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Published in:
Microbiological Reviews

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Document Version
Publisher's PDF, also known as Version of record

Publication date:
1995

Link to publication in University of Groningen/UMCG research database

Citation for published version (APA):

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The Plasma Membrane of Saccharomyces cerevisiae: Structure, Function, and Biogenesis

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INTRODUCTION

The outermost layer of the yeast cell envelope is the cell wall. The cell wall maintains the structure and the rigidity of the cell but is freely permeable for solutes smaller than 600 Da (174). The plasma membrane forms a relatively impermeable barrier for hydrophilic molecules. Specialized proteins mediate the selective uptake and/or secretion of solutes across this membrane.

Transport of solutes into yeast cells has been studied since 1930 (40), but mechanistic aspects of solute transport received substantial attention only after the proposal of the chemiosmotic theory by Mitchell (120). One of the earlier reviews on the energetics of solute transport in yeast cells came from Eddy (56). More recent reviews focused on amino acid transport (76), sugar transport (17, 107), or ion translocation (178) or tabulated the known transport systems in the plasma membrane (31). Although a considerable amount of data is available on the transport processes in the plasma membrane, the translocation mechanisms and the factors that control the rate of transport are poorly understood. The studies are often hampered by a lack of genetically well-defined mutants and/or the lack of artificial membrane systems to study translocation.
catalysis in vitro. Knowledge about the structure and function of the plasma membrane will be crucial for the manipulation of metabolic processes inside the cell.

In contrast to bacteria, in which the cytoplasmic membrane accommodates all the membrane associated processes, yeasts contain many specialized membranes: (i) the plasma membrane separates the other membranes and cell components from the external medium; (ii) the mitochondrial membrane is involved in metabolic energy generation; (iii) the endoplasmic reticulum (ER) and Golgi apparatus are involved in protein and lipid sorting and synthesis; (iv) the nuclear membrane encases and protects the DNA; and (v) the vacular and peroxisomal membranes compartmentalize special metabolic and digestive functions (Fig. 1). This review gives an overview of the different plasma membrane constituents, their origins, and their role in the maintenance and function of the plasma membrane.

**STRUCTURE OF THE PLASMAMEMBRANE**

The plasma membrane forms a lipid bilayer approximately 7.5 nm wide. It contains a mixture of polar lipids and proteins which, by their interactions, govern the structure of the membrane. The classical Singer and Nicolson model (182) describes the membrane as a continuous sea of lipids dotted with globular proteins which are able to move unrestricted within the plane of the membrane. In this model, the lipids not only diffuse freely within the plane of the membrane but also undergo rotational and transverse motions (flip-flop). The high lateral mobility of lipids in the plasma membrane, however, has recently been questioned, since the mobility of fluorescent lipid probes in the plasma membrane of *Saccharomyces cerevisiae* was found to be anomalously slow (75). Membrane proteins are often hindered in their lateral motion because of association with other proteins or association with elements of the cytoskeleton or extracellular matrix. Another dominant feature of membrane structure is the asymmetric location of the proteins. Some span the entire length of the membrane (intrinsinc), while others are only partially embedded in the membrane and protrude on one side of the membrane (extrinsic). The plasma membrane encompasses proteins involved in transport of solutes, signal transduction, anchoring of the cytoskeleton, and synthesis of outer membrane components (Fig. 2). The lipids of the plasma membrane are asymmetrically disposed across the bilayer. The inner leaflet of the *S. cerevisiae* plasma membrane is enriched in phosphatidylethanolamine (PE), phosphatidylinositol (PI), and phosphatidylserine (PS) (36). In erythrocyte membranes, PE, PI, and PS are also preferentially located in the internal leaflet, while the external leaflet is enriched in phosphatidylcholine (PC) and sphingolipids (138). A striking feature of the plasma membrane lipids is their diversity in size and composition. The major lipid classes are glycerophospholipids, sphingolipids, and sterols (Fig. 3). Glycerophospholipids consist of two fatty acid acyl chains ester-linked to glycerol-3-phosphate; various substituents such as choline (in PC), ethanolamine (in PE), serine (in PS), myo-inositol (in PI), and glycerol (in PG) can be linked to the phosphoryl group. Diphosphatidylglycerol or cardiolipin, the dimeric form of PG, is also present in yeast cells. Sphingolipids have a ceramide backbone which is composed of a long-chain base phytosphingosine that is N acylated with a hydroxy C26 fatty acid. *S. cerevisiae* contains only three major sphingolipids: inositol phosphate ceramide, mannosyl-inositol phosphate-ceramide, and mannosyl-diinositol phosphate-ceramide. Sterols are compact rigid hydrophobic molecules with a polar hydroxyl group. In contrast to higher eukaryotes, in which cholesterol is the most abundant sterol, the yeast plasma membrane contains mainly ergosterol and minor amounts of zymosterol (226).

**LIPID COMPOSITION AND ROLE OF LIPIDS IN THE PLASMA MEMBRANE**

**Phospholipids**

Most papers dealing with lipids of *S. cerevisiae* do not consider the composition of the various membrane fractions separately (86, 158). Only a few reports specifically describe the lipid composition of membrane fractions that are ≥90% pure (20, 142, 226). A limitation of these studies is the lack of uniformity in experimental conditions (choice of model organism...
ism, growth conditions, lipid extraction procedures, etc.), which makes it difficult to compare the results obtained in different studies. For instance, polar solvents are required to extract the highly polar sphingolipids (98, 143). The differences in PS and PI content (Table 1) are also quite remarkable and are most probably caused by differences in the strains, culture conditions, and/or extraction procedures used.

The lipid composition of the plasma membrane is complex...
and tightly regulated, suggesting that lipids play a role in the activity of the proteins in the plasma membrane. The annular lipids, which are in direct contact with the proteins, are likely to stabilize the proteins in a functional conformation (223). Direct evidence for a role of these annular lipids in *S. cerevisiae* has been presented in studies on two membrane proteins, a chitin synthase and the plasma membrane ATPase (100, 114, 115). It has been shown that delipidation of the ATPase results in inactivation of the enzyme (54). By reconstitution of the purified enzyme, Serrano et al. (180) showed that the ATPase requires lipids with a negatively charged polar head group for PC or PE, respectively, or to deplete the membrane for PS (100).

The influence of the bulk lipids on enzyme activity in yeast mutants with a variety of defects in phospholipid biosynthesis has been investigated. For example, choline or ethanolamine auxotrophs have been used to specifically enrich the plasma membrane for PC or PE, respectively, or to deplete the membrane of PS (4, 5). Several membrane-associated processes are affected by changes in the lipid composition; e.g., the apparent affinity constants for transport of various amino acids are increased in cells enriched with either PC or PE (198, 199). Since these studies were performed with whole cells under conditions that were poorly defined, the data should be interpreted with caution. Trivedi et al. (197) showed that the plasma membrane ATPase activity in PI-enriched cells is enhanced, which could have resulted in a higher proton motive force and, consequently, in a higher driving force for amino acid uptake.

### Fatty Acyl Chains

Oleic acid (18:1) and palmitoleic acid (16:1), together with trace amounts of palmitic acid (16:0) and stearic acid (18:0), are the principal fatty acyl chains in *S. cerevisiae* (Table 2) (41, 158). The fatty acyl packing of these chains determines to a large extent the membrane fluidity. The packing increases with increasing length of the acyl chains and decreasing extent of unsaturation, which leads to a more ordered structure and a decrease in fluidity. Perturbations of the bilayer that decrease the area of a lipid molecule, such as increased hydrostatic pressure, lowering of the temperature, or addition of sterols to phospholipids, also result in a decrease in fluidity (181). The physiological relevance of fluidity is evident from the adaptations of various yeasts to environmental stress. The plasma membrane of the psychrophilic yeast *Leucosporidium frigidum* contains a large amount of unsaturated fatty acyl chains, while the plasma membrane of the thermotolerant yeast *Torulopsis bovina* has a low content of unsaturated fatty acyl chains (216).

### Head Groups

The charge of the head groups not only affects the surface potential of the membrane (33) but also can influence the activity of membrane proteins directly (35, 53, 180). The size of the head group determines to a large extent the physical state of the membrane, which is liquid crystalline under most physiologically relevant conditions. Lipids such as PC, PS, PI, and sphingolipids, which have head groups and acyl chains with comparable cross-sectional areas, are cylindrical and organize easily in bilayers. Lipids which have smaller head groups than acyl chains, such as PE, CL, and sterols, are cone shaped and form inverted micelles in solution. High concentrations of such lipids in the membrane may locally induce a high membrane curvature and membrane-packing defect, which can create an environment into which proteins can insert without compromising the barrier function of the membrane (47).

### Sphingolipids

Sphingolipids are ubiquitous constituents of eukaryotic plasma membranes. Studies on sphingolipids started with the discovery of these molecules in the human brain in 1884 (196). Current research on sphingolipids is focused primarily on their possible role in signal transduction across the plasma membrane (68, 80, 82, 83). A clear indication for an essential role of sphingolipids in growth and viability came from the isolation of a sphingolipid-defective *S. cerevisiae* mutant. This mutant strain has an obligatory growth requirement for a sphingolipid long-chain base, such as phytosphingosine (217). The mutant lacks serine palmitoyltransferase (147), the first enzyme in sphingolipid long-chain base synthesis.

Patton and Lester (142) have shown that more than 90% of the sphingolipids are located in the plasma membrane and that the sphingolipids constitute about 30% of the total phospholipid content. Sphingolipids have not been detected in isolated mitochondria and nuclear membranes. Since glycosphingolipids have been found only in wall-bearing eukaryotes, where the molecules are presumably located in the outer leaflet of the plasma membrane (138), it is possible that these lipids have a role in wall synthesis as cell wall anchors (112). Ceramide and other products of sphingolipid turnover have been implicated as second messengers in higher eukaryotic cells (51, 82), but there is no direct evidence for a similar function in *S. cerevisiae* (122). Using suppressor strains lacking sphingolipids, Patton et al. (143) showed that these strains cannot grow at low pH, elevated temperatures, or high salt. Apparently, strains lacking sphingolipids become impaired in proton extrusion by the plasma membrane ATPase and/or the cells become more permeable to protons.

### Sterols

The content of sterols in the plasma membranes is a matter for controversy. Bottema et al. (20) reported a molar sterol-
to-phospholipid ratio of 0.365, Zinser et al. (226) gave a ratio of 3.31, while we have calculated from the data of Patton and Lester (142) a ratio of 0.94, which is comparable to the value of 0.81 reported by Rodriguez et al. (163). Since our studies indicate that it is not possible to form well-sealed liposomes with a sterol-to-phospholipid ratio higher than 1 (88a), a membrane in which each phospholipid molecule is surrounded by more than three sterol molecules seems unlikely. The sterols determine to a large extent the rigidity of the plasma membrane, which, in turn may affect the lateral movement and the activity of membrane proteins. Sterols may also create an environment into which polypeptides can insert. For this bulk function, sterol auxotrophs require relatively large amounts of sterols in the medium (15 µg/ml) (163). A further role for sterols can be found in cell proliferation, which requires the presence of specific sterols (127). The role of sterols as a trigger for cell proliferation is satisfied at concentrations of 1 to 10 ng/ml. In the region between 0.1 and 15 µg/ml, two interesting additional roles for sterols have been defined, i.e., the “critical-domain” and “domain” function. The critical-domain role is observed at 0.1 µg of ergosterol per ml and is essential for growth. Plasma membranes isolated from sterol auxotrophs grown in the presence of 0.1 µg of ergosterol per ml show a thermotropic phase transition of the lipids which is not observed at higher concentrations of ergosterol (163). At the domain concentrations, i.e., between 0.1 and 15 µg/ml, the growth yield is increased but the growth rate of a sterol auxotroph is not affected. The existence of sterol-rich and sterol-poor domains in the plasma membranes could be related to these domain functions (20). In model membrane systems, it has been shown that cholesterol has a high affinity for negatively charged phospholipids and for phospholipids which have a low transition temperature. As a result, domains of low and high cholesterol concentration are formed (48, 206). The presence of sterol-rich domains in the plasma membrane is supported by the effects of nystatin on the differences in Arrhenius kinetics of the plasma membrane ATPase and chitin synthase in wild-type and sterol mutants (without ergosterol in the plasma membrane) (20). Nystatin disrupts the bilayer structure of the membranes by complexing with ergosterol. Nystatin has no effect on the ATPase activity, while the chitin synthase activity is greatly reduced (20). It has been postulated that chitin synthase is located in a sterol-rich domain and the ATPase is located in a sterol-poor domain, which would be in accord with the differential effects of nystatin on both enzymes.

**BIOCHEMICAL PATHWAYS FOR LIPID SYNTHESIS**

The synthesis of lipids has been reviewed in several reports, most recently by Carman and Henry (30) and Paltauf et al. (141). This section focuses on some of the key enzymes of lipid synthesis and the sites of lipid synthesis in yeast cells.

**Phospholipid Biosynthesis**

The lipid matrix of *S. cerevisiae* membranes is composed of glycerophospholipids similar to those found in the membranes of higher eukaryotic cells. In mammalian cells, the majority of phospholipid biosynthetic enzymes are associated with the ER (49). For instance, PC, PE, PI, and PS are synthesized primarily at the ER. Cardiolipin and its precursor PG, as well as small amounts of PE, are synthesized in the mitochondria (43). The study by Zinser et al. (226) shows that plasma membranes of *S. cerevisiae* are largely devoid of any of the lipid-synthesizing enzymes. However, a more recent study, by Nickels et al. (129), shows that PG and PI can be synthesized by isolated plasma membranes of inositol auxotroph *S. cerevisiae* strains.

The pathways for the synthesis of phospholipids in *S. cerevisiae* have been elucidated primarily by Lester and coworkers (109, 186, 211). In *S. cerevisiae*, PE and PC are synthesized by two alternative pathways (85). In both cases, glycerol-3-phosphate is the precursor of PE and PC. In the primary pathway of phospholipid synthesis, PE and PC are derived from CDP-diaclylglycerol (CDP-DAG) (Fig. 4). The major route for PC biosynthesis in *S. cerevisiae* involves three successive methylations of PE, which sequentially results in phosphatidyl-N-monoethylethanolamine (PMME), phosphatidyl-N,N-dimethylethanolamine (PDME), and PC. In the alternative pathway, PE and PC are derived from CDP-ethanolamine and CDP-choline, respectively. PI and cardiolipin are also derived from CDP-DAG; these reactions are similar to those in higher eukaryotes. The synthesis of PS in *S. cerevisiae* is similar to that in bacteria and occurs from CDP-DAG plus serine. In higher eukaryotes, PS synthesis involves the exchange of the ethanolamine group of PE or choline group of PC for serine.

**Sphingolipid Biosynthesis**

In *S. cerevisiae*, three classes of sphingolipids are known: IPC, containing a single inositol phosphate; MIPC, containing a single inositol phosphate to which a mannose unit is attached; and the major sphingolipid, M[IP]2C, containing two inositol phosphates with a mannose unit attached to one of the inositols. The type of long-chain base, the degree of hydroxylation, and the chain length of the fatty acids give rise to a wide variety of sphingolipids in each of the three classes (184). An outline of the sphingolipid synthesis pathway is given in Fig. 5. The ceramide moiety contains the sphingolipid long-chain base phytosphingosine, linked by an amide bond to a C36 fatty acid (184). Synthesis of phytosphingosine involves the condensation of serine and palmitoyl coenzyme A in the presence of pyridoxal phosphate to yield γ-3-ketophinganine, CO2, and coen-
zyme A, which is catalyzed by serine-palmitoyltransferase. The 3-keto intermediate is converted into n-4-hydroxy-sphinganine by 3-ketosphinganine reductase and phytosphingosine synthase (146). This phytosphingosine is converted to ceramide, which then forms the backbone of the sphingolipid molecule. The ceramide is presumably synthesized in the ER. The subsequent transferase steps are most probably completed in the Golgi apparatus, since the synthesis of sphingolipids requires vesicular transport from the ER to the Golgi (154).

**Ergosterol Biosynthesis**

The branched-chain isoprenoid pathway (Fig. 6) provides a diverse class of molecules that are required for ergosterol biosynthesis but also serve purposes related to protein synthesis, protein glycosylation, and electron transport (32). In higher eukaryotes, and most probably also in *S. cerevisiae*, the ER is the principal site of sterol synthesis (159). Some evidence is available for the localization of enzymes involved in late steps of the biosynthesis in lipid particles, secretory vesicles, and the plasma membrane (225). Sterol biosynthesis starts from acetate. The principal regulatory step in the synthesis of the isoprenoids is the conversion of 3-hydroxyl-3-methylglutaryl (HMG) coenzyme A into mevalonic acid. The synthesis of ergosterol from mevalonic acid has been reviewed thoroughly elsewhere (39).

**LIPID SORTING**

Once inserted into a membrane, the lipid molecules show very little tendency to move spontaneously as monomers from one membrane via the aqueous space to another membrane (46). The variation in lipid composition of the organelles therefore requires specific lipid transport mechanisms (Fig. 7) (226). In *S. cerevisiae*, two types of phospholipid transfer proteins have been identified. One of these proteins is highly specific for PI (44), while the other protein is more specific for PC and to a lesser extent for PE, PS, and PI (21). Clear evidence for an essential role of these proteins in intracellular bulk movements of lipids is still lacking. It has also been suggested that these transfer proteins function in exchange rather than in net transport of lipids. The *PIT1/SEC14* gene encodes the PI/PC transfer protein. Temperature-sensitive mutations in *pit1/sec14* abolish phospholipid transfer in cell extracts (9). The *sec14/pit1* defects can be suppressed by mutations in structural genes that participate in the pathway of PC biosynthesis (37). These results and the observation that *PIT1/SEC14* protein copurifies with Golgi membranes suggest that *PIT1/SEC14* functions in maintaining an appropriate phospholipid composition of Golgi membranes which is essential for its secretory function (37).

The intracellular transport of proteins from the site of synthesis to their destination is mediated largely by lipid vesicles (see below). This implies that sorting of lipids can accompany the protein transport process. In most cases, however, the transport of lipids from the site of synthesis to the target organelle is not linked to protein transport (209).

**PROTEIN SYNTHESIS AND SORTING TO THE PLASMA MEMBRANE**

Plasma membrane proteins are synthesized at membrane-bound ribosomes on the rough ER; the polypeptides transit the ER and the Golgi apparatus and travel to the plasma membrane along the secretory pathway (Fig. 8). The transport from
one organelle to another is mediated by vesicular transport. A combination of biochemical studies, including reconstitution of vesicular transport in cell-free systems (7, 63), and genetic approaches, including the isolation of *S. cerevisiae* secretory mutants (132, 133, 173), has given insight into the mechanism of protein transport. Plasma membrane proteins are inserted cotranslationally into the rough ER membrane. In the ER, the polypeptides can be proteolytically processed, acquire proper folding, and/or undergo glycosylation or other types of modification. Targeting of ribosomes engaged in the synthesis of plasma membrane proteins to the ER is mediated by the signal recognition particle, which brings the nascent polypeptides to the ER membrane (81, 213). In the process of protein synthesis, the polypeptides are inserted into the rough ER membrane with the aid of an ER membrane-located protein translocation multisubunit complex that is composed of Sec61p, Sec62p, Sec63p, and two other polypeptides (50). Sec61p shows significant sequence similarity to *E. coli* SecY (74), a protein which is involved in the translocation of proteins across the cytoplasmic membrane. Transport of proteins across the ER membrane is probably made irreversible by protein folding and/or posttranslational modification. The oligosaccharyl-transferase complex, encoded by *WBPI* and *SWPI* (190, 191), has also been implicated as a component of the protein translocation pathway. Mutants with conditional mutations of the *WBPI* gene, however, are not defective in protein translocation (190).

Following synthesis and insertion into the ER, transport vesicles bud from the ER and fuse with the Golgi apparatus. Budding of the vesicles is most probably initiated by a Ras-like GTP-binding protein (Sar1p) (124, 135, 136) and a resident ER membrane protein (Sec12p) (Fig. 9). With the help of Sec12p, a GDP-GTP exchange protein (10), the Sar1 protein on the ER membrane is converted from the GDP-bound resting state to the GTP-bound active state, which promotes budding of transport vesicles from the ER. Upon completion of the vesicle formation, Sar1p hydrolyzes GTP with the help of the GTPase-activating protein Sec23p (224), after which Sar1p cycles back to the ER. These steps have been demonstrated in vitro by forming functional vesicle intermediates that are competent in fusing to the Golgi membrane (135, 169). Several proteins that mediate ER-to-Golgi transport are implicated in targeting and fusing vesicles from the ER to the Golgi. Mutations in the GTP-binding protein Ypt1p result in a block of ER-to-Golgi transport and yield accumulation of aberrant membranes and vesicles (12). In vitro studies have confirmed that Ypt1p is required for targeting of transport vesicles to the Golgi (160). Proteins encoded by the *BOS1*, *BET1*, and *SEC22* genes represent membrane proteins that are constituents of the ER-derived transport vesicles (128). Antibodies against Bos1p inhibit ER-to-Golgi transport but do not affect budding from the ER membrane (110). Mutations in the Sec22 protein cause a similar phenotype. Although the precise mechanism of the fusion process is not yet known, many details may be learned from studies with mammalian cells (185). In mammalian cells, a protein termed NSF (Sec18p in yeast cells), which is sensitive to *N*-ethylmaleimide and has ATPase activity, associates with soluble NSF attachment proteins (SNAPs; Sec17p in yeast cells). This complex binds to receptors on the vesicle (v-SNARE) and the target membrane (t-SNARE), and this attachment induces membrane fusion provided that some other, as yet uncharacterized, cytoplasmic and target membrane proteins are present. Such a mechanism of membrane fusion is likely to represent a common theme in the secretory pathway (59, 153). Many of the proteins implicated in membrane fusion in mammalian cells share sequence similarity with yeast proteins (59, 153). Sec22p, Bos1p, and Bet1p may have roles as v-SNAREs, and another membrane protein, Sec5p, may be the equivalent of the t-SNARE receptor (84).

Once associated with the Golgi apparatus, the membrane proteins undergo further processing. The Golgi is organized into three functionally distinct regions, the cis-Golgi network, the Golgi stack, and the trans-Golgi network. The cis- and trans-Golgi networks are the entry and exit sites, respectively, of the stack and are the places where the sorting takes place. Transport of proteins between Golgi cisternae is mediated by two distinct forms of transport vesicles as visualized by electron microscopy (166). These forms are called the non-
clathrin-coated vesicles and uncoated vesicles. By using a variety of blocking agents, it has been shown that the coated vesicles precede the uncoated vesicles. The role of the coat in vesicle transport remains elusive, but it is thought that the coat proteins initiate or promote membrane deformation, which is essential for the formation of the vesicle (153).

Post-Golgi secretion vesicles are transported to a specific region of the plasma membrane called the bud; membrane fusion takes place at the bud, and the formation of the daughter cell starts (133). Determination of the budding site is genetically controlled by a set of BUD genes (34). Mutations in the Sec4 GTP-binding protein cause the cell to accumulate secretory vesicles (133). The Sec4 protein with bound GTP is proposed to associate with Snclp/Snc2p on the secretory vesicle membrane (152). The complex formed recognizes an attachment site on the plasma membrane (Sso1p/Sso2p [1]) which then triggers membrane fusion (214). The Sec4 protein is subsequently released, after which it can be used for another round of membrane fusion.

One of the major questions in this process of protein flux is how the cell discriminates between proteins which are resident in an organelle and proteins which have to be exported further to other organelles. Currently, the idea in favor is that transport of proteins to the plasma membrane occurs by default (145, 221). Protein retention in a particular organelle such as the ER requires special mechanisms (130). However, this does not explain why plasma membrane proteins do not stay resident in the ER or Golgi. Bretscher and Munro (23) have proposed that targeting occurs through bilayer-mediated sorting. Hydrophobicity analysis of known Golgi membrane proteins predicts that the average length of their membrane-spanning segments is around 17 residues, while transmembrane segments of plasma membrane proteins have on the average 21 residues (23). The high content of ergosterol and sphingolipids in the plasma membrane (142, 226) favors a bilayer that is thicker than that of the Golgi membrane. Consequently, plasma membrane proteins segregate away from the energetically less favorable Golgi membrane. Since mutations in SHR3 specifically inhibit targeting of amino acid permeases to the plasma membrane but do not affect sorting of other plasma membrane proteins (111), the bilayer-mediated sorting model does not accommodate all observations with regard to transport of membrane proteins to the plasma membrane. Also, it cannot be excluded that the destination of membrane proteins by default may be the vacuole in yeast cells (162).

**PROTEIN CONTENT OF THE PLASMA MEMBRANE**

Chromosome III, which corresponds to 2.5% of the entire yeast genome, is predicted to encode 33 plasma membrane proteins. From this number, a total of more than 1,000 plasma membrane proteins can roughly be estimated to be present in *S. cerevisiae* (70, 72). It is evident that several membrane protein-encoding genes are present in multiple copies (121), and not all these proteins will be expressed at the same time. The actual number of functional plasma membrane proteins will therefore be much smaller. Indeed, using isolated and purified plasma membrane fractions, Rank and Robertson (157) estimated a total of about 150 unique polypeptides. The transport proteins are most probably the principal constituents of the plasma membrane (see below). For instance, each amino acid is transported by at least one protein (76) and the various sugars are transported by at least 15 different proteins (107). The yeast plasma membrane of a cell can contain up to $10^5$ to $10^6$ transporter molecules, which is roughly 50% of the plasma membrane proteins (178). The principal plasma membrane ATPase, encoded by *PMA1* (179), has not been taken into account in these calculations. By itself, it can account for almost 50% of the plasma membrane protein content of exponentially growing cells (178). Other plasma membrane proteins are involved in cell wall synthesis (61) or signal transduction (134) or form part of the cytoskeleton (11). In the following sections, the various transport proteins in the plasma membrane as well as information on signal-transducing enzymes pertinent to the regulation of solute transport are discussed.

**PRIMARY TRANSPORT PROTEINS**

**Plasma Membrane ATPases**

Primary transport is defined as transport in which light or chemical energy is converted into electrochemical energy (i.e., solute or ion concentration gradients). For the plasma membrane of *S. cerevisiae*, only ATP-driven primary transport systems have been described (Fig. 10). The hydrolysis of ATP by the major plasma membrane ATPase (Pma1p) results in the generation of an electrochemical gradient of protons ($\Delta \psi$). The free energy present in the $\Delta \psi$ exerts a force on the protons (the proton motive force: $\Delta F_{\text{proton}}$ or $\Delta \psi$) which is composed of an electrical potential ($\Delta \psi$) and a chemical gradient of protons across the plasma membrane $[\Delta \psi_{\text{in}} - \Delta \psi_{\text{out}}]$. This can also be expressed as $\Delta \psi = \Delta \psi_{\text{in}} - Z \Delta \psi_{\text{out}}$. The $\Delta \psi$ is used to drive membrane-associated processes such as solute transport (see below). The plasma membrane ATPase protein forms a covalent acyl phosphate intermediate as part of the reaction cycle and has two forms of the phosphorylated intermediate (E$_i$ and E$_j$) which differ in conformation (71). This type of enzyme is therefore called E$_i$E$_j$- or P-type ATPase. The catalytic mechanism of the P-type ATPase is distinct from that of the F-type ATPase of the mitochondria.

![FIG. 10. Primary and secondary transport systems in S. cerevisiae.](image-url)
and the V-type ATPase of the vacuolar membrane (3). As noted above, the plasma membrane ATPase protein (Pma1p) is the major protein in the plasma membrane (178). The ATPase is estimated to consume 10 to 15% of the ATP produced during yeast growth (67) and has a reaction stoichiometry of one proton extruded per molecule of ATP hydrolyzed (67). Because of the lack of reliable methods to quantitate the membrane potential in whole cells, it is hard to give an estimate of the $\Delta \psi$ formed by Pma1p, but values of $-200$ mV for the membrane potential have frequently been reported (178, 183). Pma1p is highly specific for Mg$^{2+}$-ATP, with rates of hydrolysis of CTP, GTP, and ITP which are less than 2% of the activity with ATP (144). The $K_{m}$ for ATP is 0.8 to 1.2 mM, and the pH optimum is around pH 6.0 (187). Addition of glucose to yeast cells causes a two- to threefold increase in plasma membrane ATPase activity (187).

The isolation of the PMA1 gene encoding the plasma membrane ATPase (179) has enabled the molecular analysis of the enzyme. The membrane-embedded part of the protein contains 8 to 12 membrane-spanning segments, with the N and C termini located in the cytoplasm (Fig. 11) (178, 183). Amino acid sequence motifs which are highly conserved among the P-type ATPases have been detected, and mutagenesis of residues in these regions has established their roles in ATPase function (178). The glutamate residue in the TGES motif at amino acid 232 (in the Pma1p amino acid sequence) is required for hydrolysis of the phosphorylated enzyme intermediate; the threonine residue in this motif is involved in the binding of vanadate (151, 178). The aspartate residue in the CSDKTGT motif at position 378 is required for the formation of the acyl-phosphate catalytic intermediate and is essential for ion pumping (151). The lysine residue at position 475 in the motif KGAP and the aspartate residue at position 534 in the motif DPPR are also important for the formation of the phosphorylated intermediate (151). Hydrolysis of the phosphorylated intermediate is facilitated by the first aspartate residue in the TGDGVND motif at position 634, while the second aspartate in this motif is important for the formation of the intermediate (151). The last 11 amino acid residues are involved in the regulation of the enzyme activity. Deletion of this part results in a constitutively activated ATPase (150). In contrast to Pma1p, the mitochondrial F-type and vacuolar V-type ATPases are composed of multiple different subunits (Fig. 12) (3, 126). The $H^+$/ATP stoichiometry of Pma1p is 1, which differs distinctly from the 3 to 4 protons pumped per ATP by the F-type ATPase. The differences in pH optima and sensitivity to inhibitors can be used to discriminate between the various ATPase activities (Table 3). In the case of the plasma membrane ATPase, the activity can be used as a marker for the isolation of the plasma membrane. The pH optima for the plasma membrane, vacuolar, and mitochondrial ATPases are pH 6, 7, and 9, respectively. The plasma membrane $H^+$-ATPase is relatively sensitive to ortho-vanadate and diethylstil-
bestrol, whereas the vacuolar and mitochondrial ATPases are not affected or only moderately affected by these inhibitors (Table 3) (202).

The genes encoding two other plasma membrane P-type ATPases have been described. The Pma1 ATPase is 90% identical to the Pma2 ATPase (175) but has distinct enzymatic properties. When overexpressed by the PMAL promoter, the Pma2 ATPase can functionally complement mutations in the PMA1 gene. The physiological function and the conditions allowing the expression of PMAL are still unknown. The high affinity for MgATP could indicate that Pma2p is a glucose-regulated ATPase that plays a role under starvation conditions, i.e., when the ATP concentration is low (187).

The gene encoding the Pmr2/Ena1 ATPase has recently been isolated by Rudolph et al. (167). The Pmr2/Ena1 protein shows 20% identity with the Pma1 enzyme (175) but has distinct enzymatic properties. Monovalent cations (Na⁺, Li⁺, and K⁺) (164). Deletion of PMR2 is not deleterious, but the cells become sensitive to high Na⁺ concentrations and elevated pH.

ABC Transporters

The Ste6 protein is a representative of the ABC superfamily (88, 105). The distinguishing feature of members of this family is a highly conserved domain of about 200 amino acids making up the ATP-binding cassette (ABC); this domain confers on these transporters the ability to bind and hydrolyze ATP (88). The Ste6 protein is required for the secretion of the transponder allowing expression of the ABC; this domain confers on the transporter the ability to bind and hydrolyze ATP (88, 105). The distinguishing feature of members of this family shows 20% identity with the Pma1 ATPase and apparently beenisolated by Rudolph et al. (167). The Pmr2/Ena1 protein i.e., when the ATP concentration is low (187). The Pmr2/Ena1 protein shows 20% identity with the Pma1 ATPase and apparently beenisolated by Rudolph et al. (167). The Pmr2/Ena1 protein i.e., when the ATP concentration is low (187). The Pmr2/Ena1 protein shows 20% identity with the Pma1 ATPase and apparently beenisolated by Rudolph et al. (167).

Deletion of PMR2 is not deleterious, but the cells become sensitive to high Na⁺ concentrations and elevated pH.

Passive Diffusion

The rate of passive diffusion of solutes across the plasma membrane is governed in part by the physical properties of the membrane such as the acyl chain length, degree of saturation of the fatty acids, membrane fluidity, and other factors (see above). A variety of sugar-alcohols such as arabinitol, erythritol, galactitold, mannitol, ribitol, sorbitol, and xylitol are thought to cross the plasma membrane by passive diffusion only (29).

Although specific transport systems have not (yet) been found for these molecules, the relatively hydrophilic nature of the sugar-alcohols makes it unlikely that the rate of diffusion is very high. More-lipophilic compounds such as fatty acids (organic acids), alkanols, and hydrocarbons are more likely to diffuse across the membrane. Various examples of compounds that can dissolve into the plasma membrane and enter the cell by passive diffusion have been discussed by Cartwright et al. (31).

Channels

Channels allow the downhill flux of solutes across the plasma membrane. To date, two distinct types of ion channels have been found in the plasma membrane of S. cerevisiae: voltage-dependent K⁺ channels (78) and rather unspecific channels that are activated by stretching of the bilayer (78).

The patch clamp technique, used to demonstrate ion channels in the yeast plasma membrane, showed that a K⁺-specific current is induced upon depolarization of the membrane (78). Alkalization of the medium, as well as a transient increase in cytoplasmic Ca²⁺ levels, which can occur in response to sugar uptake and or metabolism (15, 57), also elicits a specific K⁺ current. The translocation of some sugars induces an equally large flux of protons (assuming a sugar/H⁺ stoichiometry of 1), which could result in depolarization of the membrane potential (176). The efflux of K⁺ from the cells alleviates this depolarization. However, K⁺ efflux is also observed when glucose is taken up by uniport, i.e. without coupling ion (205). It is therefore more likely that sugar-induced K⁺ efflux is linked via a transient increase in cytoplasmic Ca²⁺ (57).

Secondary Transport Proteins

In secondary transport, the energy for translocation of one solute is supplied by (electro-)chemical gradients of other solutes (including ions). The electrochemical ion gradients are often generated by primary transport systems such as the yeast plasma membrane ATPase. Three general categories of secondary transport systems can be distinguished, i.e., uniport, symport, and antiport. Transport of a single solute which is facilitated by a carrier protein without the movement of a countertransported, the driving forces on these processes may vary considerably. For a comprehensive review on secondary transport systems, see Poolman and Konings (149). The types of transport systems detected in the yeast plasma membrane are shown in Fig. 10. The different modes of secondary transport are listed below.
Uniport

The driving force for this process is the electrochemical gradient of the transported solute. The best-known examples of electroneutral uniport in S. cerevisiae are the transporters for the monosaccharides glucose and galactose (Table 4). Until recently, glucose uptake was thought to be mediated by two kinetically distinct mechanisms: a constitutive low-affinity transport system with an apparent affinity constant for glucose ($K_a^{\text{app}}$) of approximately 20 mM and a kinase-dependent, glucose-repressible high-affinity transport system with a $K_a^{\text{app}}$ of 1 mM (18).

High-affinity glucose transport is genetically very complex, involving at least the gene products SNF3, HXT1, HXT2, HXT3, HXT4, HXT5, HXT6, and HXT7, while the presence of other genes has not been ruled out (103). High- and low-affinity transport in S. cerevisiae has been observed not only for glucose but also for various other sugars. The validity of the determined kinetic parameters of sugar uptake is still a matter of controversy. Fuhrmann and Volker (64) have suggested that the low-affinity component of transport is not carrier mediated but results from passive diffusion of the solute across the plasma membrane at the high concentrations of sugars used. Since internalized sugar is rapidly phosphorylated by a sugar kinase, the phosphorylation activity will influence the transport kinetics. Using quench flow techniques to measure initial sugar uptake rates, i.e., from the increase in radioactivity within 0.2 to 5 s, Van Dam and coworkers (204, 212) showed that the rate of glucose uptake in starved cyande-treated cells slows after 0.2 s. This suggests that depletion of ATP, caused by the starvation conditions, influences glucose uptake through the activity of hexokinase. The kinetics of glucose uptake in the subsecond time range still displays high- and low-affinity components (212). It has been suggested that regulation of glucose uptake occurs via a factor that modifies the affinity of the transporters. This factor could be the SNF3 gene product, the general glucose-sensing protein (Ggps), hexokinase PII (or P1), one of the HXT gene products, or any combination of these (212), but it could also be related to modification of the transport protein(s) by, for instance, phosphorylation. The abundance of related glucose transporters suggests that kinetic constants derived from strains that are genetically poorly defined will inevitably be the result of a combination of transport systems. In fact, Wendell and Bisson (218) have shown that the expression of the putative glucose transporter (HXT2) is regulated by the growth conditions. Since conditions that result in an increased expression of a particular transport protein may down-regulate the expression of another transporter molecule, different transporters will contribute to the transport kinetics.

Kinetic analysis of galactose transport in S. cerevisiae is also characterized by high- and low-affinity transport, but, unlike glucose transport, galactose is mediated by a single gene product (Gal2p) (200) (Table 4). It has been suggested that the different affinities are a result of an interaction of galactokinase with the transport protein (156). The regulation of expression of Gal2 involves the Gal3, Gal4, and Gal80 proteins (97).

Sympot

Ions. Solute transport in yeast cells occurs most often in symport with protons, which is in contrast to the situation in higher eukaryotes, in which Na$^+$ is often used as a coupling ion. In experiments to date, only a phosphate transport system has been reported to use Na$^+$ as a coupling ion (19). This latter observation implies that S. cerevisiae is able to generate a sodium motive force in addition to a $\Delta\psi$. Phosphate has also been shown to be transported in symport with either three (38) or two (165) protons. The gene encoding this phosphate transporter (PHO84) (see Table 6) has been sequenced and shown to be related to the family of yeast sugar transporters (26). Recently, Pho84p has been purified and functionally reconstituted into liposomes (14). The reconstituted enzyme transports phosphate in response to a $\Delta\psi$, showing that the overall transport is electrogenic, i.e., $\text{HPO}_4^{2-}/\text{H}^+$ or $\text{H}_2\text{PO}_4^-/\text{H}^+$, where $n \geq 3$ and $m \geq 2$.

Potassium transport across the plasma membrane is mediated by two kinetically distinct systems. The high-affinity transport system, encoded by TRK1 (102), is most probably a potassium/proton symporter. The low-affinity potassium transport system encoded by TRK2 (102) may not be a true secondary transport system, since its activity resembles that of a channel (see above). Deletion of TRK1 and TRK2 allowed the isolation of two genes which complement the trk1 trk2 potassium transport defect (65). Sequence analysis of these genes revealed that they are highly homologous and share high similarity with the galactose and glucose transporters encoded by GAT2 and HXT1-2, respectively. Gaber (65) postulated that these genes are sugar-dependent K$^+$ transporters involved in K$^+$ uptake. This would counteract the sugar-induced K$^+$ efflux via the K$^+$ channels described above.

Sugars. Transport of disaccharides in S. cerevisiae is mediated by proton symport systems (Table 4). Maltose is transported in symport with one proton (176, 208). Maltose transporters are encoded by at least five MAL genes, each MAL locus contains a maltose transport gene (MALX1, where $X$ is the number of the MAL locus), a maltase gene (MALX2), and at least two genes (MALX3 and MALX4) that encode proteins that regulate the expression of MalX1p and MalX2p (125). Growth of yeast cells on maltose induces synthesis of the maltose permeases by transcriptional activation. A complete description of the regulation of the MAL genes has not yet been given, since other gene products interfere with the transcription of the MAL genes. For instance, catabolite repression of the MAL genes by glucose is observed, but details of the underlying mechanism are largely unknown (125). For maltose transport, two kinetically distinct transport activities have been described (27, 36), a high-affinity
The amino acid carrier proteins are also homologous to various bacterial amino acid transporters (e.g., the *Escherichia coli* Lp, PheP, and AroP proteins) (188).

### Nucleosides

Transport of cytosine and uracil is mediated by proton symport (Table 6) (178). Amplification of the genes coding for these transporters (FCY2 for cytosine and FUR4 for uracil), using multicopy plasmids, results in at least 6- to 30-fold overexpression of proteins. In these recombinant strains, the basal rate of proton uptake is increased by a factor of at least 3 in the presence of uracil and a factor of 2 with cytosine, which corresponds with the proposed H⁺/symport mechanism for these nucleosides.

### Antiport

Antiport systems catalyze the exchange of various mono- and divalent cations for protons in the plasma membrane (56, 178). Detailed biochemical and genetic information on these antiport systems is limited, but these systems are likely to play a major role in cell volume control, regulation of cytoplasmic pH, and ion homeostasis of the cytoplasm. The recent cloning and characterization of *sod2*, a Na⁺/H⁺ antiporter of *Schizosaccharomyces pombe* (96), offers valuable prospects for further work on this class of transport systems.

The gene *ART1* was found to confer resistance to aminotrizaole, an inhibitor of the histidine biosynthetic pathway (99). On the basis of sequence comparisons, the *ART1* gene product, together with five homologs in *S. cerevisiae* (8), belongs to the major facilitator superfamily (116) and functions as an antiporter.

### Regulation of Secondary Solute Transport

*S. cerevisiae* has a number of signal-transducing pathways that enable the cell to respond to external stimuli. The cellular responses caused by these stimuli are thought to be mediated by proteins which reside in the plasma membrane. One of the best-studied examples is the cyclic AMP (cAMP) signalling pathway. If sugar-respiring or derepressed (grown on nonfermentable carbon sources) cells of *S. cerevisiae* are fed with glucose or other fermentable sugars such as fructose or sucrose, a number of metabolic changes occur very rapidly, including inhibition of gluconeogenesis (e.g., inactivation of fructose-1,6-bisphosphatase and other gluconeogenic enzymes), inhibition of various uptake systems (91), stimulation of glycolysis (activation of phosphofructokinase [131]), and mobilization of the storage sugar trehalose (203) (for reviews, see...
The addition of the fermentable sugar (first messenger) causes a rapid, transient increase in the level of the second messenger cAMP, which in turn activates (specific) protein kinases (117). Signal transduction from the first to the second messenger is mediated by the yeast RAS proteins and the RAS-activating protein, CDC25; this system is designated the RAS-adenylate cyclase pathway (117). The pathway regulates the activity of the membrane-bound adenylate cyclase, an enzyme that catalyzes the synthesis of cAMP. Knowledge about the upstream part of the pathway is limited, but the sensor of glucose-induced cAMP signalling could be one or more of the low-affinity glucose carriers or a specific glucose receptor (17, 192). The FDP1/GGS1 protein, previously thought to be the glucose sensor (193), is a subunit of the trehalose synthase complex and apparently regulates glucose transport (195).

As far as sugar metabolism is concerned, only sugar kinase activity is required for induction of the cAMP signal by glucose. Not only fermentable sugars but also intracellular acidification and nitrogen starvation can elicit a rapid activation or inactivation of enzymes known to be regulated by cAMP-dependent phosphorylation (194). Intracellular acidification, but not nitrogen limitation, constitutes an alternative means to activate the RAS-adenylate cyclase pathway. For activation of cAMP-dependent protein kinase A by the nitrogen source, a separate signal transduction pathway has been proposed which activates the enzyme at constant cAMP levels (192).

The phosphorylation of transport proteins by protein kinases, which are activated by cAMP, has been proposed to be a trigger for the controlled degradation of the protein. Alternatively, it is possible that conditions effecting cAMP-dependent protein phosphorylation coincide with those that effect transport protein breakdown. A role for cAMP-dependent protein kinase in (catabolite) inactivation of the glucose and galactose transporters is suggested from studies of mutants with different kinase activities (155). However, these results have recently been disputed by studies with similar mutants but different experimental conditions (161). For catabolite inactivation of the maltose transport protein, specific proteolysis of the protein is proposed (113), but the mechanism of this degradation has not been unravelled.

The uracil permease is stable in exponentially growing cells, but the turnover of the permease increases when the yeast cell approaches the stationary phase of growth, i.e. when the cells are starved of a nitrogen, phosphorus, or carbon source and/or when protein synthesis is inhibited (210). Recently, Galan et al. (66) showed that the substitution of an arginine by alanine in a cyclin-like destruction box in the primary amino acid sequence of the uracil permease protects the permease against stress induced degradation. A and B cyclins undergo regulated degradation at specific stages of the cell cycle, and conjugation of these proteins to ubiquitin appears to be essential for the targeting of the proteins for degradation (87). It is likely that the uracil permease is ubiquitinated, analogous to the ubiquitinated Ste6 protein (104), indicating a role of the stress-induced ubiquitin degradation pathway (60). For Ste6p and the uracil permease, the vacuole has been shown to be the site of degradation (45, 210). Both proteins are internalized from the cell surface via endocytosis, yielding endosomal membranes that travel to the vacuole. The hydrolytic enzymes of the vacuole degrade proteins via processes known as micro- and macroautophagy (6, 201). Microautophagy is the sequestration of small portions of the cytoplasm by invagination of the vacuolar membrane or by wrapping of a flapslike protrusion. Macroautophagy refers to the sequestration of organelles and cytosol within vesicles of the vacuolar system. It is very possible that the endosomal membranes containing the transporter proteins are sequestered into the vacuole by macroautophagy.

**ISOLATION OF FUNCTIONAL PLASMA MEMBRANES**

Some aspects of solute transport can be examined by using intact cells, but care should be taken of metabolic conversion and/or compartmentalization of the transported molecule. The interference of cytoplasmic processes or components with transport processes can often be restricted by using suitable substrate analogs or, even better, by using appropriate mutants in which the first step of the metabolism of a solute is blocked. However, because of complexity resulting from compartmentalization of solutes and the difficulty in manipulating energetic parameters, etc., it is often difficult to draw unequivocal conclusions regarding mechanisms of energy coupling to transport and the regulation of transport. Isolated plasma membrane vesicles, in which the effects of cellular metabolism are eliminated, have been used to study the facilitated diffusion of sugars and amino acids in yeast cells (62, 137, 139, 140, 156, 208). To isolate the plasma membrane vesicles, the membrane has to be separated from other cellular components. The first step is the removal of the cell wall, for which different strategies can be used. One of the commonly used methods involves the use of lytic enzymes that digest the b-linked glucan molecules of the cell wall. The resulting spheroplasts can be lysed, and plasma membranes are isolated by differential centrifugation and/or density centrifugation. This method has been widely used to study the composition of the plasma membrane (20, 142). Another method involves mechanical disruption of the cell wall with glass beads. This method is relatively harsh and can result in breakage of other cell organelles, which may cross-contaminate the plasma membrane fraction. After breakage of the cells, the membrane fractions are purified by differential centrifugation. In general, the mitochondria can be sedimented specifically by acid precipitation at pH 4.9, followed by centrifugation. The purity of the resulting plasma membranes can be assessed by monitoring the vanadate and azide sensitivity of the ATPase activities (Table 3). The (vanadate-sensitive) Pma1 ATPase is a marker enzyme for the plasma membrane, whereas the (azide-sensitive) F_{o}F_{1} ATPase is a marker enzyme for the mitochondria (69). By using mechanical disruption of the cell wall in combination with differential centrifugation, a plasma membrane purity of 90% can easily be achieved.

**FUSION OF PLASMA MEMBRANES WITH LIPOSOMES**

Isolated yeast plasma membranes do not constitute well-sealed vesicles but, rather, form membrane sheets, which are leaky to protons and other ions (177). Relatively well-sealed membranes can be obtained by fusing the membrane sheets with preformed liposomes (see below). However, a proton motive force cannot be easily generated in these membrane vesicles, since plasma membranes with a right-side-out configuration have the catalytic domain of the plasma membrane ATPase present at the inner surface of the membrane which is not accessible for ATP. In membranes which are inside out, ATP hydrolysis results in a reversed proton motive force (inside positive and acid), which is often not suitable for the study of membrane transport processes. Procedures have been described to generate artificially a $\Delta p$ across the membrane which has the appropriate orientation (inside negative and alkaline) (89). However, these potentials are not constant in time, which limits the applicability in the analysis of membrane transport (140). To generate a $\Delta p$ for longer periods, powerful $\Delta p$-gen-
erating systems can be functionally incorporated into mem-
brane vesicles of bacteria, fungi, and yeasts. The advantages
and disadvantages of different proton pumps and the methods
of membrane fusion have recently been reviewed (52). Cyto-
chrome c oxidase from bovine heart mitochondria is most
frequently used as an H+ pump to generate a Δp (inside
negative and alkaline), since this enzyme is most versatile in its
applicability (high activity, functional over a wide pH range).
For fusion of plasma membranes with cytochrome c oxidase-
containing liposomes, the membranes are mixed, frozen in
liquid nitrogen, and allowed to thaw undisturbed at room tem-
perature. This results in multilamellar membrane structures
that can be converted into unilamellar membranes by sonica-
tion or by extrusion of the hybrid membranes through filters of
defined pore size (205a). While bacterial membranes are rel-
atively resistant toward sonication, it appears that yeast plasma
membranes are not. For yeast membranes, the extrusion
method has proven to be superior to sonication. Moreover, the
extrusion method has the additional advantage that hybrid
membranes with a more uniform size are obtained. Typical
results of the uptake of maltose in hybrid membranes prepared
by sonication and extrusion are shown in Fig. 13.

SECRETORY VESICLES

A novel yeast protein expression system has been introduced
which takes advantage of the temperature-sensitive yeast mu-
tant with the sec6-4 mutation (215). This mutant is defective in
the final step of the vesicular secretory pathway. At the non-
permissive temperature, the sec6-4 mutant accumulates large
amounts of secretory vesicles which contain newly synthesized
plasma membrane proteins. The secretory vesicles can be iso-
lated with a high purity. The vesicles are well sealed, and the
plasma membrane Pma1 ATPase (127) and P glycoprotein
from mice (168) have been shown to be functional in these
membranes. Upon addition of ATP, a proton motive force
(inside positive and acid) is generated (127), indicating that the
orientation of the membranes is predominantly inside out with
respect to the plasma membrane. These vesicles are suitable
for the study of ATP-dependent transport and proton-linked
antiport processes.

FUNCTIONAL STUDIES IN HYBRID MEMBRANES

Studies on glucose and galactose transport in hybrid mem-
branes (62, 137, 156) have substantiated that these solutes are
indeed transported by unipart. However, a detailed character-
ization of these transport systems has not yet been undertaken.
In vitro evidence for solute-proton symport was first obtained
for the uptake of leucine (140). Transport studies of hybrid
membranes of S. cerevisiae have also been undertaken in an
attempt to estimate the proton/maltose stoichiometry of the
transport reaction (208). The CAN1 gene product, which fa-
cilitates arginine transport (90), has been studied in artificial
membranes following overexpression of the transport protein.
The $K_{app}$ values for arginine transport in the hybrid mem-
branes correspond to the values estimated in whole-cell studies
(139). By using hybrid membranes, the uptake of glutamate
and threonine has also been shown to be driven by the Δp
(205a). Furthermore, it has been demonstrated that transport
of arginine at very low substrate concentrations is reversible
upon dissipation of the Δp and that accumulated arginine can
be exchanged with excess of unlabelled arginine on the outside.
Similar observations have been made for maltose transport
(205a). These results are at variance with previous observa-
tions which indicated that transport of arginine and other
amino acids is unidirectional in S. cerevisiae (56, 139), trans
inhibition or substrate inhibition (92) following accumulation
of the substrate would form the basis for the observed irre-
versibility of transport (76). Our studies with hybrid mem-
branes indicate that kinetic asymmetry of the carriers may slow
the exit transport at high substrate concentrations but that the
transport reactions are fully reversible (205a). Finally, the
irreversibility of arginine transport in intact yeast cells is most
probably the result of the large capacity of the vacuole to
sequester basic amino acids by a mechanism of solute/proton
antiport (101, 171).

Studies on solute transport in membrane vesicles of bacteria
have revealed that the lipid composition of the membranes is
an important factor of transport activity (35, 53, 94). A study
on the influence of the phospholipid composition on transport
in yeasts, using hybrid membrane vesicles of Kluyveromyces
marxianus, suggested that transport of galactose is stimulated
by PE (207).

CONCLUDING REMARKS

The statement, made in the Introduction, that “the plasma
membrane separates the other membranes and cell compo-
nents from the external medium” is clearly an insufficient de-
scription of the many functions of the plasma membrane.
Many processes that are vital for the organism take place at the
plasma membrane. Applications of methods from both mem-
brane biochemistry and molecular genetics have been used to
analyze the molecular properties of the plasma membrane and
its constituents. The studies of the membrane biology in the
lower eukaryotes is most advanced for S. cerevisiae, but much
remains to be learned in the near future, as discussed below.

(i) The lipid composition of the plasma membrane is liable
to undergo changes under different growth conditions. It has
been shown that these changes can affect the activity of various

![Graph](image-url)
enzymes, including transporters and other plasma membrane associated proteins. For instance, enrichment of the plasma membrane with PI enhances the activity of the plasma membrane ATPase, whereas galactose transport is stimulated by PE. However, for none of these enzymes has a systematic study on lipid requirements been carried out. It is also clear that different strains of S. cerevisiae can have major differences in lipid composition, which emphasizes the need for a controllable model system which allows manipulation of the lipid composition.

(ii) The effects of the different components of the proton motive force (Δp) on the transport processes have never been investigated properly. This is a serious lack in our knowledge of the transport processes, since the Δp may not only be a driving force of the transport reaction but may also affect transport processes kinetically (148).

(iii) Unidirectional transport has been observed for almost all secondary transport systems studied to date. A thermodynamic basis for these observations has never been offered. Experiments with hybrid plasma membranes indicate that the transport processes are reversible. Kinetic asymmetry of the transporters may result in exit transport that is slow compared with uptake transport, in particular at high substrate concentrations.

(iv) The regulation of transport activity is poorly understood. The effect of protein phosphorylation on sugar transport is a matter of long-standing debate. Catabolite inactivation of various transporters is observed, but knowledge of the mechanisms of inactivation or targeting of proteins for proteolysis is lacking. The regulation of the uracil transport activity points to mechanisms of inactivation or targeting of proteins for proteolysis.

The regulation of the uracil transport activity points to mechanisms of inactivation or targeting of proteins for proteolysis. Reconstitution of purified targetsof posttranslational modification (regulation). Means may help to identify domains in the proteins that are targets of posttranslational modification (regulation).

The use of hybrid membranes and secretory vesicles will advance the molecular characterization of transport processes in yeasts. The regulation of transport activity by phosphorylation may be studied in these membranes by inclusion of phosphorylating enzymes (e.g., kinases). Reconstitution of purified transport proteins with various enzymes will allow the identification of factors that control transport activity such as phosphorylation. Detailed genetic analysis and manipulation of the genes encoding transport systems may provide insight into the molecular mechanism of transport but may also help to identify factors that affect the regulation of transport activity.

ACKNOWLEDGMENTS

This work was supported by the Foundation for Technical Sciences (Stichting Technische Wetenschappen) with financial aid from the Netherlands Organization for Scientific Research (Nederlandse Organisatie voor Wetenschappelijk Onderzoek) and by a grant from the Royal Gist-Brocades NV, Delft, The Netherlands.

We thank A. J. M. Driessen for providing some of the drawings.

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