cre12.g491600,Cre07.g325741,Cre07.g325740,Cre02.g144750,Cre02.g144700,Cre16.g655200,Cre12.g489400,Cre16.g676757,Cre02.g144600,Cre02.g144650) | Q8LP68Q8LP67A8JH07A0A2K3E3U8A8J0U2A8J994A0A2K3D267-A0A2K3E3X0A8J0U1 | P*i* transporter (Na+/P*i* family) |  |
| *Ptc1* | (Cre06.g251650) | A0A2K3DLZ3 | P*i* transporter (low affinity) |  |
| *Phox* | (Cre04.g216700) | A0A2K3DTA4 | Calcium-dependent alkaline phosphatase |  |
| *Pho1* | (Cre08.g359300) | A8JGF3 | Alkaline phosphatase |  |
| *Phod* | (Cre05.g239850) | A0A2K3DT40 | Alkaline phosphatase |  |
| *Mpa1,2,8,9,11,13* | Cre03.g146207,Cre12.g500250,Cre11.g468500,Cre11.g476700,Cre13.g578350,Cre16.g672250) | A8J2X5-A0A2K3D861--A0A2K3CVM3 | Calcineurin-like phosphatase |  |
| *Vtc1* | (Cre12.g510250) | A8IKM0 | Vacuolar transporter chaperone family (putative polyP synthesis) |  |
| *Vtc4* | Cre09.g402775 | A0A2K3DF66 |  |  |
| *Vtcx* | (Cre01.g005500, Cre10.g461500, Cre10.g461500, Cre09.g402812) | A0A2K3E503A0A2K3DBW4A0A2K3DF49 |  |  |

Table S3. Key genes involved in P acquisition and polyP metabolism in cyanobacteria with *Synechococcus sp* as reference. In prokaryotes, the genes constituting the pho regulon are controlled by the transcription factor PhoB. Based on the Pho regulon components of *Synechococcus* sp. WH8102 described here [9], we provided available data for *Synechococcus* sp. WH8102 as well as *Synechococcus* sp. strain WH7803 using Uniprot database.

| **Gene/enzyme** | **Annotation 1** | **Annotation 2** | **Remarks** | **Ref** |
| --- | --- | --- | --- | --- |
| *phoR* | SynWH7803\_1546 | Q56181 | Activated during P depletion, a regulatory component that phosphorylates phoB. Also annotated as sphS in other Synechococcus species (P39664, for S elongatus) | [10] |
| *phoB* | SynWH7803\_1545 | Q56180 | Controls transcription of the Pho regulon. Also annotated as sphR in other Synechococcus species (P39663, for S elongatus) |
| *ptrA* | SynWH7803\_1046 | A5GKK7 | Protein with a potential regulatory role under P depletion/stress |
| *phoU* | Syn7502\_00586 | K9SQ49 | A regulatory protein regulating Pi import through the Pst system by interacting with PstB and PhoB | [11] |
| *pstC* | SynWH7803\_1245 | A5GL56 | Subunits constituting the Pi import complex | [12] |
| *pstSI* | SynWH7803\_2513 | A5GPS4 |
| *pstSII* | SynWH7803\_1045 | A5GKK6 |
| *pstA* | SynWH7803\_1244 | A5GL55 |
| *pstB* | SynWH7803\_1243 | A5GL54 |
| *phnC* | SynWH7803\_1469 | A5GLT0 | Subunits consituting the phosphonate-ABC transporter |
| *phnD* | SynWH7803\_1471 | A5GLT2 |
| *phnE* | SynWH7803\_1470 | A5GLT1 |
| *phoA* | syc0750\_c | A0A0H3K146 | Alkaline phosphatases |
| *phoD* | SynWH7803\_1802 | A5GMR3 |
| *phoV* |  | Q55320 |
| *ppk1* | SYNW2495 | Q7U3D7 | Polyphosphate kinase 1 | [13]  |
| *ppx* | SynWH7803\_1855 | A5GMW6 | Exopolyphosphatase |

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