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Part of the dimer and B/C domain interface of the Escherichia coli mannitol permease (EII\textsuperscript{mtl}) has been identified by the generation of disulfide bridges in a single-cysteine EII\textsuperscript{mtl}, with only the activity linked Cys\textsubscript{384} in the B domain, and in a double-cysteine EII\textsuperscript{mtl} with cysteines at positions 384 and 124 in the first cytoplasmic loop of the C domain. The disulfide bridges were formed in the enzyme in inside-out membrane vesicles and in the purified enzyme by oxidation with Cu(II)-(1,10-phenanthroline)\textsubscript{3}, and they were visualized by SDS-polyacrylamide gel electrophoresis. Discrimination between possible disulfide bridges in the dimeric double-cysteine EII\textsuperscript{mtl} was done by partial digestion of the protein and the formation of heterodimers, in which the cysteines were located either on different subunits or on one subunit. The disulfide bridges that were identified are an intersubunit Cys\textsubscript{384}-Cys\textsubscript{124} an intersubunit Cys\textsubscript{124}-Cys\textsubscript{384}, an intersubunit Cys\textsubscript{384}-Cys\textsubscript{320} and an intrasubunit Cys\textsubscript{384}-Cys\textsubscript{324}. The disulfide bridges between the B and C domain were observed with purified enzyme and confirmed by matrix-assisted laser desorption ionization-time of flight mass spectrometry. Mannitol did not influence the formation of the disulfide between Cys\textsubscript{384} and Cys\textsubscript{124}. The close proximity of the two cysteines 124 was further confirmed with a separate C domain by oxidation with Cu(II)-(1,10-phenanthroline)\textsubscript{3} or by reactions with dimaleimides of different length. The data in combination with other work show that the first cytoplasmic loop around residue 124 is located at the dimer interface and involved in the interaction between the B and C domain.

The uptake and concomitant phosphorylation of a wide variety of carbohydrates into bacterial cells is, in many cases, accomplished by the phosphoenolpyruvate-dependent phosphotransferase system (PTS) (1). In a cascade of phosphorylation reactions (Fig. 1), the phosphoryl group is transferred from the energy donor phosphoenolpyruvate (PEP)\textsuperscript{1} via the two general components EI and HPr to the carbohydrate-specific components (Enzyme II’s), which transport and phosphorylate the carbohydrates (2). All EI’s\textsuperscript{2} have a similar architecture and consist of the cytoplasmic A and B domains and a membrane-embedded C domain. This article deals with the mannitol-specific EII (EII\textsuperscript{mtl}) of Escherichia coli, in which the three domains are covalently linked. HPr phosphorylates the A domain of EII\textsuperscript{mtl} on His\textsuperscript{554}, which subsequently phosphorylates Cys\textsubscript{384} in the B domain. Mannitol in the periplasm is bound by the C domain, transported into the cell via C and, while bound at the cytoplasmic site of C, phosphorylated by the B domain. EII\textsuperscript{mtl} is most likely a dimeric protein and the subunit interactions occur in the C domain (3–8).

Domain interactions and in particular the B/C domain interface play an important role in the catalytic cycle of EII\textsuperscript{mtl}. The energy coupling mechanism involves conformational interaction between the B and C domain. The evidence for this notion is manifold. 1) Phosphorylation of the B domain increases the rate of transport 2–3 orders of magnitude (9, 10). 2) Modification or mutagenesis of the phosphorylation site in the B domain as well as removal of the cytoplasmic domains changes the mannitol binding kinetics of the C domain (11, 12). 3) Time-resolved fluorescence and phosphorescence spectroscopy showed that, upon phosphorylation of the B domain, Trp\textsuperscript{109} in the C domain becomes immobilized whereas Trp\textsuperscript{30} in the C domain becomes more flexible (13, 14). 4) Differential scanning calorimetry showed that the thermal stability of the C domain is higher in the presence of the B domain (15). 5) Isothermal titration calorimetry experiments indicated that a significant part of the structural changes upon the binding of mannitol to the C domain reside in the B domain. Approximately 50–60 residues are removed from the bulk water upon binding of mannitol, which was much less when the same measurements were done after removal of the B domain (16). 6) Close proximity of the B and C domain has been suggested for another PTS transporter, that is the BglF system of E. coli.\textsuperscript{3}

To date, there is no structural information about the B/C domain or dimer interface of EII\textsuperscript{mtl} or any other EII. The topological model of the C domain predicts 6 membrane-spanning assistant laser desorption-ionization-time of flight mass spectrometry; DTT, dithiothreitol; PAGE, polyacrylamide gel electrophoresis.

\textsuperscript{1}The nomenclature of the enzymes is: EII, carbohydrate-specific transport protein of the PTS; EII\textsuperscript{mtl}, wild-type mannitol-specific EII of E. coli containing all four cysteines; SSCS, N-terminal His-tagged EII\textsuperscript{mtl} with Cys\textsubscript{124}, Cys\textsubscript{554}, and Cys\textsubscript{320} replaced with serine; SSCS-S124C, SSCS with Ser\textsubscript{124} in the C domain replaced with a cysteine; IIChis-CL, C-terminal His-tagged cysteine-less C domain with Cys\textsubscript{124} and Cys\textsubscript{320} replaced with serine; IIChis-S124C, IIChis-CL in which Ser\textsubscript{124} is replaced with a cysteine. Numbering of residues, even in the His-tagged mutants, is always according to the numbering in the original sequence of EII\textsuperscript{mtl}.

\textsuperscript{2}O. Amster-Choder, personal communication.

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1 The abbreviations used are: PEP, phosphoenolpyruvate; ISO, inside-out; dPEG, decyl-polyethylene glycol; CuPhe, Cu(II)-(1,10-phenanthroline)\textsubscript{3}; PTS, phosphotransferase system; mtl, mannitol; HPr, histidin-containing protein; EI, enzyme I; MALDI-TOF MS, matrix-
FIG. 1. Schematic representation of the mannitol-specific phosphoenolpyruvate-dependent phosphotransferase system of *E. coli*. Dotted arrows indicate that the phosphoryl group transfer from HPr can proceed to each of the EIImtl subunits and that inter- and intradomain phosphoryl group transfer is possible as well.

EXPERIMENTAL PROCEDURES

**Chemicals**—Decyl-polyethylene glycol (dPEG) was synthesized by B. Kwant (Kwant High Vacuum Oil Recycling and Synthesis, Bedum, The Netherlands). Bovine pancreas l-1-tosylamido-2-phenylethyl chloromethyl ketone-treated trypsin was from Sigma and endoproteinase Glu-C of *Staphylococcus aureus* V8 was from Fluka. The bismaleimides o-PDM and p-PDM were from Aldrich and BMH was obtained from Pierce. EI and HPr were purified as described previously (18, 19). All chemicals used were analytical grade.

**Construction of Plasmids for Expression of SSCS, SSCS-S124C, and IIChis-S124C**—Site-directed mutagenesis was performed with the Stratagene Quickchange mutagenesis kit. His-tagged EIImtl154 with cysteines at positions 110, 320, and 571 replaced by serine (SSCS) was constructed in pMaHisMtlAPr, which carries the gene for the N-terminal His-tagged EIImtl154.5 Subsequently, SSCS-S124C was generated by replacing Ser124 with a cysteine. IIChis-CL was generated by replacing Cys110 and Cys320 by serine in pMaMtlICHis, which carries the gene for the C domain with a C-terminal His-tag (16). IIChis-S124C was then generated by replacing Ser124 with a cysteine as described above. Mutations were identified by introducing silent restriction sites and confirmed by DNA sequence analysis.

**Generation of ISO Vesicles and Purification of SS, SSCS-S124C, and IIChis-S124C**—growth of *E. coli* LGS322 (F thi-1, hisG1, argG6, metB1, tonA2, supE44, rpsL104, lacY1, galT6, gatR49, gatR50, Δmt-IA p), ntlDF, Δ(gufR MDARec)A) carrying the various plasmids, and procedures to overexpress the mutant proteins were identical to those described for wild-type EIImtl154 (20). Inside-out (ISO) membrane vesicles containing the mutant proteins were obtained as described (21). SSCS and SSCS-S124C were purified by Ni-NTA-agarose affinity chromatography as described for 6HEIImtl154 (14), except that dPEG was used as the detergent. IIChis-CL and IIChis-S124C were purified as described (16).

**EIImtl Concentration Determination and Mannitol Binding and Phosphorylation Activities**—The dissociation constant for mannitol binding and EI or IIC concentration in vesicles was determined by flow dialysis after solubilization with 0.25% dPEG (22) with some modifications as will be described elsewhere.6 The mannitol phosphorylation activity was determined at 1 mM mannitol (23). The concentration of purified SSCS and SSCS-S124C was determined with the pyruvate burst assay, which determines the amount of PTS phosphorylation sites (24). The activities of IIChis-CL and IIChis-S124C were determined after formation of a heterodimer with EIImtl154G196D, using 33 μM mannitol as described (25).

**Disulfide Cross-linking**—A solution of ~6 μM enzyme in ISO vesicles or 1 μM purified protein was brought to a final concentration of 5 mM DTT and 20 mM EDTA from stocks of 0.1 and 0.5 mM, respectively. If appropriate, 90 nM EI was added. After pretreatment, 0.4% dPEG and PEP were added to phosphorylate the purified enzyme, provided EI was present; these additions increased the final volume by 50%. The same mixture without PEP was used to represent conditions in which the enzyme was not phosphorylated. The final concentrations of the components were 2 μM HPr, 5 mM PEP, and 5 mM MgCl2. After 5 min at 30 °C, disulfide bridge formation was initiated by oxidation with 0.1 volume of 3 mM Cu(II)-(1,10-phenanthroline)3 (CuPhc), followed by incubation at 30 °C for 30 min. The reaction was quenched by the addition of 65 mM EDTA from a stock of 0.5 M NaEDTA, pH 8.

**Partial Digestion and Reduction**—The protein was partially digested with 20 μg of trypsin or 100 μg of endoproteinase Glu-C/ml of reaction mixture for 1 h at room temperature. The digestion of the vesicles with endoproteinase Glu-C was done in the presence or absence of 0.4% dPEG. The digestion was stopped by the addition of SDS-PAGE denaturation buffer without β-mercaptoethanol. If appropriate, reduction was accomplished by the addition of 10 mM DTT after digestion.

**Heterodimer Formation**—Heterodimers between 3 μM SSCS and 1 μM IIChis-S124C or 0.2 μM SSCS-S124C and 3 μM IIChis-CL were formed by mixing purified proteins, followed by an incubation at 30 °C for 30 min. To promote heterodimer formation between SSCS-S124C and IIChis-CL, 170 mM Na2PO4 was added from a 1 M stock solution in pH 7.6. This lowers the cloudpoint of the detergent (dPEG), in which the protein is solubilized. This treatment results in dissociation of the initially homodimeric enzymes and thereby facilitates the mixing of the species (26). Subsequently, the heterodimers were treated as described above for the disulfide cross-linking procedure except that EI, HPr, MgCl2, and PEP were omitted from the mixture.

**Cross-linking with Dimaleimides of Varying Length**—1 μM Purified IIChis-S124C was reduced and demethylated as described under “Disulfide Cross-linking.” Cross-linking was initiated by adding to the protein, in 50 mM NaPi, pH 7.5, 0.1 mM EDTA plus 0.25% dPEG, 5 μM o-PDM, p-PDM, or BMH from a 10 times concentrated stock solution in N,N-dimethylformamide. The reaction was stopped with 10 mM DTT after incubation at 30 °C for 30 min.

**SDS-PAGE Analysis and Immunoblotting**—SDS-polyacrylamide gel electrophoresis was done with 10% acrylamide gels as described (27). A denaturation buffer without β-mercaptoethanol was used. The samples were not boiled in denaturation buffer, because this leads to aggregation. The proteins were visualized either by silver staining (28) or by immunodetection after the proteins were transblotted to polyvinylidene difluoride membranes by semi-dry electrophoretic blotting. Detection using the Western Light™ chemiluminescence detection kit with CSP-D™ as the substrate, was performed as recommended by the manufacturer (Tropix Inc.). The first antibody was an anti-His antibody from Amersham Pharmacia Biotech or Roche Molecular Biochemicals, and the second antibody was an anti-mouse IgG alkaline phosphatase conjugate (Sigma). MALDI-TOF Mass Spectrometry—A Coomassie-stained band containing the C domain, generated by trypsin digestion, was excised from a SDS-polyacrylamide gel and completely destained with 50 mM NH4HCO3 in 40% ethanol. Subsequently, the gel piece was washed three times with 200 μl of 25 mM NH4HCO3 and cut into pieces of ~1 mm2. A 200-μl volume of 50 mM β-mercaptoethanol in 25 mM NH4HCO3 was pipetted onto each piece and, after 2 h of mixing at room temperature, the reaction was quenched by extraction with two 200 μl volumes of 60% acetonitrile, 0.1% trifluoroacetic acid by 5 min of sonication in a bath sonicator. The β-mercaptoethanol solution and the extracts were pooled and dried in a SpeedVac. The last traces of ammonium bicarbonate were removed by adding

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5 E. Vos, personal communication.

6 E. Vos, J. Broos, and B. Poolman, unpublished data.
10 µl of 1% trifluoroacetic acid and subsequent drying in the SpeedVac. The dried samples were dissolved in 5 µl of 50% acetonitrile, 0.1% trifluoroacetic acid and sonicated for 5 min. Aliquots of 0.75 µl were applied onto the MALDI target and allowed to air dry. Subsequently, 0.75 µl of 10 mg/ml α- cyano-4-hydroxysuccinimide in 50% acetonitrile, 0.1% (v/v) trifluoroacetic acid was applied to the dried samples, which was then allowed to dry again. MALDI mass spectra were recorded with a Micromass Tofspec E MALDI time-of-flight mass spectrometer operated in reflectron mode. Spectra were calibrated externally.

RESULTS

Generation and Characterization of SSCS, SSCS-S124C, IIChis-CL, and IIChis-S124C—Two His-tagged EII^mut mutants were constructed. SSCS is a single cysteine enzyme with only Cys^384 in the B domain. SSCS-S124C contains Cys^124 in the C domain in addition to Cys^384. The phenotype of E. coli LGS322 expressing these mutants was analyzed on MacConkey agar plates with 1% mannitol. Both strains formed purple-red colonies, indicating that the mutants transport and ferment mannitol. Inside-out (ISO) membrane vesicles from LGS322 cells expressing both mutants were solubilized with 0.25% dodecanitrile, 0.1% (v/v) trifluoroacetic acid and analyzed for mannitol binding and phosphorylation activities. The dissociation constants for mannitol were 25 and 45 mM and the turnover values for phosphorylation of mannitol of these mutants were 5200 and 4900 min^-1 for SSCS and SSCS-S124C, respectively. The turn over values for mannitol phosphorylation of purified SSCS and SSCS-S124C were 3200 and 2700 per min, respectively. These activities are similar to that of wild-type EII^mut (22, 29). ISO membrane vesicles bearing IIChis-CL or IIChis-S124C, solubilized with 0.25% dodecanitrile, and analyzed for mannitol binding, displayed dissociation constants for mannitol of 32 and 70 mM, respectively. These dissociation constants are similar to previously determined values of the wild-type C domain generated by tryptic digestion of the complete protein (22) or of the separately expressed IIC (8). In addition, IIChis-CL and IIChis-S124C could both complement the mannitol-binding defective EII^mut-G196D for phosphorylation activity in an in vitro assay, a result similar to that described for IIC (8). Overall, these kinetic data clearly indicate that SSCS and SSCS-S124C are fully functional enzymes and that both mutant C domains can bind mannitol and form functional heterodimers with EII^mut.

Disulfide Bridge Formation in ISO Vesicles and Purified Enzyme—Fig. 2A shows the results of CuPhe-induced oxidation of SSCS and SSCS-S124C in ISO membrane vesicles, visualized by immunoblotting with an antibody raised against the N-terminal His-tag. The untreated proteins migrated as a major band at ~60 kDa and are indicated as EII. The band at 36 kDa is a degradation product, whereas the one at 116 kDa (band 1) is most likely the dimer. This dimer has been observed previously upon extraction of the enzyme from the membrane (3) and is most likely not held together by a disulfide bond, since it is resistant to reduction with DTT. The amount of this band 1 is the same in all lanes. The oxidation by CuPhe of both mutants resulted in the appearance of a higher molecular weight band (band 2). The molecular mass was ~200 kDa but varied depending on the concentration of acrylamide that was used (not shown). The formation of this band was almost completely reversed by reduction of the sample with DTT, suggesting that it is stabilized by a disulfide bridge. The reduction with DTT is not complete in the particular sample in lane 5. However, in lane 11 of Fig. 2A, lane 1 of Fig. 2B, and in duplicate experiments complete reduction was observed. Both high molecular weight bands (1 and 2) have been observed previously and both were denoted as dimeric species (4, 5, 30). Also in this paper we refer to band 2 as a dimeric species, but we cannot fully exclude the possibility that it represents another oligomeric state as will be discussed below. Since Cys^384 is the only candidate for disulfide formation in SSCS, the enzyme is thus capable of forming a disulfide between the two Cys^384 residues. This is an important observation, because the dimer contacts are between the C domains (8).

Partial digestion of EIImtl with endoproteinase Glu-C generated a band at 33 kDa, which corresponds to the C domain without the A and B domains. Endoproteinase Glu-C instead of trypsin was used, because it did not cleave off the N-terminal His-tag within the 1-h incubation period. The cleavage pattern of digested SSCS was the same irrespective of whether the disulfide was formed or not. In addition, the cleavage pattern was unchanged upon reduction. This shows that the disulfide bridge resides in the domains that were degraded, which is consistent with the location of Cys^384 in the B domain. However, if the same oxidation and digestion procedure was followed with oxidized SSCS-S124C, a new band at 50 kDa appeared (Fig. 2A, indicated by the arrow), irrespective of whether the digestion was done in the presence or absence of the detergent dPEG. This band disappeared upon reduction of the sample with DTT. This excludes the possibility that the protein was only partially cleaved under the oxidizing conditions. Based on its size, this band is probably the result of a disulfide bridge between Cys^124 of both monomers, indicating that residue 124 is at the dimer interface. Very vaguely, some other products, which could include a disulfide bridge between Cys^384 and Cys^124 (see below) might be visible as well.

To further examine the nature of the Cys^124-Cys^384 disulfide bridge, the CuPhe-induced oxidation was repeated with purified SSCS-S124C. Fig. 2B shows the result of this experiment, visualized by immunoblotting. The same observations were made when the gel was silver-stained (not shown). The oxidation of purified SSCS-S124C also yields the reducible dimer band 2. Almost no band 1 was observed after purification, which probably indicates that the affinity between two monomers is decreased. Upon endoproteinase Glu-C digestion, the 50-kDa fragment was not observed. Instead, a His-tagged fragment of 42 kDa was visible in addition to the 33-kDa C domain band. This 42-kDa band disappeared upon reduction of the sample with DTT (compare lanes 3 and 4). Endoproteinase Glu-C digestion of the B domain will generate a 7.9-kDa fragment containing Cys^384. The size of the 42-kDa band thus suggests that a disulfide bond is formed between the 33-kDa C domain harboring Cys^124 and the 7.9-kDa B domain fragment with Cys^384. In conclusion, the data in Fig. 2, A and B, point to the formation of two different disulfides, one intersubunit Cys^124-Cys^384 and one interdomain Cys^124-Cys^384. Further evidence for both disulfides will be supplied in the following sections.

Requirements for B/C Domain Disulfide Bridge Formation—To elucidate the composition of the disulfide bridges, the CuPhe-induced oxidation was performed with purified SSCS-S124C and SSCS (Fig. 3). The two higher molecular weight bands (1 and 2) were observed again with both proteins (lanes 2 and 14). These bands were not present upon reduction with DTT and were much less intense or absent upon phosphorylation of the protein at His^554 and Cys^384, confirming that these bands, at least in SSCS, arise from a disulfide bridge between the two Cys^384 residues in the dimeric complex. Instead of endoproteinase Glu-C, trypsin was used to define the cross-links. Trypsin first cleaves in the linker between the C and B domain and, subsequently, digests the A and B domain completely but leaves the C domain intact except for the N-terminal His-tag (22, 31). The proteolytically generated C domain can be observed on SDS-PAGE at 30 kDa, which is somewhat smaller than the endoproteinase Glu-C-generated C domain.
This is consistent with the removal of the His-tag and a different cleavage site in the linker between the B and C domain. The tryptic B domain fragment with Cys384 has a calculated mass of 1.9 kDa. Tryptic digestion of CuPhe-oxidized SSCS-S124C also showed a 30-kDa band, which was significantly broadened upwards when the sample was not treated with DTT (compare lanes 6 and 7). This suggests that the broadened 30 kDa comprises the C domain plus the 1.9-kDa fragment of the B domain, analogous with the 42-kDa band in Fig. 2B. Consistent with this conclusion are the following observations: (i) the broadening is not observed with SSCS (Fig. 3; compare lanes 17 and 18); (ii) phosphorylation prior to oxidation prevented the occurrence of the broadening (compare lanes 6 and 8); and (iii) the broadening was not observed in wild-type EII\textsuperscript{mut} or in mutants of SSCS with cysteines at positions 158 or 199 (not shown). A tryptic-generated C domain of SSCS-S124C, not treated with CuPhe, also led to some broadening, which is probably due to spontaneous oxidation (compare lanes 5 and 6).

Another point to note is that the addition of 100 mM mannitol did not have an effect on the occurrence of the broadening (lane 9). Finally, dimeric C domain was not observed in the tryptic digest of oxidized SSCS-S124C. Taken together, the broadening must be the result of a disulfide bridge between Cys\textsuperscript{384} and Cys\textsuperscript{124}. To exclude the possibility that this disulfide bridge is an aspecific reaction between two accessible cysteines, another control experiment was performed (Fig. 3, lanes 11 and 12). With the sample in lane 11, oxidation was carried out after trypsin treatment, whereas in lane 12 it was carried out before trypsinolysis. Clearly, the broadening of the C domain band is no longer observed when the trypsin digestion preceded the oxidation. Thus, Cys\textsuperscript{124} is not capable of reacting with just any cysteine-
containing peptide, present at the same concentration.

**MALDI-TOF Mass Analysis**—To demonstrate that the fragment, which caused the broadening of the tryptic-generated C domain, originated from the B domain, the protein was excised from the SDS-polyacrylamide gel, reduced with β-mercaptoethanol to cleave the disulfide bond between the C domain and the B domain peptide, the peptides were extracted with organic solvents, and the extract was analyzed with MALDI-TOF MS. Fig. 4 shows the mass spectrum of the extracted peptides. The spectrum only contained 4 peaks, all of which could be assigned to tryptic B domain fragments that contain Cys384. The peak at \( m/z \) 1879.05 is the fully cleaved peptide with residues 380–399 (expected \( m/z \) 1878.92), and the peak at \( m/z \) 2007.05 represents the partially cleaved fragments of residues 379–399 and/or 380–400 (expected \( m/z \) 2007.02). This partial cleavage is due to the presence of the RK and RKK sequences at the N and C terminus of these peptides, respectively, that cannot be fully cleaved by trypsin. The peaks at \( m/z \) 1954.79 and 2083.05 represent the same peptides but with a β-mercaptoethanol adduct, which gives a mass increase of 76 Da. If the same procedure was applied to the C domain band that was reduced prior to SDS-PAGE and excised from the gel following the same procedure no peptides were observed.

**The B/C Disulfide Bridge Can Cross the Dimer Interface**—To this point, we have provided evidence for a B/C interdomain cross-link between Cys384 and Cys124 in purified SSCS-S124C, and a cross-link between the Cys 124 of both monomers in the enzyme in iso membrane vesicles. In addition, the data on SSCS provide unequivocal evidence for a disulfide across the dimer interface between the Cys384 residues on each B domain. To establish whether the disulfide between Cys384 in the B domain and Cys124 in the C domain could be formed within one monomer. For this purpose, heterodimers of SSCS-S124C and a cysteine-less IIChis (IIChis-CL) were formed. It is crucial for this experiment that all the SSCS-S124C monomers are forming a heterodimer with a IIChis-CL monomer, such that only the intrasubunit disulfide bridge is possible. Therefore, an ~15-fold excess IIChis-CL was added and the het-
erodimer formation was facilitated by the addition of 170 mM Na$_3$PO$_4$, pH 7.6, which lowered the cloud point of the solution (see “Experimental Procedures”). Na$_3$PO$_4$ alone did not have an influence on the cross-linking behavior of SSCS-S124C (not shown). As can be seen in Fig. 5B, homodimers were no longer present upon oxidation with CuPhe, which is indicative of complete heterodimer formation (compare Fig. 2B, lane 2, and Fig. 5B, lane 2). Endoproteinase Glu-C digestion of the oxidized sample generated the 33-kDa C domain and the additional 42-kDa band (arrow in lane 4 of Fig. 5B); the latter is absent upon reduction of the sample with DTT. This experiment, therefore, proves that the B/C disulfide bridge can also be formed within one subunit.

Residue 124 Is Located Near the Dimer Interface—The CuPhe-induced cross-linking of SSCS-S124C in ISO membrane vesicles corresponds most likely to a disulfide bridge between Cys$^{124}$ of both monomers. The CuPhe-induced oxidation was repeated with purified IIChis-S124C (Fig. 6). IIChis-S124C migrates as a monomer with an apparent molecular mass of 28 kDa in the presence of DTT. Upon oxidation, a dimeric IIChis-S124C with an apparent molecular mass of 50 kDa was observed. To confirm the close proximity of both Cys$^{124}$ residues in one dimer, reduced IIChis-S124C was subjected to cross-linking with dimaleimides of different lengths, ranging from 7.7 to 15.1 Å. Fig. 6 shows that all three dimaleimides also yielded the formation of the 50-kDa dimer. These data indicate that the residue at position 124 is located at the dimer interface in purified IIChis-S124C.

**DISCUSSION**

In this article we describe the generation of several disulfide bridges, indicative for close proximity, between two cysteines in the dimeric EII$^{mtl}$. In the enzyme in ISO membrane vesicles, intersubunit disulfide bridges between both Cys$^{384}$ residues and between both Cys$^{124}$ residues are formed. Upon purification in the detergent dPEG, the intersubunit disulfide between both Cys$^{384}$ residues is still formed. In addition, an interdo-

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**Fig. 5.** Heterodimer experiments to determine whether the Cys$^{384}$-Cys$^{124}$ disulfide can be formed intra- and intermolecularly. A, immunoblot of CuPhe-induced oxidation of homo- and heterodimers of purified SSCS (3 μM) and IIChis-S124C (1 μM). After CuPhe-induced oxidation, the samples were split and either reduced with 10 mM DTT or left untreated. Due to a poor blotting efficiency of the C domain alone, the apparent concentrations on the PVDF of EII$^{mtl}$ and the C domain differ. B, immunoblot of CuPhe-induced oxidation of heterodimers formed between purified SSCS-S124C (0.2 μM) and IIChis-CL (3 μM) in the presence of 170 mM Na$_3$PO$_4$, pH 7.6. After CuPhe-induced oxidation, the samples were reduced with DTT (lane 1), left untreated (lane 2), endoproteinase Glu-C digested and, subsequently, reduced with DTT (lane 3), or endoproteinase Glu-C digested (lane 4). The arrow indicates the 42-kDa band. Approximately 0.15 μg (A) and 0.075 μg (B) of EII$^{mtl}$ was loaded per lane.

**Fig. 6.** Immunoblot of cross-linking experiments with purified IIChis-S124C. IIChis-S124C (1 μM) was reduced and subjected to cross-linking by oxidation with CuPhe (lanes 1 and 2) or with α-PDM, p-PDM, and BMH, which can span 7.7, 12.0, and 15.1 Å, respectively. Lane 1 represents the sample in which DTT after CuPhe oxidation. Approximately 0.1 μg of IIChis-S124C was loaded per lane.

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main cross-link between Cys$^{384}$ and Cys$^{124}$ is observed, which either can be formed as an intrasubunit or an intersubunit disulfide. The intersubunit disulfide between both Cys$^{124}$ residues is not formed in purified EII, but it is formed in purified C domain harboring Cys$^{124}$. It is important to stress that both the detergent-solubilized EII and IIC retain full binding capacity, and the soluble EII retains full mannitol phosphorylation activity. The observations made with the detergent-solubilized enzymes thus reveal structural information of functionally relevant conformations of the protein.

To form a disulfide bond, the C$_S$ atoms of the cysteines have to come within 3.8–4.5 Å of each other (32). The two Cys$^{384}$ and two Cys$^{124}$ residues are thus in very close proximity both at the
B/C domain interface and the dimer interface of EIImtl. The multiplicity of possible disulphides is easy to understand in the light of the interdomain dynamics that are essential for the entire phosphorylation and transport cycle. The architecture and functioning of EIImtl necessitates an interdomain flexibility in which the B domain interacts with various domains at different stages in the catalytic cycle. (i) The active sites of the A and B domains, each of which are proteins of ~15 kDa, must approach one another to transfer the phosphoryl group from His554 on the A domain to Cys384 on the B domain, then (ii) this same region of the B domain, containing a phosphorylated Cys384, must interact with the C domain to effect the conformational energy coupling which enables the translocation and subsequent phosphorylation of mannitol. (iii) The phosphoryl group can cross the dimer interface from the A domain of one monomer to the B domain of the other monomer (illustrated in Fig. 1) (33, 34) or from the B domain of one monomer to the mannitol bound by the C domain of another monomer (25, 35). It is, therefore, logical that the active site Cys384 in the B domain is in close proximity with different regions of the enzyme at different steps in the catalytic cycle and that, during the cross-linking process, these various domain interactions transiently occur and lead to the cross-links observed. Upon purification in detergent, a different pattern of the disulphide bridges is observed, which is additional evidence for this dynamic situation.

The observation of different higher aggregated forms of EIImtl, all denoted as dimeric forms, is not new. Band 1 was observed upon extraction of the enzyme from the membrane, whereas band 2 appeared upon cross-linking via disulphides, dimaleimides, or lysine-specific cross-linkers (3–5, 30). Band 1 is insensitive to reduction suggesting that it is stabilized by noncovalent interactions rather than disulphides. In this regard, it is noteworthy that most observations of band 1 stem from measurements on protein extracted from the membrane but it is likely that its aggregation state is stabilized by lipids complexed to the protein. Band 2’s position and, thus, its estimated mass varies with the degree of cross-linking in the polyacrylamide gel, but it is close to that of a tetramer. In a single-cysteine EIImtl, the tetramer can be generated when a single disulphide bond cross-links two dimers whose subunits are held together by native-like interactions, as in the case of band 1. The tetramer could also arise from two disulphide-bonded dimers that come together to form a tetramer. The band in between 1 and 2 (lane 3, Fig. 2A) could represent the loss of a monomer from a tetramer, which is only possible in the interdimer cross-linked tetramer. A possible tetrameric state of the enzyme, however, does not lead to other conclusions for the close proximity of the cysteines at positions 384 and 124. In the future we will examine the possible tetrameric nature of EIImtl in more detail with analytical ultracentrifugation as has been done for the lactose carrier of Streptococcus thermophilus (36).

As summarized in the Introduction, there is a lot of kinetic and thermodynamic evidence for conformational coupling at the B/C domain interface. However, there was no direct structural information about the location of this interface. Here, we present for the first time the location of at least part of the B/C domain interface, which is formed by the first cytoplasmic loop in the C domain and the region around the active-site cysteine in the B domain. The first evidence for the importance of this loop in the interaction with the B domain came from time-resolved fluorescence spectroscopy studies on a series of single-tryptophan containing mutants (13). Notably, a change in the time-resolved anisotropy of tryptophan 109 was observed upon phosphorylation of the B domain. The location around residue 124 is in a region which is conserved among mannitol-specific EIIs of different origin (37). Close proximity of this region of the C domain and the B domain active site was already suggested by photocross-linking experiments. Recent kinetic data on a series of phenylalanine to tryptophan replacements in this first cytoplasmic loop suggest that residues 126 and 133 are critical for the phosphorylation of mannitol but not for mannitol binding. The data suggest that these residues are located at or near the dimer interface and involved in the B/C domain interaction, which is consistent with the data presented here.

The location of the interface in the first cytoplasmic loop is very interesting, because all previously described mutations that have an influence on the functioning of EIImtl are located in the predicted second cytoplasmic loop. This is also the location of the GIXE motif (residues 254–257), which is highly conserved in all EIIs and speculated to be involved in substrate binding (38). Replacement of Glu257 in this motif led to enzymes with no or only low affinity mannitol binding, depending on the substituent, as well as defective transport (39). Another region in the same loop is also important for activity. For instance, replacement of Gly1396 or His1395 led to enzymes, which exhibited no or low affinity binding for mannitol (25, 34, 40). Interestingly, a heterodimer of the inactive mutants E257A and H195A was significantly active in transport and phosphorylation of mannitol, suggesting that these residues are in close proximity (35). Also data on the glucose transporter of E. coli point to a role for the second cytoplasmic loop in substrate binding (41).

In conclusion, the data presented here suggests that residues 124 and 384 of both subunits can come within 5 Å of each other and are located at the B/C domain and dimer interface. An intriguing question is what happens at the B/C domain interface upon phosphorylation. Phosphorescence data of single tryptophan mutants in the C domain show that a conformational change takes place upon phosphorylation of Cys384, different from that upon mannitol binding (14). With the current pairs of cysteines, however, it is not possible to figure out what is happening precisely, because phosphorylation prevents Cys384 from forming a disulphide. In the future, we will screen several cysteine mutants in these regions of the protein to determine the exact borders of the B/C domain and dimer interface and changes therein upon mannitol binding and/or B domain phosphorylation. Eventually this will lead to a more detailed understanding of the energy coupling mechanism at the B/C domain interface in EIImtl.

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