Gln-222 in Transmembrane Domain 4 and Gln-526 in Transmembrane Domain 9 Are Critical for Substrate Recognition in the Yeast High Affinity Glutathione Transporter, Hgt1p*

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Jaspreet Kaur1 and Anand K. Bachhawat2

From the Institute of Microbial Technology, Sector 39-A, Chandigarh 160 036, India

Hgt1p, a member of the oligopeptide transporter family, is a high affinity glutathione transporter from the yeast Saccharomyces cerevisiae. We have explored the role of polar or charged residues in the putative transmembrane domains of Hgt1p to obtain insights into the structural features of Hgt1p that govern its substrate specificity. A total of 22 charged and polar residues in the predicted transmembrane domains and other conserved regions were subjected to alanine mutagenesis. Functional characterization of these 22 mutants identified 11 mutants which exhibited significant loss in functional activity. All 11 mutants except T114A had protein expression levels comparable with wild type, and all except E744A were proficient in trafficking to the cell surface. Kinetic analyses revealed differential contributions toward the functional activity of Hgt1p by these residues and identified Asn-124 in transmembrane domain 1 (TMD1), Gln-222 in TMD4, Gln-526 in TMD9, and Glu-544, Arg-554, and Lys-562 in the intracellular loop region 537–568 containing the highly conserved proline-rich motif to be essential for the transport activity of the protein. Furthermore, mutants Q222A and Q526A exhibited a nearly 4- and 8-fold increase in the Km for glutathione. Interestingly, although Gln-222 is widely conserved among other functionally characterized oligopeptide transporter family members including those having a different substrate specificity, Gln-526 is present only in Hgt1p and Pgt1, the only two known high affinity glutathione transporters. These results provide the first insights into the substrate recognition residues of a high affinity glutathione transporter and on residues/helices involved in substrate translocation in the structurally uncharacterized oligopeptide transporter family.

Hgt1p or ScOpt1p, a polytopic membrane protein, from the yeast Saccharomyces cerevisiae, was the first high affinity glutathione transporter to be identified in any system (1). Hgt1p belongs to a relatively novel family of transporters, the oligopeptide transporter (OPT)3 family, that contains a large number of fungal, plant, and prokaryotic members (2). The functional characterizations of a few of the fungal and plants members have demonstrated their ability to transport oligopeptides, glutathione, and metal-secondary amino acid conjugates by harnessing the proton gradient across the plasma membrane (3–7). Furthermore, these studies have also highlighted the physiological significance of this family in assimilation/mobilization of oligopeptides as nutrients in fungi and plants and in maintenance of metal homeostasis in plants. However, the majority of the members are yet uncharacterized and need to be defined with respect to their substrate specificity and physiological role.

A complete lack of information on the structural features of the OPT family further limits our understanding of this large, uncharacterized family. Identification of residues or motifs critical for substrate recognition among the functionally characterized members would enable functional characterization of the new members within the family. This has prompted us to initiate a systematic study on the structure-function characterization of Hgt1p as a representative of the OPT family. Not only is Hgt1p the best characterized member of the OPT family in terms of its substrate specificity, being also able to transport some oligopeptides albeit with low affinity (1, 7, 8), its native host S. cerevisiae is a well established model system and easily amendable for mutagenesis-based structure-function studies. We have recently investigated the role of the 12 native cysteine residues in the structural stability and the transporter activity of the protein where 2 of the cysteines were found to be essential for functionality (9). However, no hints on the important motifs or conserved amino acids of Hgt1p (or any other member of the OPT family) that could be involved in substrate recognition have been obtained so far. In the current study we have focused on the polar and charged residues in the transmembrane domains of Hgt1p to explore their role in substrate recognition.

Glutathione, the substrate for Hgt1p, is a hydrophilic substrate. Prior studies on structural characterization of transporters of the other hydrophilic substrates using biochemical and genetic strategies, such as site-directed mutagenesis and random mutagenesis, have established the role of polar and

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† The on-line version of this article (available at http://www.jbc.org) contains supplemental Table 1 and Fig. 1.

1 Recipient of a research fellowship from the Council of Scientific and Industrial Research, Government of India.

2 To whom correspondence should be addressed. Tel: 91-172-2636681; Fax: 91-172-2690585 or 91-172-2690632; E-mail: anand@imtech.res.in.

3 The abbreviations used are: OPT, oligopeptide transporter; HA, hemagglutinin; PT, peptide transport; TMD, transmembrane domain; MRP, multidrug-associated resistance protein.
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charged residues in the transmembrane domains of transporters in recognition, binding, and translocation of substrates (10–18). The availability of the crystal structures of a few transporter proteins has further enabled direct visualization of such interactions between the key residues in the transmembrane domains and the substrate molecule (19–22). In light of these studies we anticipated that few of the charged or polar residues in the predicted transmembrane domains of Hgt1p would be involved in substrate recognition and translocation across the membrane. Hence, a total of 22 polar or charged amino acids spanning the predicted transmembrane domains of Hgt1p were subjected to alanine scanning and functionally characterized. Detailed biochemical characterizations of these mutants revealed that Asn-124, Gln-222, Gln-526, Glu-544, Arg-554, and Lys-562 are key residues for the transport activity of Hgt1p. As replacement of Gln-222 in TMD4 and Gln-526 in TMD9 with alanine resulted in a significant decrease in the affinity of the transporter for glutathione, it suggested that the two residues might directly participate in glutathione recognition as a substrate. These observations provide the first insights into substrate binding residues in Hgt1p, a member of a novel and important transporter family (OPT family).

EXPERIMENTAL PROCEDURES

Chemicals and Reagents—All the chemicals used in this study were obtained from commercial sources and were of analytical grade. Media components, fine chemicals, and reagents were purchased from Sigma Aldrich, HiMedia (Mumbai, India), Merck, USB Corp., or Difco. Oligonucleotides were purchased from Sigma Aldrich, HiMedia (Mumbai, India), Merck, USB Corp., or Difco. Oligonucleotides were purchased from Sigma Aldrich, HiMedia (Mumbai, India), Merck, USB Corp., or Difco. Oligonucleotides were purchased from Sigma Aldrich, HiMedia (Mumbai, India), Merck, USB Corp., or Difco. Oligonucleotides were purchased from Sigma Aldrich, HiMedia (Mumbai, India), Merck, USB Corp., or Difco.

Site-directed Mutagenesis and Plasmid Construction—The double-tagged HGT1, tagged with hexahistidine epitope at the N terminus and HA tag at the C terminus (9), was subcloned downstream of the TEF promoter at BamHI and EcoRI site of a modified p416TEF vector (p416M1-TEF) in which all the restrictions sites flanking the BamHI and EcoRI restriction sites have been removed by blunting and re-ligation.

The resulting plasmid pTEFM1-His-HGT1-HA was used as a template to introduce two silent mutations to generate the restriction sites—Mscl (1366) and XbaI (1584) in the wild-type HGT1 gene using the QuikChange® site-directed mutagenesis kit with respective mutagenic oligonucleotides pairs given in supplemental Table 1. This modification generated a recombinant HGT1 gene that was unaltered in the encoded protein product but had additional restriction sites to facilitate cloning and screening of mutant DNA (Fig. 1). This modified gene product was used as a template for site-directed mutagenesis for creation of different site-directed mutants of Hgt1p using either the QuikChange® site-directed mutagenesis kit or the splice overlap extension strategy. The different mutagenic oligonucleotides pairs used for generation of these mutants are given in supplemental Table 1.

For using the QuikChange® site-directed mutagenesis kit to generate the mutants, the double-tagged HGT1 (N-His-HGT1-HA) was subcloned into pBSK vector and used as a template together with different mutant primer pairs (supplemental Table 1) in mutagenic PCR set up as per the manufacturer’s instructions. The resulting mutants were sequenced to confirm the presence of the desired nucleotides changes and rule out any undesired mutations introduced during the mutagenic procedure. The fragments containing the mutations were subcloned back into the TEF vector background (pTEFM1-His-HGT1m-HA) using the appropriate restriction sites for subsequent analyses. While using the splice overlap extension strategy, the mutations were directly generated in the TEF vector background, and the resulting mutations were confirmed by sequencing the appropriate regions.

The Plate “Dual Complementation-cum-toxicity” Assay—The development of the assay and procedure has been described previously (9). Briefly, the yeast strain met15∆glt1Δ (ABC 817) was transformed with a single copy, centromere vector expressing wild type, or different HGT1 mutants expressed downstream of the TEF promoter. Transformants were grown in minimal media containing methionine and other supplements without uracil overnight. These cultures were reinoculated in the same media and allowed to grow till they reached exponential phase. Equal numbers of cells were harvested, washed with water, and resuspended in sterile water to an A600 of 0.2. These were serially diluted 1:10, 1:100, and 1:1000. 10 μl of these cell resuspensions were spotted on minimal medium containing different concentrations of glutathione (15, 30, 50, 100, 150, 200 μM) or methionine (200 μM) as the sole organic sulfur source. The plates were incubated at 30 °C for 2–3 days, and photographs were taken. Only the data obtained with 15, 50, and 200 μM GSH have been shown.

Strains, Media, and Growth Conditions—The Escherichia coli strain DH5α was used as a cloning host. The S. cerevisiae strain (ABC 817) bearing an HGT1 disruption in BY4741 background (MATa his3Δ1 leu2Δ0 met15Δ1 ura3Δ0 ght1Δ::LEU2) is deficient in glutathione uptake ability and was used in the experimental studies (1). The yeast strain was regularly maintained on yeast extract, peptone, and dextrose medium and grown at 28–30 °C. The yeast transformants were selected and maintained on synthetic defined minimal medium containing yeast nitrogen base, ammonium sulfate dextrose supplemented with adenine, histidine, leucine, lysine, methionine, tryptophan, and uracil at 50 mg/liter as per requirement. Growth, handling of bacteria and yeast, and all the molecular techniques used in the study were according to standard protocols (23, 24).

The availability of the crystal structures of a few transporter proteins has further enabled direct visualization of such interactions between the key residues in the transmembrane domains and the substrate molecule (19–22). In light of these studies we anticipated that few of the charged or polar residues in the predicted transmembrane domains of Hgt1p would be involved in substrate recognition and translocation across the membrane. Hence, a total of 22 polar or charged amino acids spanning the predicted transmembrane domains of Hgt1p were subjected to alanine scanning and functionally characterized. Detailed biochemical characterizations of these mutants revealed that Asn-124, Gln-222, Gln-526, Glu-544, Arg-554, and Lys-562 are key residues for the transport activity of Hgt1p. As replacement of Gln-222 in TMD4 and Gln-526 in TMD9 with alanine resulted in a significant decrease in the affinity of the transporter for glutathione, it suggested that the two residues might directly participate in glutathione recognition as a substrate. These observations provide the first insights into substrate binding residues in Hgt1p, a member of a novel and important transporter family (OPT family).
Transport experiments were carried out with [35S]GSH as ice in a MES-buffered medium until the transport was initiated. Cells were harvested and washed and put on supplemented in the same media and allowed to grow till they reached exponential phase. Cells were harvested and washed and put on supplemented without uracil overnight. These cultures were reinoculated in minimal media containing methionine and other supplements. The resulting signal intensity was normalized with reference to the band surface area (in square pixels) and expressed in arbitrary units. The relative protein expression levels in the mutant Hgt1p were represented as percentage expression relative to wild-type Hgt1p.

**Cellular Localization of the Mutants by Confocal Microscopy**—To localize Hgt1p and its different alanine mutants, indirect immunofluorescence was performed using a published protocol (26). Images were obtained with an inverted LSM510 META laser scanning confocal microscope (Carl Zeiss) fitted with a Plan-Apochromat ×100 (numerical aperture, 1.4) oil immersion objective. The 488-nm line of an argon ion laser was directed over an HFT UV/488 beam splitter, and fluorescence was detected using an NFT 490 beam splitter in combination with a BP 505–530 band pass filter. Images obtained were processed using Adobe Photoshop Version 5.5.

**Sequence Analysis**—The HGT1 open reading frame and Hgt1p sequences were retrieved from the Saccharomyces genome data base. The multiple sequence alignment of the protein sequences was generated using ClustalX program using default parameters (27). For the prediction of transmembrane domains in Hgt1p, five different transmembrane prediction software programs were used: HMMTOP (28), TMHMM (29), MEMSAT (30), PHDHTM (31), and TopPRED II (32). The Hgt1p amino acid sequence was submitted as a query sequence, and predictions were made in default settings.

**RESULTS**

**Selection of Amino Acid Residues in TMDs of Hgt1p for Alanine Scanning**—A reasonably reliable topology model is a prerequisite for probing the role of amino acids in the transmembrane domains of Hgt1p. Previously, Becker and co-workers (33) predicted a topology model of Hgt1p with 12 transmembrane domains and extracellular N and C termini using topology prediction software in combination with multiple sequence alignment of the functionally characterized members of the OPT family (Fig. 1). Although the software predicted 14 transmembrane domains, the authors had omitted two of the predicted domains corresponding to the regions 537–568 and 707–724 citing the presence of conserved proline-rich motifs EXIGYX2PG(R/K)PXX4KX3G and PPXN(T/P), respectively, in these regions. These motifs consist of proline residues in proximity to each other or a glycine residue, which theoretically disfavors a helix formation and, hence, were predicted to
form loops in the predicted topology model (33). We have carried out an independent topology prediction analysis using also additional membrane protein topology prediction software reported in the literature. Our analysis leads us to concur with the Becker topology model of Hgt1p with the 12 transmembrane domains (data not shown). Hence, the predicted topology model has been used as a platform for the structure-functional analysis of Hgt1p. However, in the absence of any firm experimental evidence for excluding the two likely transmembrane domains spanning the regions 537–568 and 707–724 in Hgt1p, we have included these regions for our mutational study, while staying with the Wiles et al. (33) topology model of Hgt1p.

In the absence of any previous hints on the important motifs or conserved amino acids in the transmembrane domains of Hgt1p (or any other member of the OPT family) that could be involved in substrate recognition, we adopted a comprehensive approach to identify the important residues or domains in Hgt1p that may play a specific role in substrate translocation. Glutathione, the substrate for Hgt1p, is a hydrophilic substrate, and prior studies on structural characterization of transporters of the other hydrophilic substrates have established that transmembrane domains lining the channels are rich in charged and polar residues. An examination of the 12 predicted transmembrane domains of Hgt1p revealed that each of these domains had at least one charged/polar residue in it, resulting in a total of 49 residues (Table 1). As the charged and polar residues that form a part of the permeability channel show a characteristic distribution where they often tend to cluster on one face of the helix (amphiphilic arrangement), helix wheel projections were drawn for each of the 12 transmembrane domains (supplemental Fig. 1). These helix wheel projections were analyzed for the presence and distribution of the charged and polar residues in these domains (supplemental Fig 1 and Table 1). Two of the 12 transmembrane domains (TMD 5 and TMD11) contained only a single polar residue, and hence, were not included in this study. TMD8 contains three polar residues, Gln-489, Cys-501, and Cys-502. However, the two cysteine residues in TMD8 are not crucial for the functional activity of Hgt1p (9), and hence, the TMD8 was also not included in our mutational analysis of Hgt1p. Of the remaining 9 transmembrane domains, TMDs 1, 2, 4, 6, 7, 9, 10, and 12 have a clear distinction between the polar and nonpolar phase, and TMD3 is very rich in polar residues, which are scattered all around the helix. Hence, from these nine transmembrane domains, all the five charged residues in the predicted transmembrane domains (Glu-135, Arg-150, His-445, Glu-612, and Glu-744) were selected for mutational analysis in this study. With the remaining polar residues in the transmembrane domains, the following two criteria were used to select the residues; (a) restriction was made with respect to number of residues, selecting one or at the most, two residues from each transmembrane domain so as to cover all the remaining nine transmembrane domains in Hgt1p, and (b) when picking more than one polar residue in a transmembrane domain, residues present in different faces of the helices were selected.

In addition, three of the highly conserved charged residues, Glu-544, Arg-554, and Lys-562, were selected from the region spanning 537–568, and two polar residues (Asn-710 and Asn-722) were selected from the region spanning 707–724. Thus a total of 22 residues were selected from TMD 5, 7, 9, 10, and 11 for mutational analysis. From the TMD 12, 2, 4, 6, 7, 9, and 10, the charged residues Glu-135, Arg-150, His-445, Glu-612, and Glu-744 were selected. In addition, 49 residues (Table 1). As the charged and polar residues that form a part of the permeability channel show a characteristic distribution where they often tend to cluster on one face of the helix (amphiphilic arrangement), helix wheel projections were drawn for each of the 12 transmembrane domains (supplemental Fig. 1). These helix wheel projections were analyzed for the presence and distribution of the charged and polar residues in these domains (supplemental Fig 1 and Table 1). Two of the 12 transmembrane domains (TMD 5 and TMD11) contained only a single polar residue, and hence, were not included in this study. TMD8 contains three polar residues, Gln-489, Cys-501, and Cys-502. However, the two cysteine residues in TMD8 are not crucial for the functional activity of Hgt1p (9), and hence, the TMD8 was also not included in our mutational analysis of Hgt1p. Of the remaining 9 transmembrane domains, TMDs 1, 2, 4, 6, 7, 9, 10, and 12 have a clear distinction between the polar and nonpolar phase, and TMD3 is very rich in polar residues, which are scattered all around the helix. Hence, from these nine transmembrane domains, all the five charged residues in the predicted transmembrane domains (Glu-135, Arg-150, His-445, Glu-612, and Glu-744) were selected for mutational analysis in this study. With the remaining polar residues in the transmembrane domains, the following two criteria were used to select the residues; (a) restriction was made with respect to number of residues, selecting one or at the most, two residues from each transmembrane domain so as to cover all the remaining nine transmembrane domains in Hgt1p, and (b) when picking more than one polar residue in a transmembrane domain, residues present in different faces of the helices were selected.

In addition, three of the highly conserved charged residues, Glu-544, Arg-554, and Lys-562, were selected from the region spanning 537–568, and two polar residues (Asn-710 and Asn-722) were selected from the region spanning 707–724. Thus a total of 22 amino acids representative of 9 transmembrane domains of Hgt1p and 2 intracellular loops were mutagenized to the alanine residue and evaluated for the functional activity (Fig. 1 and Table 1).

**Functional Evaluation of the Alanine Mutants of Hgt1p**—A preliminary characterization of the alanine mutants of Hgt1p was done using a plate-based dual complementation–cum-toxicity assay, previously designed for the rapid evaluation of the functional activity of the mutants of the transporter (9). Briefly, the assay is based upon the dual behavior of Hgt1p, expressed from TEF promoter in a met15Δ strain, an organic sulfur auxotroph defective in glutathione uptake. While at low glutathione concentrations (15 μM or lower), HGT1I expressed under the TEF promoter complements the growth defect in a met15Δ strain very well (1), the same construct results in toxicity when cells are grown in medium containing 30 μM or higher glutathione concentrations (34). Thus, the assay is used to evaluate the functional activity of Hgt1p with respect to two parameters. (a) ability to complement the GSH transport defect of the strain met15Δ in low concentrations of GSH and (b) the ability to cause toxicity in media containing higher concentrations of GSH.

The plasmids bearing wild-type Hgt1p or with the mutated residue in Hgt1p were individually transformed into the met15Δ strain (ABC 817) and checked for growth by dilution spotting on minimal media containing a range of glutathione concentrations as the sole source of organic sulfur (Fig. 2). Functional evaluation of the mutations in Hgt1p using the plate assay identified four subgroups, (a) severe effect (complemen-
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FIGURE 2. Functional characterization of alanine mutants of the polar/charged residues in the putative transmembrane domains of Hgt1p. The met15Δhgt1Δ strain (ABC 817) was transformed with wild-type (WT) Hgt1p and the different alanine mutants of Hgt1p expressed under the TEF promoter along with control vector (p416M1-TEF) and used for plate-based dual complementation-cum-toxicity assay by dilution spotting on minimal media containing different concentration of glutathione as described under “Experimental Procedures.” The functional analysis of the alanine mutants of polar residues is shown in A and B and, for the charged residues, in C.

Reduction in Protein Levels
—The decreased activity of the alanine mutants of Hgt1p, and these residues were located in TMD4 (Gln-222), TMD9 (Gln-526), the intracellular loop between TMD9 and TMD10 (Glu-544, Arg-554, Lys-562) and TMD12 (Glu-744). In contrast, five of the residues located in TMD1 (Thr-114, Asn-124), TMD2 (Asn-137), TMD6 (Asn-357), and TMD7 (His-445) led to a moderate effect on the functional efficiency of Hgt1p upon being mutated to alanine. To define the role of these residues in the function of Hgt1p, we undertook a detailed biochemical characterization of these 11 mutants.

Among the 22 amino acids initially selected, we were able to identify 11 residues in the different transmembrane domains of Hgt1p, which when replaced by a relatively inert residue (alanine) resulted in a significant decline in glutathione uptake activity for all the mutants that fell into the last group.

To corroborate these spotting assays with actual transport data, we measured the initial rate of [35S]glutathione uptake in the met15Δhgt1Δ strain (ABC 817) transformed with the alanine mutants of Hgt1p (Table 2). Interestingly, the quantitative information generated from the biochemical assay also defined four groups of activity which correlated closely with the plate assay; (a) those with severe effect showed <20% that of the activity compared with the wild-type protein, (b) those with moderate effect fell into roughly 20–30% activity bracket, (c) those with mild effect retained nearly 50% activity, and (d) those with very mild to no effect showed >75% activity. The only exception in this grouping was the N124A mutant, which despite showing complementation ability comparable with wild-type Hgt1p, exhibited only 16% transport activity; nonetheless, it was placed in Group II based upon its behavior in the plate based dual-complementation assay. Furthermore, as the plate assay generated a reliable picture of the activity of the different mutants, we did not determine the [35S]glutathione uptake activity for all the mutants that fell into the last group.
transformed with the plasmids bearing the alanine mutants of Hgt1p were loaded onto the SDS-PAGE gels, electrobotted to the membrane, and probed with anti-HA monoclonal antibody. As shown in Fig. 3, an 85-kDa band corresponding to the wild-type Hgt1p was visualized for all the mutants, although the mutants showed variation in the expression levels. Densitometry analysis of unsaturated band signals revealed that in particular T114A mutant showed a drastic fall in protein expression levels, suggesting that the residue might be crucial for protein folding and stability (Fig. 3). However, for the other mutants, the protein expression levels did not appear to be significantly altered. The protein expression levels ranged between 50 and 90% relative to the wild-type protein levels, indicating that these mutants did not significantly perturb the protein structure and stability, and the significant loss in glutathione uptake ability of these mutants was not a consequence of decreased protein stability and protein expression levels.

Analysis of Cell Surface Trafficking of Mutants with Loss in Functional Activity Reveals E744A Is Defective in Trafficking—Hgt1p is a plasma membrane-localized transporter, and localization studies with Hgt1p expressed from its native promoter as well as from the constitutive TEF promoter has revealed exclusive plasma membrane localization for the transporter.

As any mutation that affects trafficking could also explain the loss in functional activity, we examined all 11 mutants expressed from the met15Δhgt1Δ strain (ABC 817) transformed with plasmids bearing the different alanine mutants of Hgt1p were prepared, and ~20 μg of total protein was resolved using 9% SDS-PAGE, electrobotted to a nitrocellulose membrane. The blot was probed with mouse anti-HA (Cell Signaling) at 1:1000 dilution as primary antibody and goat anti-mouse IgG horseradish peroxidase-conjugated antibody (Cell Signaling, at 1:2500 dilution) as secondary antibody. The signal was detected using ECL kit (Amersham Biosciences). Molecular weight markers (SM0431, MBI Fermentas) were used to estimate the protein molecular weight. The total protein was quantified by densitometry analysis of protein bands. The data are expressed as percentage protein expression normalized to the wild-type (WT) expression level and are the mean of the protein expression levels obtained in three independent experiments. A representative blot is shown in the inset. Equal loading of the proteins (20 μg) in each well of the gel was visually monitored by Coomassie staining of a duplicate gel and Ponceau S staining of the membrane after transfer (data not shown).

### TABLE 2

<table>
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<tr>
<th>Mutant (TMD)</th>
<th>Complementation (15 μM GSH)</th>
<th>Toxicity (&gt;50 μM GSH)</th>
<th>Transport activity (mean ± S.E.)</th>
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<tr>
<td>WT-Hgt1p</td>
<td>+</td>
<td>+</td>
<td>100.0 ± 1.6</td>
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<td>Severe effect-Group I</td>
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<td>Q222A (TMD 4)</td>
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<td>–</td>
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<td>–</td>
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</table>

FIGURE 3. Quantification of the total protein expression levels of alanine mutants of Hgt1p showing severe effect on activity (Group I mutants) (A) and moderate effect on activity (Group II) (B). The crude extracts prepared from the met15Δhgt1Δ strain (ABC 817) transformed with plasmids bearing the different alanine mutants of Hgt1p were prepared, and ~20 μg of total protein was resolved using 9% SDS-PAGE, electrobotted to a nitrocellulose membrane. The blot was probed with mouse anti-HA (Cell Signaling) at 1:1000 dilution as primary antibody and goat anti-mouse IgG horseradish peroxidase-conjugated antibody (Cell Signaling, at 1:2500 dilution) as secondary antibody. The signal was detected using ECL kit (Amersham Biosciences). Molecular weight markers (SM0431, MBI Fermentas) were used to estimate the protein molecular weight. The total protein was quantified by densitometry analysis of protein bands. The data are expressed as percentage protein expression normalized to the wild-type (WT) expression level and are the mean of the protein expression levels obtained in three independent experiments. A representative blot is shown in the inset. Equal loading of the proteins (20 μg) in each well of the gel was visually monitored by Coomassie staining of a duplicate gel and Ponceau S staining of the membrane after transfer (data not shown).
cells, suggesting a partial defect in trafficking of the mutant. However, very poor cell surface signal was detected for T114A and E744A mutant. The staining pattern for E744A suggested that the protein was trapped in the endoplasmic reticulum. These findings suggest that replacement of Glu-744 residues with alanine interfered with the trafficking of the protein to the cell surface, and this may be the principal reason for the observed loss in functional activity of the mutant.

In the case of T114A a diffused and relatively weak cytosolic signal was observed, which probably reflects the decreased protein expression levels observed earlier for this mutant in the Western blot. These findings further confirm that loss in activity of the T114A mutant is mainly a consequence of decreased protein expression levels.

Kinetic Analysis of the Mutants Reveals a Critical Role of Asn-124 (TMD1), Gln-222 (TMD4), and Gln-526 (TMD9) in Glutathione Transport by Hgt1p—The analysis of total protein expression levels and cell surface localization of the mutants in Group I and Group II revealed that with the exception of T114A and E744A, the remaining mutations did not bear a significant effect on the protein expression or its cell surface localization. This suggests that loss in functional activity of these mutants might be because of some specific defect related to the ability of the mutants to transport glutathione. Hence, to characterize these residues for their role in substrate binding or translocation, we undertook the measurement of kinetic parameters of the mutants by measuring the initial rates of glutathione uptake over a range of glutathione concentrations. As K562A and E744A had very poor activity, these could not be included for the kinetic study. The apparent $K_m$ and $V_{max}$ values and the $K_m/V_{max}$ ratios (transport efficiencies) obtained for the rest of the mutants are summarized in Table 3. The $K_m$ and $V_{max}$ values for wild-type Hgt1p were estimated to be $48.1\pm 10.5 \, \mu M$ and $57.8 \pm 3.9 \, \text{nmol of glutathione} \cdot \text{mg protein}^{-1} \cdot \text{min}^{-1}$. Although the $K_m$ was in close agreement with the previously reported value ($53.8 \pm 5.5 \, \mu M$), the $V_{max}$ differed significantly from the previously reported value ($10.0 \pm 0.6 \, \text{nmol of glutathione} \cdot \text{mg protein}^{-1} \cdot \text{min}^{-1}$).

### Table 3

<table>
<thead>
<tr>
<th>Mutant (TMD)</th>
<th>Protein expression</th>
<th>Kinetic parameters</th>
<th>Corrected $V_{max}$</th>
<th>Corrected $V_{max}/K_m$</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>%</td>
<td>$K_m , \mu M$</td>
<td>$V_{max} , \text{nmol of glutathione} \cdot \text{mg protein}^{-1} \cdot \text{min}^{-1}$</td>
<td>$V_{max}/K_m , \mu M$</td>
</tr>
<tr>
<td>WT-Hgt1p</td>
<td>100</td>
<td>$48.1 \pm 10.5$</td>
<td>$57.8 \pm 3.9$</td>
<td>1.2</td>
</tr>
<tr>
<td>Severe effect (complementation defective)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Q22A (TMD4)</td>
<td>91</td>
<td>$213.9 \pm 69.5$</td>
<td>$11.4 \pm 1.9$</td>
<td>12.5</td>
</tr>
<tr>
<td>Q562A (TMD9)</td>
<td>62</td>
<td>$372.3 \pm 106.7$</td>
<td>$38.0 \pm 6.5$</td>
<td>61.3</td>
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<tr>
<td>E544A (ICL9–10)</td>
<td>86</td>
<td>$85.2 \pm 25.1$</td>
<td>$10.5 \pm 1.2$</td>
<td>12.2</td>
</tr>
<tr>
<td>R554A (ICL9–10)</td>
<td>74</td>
<td>$116.6 \pm 53.1$</td>
<td>$16.5 \pm 3.1$</td>
<td>22.3</td>
</tr>
<tr>
<td>Moderate effect (no toxicity)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>T114A (TMD1)</td>
<td>11</td>
<td>$40.2 \pm 19.0$</td>
<td>$8.3 \pm 1.1$</td>
<td>75.5</td>
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<tr>
<td>N124A (TMD1)</td>
<td>58</td>
<td>NM</td>
<td>NM</td>
<td>33.2</td>
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<tr>
<td>N137A (TMD2)</td>
<td>51</td>
<td>$29.3 \pm 17.0$</td>
<td>$21.7 \pm 3.3$</td>
<td>42.5</td>
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<tr>
<td>N357A (TMD6)</td>
<td>59</td>
<td>$24.3 \pm 11.6$</td>
<td>$19.6 \pm 2.3$</td>
<td>33.2</td>
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<tr>
<td>H445A (TMD7)</td>
<td>67</td>
<td>$28.5 \pm 11.1$</td>
<td>$23.6 \pm 2.4$</td>
<td>35.2</td>
</tr>
</tbody>
</table>

$^a$ $V_{max}$ was adjusted to the protein expression levels.
glutathione\textpercnt \textpercnt protein\textsuperscript{-1}min\textsuperscript{-1}) (1). The difference in the \( V_{\text{max}} \) is likely to be a consequence of growing the yeast cells in medium additionally supplemented with adenine, leucine, tryptophan, and lysine (in addition to the required supplements histidine and methionine). This medium leads to significantly better growth that could have resulted in better protein expression. As \( K_m \) is an intrinsic property of the protein whereas \( V_{\text{max}} \) can vary with the protein expression levels and experimental conditions, the results were considered to be reliable and used for evaluation of the mutants.

The kinetic characterization of the mutants revealed interesting insights into the roles of residues in the functional activity of the transporters. In particular, the Q526A mutant in TMD9 showed a nearly 8-fold increase in its \( K_m \) for glutathione, with the corrected \( V_{\text{max}} \) value nearly the same as the wild-type \( V_{\text{max}} \) value, thereby resulting in nearly a 7-fold decrease in the transport capacity. A nearly 4-fold increase in \( K_m \) for glutathione was also observed for another glutamine residue, Gln-222, in TMD4. However, Q222A also exhibited a significant loss in corrected \( V_{\text{max}} \) value such that the transport efficiency of the mutant Hgt1p fell by nearly 20-fold. The significant decrease in affinity for glutathione upon mutation of the Gln-222 and Gln-526 to alanine suggests these residues play a critical role in interacting with the substrate.

In contrast, the kinetic analysis of E544A and R544A revealed that mutant yielded a nearly 2-fold increase in \( K_m \) values but a drastic loss in the catalytic activity. The corrected \( V_{\text{max}} \) values for E544A and R554A mutants were 12.2 and 22.3 nmol of glutathione\textpercnt \textpercnt protein\textsuperscript{-1}min\textsuperscript{-1}, respectively, resulting in a nearly 8- and 6-fold decrease in transport efficiency of the mutants. The decreased \( V_{\text{max}} \) values obtained for the three mutants, Q222A, E544A, and R554A, which could not be attributed to the decreased protein levels for the mutants, suggest that these residues might play some critical role in the conformation changes associated with translocation of the substrate by the protein or, alternatively, in binding of protons to drive the translocation of the substrate.

Among the mutants that were moderately affected in activity (Group II, Table 2), T114A showed a drastic fall in its \( V_{\text{max}} \) value, which was in agreement with its decreased protein expression level. In contrast, mutants N137A, N357A, and H445A showed a nearly 2-fold decrease in \( K_m \) and corrected \( V_{\text{max}} \) values such that the transport efficiency for these mutants remained nearly similar to the wild type. Considering the observed alterations in the kinetic parameters for these three mutants, it appears likely that these residues are not directly involved in interacting with the substrate. Instead, the introduction of alanine at these positions most likely leads to minor conformation changes in the transporter leading to decreased protein stability and, hence, protein expression levels and indirectly affects the substrate binding.

In contrast, the N124A mutant showed non-saturating binding even at 400 \( \mu \text{M} \) glutathione concentration, making it difficult to obtain a reliable estimate of the kinetic parameters of the mutant. Moreover, the initial rate of glutathione uptake at different concentration was marginally more than the background values (measured in the vector transformed cells), implying a significant defect in the substrate binding or translocation mechanism of the protein for this particular mutant.

**Functional Analysis of K562R and K562L Reveals the Lysine Residue Is Mandatory at Position 562 in Hgt1p**—The drastic fall in activity of K562A, which otherwise exhibited total and surface protein expression levels comparable with the wild-type Hgt1p, suggested that this residue might play an important role in the transport activity of the protein. As the kinetic parameters could not be measured for this mutant, we tried to further probe the importance of this residue by construction and functional evaluation of K562L and K562R mutants. By substitution of Lys-562 with a conservative residue (Arg) and a non-conservative residue (Leu), we hoped to distinguish between the requirement for positive charge and/or steric (side-chain volume) properties at the position 562 for the transport activity of Hgt1p.

As shown in Fig. 5, replacement of Lys-562 either with positively charged Arg or iso-steric Leu led to drastic loss in the protein activity. The K562L, like K562A mutant, failed to complement the \( hgt1 \Delta \) defect of \( met15 \Delta hgt1 \Delta \) strain (ABC 817) even at as high as 200 \( \mu \text{M} \) GSH and exhibited virtually no glutathione uptake activity in the radiolabeled GSH assay (Fig. 5A and B). In contrast, K562R exhibited very poor complementation ability, with the mutated protein supporting growth of \( met15 \Delta hgt1 \Delta \) strain (ABC 817) at 50 \( \mu \text{M} \) or higher glutathione concentrations only, and no toxicity was observed (Fig. 5A). The poor activity of the mutant was also reflected in the quantitative assay, where it recorded only 8–12% GSH uptake ability relative to the wild-type protein at 100 \( \mu \text{M} \) GSH (Fig. 5B). Radiolabeled GSH uptake assay of K562R at higher GSH concentrations (400 \( \mu \text{M} \) GSH) also failed to exhibit any significant glutathione uptake into the cells (data not shown). An examination of the total protein expression levels (data not shown) and cell surface expression levels (Fig. 5C) revealed that the observed loss in activity of the mutants could not be attributed to defective protein expression levels or trafficking.

Thus, the complete lack of activity of the K562A/L mutants coupled with the inability of a positively charged residue (Arg) to efficiently compensate for the lysine residue at position 562 suggests that presence of lysine \textit{per se} is mandatory for the functional activity of the transporter. Furthermore, the lack of transport capability of K562R even at high GSH concentrations implies that Lys-562 could be a key catalytic residue during the substrate translocation process of the transporter.

**Conservation Pattern of Residues Important for Hgt1p Function by Multiple Sequence Alignment with Other Oligopeptide Transporters**—Comparative sequence analysis can yield valuable insights into the functional significance of a residue. Hence, it was of interest to examine the status of the critical residues found essential for the functional activity of Hgt1p in the other peptide transport (PT) members, which have been characterized in terms of their substrate specificity.

The OPT family contains two distinct clades, the peptide transporting (PT) clade and the yellow stripe (YS) clade that are only remotely related to each other and are distinguished on the basis of their substrate specificity and phylogenetic analysis (3). The PT clade that contains 205 members, including Hgt1p, has only four other members for which...
physiological substrate preference have been clearly established. These include Pgt1, CaOpt1, Isp4, and AtOpt4. Pgt1 has been recently characterized as a high affinity glutathione transporter from *Schizosaccharomyces pombe* (4), whereas AtOpt4 from *Arabidopsis thaliana*, CaOpt1 from *Candida albicans*, and Isp4 from *S. pombe* have been shown to specifically mediate uptake of oligopeptides (7, 35, 36).

Multiple sequence alignment of these five PT family members revealed a number of polar/charged residues conserved across the PT members within the predicted transmembrane domains (Fig. 6). Interestingly, four of the six residues, Asn-124 (TMD1), Gln-222 (TMD4), and Glu-544 and Lys-562 (ICL 537–568) identified to be crucial for the substrate translocation are completely conserved among the five PT members. The high degree of conservation of Asn-124, Gln-222, Glu-544, and Lys-562 among the evolutionary distant members of the PT member suggests that these key residues could be important for the catalytic activity of the PT clade transporters in general. In contrast to the high degree of conservation of Gln-222 across the PT members, Gln-526 in TMD9, the only residue which exhibited a significant increase in $K_m$ for GSH without any significant effect on $V_{\text{max}}$ was conserved only among the glutathione transporters (Hgt1p and Pgt1).

The mutants R554A and E744A (TMD12), which exhibited a significantly decreased transport activity, displayed a complete conservation of positive and negative charge conservation at the respective positions in the five OPT members (Fig. 6). In the case of Glu-744, sequence alignment revealed that the glutamate residue was found exclusively in Hgt1p and was not conserved among the other members. Even the *S. pombe* glutathione transporter lacked Glu-744 and contained an Asp at this residue, like the other oligopeptide transporter members. As the drastic loss in activity of E744A mutant was attributed to the entrapment of the mutant transporter in endoplasmic reticulum, we investigated the residue further in the light of the sequence analysis. We created an E744D mutation and evaluated it for functionality. The E744D mutant, unlike E744A mutant, exhibited functionality like the wild-type protein, as seen from the plate assay, and exhibited around 65% transport activity in the radiolabeled GSH assay (Fig. 5, A and B). The E744D mutant was also able to traffic to the cell surface efficiently, further underlining the requirement for a negative charge at the amino acid position corresponding to 744 in Hgt1p among the PT members.

**FIGURE 5.** Functional analysis of K562L, K562R, and E744D mutants reveal significant loss in activity for K562L and K562R mutants. A, the strain met15Δhgt1Δ (ABC 817) was transformed with plasmids bearing the K562L, K562R, and E744D mutations in Hgt1p and used for plate-based dual-complementation-cum-toxicity assay by dilution spotting on minimal media containing different concentrations of glutathione as described under “Experimental Procedures.” B, measurement of the rate of radiolabeled glutathione uptake. The data are represented as percentage of rate of uptake by the mutants relative to wild-type Hgt1p (WT). The rate of GSH uptake in wild-type Hgt1p was $38.1 \pm 2.8$ nmol min$^{-1}$mg protein$^{-1}$. Experiments were repeated twice, in triplicate, and representative data are shown as the mean $\pm$ S.D. C, cell surface localization analysis by indirect immunofluorescence using mouse anti-HA (Cell Signaling) primary antibody (at 1:100 dilution) and goat anti-mouse IgG horseradish peroxidase-conjugated antibody (Cell Signaling) secondary antibody (at 1:500 dilution). Cells were visualized using confocal microscope, as described under “Experimental Procedures.” Only fluorescence images have been shown.
DISCUSSION

The OPT transporter family catalyzes the uptake of oligopeptides or peptide-like substrates such as metal-secondary amino acid conjugates or glutathione in a proton-dependent manner (3, 7). However, how the transport occurs, the TMD helices, and the residues involved in either the recognition or the translocation process are not known and have not been investigated. A systematic effort was, therefore, initiated in this study for the first time to obtain insights into this process in this large, uncharacterized family of transporters.

Hgt1p, the high affinity glutathione transporter of S. cerevisiae, the best studied member of this family (1, 7, 8, 34, 37), seemed ideally suited to yield insights with a simple plate assay (9) and the ready availability of glutathione and radiolabeled glutathione (in contrast to other substrates of the OPT members). The substrate of Hgt1p, glutathione, is hydrophilic in nature, and therefore, charged and polar residues within the transmembrane domains appeared to be logical candidates for participating in the substrate binding and translocation while also possibly playing other structurally significant roles. This assumption has been the basis of our strategy for selecting a set of 22 polar and charged amino acids across the predicted transmembrane domains in Hgt1p for alanine mutagenesis in this study.

A detailed functional analysis of these residues has revealed that mutation of several of these residues to the nonpolar residue alanine led to a drastic reduction of activity. Those showing a significant effect were found in TMD1 (Thr-114, Asn-124), TMD4 (Gln-222), and TMD9 (Gln-526), implying these as clearly very important domains for the functional activity of Hgt1p. An examination of the helix wheel projection of these transmembrane domains shows that whereas Thr-114 and Asn-124 in TMD1 and Gln-526 in TMD9 clearly tend to cluster with the other hydrophilic residues in the domain, Gln-222 in TMD4 tends to lie just at the interface between the polar and non-polar faces of the transmembrane domain (Fig. 7). Furthermore, Thr-114 and Gln-222 are right in the center of the helices, whereas Asn-124 and Gln-526 are much deeper, toward the cytoplasmic end of the transmembrane domains (Fig. 7). Considering the strong affect of these mutants on the kinetic parameters coupled to their positioning in the amphiphatic face of the helices, it appears likely that these domains line the translocation channel of the transporter. Among the remaining transmembrane domains targeted in this study, one of the residues targeted in TMD2, TMD6, and TMD7 showed a moderate defect, whereas a second residue in this domain showed a mild or negligible loss in functional activity. These domains might, thus, be peripherally or indirectly involved in the transport process. In contrast, although we targeted two residues in TMD3 and three residues in TMD10 mutation to alanine, none of these mutations seemed suited to yield insights this process in this study.

A multiple sequence alignment for the protein sequences of the 5 PT members with defined substrate specificity.

Sequences of Hgt1 (gi 6322244), Pgt1 (gi 19115899), CaOpt1 (gi 2367386), Isp4 (gi 1827508), and AtOpt4 (gi 15237689) were retrieved from Entrez at the NCBI website and aligned using ClustalX program (27). The sequence alignment has been edited to show only the 12 putative transmembrane domains in Hgt1 and the two putative transmembrane domains, excluded in the Becker’s group topology (33) (shaded gray). The numbers corresponding to amino acids sequence of Hgt1 have been shown. The conserved polar and charged residues are shaded yellow, and the residues conserved in the glutathione transporters (Hgt1 and Pgt1), although absent in non-glutathione transporters, are shaded cyan blue. The residues subjected to alanine scanning in this study are marked with an arrow.

FIGURE 6. Multiple sequence alignment for the protein sequences of the 5 PT members with defined substrate specificity. Sequences of Hgt1 (gi 6322224), Pgt1 (gi 19115899), CaOpt1 (gi 2367386), Isp4 (gi 1827508), and AtOpt4 (gi 15237689) were retrieved from Entrez at the NCBI website and aligned using ClustalX program (27). The sequence alignment has been edited to show only the 12 putative transmembrane domains in Hgt1 and the two putative transmembrane domains, excluded in the Becker’s group topology (33) (shaded gray). The numbers corresponding to amino acids sequence of Hgt1 have been shown. The conserved polar and charged residues are shaded yellow, and the residues conserved in the glutathione transporters (Hgt1 and Pgt1), although absent in non-glutathione transporters, are shaded cyan blue. The residues subjected to alanine scanning in this study are marked with an arrow.
showed a significant effect on activity, leaving these domains open for further exploration for their role in forming the translocation channel.

Among the two intracellular regions 537–568 and 707–724 selected for mutational analysis in this study, only the domain stretching the region 537–568 was found to be crucial for the transporter activity. These two regions, although weakly predicted as putative transmembrane domains, have not been considered as TMDs in the final model because of their proline-rich nature (33). However, three of the charged residues, Lys-562, Glu-544, and Arg-554, belonging to the highly conserved proline rich motif, $^{544}\text{EXLGYX}_2\text{PG}(R/K)\text{PXAX}_4\text{KXX}_2\text{G}$, in this region were found to be critical for the translocation activity of the protein (Table 3). Previously, experimental characterization of the conserved proline residues in the transmembrane domains of the voltage-gated potassium (Kv) channels and ligand gated channels has revealed that these proline residues provide a hinge or kink that is proposed to act as a molecular switch to link the conformational changes in the protein with the substrate translocation (38). Similarly, the conserved prolines in the vicinity of the catalytic cysteines as $^{\text{PCX}_2\text{P}}$ motif in the transmembrane domain of DsbD, an integral membrane oxidoreductase in *E. coli*, have been shown to be critical for the functionally important conformational flexibility of the protein (39). The results of the mutational analysis in our study and the high degree of conservation of the region 537–568 in Hgt1p (Fig. 6 and data not shown) seem to point toward an important role of this proline-rich region in protein activity, and indeed, we have recently observed that Pro-555 is important for transport activity of Hgt1p. It is likely that the presence of the conserved proline residues in the region might confer a high degree of conformational flexibility to this region needed for substrate translocation or enable the domain to partially transverse the membrane, forming an inverted loop that could be critical for substrate binding or translocation.

4 C. V. Srikanth and A. K. Bachhawat, unpublished data.
Of particular interest were the two glutamine residues, Gln-222 in TMD4 and Gln-526 in TMD9. Although replacement of the former with alanine resulted in a nearly 4-fold increase in $K_m$ value and almost a complete loss in the catalytic turnover of the transporter, Q526A mutant showed a nearly 8-fold decrease in the $K_m$ values without a significant effect on $V_{max}$. Furthermore, Gln-222 was found conserved among different OPT members, whereas Gln-526 was present only in Pgt1 but not in the other functionally characterized oligopeptide transporters. This differential pattern of conservation and effect of mutations of Gln-222 and Gln-526 becomes particularly remarkable as Pgt1, like Hgt1p, is the only other PT member characterized to transport glutathione with high affinity, whereas all the other three PT members, AtOpt4, CaOpt1, and lSp4, have been shown to transport tetrapeptides and pentapeptides but do not transport glutathione (4, 7, 35, 36). Taken together, the results suggest that although both glutamine residues participate in substrate transport, Gln-526 is critical in identifying glutathione as substrate, whereas Gln-222 recognizes a structural feature common to oligopeptides, including glutathione, a modified tripeptide. In further considering the dramatic effect of mutation on Gln-222 on $K_m$ and $V_{max}$, it could be that the residue might not be directly involved in substrate binding but might be needed for the translocation of substrate and, hence, its influence on substrate binding as well. In contrast Gln-526 appears to be strictly important for glutathione binding/recognition.

Considering the role of Gln-526 as a key residue in identification of glutathione as a substrate, it might be interesting to probe the role of the other polar residues with limited conservation only among the glutathione transporters (Fig. 6). Such residues with limited conservation across the family have been shown to be critical determinants of substrate selectivity among the other transporters. For instance, among 18 homologues of the sugar transporting family in S. cerevisiae, only the high affinity galactose transporter (Gal2p) contains tyrosine as a central aromatic acid in TMD10, whereas all the other 17 homologues, including Hxt2p, a high affinity glucose transporter, contain phenylalanine at the corresponding site. Experimental studies have shown that the presence of tyrosine in Gal2p is crucial for differential recognition of galactose and glucose between the two transporters (40, 41). Similarly, a single difference of a glycine residue in TMD6 of GLYT1 for a serine residue at the corresponding position in GLYT2 is sufficient to explain the ability of GLYT1 to transport glycine and its N-methyl derivative, sarcosine, whereas GLYT2 transports only glycine (16).

Although Hgt1p and the S. pombe orthologue of the same family, Pgt1, are the only two high affinity glutathione transporters known ($K_m$ in the range of 45–65 μM), low affinity transporters of glutathione have been described and include the MRP family of transporters (MRPs in mammals, Ycf1p in yeast) that transport glutathione with low affinity ($K_m$ in the range of 10 mM) and glutathione conjugates but belong to a very distinct family, the ABC transporter superfamily (42). Interestingly, mutational analysis of charged residues in MRP1 led to the identification of key lysine residues that upon replacement with either Asp or Leu results in selective loss of transport of glutathione or its conjugate cysteinyl leukotriene 4 (LTC4), with no discernible effect on the transport of other organic acids or methotrexate drug (17). This is particularly interesting when one considers that even more direct evidence for a role of glutamine and lysine residues in glutathione binding has also been obtained from the crystal structure of a S. cerevisiae glutaredoxin (Grx1) bound to glutathione (43), where it was observed that a conserved glutamine and lysine residue are involved in anchoring the glycine moiety of the substrate by a hydrogen-bonding network. A similar role for a glutamine residue has been identified in other glutaredoxins and glutathione S-transferases (44–46).

In conclusion, the findings described in this report have enabled us to generate the first structural insights into the functioning of a high affinity glutathione transporter, Hgt1p, laying a platform for a more detailed investigation into the importance of these residues and the TMDs 1, 4, and 9 in the transporter activity of Hgt1p. Considering that members of the OPT family have been implicated in metal and oligopeptide distribution and development processes in plants and mating and survival under adverse conditions in fungi, the insights gained with Hgt1p could pave the way for future efforts to understand and even manipulate the other OPT members.

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