

Supplementary Materials.

Phosphorus deficiency induces sexual reproduction in the dinoflagellate *Prorocentrum cordatum*.

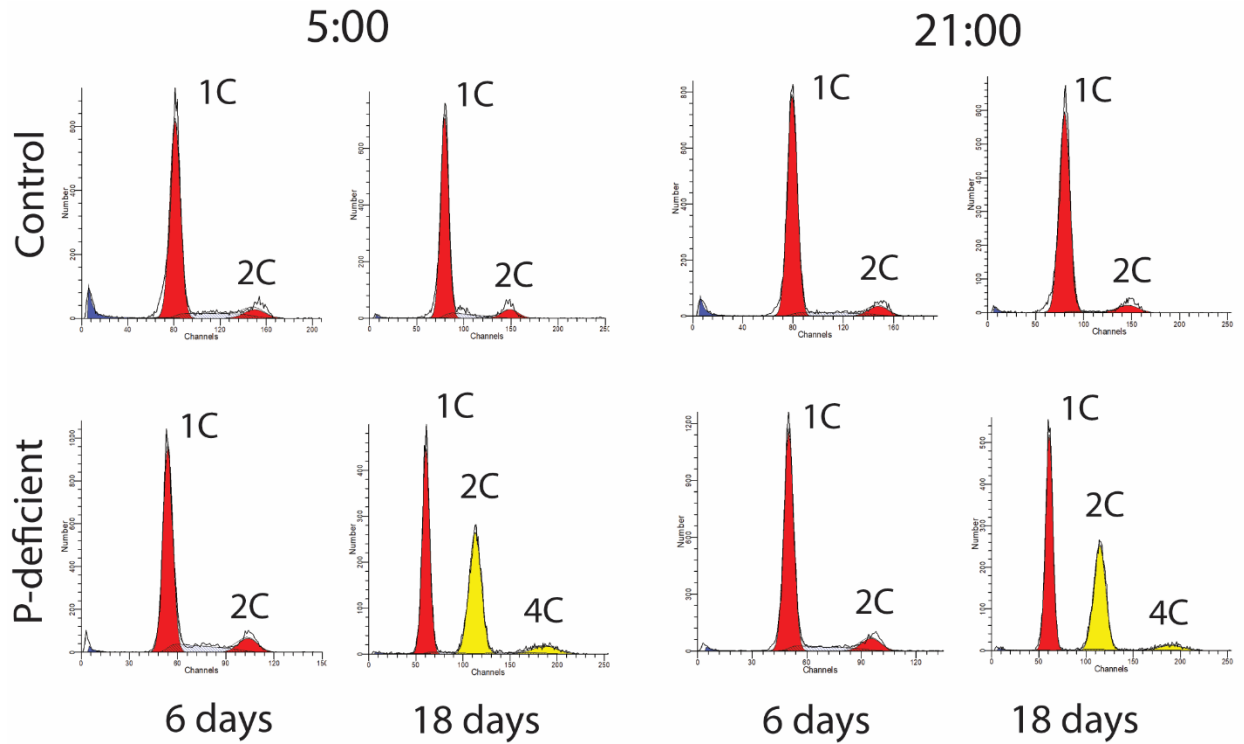
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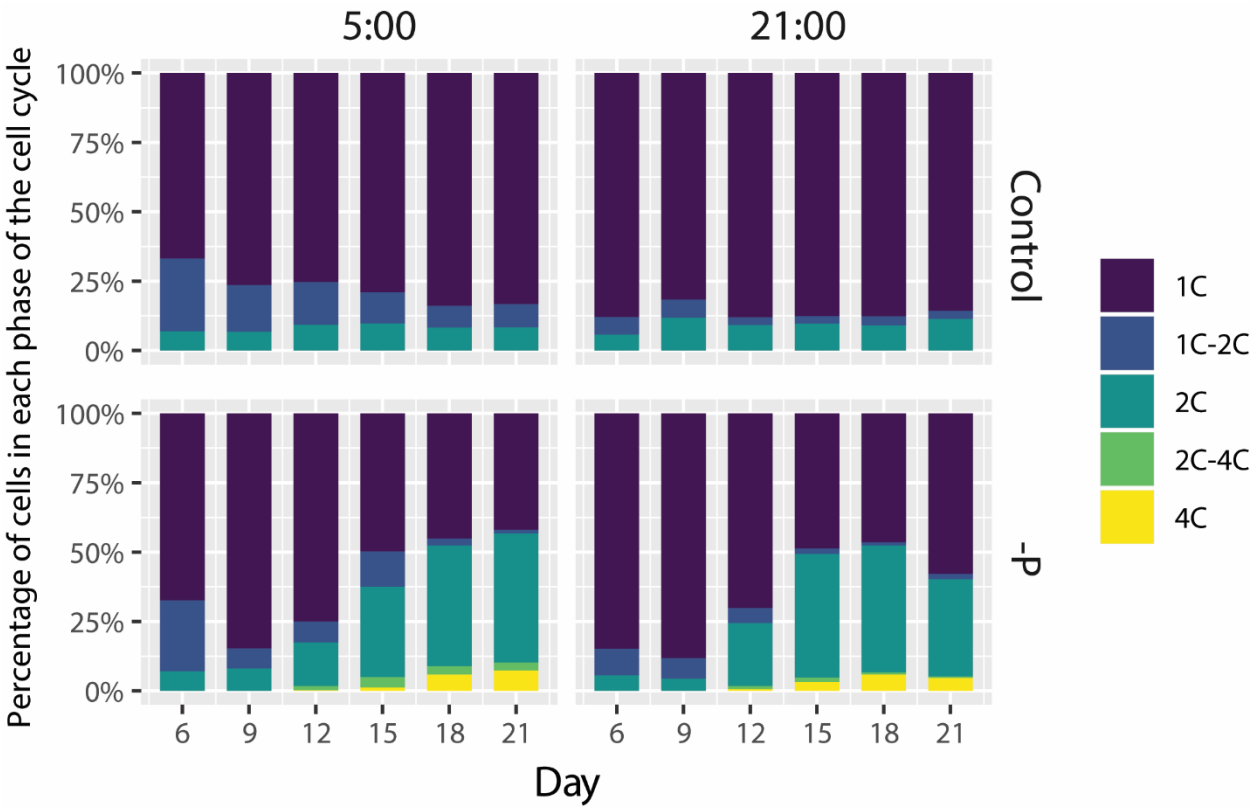
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Suppl. Fig.1. Examples of raw flow cytometry data. Flow histograms showing DNA intensity of the samples taken at the time points 6 days and 18 days at 5:00 **(a)** and 21:00 **(b)** in the control and P-deficient cultures.



Suppl. Fig. 2. Percentage of cells in the different phases of the cell cycle during 21-day experimental period. Shown are means from the triplicated experiments in the control and P-deficient cultures.



Suppl. Fig. 3. Multiple sequence alignment of *P. cordatum* PHO84 homologs with homologous sequences from various species. The sequences used in the alignment are: *Saccharomyces cerevisiae* (Sc_Ph084, GenBank ID: QHB10616.1), *Pholiota nameko* (Pn, UniProtKB ID: Q96X52), *Arabidopsis thaliana* (At, GenBank ID: AED94948.1), *Oryza sativa* (Os, UniProtKB ID: Q8GSD9). Conserved sequences of proton-coupled transporters generated by the motif-building program MEME are black-boxed. The glycine-rich phosphate binding motif GXGXGG shared by proton-coupled phosphate transporters in plants, fungi, bacteria, and mammals shown in the red box. Sites corresponding to *S. cerevisiae* Arg168, Asp358 and Lys492 are shown in purple boxes and marked with arrows.

101 200

At_AED94948.1 AKPGSLPPH---VAAAVNGVALCGTSLGGQFFGWLGDXLGRKKVYGLTLVMILCSVASG--LSFGHEAKGVMITLCFRFWLGFIGGGDYPLSATIMS
 Os_Q8GSD9.1 PNPGLTLPN---VSSAVTGVALCGTLAQQLFFGWLGDXLGRKSVYGFITLIMVVCSTASG--LSFGHTPKSVIATLCFRFWLGFIGGGDYPLSATIMS
 Sc_Ph84 G-----P-----SQTLKVSISVGTVIGQFGFTLADIVGRKRIYGMELIIMIVCTILT--TVAHSPAINFVAVLTPYRIVMGIGIGGGDYPLSSIIIS
 Pn_Q96X52 ALK-ALNKQ---QDLGVKVAIPVGTILVGQLLEGLLADLGRKKMYGMELMIITATFAQA--LSEAPAVHIIGVLVVRIVMGVIGGGDYPLSAVISS
 0191095568 DADDCEEDFKGFLMLSSAALLGAIAGQITFGVLADIRRRITFIVTGSLLVFGAVLSASCOTFGGGRFMYQLVVRIGILSFGIGGVEPLSATICA
 0191156728 -----XALSILGALVSFAFVPVGDAESSVFTFLSLSRVLGVGVGGVYPLAAITIAA
 0191040874 -----XGALVSFAFVPVGDAESSVFTFLSLSRVLGVGVGGVYPLAAITIAA
 0190869834 PSDK-----SMMVSMMLAGVVTGQLTFGYVADLMCRKPTTFIAVLTIVGALLSASCMAE-ETMFDLPLQLSLRLLGVGVGGVEYPLAAITIA
 0191146536 PTDR-----SLVGGATLAGAVAGQLFGGLLGSCLCRKATFLACVLIITAGAVLSGGVLNGLGLPLSLVHCLALCRFALGVGVGGVEYPLAAITIAA

201 300

At_AED94948.1 EYAN-KKTRGA-IAAVFAVQGVGILAGGFVALAVSSIFDKKFPAPTYAVNRALSTPPQVDYLRITIVMEGALPAALTYWRMKMPETARYTALVAKNIKQ
 Os_Q8GSD9.1 EYAS-KKTRGA-IAAVFAVQGVGILFGAIVALVVSAGFRHAYPAPSYAQNPAASLAPADYTWRLILMFGTIPAGLTYWRMKMPETARYTALVARNAKQ
 Sc_Ph84 EFAT-TKMRGAIMGAVFANCAQGISGGIITALILVAAYKGELEYANSGAECDAQCQACQWRILIGLGTVLGLACLYFRLTIPESPRYQLDNAKLEL
 Pn_Q96X52 EFAS-TKTRGRMTTAVFASQGNFTAAALVGFIITAAVKSILKEA-----SITNLHSDVMWRLLIGLGAVPGVVLYFRLTIPETPRFTMDLERNIDQ
 0191095568 EGTA-PRKRATMMSLVFANQGLGYLLAASIVILAYMEVS-----LEFFWRFPFAGAILPGISLFFRMYKHESDDFSKVLKSRAG
 0191156728 ESSD-AANRGRSTALVFSVOGVTLLVPLVGMVFLYSEGTY-----EHRKTEDLPMPDISMRMLGVGALPGILLIPFKTVPDSONRLHITQSPESF
 0191040874 ESSD-AANRGRSTALVFSVOGVTLLVPLVGMVFLYSEGTY-----EHRKTEDLPMPDISMRMLGVGALPGILLIPFKTVPDSONRLHITQSPESF
 0190869834 ESADDEIRGRFMAVVISQGFGMLLSSTVAIAALSAQAS-----LETTWRLLLGFGAIPSLVAFGLRWPHHETSFAKE---DRSRR
 0191146536 EDSVVGSGRGRLVAAVFSVOGGMLLSCLLSLLLLAAGLP-----LEHWRLLLVGAIPPAAVIYARSKHESELFLA---AKEGA

301 400

At_AED94948.1 ATADMSKVLQTDIELEER-----VEDDVKDPKQNYGLFSKEFLRR-HGLHLLGTTSTWFLLDIAFYSONLFQKDFSAIGWIPKAA--TM
 Os_Q8GSD9.1 AAADMSKVLHAEIERPE-----VVESQVAGETKGLFSROFMKR-HGMHLLATTSTWFLLDIAFYSONLFQKDFSKGVWIPPAK--TM
 Sc_Ph84 AAAAQEQDGEKKIHDTSDDEMAINGLERASTAVESLDNHPKASFKDFCRHFGQWYKILLGTAGSWFTLDVAFYGLSLNAPVILQITGYA--GSK
 Pn_Q96X52 AATDIAQAVLAGRK-SHVDDDA-----FIQRIEAPKASWADFRHFQKFNFKILFGTAYSWFALDAFYGLGLSLGIIQAIGFGNPTSTGTQ
 0191095568 A-----R--GVGTASTAYFYANHVLTAGNWFDFIVFYANSLFNADVLRLVIDVPGG--
 0191156728 N-----SQTIVTRVNRNRYWPKIIGCAGGWLFDFITFYGNLTLPATVILKNVHTSGG--LTP
 0191040874 N-----SQTIVTRVNRNRYWPKIIGCAGGWLFDFITFYGNLTLPATVILKNVHTSGG--LTP
 0190869834 I-----TGESSGVETMAAFWRLLLGTAFTWFLMNTFOYSIGSKSTILNDAMSQ-VGPGRAS
 0191146536 TI-----SAGAGSAWQAIRKYWHPILGTTSTWFILDITFYGTGSKTRIGSFLMGSRASPREE

401 500

At_AED94948.1 NATHEVFRIARQTLIALCSTVPGYWFVAFIDTIGRFKIQNGFFMMTVFMFAIA-PPYNHMK-PENRIGFVWYSLTFFFAFNGPVATTFIVPAEIE
 Os_Q8GSD9.1 NALEEYRISRQALIALCETIPGYWFTVAFIDTIGRFKIQNGFFMMTVFMFAIALG-VPYDHWTH-PAHHTGFVVLVYALTFFFAFNGPNSSTTFIVPAEIE
 Sc_Ph84 NVYKKLYDTAVGNLILCAGSLPGYWVSFTVDIIGRKPIQLAGFIILITALEVIG-FAVHKLGD-----HGLLALVYICQFFQNGPNTTTFIVPGEIE
 Pn_Q96X52 AIYDNKNICVGNLILSAGLIPGYWVSFLIDKWRKPIQLMGFIALITLFTVLG-FGYDKLISTPSKKAFVFLYCLADFFQNGPNTTTFIVPGEIE
 0191095568 -----LKSMMKLTLVVVLIMLPGYFVGVALINRLGRKATQIGYCNMILWFGVCG-IFYSSLKD--MP-GLFVIIYGLTFFFAFNGPNTTTFIVPGEIE
 0191156728 VIGDGLPNNLCLQTLTILALIGLPYVSVYFMSMRKNIQNGFVVMVAVLYASLG-VFYDDLKN--SA-GLLLTYGLTYFSSNFGPNSSTTFILPSEIE
 0191040874 VIGDGLPNNLCLQTLTILALIGLPYVSVYFMSMRKNIQNGFVVMVAVLYASLG-IFYDDLQD--SA-GLLVALYGLTYFSSNFGPNSSTTFILPSEIE
 0190869834 YMRQAKFA-----NATSGEATLGFAGHVLISRASRFQMGFAAVGMVFATVGAHSVQMP--NG-GMLLVLLGLVFFFLNAGPNTTTFILPAEIE
 0191146536 IWDFAVFA-----SVCCCLAIPGYLLAVAFMDRIGRYNLQNGFLALAAANFFTIGAVYRDDLPE--GARWGLLVGFLGTLFSNFGPNTTTFIVPITETIY

501 600

At_AED94948.1 PARLRSTCHGISAAAGXGAIVGA-GLYAAQSQDKAKVDAGYPPGIGVKNLSIMLGVLNFIGMLFTFLVPEPKGMSLEEL-SGEAEVSHDEK-----
 Os_Q8GSD9.1 PARLRSTCHGISAAAGXGAIIIGA-GLYAAQDQ--HNPDAGYSRGIGRNALFVLAGTNFLGMLMTLLVPESKGSLSEEM-SKDNVDETAQEAIAQA-
 Sc_Ph84 PTRYRSTAHGISAAAGXGAIIAQITALGTLLD--HNCARDGKPTNCLPHVMEIFALFLLGIFTILLIPETKRTLEET-NELYHDEIDPATLNRNK
 Pn_Q96X52 PTRYRSTAHGISAAAGXGAIVAQVGSQDKD-----IGGSAWVKHILEIFAFNLTIGIGSTLLLPETKNTLEDL-SNENQEGFVRGTSNKTA-
 0191095568 PSQAKATLIGCSAAAGXGAATGSVMVPFVTG-----QPATPDGRLAMLICGLAIGGLILTFLTPSYGPDLEPQSEETVGFVPLFFQRKMK
 0191156728 PREVRITSLNGCAASGXGAVLGSCKKPL-----SDSYGRSVAFYMCAYCAGVGFVLTFF-----
 0191040874 PREVRITSLNGCAASGXGAVLGAFCFKPV-----SDSYGRSVAFHMCAACAAGVFLVTCFVEDRRGLAMEERAILL-----AL-----
 0190869834 PTRIRATCHGISAAAGXGALVGTALLSPA-----EAFAGMPVYFACAILAISAAATYLFTRHVSQSLQEGSVEEC-----AVKAQRK
 0191146536 PTLLIRATCHGISAAAGXGAVAGVVAAPC-----EQAFGLRAVLGFCGAVCLGGAAVTFCFTREPVEDLRX-----

Suppl. Fig. 4. Multiple sequence alignment of *P. cordatum* PAPs with homologous sequences of *A. thaliana* PAP11 (GenBank ID: AEC06729.1) and PAP12 (GenBank ID: AEC07951.1). The conserved sequence motifs of PAPs identified by Schenk et al.³⁶ are boxed.

