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Plant Biology:
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A Bacterial Glucanotransferase Can Replace the Complex Maltose Metabolism Required for Starch to Sucrose Conversion in Leaves at Night*

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Christian Ruzanski, Julia Smirnova, Martin Rejzek, Darrell Cockburn, Henriette L. Pedersen, William G. T. Williams, Birte Svensson, Martin Steup, Oliver Ebenhöh, Alison M. Smith, and Robert A. Field

From the The John Innes Centre, Norwich Research Park, Norwich NR4 7UH, United Kingdom, the Institut für Biochemie und Biologie, Universität Potsdam, Karl-Liebknecht-Strasse 24-25, 14476 Potsdam-Golm, Germany, the Department of Systems Biology, Technical University of Denmark, 2800 Lyngby, Denmark, the Department of Plant Biology and Biotechnology, University of Copenhagen, Thorvaldsensvej 40, 1871 Frederiksberg C, Denmark, and the Institute for Complex Systems and Mathematical Biology, University of Aberdeen, Meston Walk, Old Aberdeen, Aberdeen AB24 3UE, Scotland, United Kingdom

Background: Maltose metabolism during leaf starch degradation requires a multidomain glucanotransferase and a complex polysaccharide.

Results: A conventional bacterial glucanotransferase rescues an Arabidopsis mutant lacking the multidomain glucanotransferase.

Conclusion: Both the plant glucanotransferase-polysaccharide couple and the bacterial enzyme provide a glucosyl buffer in the starch degradation pathway.

Significance: New light is shed on the regulation and evolution of maltose metabolism.

Controlled conversion of leaf starch to sucrose at night is essential for the normal growth of Arabidopsis. The conversion involves the cytosolic metabolism of maltose to hexose phosphates via an unusual, multidomain protein with 4-glucanotransferase activity, DPE2, believed to transfer glucosyl moieties to a complex heteroglycan prior to their conversion to hexose phosphate via a cytosolic phosphorylase. The significance of this complex pathway is unclear; conversion of maltose to hexose phosphate in bacteria proceeds via a more typical 4-glucanotransferase that does not require a heteroglycan acceptor. It has recently been suggested that DPE2 generates a heterogeneous series of terminal glucan chains on the heteroglycan that acts as a “glucosyl buffer” to ensure a constant rate of sucrose synthesis in the leaf at night. Alternatively, DPE2 and/or the heteroglycan may have specific properties important for their function in the plant. To distinguish between these ideas, we compared the properties of DPE2 with those of the Escherichia coli glucanotransferase MalQ. We found that MalQ cannot use the plant heteroglycan as an acceptor for glucosyl transfer. However, experimental and modeling approaches suggested that it can potentially generate a glucosyl buffer between maltose and hexose phosphate because, unlike DPE2, it can generate polyanhydro maltosaccharides from maltose. Consistent with this suggestion, MalQ is capable of restoring an essentially wild-type phenotype when expressed in mutant Arabidopsis plants lacking DPE2. In light of these findings, we discuss the possible evolutionary origins of the complex DPE2-heteroglycan pathway.

Starch mobilization in leaves at night is one of the major metabolic fluxes in the biosphere. In many plants, up to half of the carbon assimilated via photosynthesis is stored as starch. The conversion of starch to sucrose during the night supplies the plant with carbon for metabolism and growth. In Arabidopsis grown in controlled conditions, night time conversion of starch to sucrose occurs at a constant rate that exhausts the starch reserves almost exactly at dawn. Mutants with reduced or accelerated rates of starch mobilization at night grow slowly and may exhibit symptoms of starvation. The main product of starch mobilization in the chloroplast is maltose, which is exported to the cytosol for conversion to hexose phosphates. These are used in cellular metabolism and for synthesis of sucrose for export to non-photosynthetic parts of the plant (1, 2). Despite the importance of night time starch mobilization for plant productivity, major questions remain over the pathway from maltose to hexose phosphate in the cytosol. The current state of knowledge is as follows.

In the cytosol, maltose is acted on by a 4-α-glucanotransferase (DPE2), which is vital for the normal metabolism and
Glucanotransferases and Maltose Metabolism in Leaves

FIGURE 1. Maltose metabolism in *E. coli* and *Arabidopsis* and the proposed pathway in the *Arabidopsis* dpe2 mutant expressing MalQ. **A**, in both *E. coli* and *Arabidopsis*, maltose enters the cytoplasm/cytosol, where it is disproportionated to yield glucose and a glucosylated acceptor molecule. Phosphorylation of glucose and phosphorolysis of the glucosylated acceptor then yield hexose phosphates. The pathway in *E. coli* is on the right; the putative pathway in leaf cells at night is on the left. *E. coli*-specific reactions are dark red, and plant-specific reactions are green. **B**, starch is metabolized to maltose and glucose in the chloroplast. Both metabolites are exported via specific transporters into the cytosol. In wild-type plants (*green*), maltose is disproportionated via DPE2 to yield glucose and glucosylated SHG. Pho2 can catalyze conversion of the glucosyl moiety to hexose phosphate. Free glucose is converted to hexose phosphate via hexokinase. In dpe2MalQ plants (*brown*), maltose is disproportionated via MalQ to yield glucose and malto-oligosaccharides. PHS2 can catalyze conversion of malto-oligosaccharides to hexose phosphate. As in wild-type plants, free glucose is converted to hexose phosphate via hexokinase. MEX1, maltose transporter; MOS, malto-oligosaccharide; Glk, glucokinase; MalP, *E. coli* glucan phosphorylase; BAM, β-amylase; ISA3, isoamylase 3.

growth of the plant. In *dpe2* mutants, maltose accumulates to very high levels, and growth is strongly reduced. DPE2 catalyzes the release of the reducing glucosyl moiety of maltose as free glucose, which can be phosphorylated via hexokinase to yield glucose 6-phosphate. The non-reducing glucosyl moiety of maltose is transferred onto an acceptor molecule (3–7). The nature of the acceptor *in vivo* is not known with certainty, but several lines of evidence indicate that it is a complex, soluble heteroglycan (SHG)9 widely distributed in plant species and organs (8–12). SHG is a heterogeneous mixture of glycans mainly composed of galactose and arabinose with minor amounts of glucose, fucose, mannose, rhamnose, and xylose. A defined proportion of SHG, which has been designated as subfraction I, comprises molecules larger than 10 kDa and is largely or exclusively cytosolic (8, 9, 13). In *vitro*, subfraction I both binds to recombinant DPE2 and acts as an acceptor of glucosyl moieties transferred by DPE2 from maltose. These glucosyl residues can be further metabolized by recombinant cytosolic phosphorylase isozyme (designated PHS2 in *Arabidopsis* and Pho2 in other species) to yield glucose 1-phosphate (6, 7). Thus, DPE2, cytosolic heteroglycan, and PHS2 together provide a route by which the non-reducing glucosyl moiety of maltose can be converted to hexose phosphate (Fig. 1A).

There is good circumstantial evidence that this pathway operates *in vivo*. First, mutant *Arabidopsis* and transgenic potato plants lacking DPE2 have up to 200 times more maltose than wild-type plants and reduced rates of starch degradation (3–5). In the Arabidopsis *phs2* mutant, maltose levels are elevated about 4-fold at night. Second, the structure of cytosolic heteroglycans is dependent on metabolic conditions. For example, the glucose content of these molecules in *Arabidopsis* leaves differs between night and day and is altered in *dpe2* mutants and lines with altered expression of cytosolic phosphoglucomutase (6, 10). Third, in short term experiments performed with potato tuber discs incubated with glucose 1-phosphate, the glucosyl content of cytosolic heteroglycans reflects the expression level of the cytosolic phosphorylase isozyme, Pho2 (10). Finally, there is no evidence for the existence in the cytosol of plant cells of glycogen or longer malto-oligosaccharides that could act as acceptors for the DPE2-mediated transfer of the non-reducing glucosyl residue from maltose. Soluble heteroglycans are the only cytosolic carbohydrates known to act as DPE2 acceptors.

The plant pathway of maltose metabolism is superficially similar to that of bacteria, including *Escherichia coli* (7, 14, 15). Maltose in *E. coli* is also metabolized to hexose phosphates via a 4-α-glucanotransferase (MalQ), a hexokinase, and a glucan phosphorylase (MalP) (Fig. 1A). The similarities are illustrated by the fact that an *E. coli* strain lacking MalQ was partially complemented with respect to growth on maltose by introduction of DPE2 from *Arabidopsis* (7). However, MalQ differs radically from DPE2 in that it appears to use maltose for a variety of transfer reactions leading to glucose and a series of malto-oligosaccharides (16, 17). There is no evidence that acceptors such as the cytosolic heteroglycans are involved in the bacterial pathway. Both enzymes belong to family 77 of glycoside hydrolases (GH77) (18), but whereas the GH77 domain is uninterrupted in MalQ, the domain in DPE2 contains an insertion of about 170 amino acids. DPE2 also possesses two N-terminal carbohydrate binding modules of the CMB20 family, but MalQ does not (19) (see Fig. 8A).

9 The abbreviations used are: SHG, soluble heteroglycan; CBM, carbohydrate binding module; SPR, surface plasmon resonance; GH77, glycoside hydrolase family 77; TEV, tobacco etch virus; HPAEC, high performance anion exchange chromatography; PAD, pulsed amperometric detection; Tricine, N-[2-hydroxy-1,1-bis(hydroxymethyl)]ethyl]glycine; IMAC, immobilized metal affinity chromatography.
Little is known about the functional significance of the DPE2-cytosolic heteroglycan pathway in plants or the selective advantage that it confers over biochemically and genetically less complex pathways, such as that in *E. coli*. It has recently been proposed that cytosolic heteroglycan can act as a “glucosyl buffer” between maltose export from the chloroplast and hexose phosphate utilization in the cytosol (11). The combined action of a glucanotransferase and a phosphorylase both operating close to equilibrium is presumed to form a heterogeneous series of terminal glucan side chains of cytosolic heteroglycans. Modeling reveals that, due to heterogeneity in length (i.e. in glucosyl content), side chains permit temporary variation in one of these fluxes without significantly affecting the other flux (20). Such buffering may be vital for a steady and sustained supply of carbon from starch for night time metabolism in the leaf. However, there is no a priori reason why buffering between maltose and hexose phosphates should require proteins and substrates with the complexity of DPE2 and the cytosolic heteroglycan. It remains possible that these molecules have specific functions in the conversion of starch to hexose phosphate other than or in addition to providing a glucosyl buffer.

To shed light on the significance of the DPE2-cytosolic heteroglycan pathway, we compared key properties of DPE2 from *Arabidopsis* and MalQ from *E. coli*. We uncovered striking differences in substrate specificity and affinity, consistent with the idea that MalQ cannot use cytosolic heteroglycan as a substrate. However, simulations of our mathematical model demonstrated that a hypothetical plant pathway containing MalQ rather than DPE2 would retain a “glucosyl buffer” function without a requirement for cytosolic heteroglycan because, unlike DPE2, MalQ can convert maltose into a polydisperse series of malto-oligosaccharides. Thus, if the main function of the DPE2-cytosolic heteroglycan pathway in vivo is to provide a glucosyl buffer, introduction of MalQ might be expected to bypass the requirement for DPE2 in planta. To test this idea, we examined the impact of expression of MalQ in dpe2 mutant plants. The transgenic plants regained metabolic functions and growth rates close to those of wild-type plants. The results have important implications for understanding the control of starch degradation and shed new light on the evolutionary origins of the starch degradation pathway.

### EXPERIMENTAL PROCEDURES

#### Plant Growth and Transformation

* Arabidopsis thaliana* plants were grown in compost at 20 °C and 75% relative humidity with 12 h of dark, 12 h of light at 160 µmol quanta m⁻² s⁻¹. The dpe2 mutant was dpe2-3 (Wasilewskija, 3). For transformation, the MalQ gene from *E. coli* was synthesized with codon usage optimized for *Arabidopsis* (GeneArt®) and cloned into the vector plasmid pEarleyGate 202, which added a 35S promoter and an N-terminal FLAG tag to the protein and contained a glufosinate resistance gene cassette. The resulting plasmid was stably transferred into dpe2-3 via *Agrobacterium tumefaciens* GV3101-mediated floral dip transformation. T0 plants were sprayed with glufosinate. Survivors were allowed to self-fertilize and were used to select homozygous lines.

**TABLE 1**

| Purpose of construct | Description | Amino acids | Primers |
|----------------------|-------------|------------|---------|
| Cloning of full-length DPE2 into pET151 | Production of full-length DPE2 with N-terminal His6-TEV | DPE2 1-955 | 5′-CACCATGATATCTAATAGCA-3′ |
| Cloning of CBM20-1 into pET151 | To produce first CBM20 module with N-terminal His6-TEV | DPE2 1-143 | 5′-CACCATGATATCTAATAGCA-3′ |
| Cloning of CBM20-2 into pET151 | Production of second CBM20 module with N-terminal His6-TEV | DPE2 144-240 | 5′-CACCATGATATCTAATAGCA-3′ |
| Cloning of Dpe2 into pET20a | Production of Dpe2 mutant in which coiled-coil motif is interrupted by insertion of LPAGS motif | DPE2 1-365 | 5′-CACCATGATATCTAATAGCA-3′ |
| Cloning of Dpe2 into pET20a | Production of Dpe2 mutant in which coiled-coil motif is deleted completely | DPE2 1-351Δ 386-955 | 5′-CACCATGATATCTAATAGCA-3′ |
| Cloning of Dpe2 into pET20a | Production of Dpe2 mutant in which catalytic domain insertion is deleted completely | DPE2 1-359Δ 745-955 | 5′-CACCATGATATCTAATAGCA-3′ |
| Cloning of Dpe2 into pET20a | Production of Dpe2 active site mutant D563N | DPE2 1-955 | 5′-CACCATGATATCTAATAGCA-3′ |
| Cloning of Dpe2 into pET20a | Production of Dpe2 active site mutant D563A | DPE2 1-955 | 5′-CACCATGATATCTAATAGCA-3′ |
| Cloning of Dpe2 into pET20a | Production of Dpe2 active site mutant D810N | DPE2 1-955 | 5′-CACCATGATATCTAATAGCA-3′ |
| Cloning of Dpe2 into pET20a | Production of Dpe2 active site mutant D810A | DPE2 1-955 | 5′-CACCATGATATCTAATAGCA-3′ |
| Cloning of full-length DPE2 into pET20a fusion to MalQ | Forward and reverse primers for all of the above pET20a constructs | DPE2 1-955 | 5′-CACCATGATATCTAATAGCA-3′ |
| Cloning of full-length PHS2 into pET20a fusion to MalQ | Production of full-length DPE2 with N-terminal His6-TEV | PHS2 1-841 | 5′-CACCATGATATCTAATAGCA-3′ |
Expression of Recombinant Proteins—Primers are shown in Table 1. DPE2 (At2g40840) cDNA was as described (3). PHS2 (At5g46970) cDNA was prepared from Arabidopsis (Col-0) leaf mRNA with the primers described previously (7).

For protein expression, cDNA was cloned into pET151 to give a construct encoding an isopropyl 1-thio-β-D-galactopyranoside-inducible, N-terminally His6-tagged protein with a TEV protease cleavage site C-terminal to the His tag. E. coli Rosetta II cells containing the constructs were grown overnight at 16 °C after induction. Cells were harvested by centrifugation and lysed with a cell disrupter in the presence of DNase, lysozyme, and Complete Protease Inhibitor EDTA-free (Roche Applied Science). After centrifugation and filtration to remove debris, extracts were subjected to chromatography on a HiLoad Superdex S-200 16/60 preparation grade column (GE Healthcare), as described in the figure legends. Samples were loaded onto HiTran columns in 100 mM HEPES (pH 7.5), 500 mM NaCl, 2 mM DTT, Complete Protease Inhibitor, and 60 mM imidazole, and bound proteins were eluted with this medium containing 500 mM imidazole. Superdex chromatography was in 25 mM HEPES (pH 7.5), 50 mM NaCl.

For dynamic light scattering, 20 μg of protein was filtered (0.1-μm membrane) and then analyzed in a 12-μl quartz cuvette in a dynamic light scattering device (Dynapro, Wyatt Technology Corp.). Measurements were taken every 5–10 s at 25 °C. Data were analyzed with the Dynamics™ software package.

Circular dichroism measurements were made in a 0.1-mm quartz cuvette in a Jasco J-715 spectropolarimeter between 26 and 185 nm, in 0.5-nm steps. Data were analyzed with software from the DICHROWEB server.

Enzyme Assays—Unless otherwise stated, stopped assays of recombinant enzymes were in 100 μl of 100 mM Hepes (pH 7.0) at 37 °C, using enzyme and substrate concentrations stated in legends. Coupled assays in which glucose production was monitored were at pH 7.9, in the presence of 1 mM each of ATP, NAD, and MgCl2; 3 units of hexokinase; and 1 unit of glucose-6-phosphate dehydrogenase (NAD-linked, from Leuconostoc mesenteroides). Measurements from coupled assays were used to estimate K_m values from Hanes plots.

Sugar Linkage Analysis—Analysis was as described previously (21, 22). Samples were per-O-methylated, hydrolyzed with trifluoroacetic acid, reduced with deuterated borohydride, and then per-O-acetylated with acetic anhydride. The resulting alditol acetates were solubilized in dichloromethane and analyzed by gas chromatography–mass spectrometry (23).

Binding of Recombinant Proteins to Starch—Starch granules were washed with 100 mM PIPES (pH 6.8) at 4 °C. Samples of 20 μM protein were mixed with 20 μg of starch glucan in 500 μl of this buffer, shaken for 30 min on ice, and then centrifuged at 22,000 × g for 5 min. The pellet was washed extensively with phosphate-buffered saline and then incubated at 100 °C for 10 min in 500 μl of SDS-PAGE loading buffer. Soluble and pellet fractions were analyzed on 4–12% SDS-polyacrylamide gels.

Analysis of Actions on Maltose—Maltose (5 mM) in 50 μl of [18O]water was incubated for 5 min at 37 °C with 1 μg of recombinant protein or bovine serum albumin. The mixture was boiled and analyzed on a 100 × 2-mm Luna NH2 column (Phenomenex) run in HILIC (hydrophilic interaction liquid chromatography) mode at 200 μl min⁻¹ and 30 °C with a gradient from 90 to 10% acetonitrile in 20 mM ammonium acetate (pH 9.45) over 15 min. Detection of [18O]glucose was by electrospray mass spectrometry.

Carbohydrate Microarrays—Polysaccharides (obtained either by enzymatic fragmentation of large cell wall polymers followed by purification or by chemical synthesis of various glycans) (24) were spotted onto nitrocellulose membranes (4 × 3 or 4 × 2 cm) using a microarray printer (24–26). Membranes were incubated with recombinant protein (5 mg) and 14C-labeled substrate (1 mM, either 37 GBq mol⁻¹ (maltose) or 18 GBq mol⁻¹ (glucose 1-phosphate)) in 5 ml of phosphate-buffered saline (PBS) for 4 h at 25 °C and then washed three times in PBS and twice in PBS with 0.05% (v/v) Tween 20 before fluorescence scanning in a PhosphorImager.

Surface Plasmon Resonance—Recombinant protein (2 mg ml⁻¹) was mixed with a 20-fold molar ratio of 20 mM EZ-link Sulfo NHS-LC biotin (Pierce), incubated at room temperature for 30 min, and then passed twice through a Sephadex G20 gel filtration spin column (GE Healthcare). Eluted protein at 10 μg ml⁻¹ in 10 mM HEPES (pH 7.0), 150 mM NaCl was applied to a Series S sensor chip SA (GE Healthcare), activated with 50 mM NaOH, 1 mM NaCl, to give 3000 bound response units. For measurements with maltotriose and maltotetraose, recombinant MalQ was directly immobilized on a Series S Sensor chip CM5 activated with 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide and N-hydroxysuccinimide. Protein was applied at 100 μg ml⁻¹ in 10 mM sodium acetate (pH 5.0), 150 mM NaCl and immobilized with an amine coupling kit (GE Healthcare) to give 6000 bound response units. The surface was then quenched with ethanolamine.

Analyses were applied to chips at 30 μl min⁻¹ at 25 °C in 10 mM HEPES (pH 7.0). Contact time was 90 s; dissociation time was 30 s; and regeneration was with 10 mM HEPES (pH 7.0), 1 mM NaCl for 90 s. Measurements were in triplicate on each of two chips. Analyte concentrations ranged from 50 nM to 10 mM. Experiments were performed on a Biacore T100 (GE Healthcare).

Experiments with SHG1 and SHG2 were purified from Arabidopsis (Ws) leaves harvested at the end of the light period as described previously (13). For experiments with unlabeled SHG1 and labeled maltose, samples of 30 μg were incubated in 150 μl of 100 mM citrate/NaOH (pH 7.0), 5 mM MgCl2, 10 mM dithioerythritol with recombinant protein and 12 mM [14C]maltose at 37 °C. For experiments with [14C]SHG1, prelabeling was by incubation of 40 μg of SHG1 with 6 μg of recombinant DPE2 and 12 mM [14C]maltose in 100 μl at 37 °C, followed by heating (95 °C for 5 min), centrifugation (20,000 × g for 10 min at 4 °C), and washing on a 10-kDa membrane filter. Samples of 20 μg of [14C]SHG1 were incubated with recombinant protein as above except that maltose was 10 mM and unlabeled. After incubations, mixtures were centrifuged and washed on a filter as above. Radioactivity in the filtrate and retentate was measured. For experiments in which neither SHG1 nor maltose was labeled, incubations contained recombinant MalQ, 200 μg of SHG1 (∼8 nmol of glucosyl moieties), and 8 nmol of maltose. After incubation, the mixture was...
heated, centrifuged, and passed through a 10-kDa filter. The filtrate was analyzed by HPAEC-PAD.

Native Gels for Enzyme Activity—For DPE2 and MalQ activity, leaves (~1 g) were harvested into liquid N₂ midway through the light period (unless stated otherwise), powdered in liquid N₂, and then homogenized in 5 ml of 100 mM MOPS (pH 7.0), 150 mM NaCl, 10% (v/v) glycerol, 0.1% (v/v) Triton X-100, 50 μM DTT, and 10 μl ml⁻¹ protease inhibitor (Roche Applied Science) at 4 °C and centrifuged at 20,000 × g. For PHS2 activity, extraction was as above except the medium was 2 ml of 100 mM Tricine-NaOH (pH 6.5), 5 mM MgCl₂, 10 mM dithioerythritol, 0.5 mM PMSF, 2 mM benzamidine, 2 mM aminocaproic acid, 10% (v/v) glycerol. Samples (2.5–5 mM Glc₇ for MalQ, or 20 mM glucose 1-phosphate for PHS2, 100 mM NaCl, 10% (v/v) glycerol, 0.1% (v/v) Triton X-100, 50 mM Tricine-NaOH (pH 7.8), 5 mM MgCl₂, 10 mM dithioerythritol, 0.5 mM PMSF, 2 mM benzamidine, 2 mM aminocaproic acid, 10% (v/v) glycerol. Samples (2.5 μg of protein for DPE2 and MalQ, 10 μg for PHS2) were mixed with native sample buffer and loaded onto acrylamide gels containing 0.5% (w/v) glycerol (for DPE2), 0.2% (w/v) glycerol (for PHS2), or no glycerol (for MalQ). After electrophoresis, gels were washed with 100 mM MOPS (pH 7.0) (for DPE2 and MalQ) or 100 mM citrate-NaOH (pH 6.5) (for PHS2) and then typically incubated for 2 h at 37 °C in the same buffer plus 5 mM maltose for DPE2, 5 mM Glc7 for MalQ, or 20 mM glucose 1-phosphate for PHS2, prior to staining with aqueous 0.67% (w/v) I₂ and 3.33% (w/v) KI.

Carbohydrate Analyses—A representative 50–150-mg sample of a single rosette was harvested into liquid N₂ and powdered in a ball mill. Extraction in dilute perchloric acid, starch solubilization and hydrolysis, enzymatic assay of sucrose and hexoses, and analysis of malto-oligosaccharides by HPAEC-PAD were as described previously (27, 28).

Simulations of the NAD(H)-coupled MalQ Assays—For the simulation of the NAD(H)-coupled in vitro assays of MalQ, the hexokinase reaction,

\[ G_1 + ATP \rightarrow G6P + ADP \]

was additionally represented as a simple first-order reaction with rate constant \( k_{\text{HXK}} \), corresponding to the assumption that ATP concentration is large and remains approximately constant throughout the reaction and that the reaction is practically irreversible under the chosen conditions. The number of glucose 6-phosphate molecules produced was recorded and plotted in Fig. 9A. The following initial conditions and parameters were used for the in vitro simulation: at time \( t = 0 \), \( G_3 = 10,000, G_n = 0 \) for \( n \neq 2, E_1 = 59, E_2 = E_3 = E_4 = E_6 = 1 \); rate constants, \( k_{\text{MalQ}} = 0.0006 \, s^{-1}, k_{\text{HXK}} = 0.02 \, s^{-1} \).

Simulations of the MalQ/PHS2 Buffer—To simulate an in vivo function of the MalQ-mediated buffer, the phosphorylase PHS2 was also represented in the simulations. The forward and backward reactions

\[ G_n + P_i \rightarrow G_{n-1} + G1P \quad (n \geq 4) \]
\[ G_n + G1P \rightarrow G_{n+1} + P_i \quad (n \geq 3) \]

were represented as second order mass action reactions. The ratio of the forward and backward rate constants \( k^{+}_{\text{PHS}} \) and \( k^{-}_{\text{PHS}} \) was assumed to be \( K_{E} = k^{+}_{\text{PHS}} / k^{-}_{\text{PHS}} = 0.19 \), in agreement with the findings reported in Ref. 20. The concentration of inorganic phosphate was assumed to be constant. Further, for the sake of simplicity, no distinction was made between glucose 1-phosphate and glucose 6-phosphate, and both were lumped into one variable representing the total pool of glucose phosphates.

To simulate an open system, an influx of maltose from an external source was represented as a zero order reaction (rate \( v_{\text{in}} \)). A consumption of glucose phosphate was represented as a first order reaction with rate constant \( k_{\text{out}} \).

For Fig. 9, B–D, maltose influx was simulated as a fluctuating function according to the equation

\[ v_{\text{in}} = v_{\text{in}}^0 + A \cdot \sin(\omega t) \]  

(Eq. 1)

The following parameter values were used: \( k_{\text{MalQ}} = 0.01 \, s^{-1}; k_{\text{HXK}} = 0.1 \, s^{-1}; k^{+}_{\text{PHS}} = 10^{-5} \, s^{-1}; k_{\text{out}} = 0.2 \, s^{-1}; v_{\text{in}}^0 = 100 \, s^{-1}; A = 100 \, s^{-1}; \omega = 0.2 \, s^{-1} \) (rapid), 0.02 s⁻¹ (medium), or 0.002 s⁻¹ (slow fluctuations); \( P_i = 50,000 \).
RESULTS AND DISCUSSION

Diverse Heteroglycans Are Acceptors for DPE2 but Not MalQ—In in vitro studies, recombinant DPE2 uses glycogen and cytosolic heteroglycans as acceptors for the transfer of the non-reducing glucosyl moiety from maltose. In addition, a glucosyl transfer from glycogen to monosaccharides, including mannose and xylose, was demonstrated (3, 6). These kinetic properties are consistent with the idea that DPE2 transfers glucosyl moieties from maltose onto glucosyl and other terminal residues of cytosolic heteroglycan in vivo. We investigated whether MalQ shares this broad acceptor specificity.

Recombinant DPE2 and MalQ (purification shown in Fig. 2, A–C) both formed disaccharides with D-glucose, D-mannose, D-xylose, D-allose, N-acetyl-D-glucosamine, and 2,3-dideoxy-D-glucose but not with L-rhamnose, D-galactose, D-fucose, or L-arabinose (Fig. 3, A and B). Thus, both DPE2 and MalQ can use a relatively wide range of monosaccharides as glucosyl acceptors. Consideration of the structures of these sugars suggests that efficient monosaccharide acceptors have both a D-configured pyranose ring and an equatorial orientation of the hydroxyl group at C4.

To investigate the actions of DPE2 and MalQ on complex polysaccharides, we used carbohydrate microarrays consisting of fragments of plant and algal carbohydrates printed onto nitrocellulose membranes (24–26, 30) (Tables 2 and 3). After incubation with recombinant protein and [14C]maltose, membranes were washed to minimize nonspecific binding and then subjected to fluorescence scanning. Recombinant DPE2 transferred 14C from [14C]maltose onto diverse carbohydrates, including the sulfated algal carbohydrate carrageenan, rham-
nogalacturonan I, rhamnogalacturonan II-enriched pectin, fucosylated xyloglucan, cellulose, glucomannan, and β 1,3-linked β-D-glucan (Fig. 3C). In contrast, recombinant MalQ transferred 14C from [14C]maltose only onto α1,4- and α1,4-, α1,6-linked glucans (maltose, maltopentaose, α-(1,6)-D-glucosyl-α-(1,4)-β-D-maltotriose, and α-(1,6)-D-glucosyl-α-(1,4)-β-D-maltosyl-maltose) (Fig. 3C). Neither of the latter two branched oligoglucans was used by DPE2 as an acceptor.

We also used the carbohydrate microarrays to examine the acceptor specificity of the cytosolic phosphorylase isozyme PHS2. Recombinant PHS2 mediates the reversible glucosyl transfer between cytosolic heteroglycans and glucose 1-phosphate in vitro (6–9, 13). The enzyme (purification shown in Fig. 2I) transferred 14C from [14C]glucose 1-phosphate to diverse carbohydrate fragments on the microarrays. Intriguingly, the pattern of labeling was very similar to that of DPE2, including...
labeling of carrageenan, rhamnogalacturonan I, rhamnogalac-
turonan II, and fucosylated xyloglucan (Fig. 3C). These data are consistent with the idea that DPE2 and PHS2 may act on a common, complex polysaccharide substrate in vivo.

The fact that MalQ used only \( \beta(1\rightarrow4) \)- and \( \beta(1\rightarrow6) \)-linked D-glucans as substrates on the carbohydrate microarrays indicated that, unlike DPE2, it may be unable to use plant cytosolic heteroglycans as a substrate. To test this idea, SHG\(_L\) isolated from wild-type Arabidopsis leaves was incubated with recombinant MalQ and \([14C]\)maltose. Incorporation of \( ^{14}C \) into SHG\(_L\) was extremely low (Fig. 4). In contrast, and as expected (6, 13), both DPE2 and PHS2 labeled SHG\(_L\) extensively (from \([14C]\)maltose and \([14C]\)glucose 1-phosphate, respectively).

After 60 min of incubation with 10 \( \mu \)g of recombinant protein, labeling of SHG\(_L\) via DPE2 and PHS2 was 230 and 560 times greater, respectively, than labeling via MalQ. In further experiments, we examined whether MalQ has significant hydrolytic activity toward either SHG\(_L\) or maltose. We found that the enzyme can release glucose and malto-oligosaccharides from preglycosylated SHG\(_L\) in the absence of any acceptor other than water (Fig. 5, A and B). This action may be hydrolytic, but as we discuss below, it might also reflect the possession by MalQ of tightly bound malto-oligosaccharides that can act as initial substrates of the reaction. MalQ has very limited hydrolytic activity on maltose, as demonstrated by \( ^{18}O \) labeling of glucose by recombinant MalQ in the presence of maltose and \([18O]\)water (Fig. 5, C–F), but by far its predominant action on maltose is disproportionation (see below).

These results show that although MalQ and DPE2 have similar, relaxed specificities toward monosaccharides as acceptors, only DPE2 can use complex heteroglycans as acceptors. MalQ exclusively uses \( \alpha \)-glucans as acceptors.

Maltose and Small Malto-oligosaccharides Are Good Acceptors for MalQ but Not DPE2—DPE2 and MalQ differ profoundly in their actions on small malto-oligosaccharides. It has been reported that DPE2 has no activity on maltose alone, whereas MalQ can use maltose as both donor and acceptor. Thus, MalQ acts on maltose when added as the only exogenous carbohydrate, leading to the formation of glucose and a series of malto-oligosaccharides. By contrast, DPE2 efficiently metabolizes maltose only when provided with a distinct acceptor molecule (6, 16, 17, 19). To probe these differences further, we compared the actions of MalQ and DPE2 on malto-oligosaccharides of different lengths.

In short incubations, no disproportionation of maltose was detected with DPE2 (Fig. 6, A and B). In long incubations at high enzyme concentrations, both enzymes disproportionated all of these molecules, although DPE2 action on maltose was very limited (Fig. 6, C and D). From each malto-oligosaccharide, MalQ produced glucose and a series of longer malto-oligosaccharides (Fig. 6, E and F). This was an exception; the main products were glucose and maltotetraose (Glc4) rather than maltose and Glc4.
This distribution probably reflects the use of the maltose product as a donor for glucosylation of Glc3 to produce glucose and Glc4. Indeed, maltose was one of the least abundant DPE2 products in all incubations. This experiment shows that DPE2 preferentially transfers single glucosyl residues, consistent with the restriction of substrate binding beyond subsite \(-1\), as proposed previously (19).

We used surface plasmon resonance (SPR) to measure binding affinities of MalQ and DPE2 for malto-oligosaccharides. Immobilized recombinant proteins were exposed to various concentrations of malto-oligosaccharides. MalQ displayed a very high affinity (i.e. low dissociation constant) for Glc3 and Glc4 and progressively lower affinities for Glc5, Glc6, and Glc7. DPE2 had much lower affinity for malto-oligosaccharides in general and bound malto-oligosaccharides Glc5, Glc6, and Glc7 more strongly than Glc4 (Fig. 7). The dissociation constant of MalQ for Glc4 was more than 10,000 times lower than that of DPE2, whereas its dissociation constant for Glc7 was only 170 times lower than that of DPE2. Overall, these data show that MalQ can rapidly generate a wide range of malto-oligosaccharides from single, small malto-oligosaccharide species, including maltose, whereas DPE2 has only a very low affinity for and action on small malto-oligosaccharide acceptors. Despite these profound differences in acceptor specificity, we found that MalQ and DPE have very similar affinities for maltose as a donor. For two separate preparations of the enzymes, MalQ had $K_m$ values of 2.1 and 1.9 mM (with Glc7 as an acceptor), and DPE2 had $K_m$ values of 2.9 and 2.3 mM (with glycogen as an acceptor).

**FIGURE 4.** Transfer of glucosyl residues onto SHG by PH52, DPE2, and MalQ. Purified SHG was incubated with recombinant enzyme and either [14C]maltose (for DPE2 and MalQ) or [14C]glucose 1-phosphate (for PH52) for 10 min (gray bars) or 60 min (black bars), and then dpm in SHG, were determined. Values are means of values from two separate incubations. A, incorporation catalyzed by 10 μg of each enzyme. B, incorporation catalyzed by 10 and 90 μg of MalQ. Values for 10 μg are the same as those shown in A. Note the very low values and lack of proportionality of incorporation with time or amount of enzyme.

**TABLE 3**

| Glycans on the array shown at the right in Fig. 3C and in Fig. 3E are listed. | A | B | C | D | E | F | G | H | I |
|---|---|---|---|---|---|---|---|---|---|
| α-(1→4)-D-glucopyranose (DE 0%) | β-D-glucosidase | β-(1→4)-D-glacto-tetraose | Lime pectin, DE 11% (Danisco #E11) | Lime pectin, DE 4% (Danisco #F3) | Lime pectin, DE 0% (Danisco #B00) | Lime pectin, DE 16% (Danisco #P16) | Sugar beet pectin (Danisco #BP6232) |
| α-L-arabinose | α-(1→4)-D-glucanase | α-(1→5)-L-arabinose-ribose | Peptic galactan #1 (lupin) | Peptic galactan #2 (potato) | Peptic galactan #3 (lupin) | Peptic galactan #4 (tomato) | RGII enriched pectin (red wine) |
| α-(1→5)-L-arabinose-ribose | β-(1→2)-D-glucanase | β-(1→3)-D-glucanase | β-(1→6)-D-glucanase | β-(1→3)-D-glucanase | (1→6)-(1→3)-β-D-glucan (laminarin) | (1→3)-β-D-glucan (pachyan) |
| β-(1→3)-D-mannobiose | α-(1→2)-D-mannosidase | β-(1→4)-D-mannosidase | Xylan (birch wood) | Xylan (birch wood) | 4-Methoxy-glucoronarabinoxylan (birch) | Xyloglucan, non-fucosylated (tamarind seed) | Xyloglucan, nearly fucosylated (pea) |
| β-D-mannose | β-(1→4)-D-mannanotriose | β-(1→4)-D-mannotetraose | 6-O-methyl-d-galactosyl-β-(1→4)-D-mannobiose | 6-O-methyl-d-galactosyl-β-(1→4)-D-mannobiose | β-glucan #1 (lichenan, Iceland moss) | β-glucan #2 (barley) | β-glucan #3 (yeast) | (1→6)-(1→4)-α-D-glucan (pullulan) |
| β-D-xylose | β-(1→4)-D-xylosidase | β-(1→4)-D-xylopentase | 3-O-methyl-d-galactosyl-β-(1→4)-D-glucanase | 3-O-methyl-d-galactosyl-β-(1→4)-D-glucanase | Glycogen | Alginic acid | Alginic acid | Alginic acid |
| Conjugate of Xyloglucan | Conjugate of Xyloglucan | Conjugate of Xyloglucan | Conjugate of Xyloglucan | Conjugate of Xyloglucan | Conjugate of Xyloglucan | Conjugate of Xyloglucan | Conjugate of Xyloglucan | Conjugate of Xyloglucan |
| XXX(G)- | XXX(G)- | XXX(G)- | XXX(G)- | XXX(G)- | XXX(G)- | XXX(G)- | XXX(G)- | XXX(G)- |
| (1→3)-(1→4)-β-D-glucan- [G3G4](G)- | (1→3)-(1→4)-β-D-glucan- [G3G4](G)- | (1→3)-(1→4)-β-D-glucan- [G3G4](G)- | (1→3)-(1→4)-β-D-glucan- [G3G4](G)- | (1→3)-(1→4)-β-D-glucan- [G3G4](G)- | (1→3)-(1→4)-β-D-glucan- [G3G4](G)- | (1→3)-(1→4)-β-D-glucan- [G3G4](G)- | (1→3)-(1→4)-β-D-glucan- [G3G4](G)- | (1→3)-(1→4)-β-D-glucan- [G3G4](G)- |
| α-(1→4)-D-glucan- [G3G4](G)- | α-(1→4)-D-glucan- [G3G4](G)- | α-(1→4)-D-glucan- [G3G4](G)- | α-(1→4)-D-glucan- [G3G4](G)- | α-(1→4)-D-glucan- [G3G4](G)- | α-(1→4)-D-glucan- [G3G4](G)- | α-(1→4)-D-glucan- [G3G4](G)- | α-(1→4)-D-glucan- [G3G4](G)- | α-(1→4)-D-glucan- [G3G4](G)- |
| β-D-glucose | β-(1→3)-D-glucan- [G3G4](G)- | β-(1→3)-D-glucan- [G3G4](G)- | β-(1→3)-D-glucan- [G3G4](G)- | β-(1→3)-D-glucan- [G3G4](G)- | β-(1→3)-D-glucan- [G3G4](G)- | β-(1→3)-D-glucan- [G3G4](G)- | β-(1→3)-D-glucan- [G3G4](G)- | β-(1→3)-D-glucan- [G3G4](G)- |

**FIGURE 4.** Transfer of glucosyl residues onto SHG by PH52, DPE2, and MalQ. Purified SHG was incubated with recombinant enzyme and either [14C]maltose (for DPE2 and MalQ) or [14C]glucose 1-phosphate (for PH52) for 10 min (gray bars) or 60 min (black bars), and then dpm in SHG, were determined. Values are means of values from two separate incubations. A, incorporation catalyzed by 10 μg of each enzyme. B, incorporation catalyzed by 10 and 90 μg of MalQ. Values for 10 μg are the same as those shown in A. Note the very low values and lack of proportionality of incorporation with time or amount of enzyme.
many organisms but absent from the chloroplastic 4-α-glu
canotransferase DPE1 and from MalQ (Fig. 8B). Coiled-
coiled motifs facilitate protein-protein interactions, in par-
ticular homodimer formation (31). Results from analyses of
pure recombinant DPE2 by size exclusion chromatography,
dynamic light scattering, and non-denaturing PAGE were all
consistent with its existence as a homodimer (Figs. 2,
A and B, and 8C). Previous research also suggested that DPE2 exists
as a dimer or larger multimer in Arabidopsis and maize leaf
extracts (32).

We attempted to discover the importance for DPE2 proper-
ties of the coiled-coil motif and the insertion in the GH77
domain by producing recombinant proteins in which these fea-
tures were altered or missing. Proteins that lacked the coiled-
coil motif or possessed a mutated form with an inserted
motif predicted to ablate its function (33) were insoluble, sug-
gest that the motif is important for protein structural integ-


despite the insertion, we established through mutagenesis that the enzyme requires for activity two of the three invariant res-
ides that make up the catalytic triad of GH77 enzymes (Fig.
8D); a requirement for the third of these residues had been
established previously (19). These data suggest that DPE2 has
the same catalytic mechanism as other GH77 enzymes and thus
that the amino acid insertion plays no major role in catalysis.

A previous study showed that the CBM20 domain of DPE2 is
important for its actions on malto-oligosaccharides and its
affinity for glucans. A mutant form of DPE2 lacking the N-ter-
minal CBM20 had much higher disproportionation activity
when supplied with maltose and short malto-oligosaccharides
(Glc3 to Glc7) than native DPE2 and much lower activity when
supplied with maltose and glycogen (19). Whereas the native
enzyme bound to starch, the mutant did not. Steichen
et al. (19)
proposed that the CBM20 domain confers affinity for large glu-
cans but also limits the use of small malto-oligosaccharides
because it restricts the binding of substrate beyond subsite −1,
as discussed above.

We extended these investigations by comparing the glucan-
binding capacity of the CBM20s with that of native DPE2.
Recombinant CMB20-1 (the N-terminal module) and native DPE2 both bound to starch and starch polymers, but CBM20-2 did not bind to these glucans (Fig. 8, E and F; purification shown in Fig. 2, H and I). These results suggest that the glucan-binding properties of DPE2 are largely conferred by CBM20-1. A similar conclusion was drawn by Steichen et al. (19), who reported that loss of CMB20-1 alone was sufficient to abolish the glucan binding properties of DPE2.

Given the influence of the CBM20 domain on the properties of DPE2, we investigated the impact on MalQ of the addition of this domain (containing both CBM20-1 and CBM20-2; purification shown in Fig. 2 G). As expected, the domain conferred the ability to bind to starch and amylose (Fig. 8 G). However, the fusion protein resembled MalQ rather than DPE2 with respect to its affinity for small malto-oligosaccharides. Using SPR, we found that the fusion protein had a very high affinity for Glc3 and Glc4 and progressively lower affinities for Glc5, Glc6, and Glc7 (Fig. 7). Although dissociation constants for the fusion protein were higher than for MalQ, they were at least 80 times lower than the dissociation constants of DPE2 for the same molecules.

These results confirm that the major structural difference between DPE2 and MalQ, the presence of CBMs on DPE2, confers the capacity to bind to polyglucans. It also influences the affinity of the protein for small malto-oligosaccharides, but it does not confer the very low affinity for small malto-oligosaccharides seen in DPE2. Importantly, it does not confer the capacity to use heteroglycans. Thus, the use of heteroglycans as substrates must be attributable to some structural difference between MalQ and DPE2 other than the CBM20 domain. Future identification of this feature will be facilitated by our observation that the cytosolic glucan phosphorylase PHS2, which lacks obvious carbohydrate binding modules, can act on carbohydrates other than glucans as acceptors. When incubated with the carbohydrate microarrays and [14C]maltose, the fusion protein labeled the same glucans as MalQ. It did not use any of the diverse carbohydrates used by DPE2, and it retained the ability to use the branched malto-oligosaccharides that were not used by DPE2 (Fig. 3 C).

These results confirm that the major structural difference between DPE2 and MalQ, the presence of CBMs on DPE2, confers the capacity to bind to polyglucans. It also influences the affinity of the protein for small malto-oligosaccharides, but it does not confer the very low affinity for small malto-oligosaccharides seen in DPE2. Importantly, it does not confer the capacity to use heteroglycans. Thus, the use of heteroglycans as substrates must be attributable to some structural difference between MalQ and DPE2 other than the CBM20 domain. Future identification of this feature will be facilitated by our observation that the cytosolic glucan phosphorylase PHS2, which lacks obvious carbohydrate binding modules, can act on...
Despite Their Different Properties, both DPE2 and MalQ Can Potentially Generate Glucosyl Buffers in Vivo—Our results lend weight to the current view that conversion of maltose to hexose phosphate in the cytosol at night uses the cytosolic heteroglycan as an intermediate. Although DPE2 has the general properties of a GH77 glucanotransferase, it is more complex than most GH77 enzymes, and it possesses a capacity to transfer glucosyl moieties from malto-oligosaccharides onto complex glycans that is thus far unique among GH77 enzymes. In addition, DPE2 cannot use small malto-oligosaccharides effectively as acceptor substrates; it requires a larger glucan or glycan as an acceptor. All of these features are consistent with the use of the cytosolic heteroglycan as an acceptor substrate by DPE2. Our results also show that MalQ could not directly substitute for DPE2 in the plant, because it lacks the capacity to transfer glucosyl moieties from maltose to cytosolic heteroglycan.

However, although MalQ could not replace the DPE2 function directly, it might be able to substitute for the proposed glucosyl buffer function of the pathway. Fettke et al. (11) suggested that in wild-type plants, cytosolic heteroglycan acts as a glucosyl “buffer” between maltose export from the chloroplast and hexose phosphate utilization in the cytosol, so that temporary fluctuations in one of these fluxes does not impact the other flux. Kartal et al. (20) provided a mechanism for this buffering action. They showed that DPE2 and PHS2 together can maintain polydispersity of glucosyl chains on cytosolic heteroglycan, in a system driven largely by entropy gradients. Comparison of the theoretical performance of this entropy-driven
cytosolic heteroglycan pathway with an alternative hypothetical pathway in which maltose is metabolized to hexose phosphate without a polydisperse glucan intermediate showed that the former pathway can maintain a constant output of hexose phosphate in the face of fluctuations in maltose export from the chloroplast, but the latter, hypothetical pathway lacks this buffering capacity.

We reasoned that MalQ might provide a glucosyl buffer by disproportionating maltose to yield glucose and a polydisperse pool of malto-oligosaccharides. Glucose could be further metabolized by hexokinase, and malto-oligosaccharides could be further metabolized by cytosolic phosphorylase PHSI (analogous to the metabolism of imported maltose in *E. coli*; see Fig. 1, A and B). We examined this possibility using the modeling approach described by Kartal et al. (20) (see “Experimental Procedures”).

We first examined under which conditions MalQ can create a polydisperse pool of malto-oligosaccharides from pure maltose. Early work on MalQ (34) suggested that maltose cannot act as a glucosyl donor for this enzyme. Without further assumptions, this suggestion is not compatible with subsequent observations that the recombinant enzyme catalyzes disproportionation with pure maltose as initial substrate, in the absence of any added donor (16, 17) (experiments above). However, as discussed above, MalQ displays an extremely high affinity for short malto-oligosaccharides (dissociation constants of 0.26 and 0.41 μM for Glc3 and Glc4, respectively; Fig. 7). It can be assumed that both *in vivo* and *in vitro*, at least some MalQ proteins are bound to malto-oligosaccharides that can act as initial donors, allowing formation of free malto-oligosaccharides from maltose. These then act as donors and initiate the disproportionation reaction. With this assumption, the time course of glucose production observed from added maltose in *in vitro* assays with purified recombinant MalQ can readily be explained (Fig. 9A).

Once a polydisperse pool of malto-oligosaccharides is established, it can potentially act as a buffer between maltose influx and glucose-phosphate utilization, analogous to the cytosolic heteroglycan buffer (20). To explore the functioning of the malto-oligosaccharide buffer, we simulated a highly fluctuating maltose influx and a constant demand for glucose phosphate through a rapidly changing function representing the provision of maltose and a fixed rate constant for the glucose phosphate-removing reaction. Fig. 9B shows that a constant provision of glucose phosphate is maintained despite the highly variable maltose influx. An interesting property of the buffering mechanism is revealed by simulating slow fluctuations. The outflux of glucose phosphates follows the influx of maltose with a certain delay (Fig. 9D). This can be explained by the fact that any (slow) change in either supply or demand leads to an adaptation of the buffer size. As a consequence, such changes do not have an immediate effect on other processes but rather lead to a slow adaptation of the polydisperse buffer.

From these considerations, it seems likely that MalQ could bypass a requirement for DPE2 *in planta* if the primary function of the DPE2-cytosolic heteroglycan pathway is to provide a glucosyl buffer in the pathway of starch degradation. However, if DPE2 and/or cytosolic heteroglycan have other essential functions specific to their properties and structures, MalQ could not substitute for DPE2. We tested these ideas by introducing a construct encoding MalQ from *E. coli* into the *dpe2* mutant of *Arabidopsis* and examining the extent to which a wild-type phenotype was recovered in homozygous, MalQ-expressing transgenic lines.

Expression of MalQ Can Restore a Wild-type Phenotype in *dpe2* Mutant Plants—*dpe2* mutant plants have up to 200 times more maltose than wild-type plants, elevated levels of starch, altered sugar metabolism, and reduced growth rates (3, 4). Among *dpe2* lines expressing MalQ, we found several with starch contents similar to wild-type rather than *dpe2* plants (Fig. 10A). End-of-night starch content was correlated with rosette fresh weight across the transgenic lines. The line with the lowest starch content (*dpe2* MalQ9) had the same fresh weight as wild-type plants, whereas lines with high starch contents had fresh weights comparable with *dpe2* (Fig. 10B). Two lines selected for further study had end-of-night starch contents of 3.3 (*dpe2* MalQ9) and 6.0 (*dpe2* MalQ11) mg of starch g⁻¹ fresh weight, compared with wild-type and *dpe2* values of 1.5 and 15.3, respectively.

DPE2 and MalQ activities in extracts of the selected transgenic lines were analyzed by detection of iodine staining bands in glycogen-containing native gels incubated with maltose (for DPE2) or Glc7 (for MalQ) after electrophoresis (3). As expected, DPE2 activity was present in wild-type plants but absent from *dpe2* plants and the *dpe2* MalQ lines. MalQ activity was absent from wild-type and *dpe2* lines but present in the transgenic lines (Fig. 10C). Immunoblot analysis detected DPE2 protein in wild-type plants but not in *dpe2* or transgenic plants, and MalQ protein was detected only in transgenic plants (Fig. 7D; validation of antisera shown in Fig. 2E). Both native gel and immunoblot analyses indicated that the level of MalQ activity/protein was higher in *dpe2* MalQ9 than in *dpe2* MalQ11.

Expression of MalQ strongly reduced the levels of maltose in *dpe2* mutant plants. In *dpe2* MalQ9, levels were at least 100-fold lower than in the *dpe2* mutant, and the daily pattern of change was similar to that of wild-type plants. In *dpe2* MalQ11, maltose was at least 10-fold higher than in wild-type plants but about 8-fold lower than in the *dpe2* mutant (Fig. 11, A and B). Levels of Glc3, Glc4, and Glc5 were similar in *dpe2* MalQ9 and wild-type plants and much lower than in *dpe2* plants. Levels rose at night and fell during the day in both genotypes. In *dpe2* MalQ11 plants, levels of these compounds were higher than in wild-type plants and like those of *dpe2* plants, they rose during the day and fell at night (Fig. 11, C–F). Levels of starch and sugars were similar in *dpe2* MalQ9 plants and wild-type plants, whereas levels in *dpe2* MalQ11 plants were more similar to those of *dpe2* plants (Fig. 11, G–J).

We reported previously that the *dpe2* mutation changes the composition of leaf cytosolic heteroglycans; the contents of xylose, mannose, and in particular glucose are higher in relation to arabino and galactose than in wild-type plants (6). Expression of MalQ in *dpe2* plants reversed these changes. The composition of SHG₆ from *dpe2* MalQ plants with high levels of MalQ resembled that of wild-type rather than *dpe2* plants (Fig. 12, A and B). *dpe2* plants contained more SHG₆ than wild-type
Glucanotransferases and Maltose Metabolism in Leaves

A

produced glucose (normalised)

time, min

B

\( \omega = 0.2 \)

fluxes (a.u.)

maltose influx (a.u.)

time, min

C

\( \omega = 0.02 \)

fluxes (a.u.)

maltose influx (a.u.)

time, min

D

\( \omega = 0.002 \)

fluxes (a.u.)

maltose influx (a.u.)

time, min
Glucanotransferases and Maltose Metabolism in Leaves

plants, and dpe2MalQ plants contained amounts intermediate between those of dpe2 and wild-type plants (Fig. 12C).

Loss of dpe2 increases glucan phosphorylase activity in Arabidopsis leaves (3). Using a native gel assay, we found that activities of both plastidial (PHS1) and cytosolic (PHS2) isoforms of phosphorylase were higher in dpe2 than in wild-type extracts but were restored to nearly wild-type levels in both dpe2MalQ lines (Fig. 12D).

Our results thus far indicated that MalQ can largely replace the functions of DPE2/cytosolic heteroglycan, allowing nearly normal plant metabolism and growth in 12-h light, 12-h dark cycles. However, shortfalls in the capacity of MalQ to replace the endogenous pathway might be more obvious under long night conditions, in which plant growth is strongly dependent on optimal conversion of starch to hexose phosphates. Accordingly, we grew dpe2MalQ plants at a range of day lengths. Day length had no obvious effect on the relationship between the fresh weights of wild-type and dpe2MalQ plants. In batches of 28-day-old plants grown with 18-, 16-, and 8-h night periods, dpe2MalQ9 plants had 108, 89, and 92% of the fresh weight of wild-type plants, respectively (see also the independent experiment in Fig. 13). Thus, MalQ can effectively replace the functions of DPE2 and the cytosolic heteroglycan even in conditions in which growth is highly dependent on this pathway.

Possible Evolutionary Origins of the DPE2-Cytosolic Heteroglycan Pathway—Our results indicate that DPE2 and the cytosolic heteroglycan have no specific structural or functional properties that are essential for the conversion of maltose to hexose phosphate (or indeed other aspects of cellular metabolism) in planta. This conclusion arises because, under the range of growth conditions we examined, DPE2/heteroglycan can be replaced by MalQ without obvious detrimental effects on plant growth.

This finding is surprising in light of the genetic and biochemical complexity of the heteroglycan (its synthesis must require numerous enzymes of sugar interconversion and polymerization).
tion) and the high level of conservation of the pathway among photosynthetic organisms. Phylogenetic analyses by Ball and colleagues (35–39) offer a possible evolutionary explanation for this conundrum. These authors propose a complex evolutionary origin of chloroplastic starch metabolism, in which pathways of glucan metabolism derived from the eukaryotic host and the prokaryotic symbiont have been "rewired" by modification, duplication, and subcellular relocation. Their analyses indicate that DPE2 was acquired by the Archaeplastida from their eukaryotic ancestor, in which it may have been involved in maltose metabolism associated with cytoplasmic $\alpha$-glucan turnover. In this ancestral organism, the acceptor substrate for DPE2 would have been an $\alpha$-glucan rather than heteroglycan, and the CBMs of DPE2 may have had a role in determining its affinity for $\alpha$-glucan. During the evolution of the Chloroplastida, it is proposed that $\alpha$-glucan turnover relocated to the plastid. Evolution of the plastid envelope maltose transporter MEX1 (found only in the Chloroplastida) (36) meant that cytosolic DPE2 continued to provide the route for metabolism of maltose produced by starch degradation but no longer had access to $\alpha$-glucan as an acceptor substrate. Presumably, the use of cytosolic heteroglycan as an acceptor substrate arose at

FIGURE 11. Metabolite contents of transgenic lines. Measurements were made on whole rosettes of 21-day-old plants grown in 12-h light, 12-h dark over a single day-night cycle. Values are means of measurements on five individual plants for each line. Error bars, S.E. A, maltose levels in dpe2 mutant (open circles), dpe2MalQ11 (closed triangles), dpe2MalQ9 (open triangles), and wild-type (closed circles) plants. B, data for wild-type and dpe2MalQ9 plants from A, on an expanded scale. C–F, Glc3 (dark gray), Glc4 (light gray), and Glc5 (white) levels in dpe2 mutant (C), dpe2MalQ11 (D), wild-type (E), and dpe2MalQ9 (F) plants. Note the different y axis scales. G–J, starch, sucrose, glucose, and fructose levels in dpe2 mutant (open circles), dpe2MalQ11 (closed triangles), dpe2MalQ9 (open triangles), and wild-type (closed circles) plants.

FIGURE 12. Effects of MalQ expression on SHGL and PHS2 in transgenic lines. SHGL was purified from mature leaves of dpe2 mutant and wild-type plants and transgenic lines dpe2MalQ11 and dpe2MalQ9. The sugar composition of hydrolyzed SHGL was analyzed by HPAEC-PAD. A and B, plants harvested at the end of the night (A) and the end of the day (B). Fuc, fucose; Ara, arabinose; Rha, rhamnose; Gal, galactose; Glc, glucose; Xyl, xylose; Man, mannose. C, amounts of SHGL in mature leaves at the end of the day (white) and the end of the night (black). Values are means of three biological replicates. Error bars, S.D. D, phosphorylase activity in transgenic lines. Extracts containing 10 $\mu$g of protein were subjected to discontinuous native PAGE and developed for phosphorylase activity (9). Closed arrows, PHS2 (cytosolic) activity; open arrows, PHS1 (plastidial) activity (see Refs. 13, 41, and 42).
this point. DPE2 either already possessed the capacity to use glycans as substrates or acquired features that enhanced affinity for existing cytosolic heteroglycans in response to relocation of α-glucan metabolism to the plastid.

As a parallel evolutionary scenario, we raise the possibility that the cytosolic heteroglycan might reflect a form in which the eukaryotic host initially acquired carbon from the photosynthetic symbiont. Ball et al. (38) have argued persuasively that the main form in which carbon was exported from the cyanobacterial symbiont was ADP-glucose, fuelling an existing pathway of α-glucan synthesis in the cytosol of the host cell. We suggest that the cyanobacterial symbiont may also have continued to export the glycans that would have constituted its exopolysaccharides in the free-living state. Many modern cyanobacteria release exopolysaccharides with compositions similar to that of cytosolic heteroglycan; arabinose, xylose, galactose, fucose, rhamnose, and glucose are all common residues (40). Perhaps catabolism of these exopolysaccharides provided an important source of carbon for the host cell, and cytosolic heteroglycan is an evolutionary remnant of this first interface between photosynthetic and host cell metabolism.

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