The Nha1 antiporter of *Saccharomyces cerevisiae* mediates sodium and potassium efflux

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The NHA1 gene of *Saccharomyces cerevisiae*, transcribed into a 3-5 kb mRNA, encodes a protein mediating Na\(^+\) and K\(^+\) efflux through the plasma membrane that is required for alkali cation tolerance at acidic pH. Deletion of the gene in a wild-type strain resulted in higher sensitivity to both K\(^+\) and Na\(^+\) at acidic pH. Measurements of cation loss in strains carrying deleted or overexpressed alleles of NHA1 demonstrated its role in K\(^+\) and Na\(^+\) efflux. In addition, high K\(^+\) and Na\(^+\) efflux observed upon alkalinization of the cytoplasm implies a role of Nha1p in the regulation of intracellular pH. Moreover, the overexpression of ENA1 and NHA1 genes in an ena1Δ-nha1Δ strain showed that the Nha1 alkalinization antiporter is responsible for growth on high concentrations of KCl and NaCl at acidic pH, and Ena alkali-cation ATPases are necessary at higher pH values. Both systems have a complementary action to maintain the intracellular steady-state concentration of K\(^+\) and Na\(^+\).

**Keywords**: K\(^+\)/H\(^+\) antiporter, Na\(^+\)/H\(^+\) antiporter, salt tolerance, yeast

INTRODUCTION

The most abundant cation in *Saccharomyces cerevisiae* cells, as well as in most other eukaryotic and prokaryotic organisms, is K\(^+\), which is involved in numerous enzymic activities. In contrast, a high intracellular concentration of Na\(^+\) ions is toxic for most organisms, including yeast. Thus, organisms which lack the capacity to escape the environmental stress of increased NaCl concentrations, for example plants and fungi, must possess very efficient mechanisms for controlling the optimal intracellular concentrations of this cation. As K\(^+\) is capable of preventing most intracellular Na\(^+\) inhibitory effects, it seems clear that the intracellular K\(^+\)/Na\(^+\) ratio, which is proportional to net uptakes, i.e. differences between influx and efflux, plays a crucial role in the maintenance of cellular ionic homeostasis and reducing Na\(^+\) toxicity (Haro et al., 1991; Gómez et al., 1996; Rios et al., 1997).

An extensive study of potassium uptake in *Sacch. cerevisiae* revealed at least two genes which are thought to be components of a complex K\(^+\) transport system or independent potassium transporters: TRK1 and TRK2 (Ko & Gaber, 1991; Ramos et al., 1994). In addition, a K\(^+\) uptake channel has been detected in *Sacch. cerevisiae* by patch-clamp experiments (Bertl et al., 1995), but not yet genetically characterized. Less is known about potassium efflux, which is also an important component of ionic homeostasis. In *Sacch. cerevisiae*, about two-thirds of the K\(^+\) taken up is returned to the external medium (Rodríguez-Navarro & Ramos, 1984; Ortega & Rodríguez-Navarro, 1985). In depolarized *Sacch. cerevisiae*, potassium efflux is mediated by a channel encoded by a gene identified in the yeast sequencing programme (André, 1995) and characterized as TOK1 (Ketchum et al., 1995) or YCK1 (Zhou et al., 1995) by patch-clamp analyses in *Xenopus* oocytes and yeast, respectively. In addition, several reports have described in *Sacch. cerevisiae* an active K\(^+\) efflux mediated by a K\(^+\)/H\(^+\) antiporter (Ortega & Rodríguez-Navarro, 1985; Peña & Ramírez, 1991; Camarasa et al., 1996; Ramírez et al., 1996), but the gene(s) responsible has not yet been identified. Finally, it must be noted that the ENA1 gene involved in Na\(^+\) efflux (see below) could also be involved in K\(^+\) efflux, as has been suggested after characterization of ena1Δ-4 mutants (Haro et al., 1991) and in a biochemical study of Ena1p phosphorylation (Benito et al., 1997).

Concerning Na\(^+\), under non-stressed conditions, the amount of Na\(^+\) entering cells is very low. Upon salt...
stress this cation is believed to be taken up with low affinity by systems involved in transport of K⁺ and other ions. To prevent toxic effects, Na⁺ must be in turn efficiently extruded. The main system eliminating Na⁺ affinity by systems involved in transport of K⁺ and other ions from Sacch. cerevisiae cells is a Na⁺ ATPase encoded by the ENA1 gene allelic to PMR2 (Haro et al., 1991; Wieland et al., 1995). In most Sacch. cerevisiae strains, ENA1 is the first unit of a tandem array of four or five genes, depending on the strain (Garcia-de-la-Iglesia et al., 1993; Wieland et al., 1995). ENA2, ENA3 and ENA4 are expressed constitutively at low levels and ENA1 is induced by Na⁺, Li⁺ and high pH values (Garcia-de-la-Iglesia et al., 1993).

Considering that Ena1p is active mainly at alkaline pH values, a putative Na⁺/H⁺ antiporter active at acidic pH has been postulated (Rodriguez-Navarro & Ortega, 1982). This hypothesis was strengthened by two other observations: (i) the small residual Na⁺ efflux observed in ena1Δ mutants (Haro et al., 1991) and (ii) the characterization of Na⁺/H⁺ antiporters in other yeasts. In Schizosaccharomyces pombe, the efflux of intracellular Na⁺ is mediated by a Na⁺/H⁺ antiporter encoded by the sod2 gene (Jia et al., 1992). This protein shows some similarity to the human and bacterial Na⁺/H⁺ antiporters, and extensive homology to the product of the Zygosaccharomyces rouxii Z-SOD2 gene (Watanabe et al., 1995). In both yeasts, these antiporters are probably major systems for eliminating toxic Na⁺ cations from cells as the Na⁺ tolerance observed depends on the level of sod2 (Z-SOD2) expression. Recently, we have selected a Na⁺-resistant clone containing a truncated allele of the ORF YLR138w. Since the corresponding putative protein was highly similar to Schiz. pombe and Z. rouxii antiporters, we proposed that the cloned locus encoded a putative Na⁺/H⁺ antiporter and designated it NHAI (Prior et al., 1996).

This paper describes a functional study of the NHAI gene. In the first part, we report the cloning of the complete NHAI gene, characterization of its mRNA and attempts to increase its expression. In the second part, Western blots using a tagged Nha1p suggest that the protein is localized in the plasma membrane. In addition, the phenotypes of different strains with disrupted or overexpressed NHAI were determined and evidence for a pH-dependent role of Nha1p in Na⁺ and K⁺ tolerance was presented. Finally, results of Na⁺ and K⁺ efflux measurements demonstrate that, as previously assumed, the NHAI gene product is not only a Na⁺/H⁺ antiporter but is also an efficient K⁺/H⁺ antiporter.

**METHODS**

**Strains and media.** All Sacch. cerevisiae strains used in this work were derivatives of W303.1A (MATα ura3-1 trpl-1 his3-11/15 ade2-1 can1-100) and W303.1B (MATα) (Wallis et al., 1989); G19 (MATα) containing the deletion ena1Δ::HIS3::ena4Δ (Bañuelos et al., 1995); B31 (ena1Δ::HIS3::ena4Δ nha1Δ::LEU2) derived from G19 by substituting the 11 kb SnaBI-HincII fragment of NHAI by the LEU2 gene (a gift from A. Rodriguez-Navarro, Polytechnic University of Madrid, Spain); and C25 (MATα-nha1Δ::LEU2), obtained by crossing strains W303.1A and B31. In all experiments, strains were transformed either with appropriate 'empty' vector or with one of the plasmids described below. The strains were routinely grown in YNB minimal medium (2% glucose, 0.7% Bacto yeast nitrogen base without amino acids and nutritional requirements), or in complex YPD medium (1% yeast extract, 2% peptone, 2% glucose) at 30 °C. The K⁺ and Na⁺-free minimal liquid medium used in this study was arginine phosphate medium (AP) (Rodriguez-Navarro & Ramos, 1984) supplemented with KCl and NaCl as indicated.

**Plasmids.** To construct all the plasmids listed below we used the original pCS1 and two DNA fragments obtained by PCR. The complete NHAI ORF was amplified using primers 1 (5' GCTCTAGATATTTAGGCTATCTG 3') and 2 (5' GCTCTAGATATTTAGGCTATCTG 3'), and a DNA fragment corresponding to the last 2098 nucleotides of the truncated ORF was obtained with primers 3 (5' GGTAGGTCGACAGATGC 3') and 4 (5' CCATCGTACTTGGGAAATGAC 3'). Both DNA fragments were first cloned in pBluescript (Short et al., 1988) and sequenced. The plasmids were as follows: pCSMCY, complete NHAI gene with its own promoter and CYC1 terminator in YEp352 (Hill et al., 1986); pCSCY, truncated NHAI gene with its own promoter and CYC1 terminator in YEp352; pBS2, complete NHAI gene with its own promoter and CYC1 terminator in a single-copy vector derived from p416ADH (Mumberg et al., 1993); pMA52, complete NHAI gene with PGK1 promoter and PGK1 terminator in pYEPG15 (Brunelli & Pall, 1993); pMAADH426, complete NHAI gene with ADH1 promoter and CYC1 terminator in p426ADH (Mumberg et al., 1995); pMAPDP426, complete NHAI gene with GPD1 promoter and CYC1 terminator in p426GPD (Mumberg et al., 1995). For epitope tagging of NHAI, a Smal site was introduced by PCR before its stop codon using oligonucleotides 3 and 5 (5' TATAGCATGCTAATCCGCGGATCTCCTCGGTTGCGG 3') for the truncated version and oligonucleotides 3 and 6 (5' TATAGCATGCTAATCCGCGGATCTCCTCGGTTGCGG 3') for the complete NHAI version (Fig. 1). The following plasmids were then constructed: pCSEmyc, (truncated NHAI gene with its own promoter and c-myc epitope in its C terminus in YEpmyc181 (Reisdorf et al., 1993); pCSMEmyc, complete NHAI gene with its own promoter and c-myc epitope in its C terminus in YEpmyc181; pGB34, ENA1 gene with its own promoter in a single-copy vector, YCp50 (Haro et al., 1993).

![Fig. 1. Restriction map of the NHAI locus in chromosome XII of Sacch. cerevisiae and in the pCS1 plasmid. Arrows with numbers correspond to oligonucleotides used for PCR amplifications (see Methods).](image-url)
Salt tolerance determination. The growth capacity of yeast strains in the presence of NaCl or KCl was tested on solid YPD or YNB media inoculated with serial 10-fold dilutions of saturated cultures. Growth was recorded after 4 d. At the concentrations reported in Tables 1 and 2, no appreciable growth was observed. When growth was tested at pH 6.6 or 7.0, media were supplemented with 20 mM HEPES. To attain pH 5.5, HCl was added to the media, and for pH 3.6 tartaric acid was used after autoclaving.

Cation loading of cells. For slow K+ or Na+ loading, cells were grown overnight in AP medium pH 5.5 supplemented with the concentrations of KCl and NaCl. For rapid Na+ loading, cells grown in AP were transferred to 10 mM MES buffer adjusted to pH 5.5 with Ca(OH)₂ containing 2% glucose, 0.1 mM MgCl₂, 1 mM KCl and 50 mM NaCl and incubated in this medium for 10 min at 30°C.

Cation contents and loss. Samples of cells were withdrawn from the incubation mixtures at various time intervals, cells were collected on Millipore membrane filters, rapidly washed with a 20 mM MgCl₂ solution, acid-extracted and analysed by atomic emission spectrophotometry as described by Rodriguez-Navarro & Ramos (1984) and Haro et al. (1991). Measurements of Na+ or K+ loss were carried out in incubation buffer consisting of either 10 mM MES adjusted to pH 5.5 with Ca(OH)₂, or 10 mM TAPS [N-tris(hydroxymethyl)methyl-3-aminopropanesulfonic acid] adjusted to pH 8.0 with Ca(OH)₂. In both cases buffers contained 0.1 mM MgCl₂ and 2% glucose and were supplemented with KCl, RbCl or NH₄Cl as indicated. Results are reported as the means of at least four independent experiments. The standard errors of the means were 20% lower than the corresponding mean.

DNA and RNA manipulation. Manipulation of nucleic acids was done by standard protocols (Sambrook et al., 1989) or, where appropriate, following the manufacturer’s instructions. For Northern blots, total RNA was extracted as described by Carlson & Botstein (1982) and the probe was prepared as an in vitro run-off transcript (Quillet et al., 1989).

Western blot analysis. Yeast cells in the exponential phase of growth were harvested by centrifugation. Extracts from whole cells and plasma membranes were prepared and immuno-blotting performed as described previously (Matejcková & Sychrova, 1997). The primary antibody, monoclonal anti-c-myc 9E10 (1:250, Santa Cruz Biotechnology) was detected by chemiluminescence (ECL, Amersham) using HRP-conjugated anti-mouse IgG secondary antibody (1:2500, Sigma).

RESULTS
Cloning of the complete NHA1 gene and its expression in different vectors

The original plasmid (pCS1) selected by complementation of Na⁺ sensitivity of the strain HS100-3C (Prior et al., 1996) contained a truncated allele of NHA1 in which the 3’ terminal 294 bp of the coding sequence were missing, according to the GenBank/EMBL nucleotide sequence database (Fig. 1). In addition, the insert was a chimera, containing two short fragments from other chromosomes at both ends of the NHA1 insert. To study gene expression and to establish the role of the gene product, we amplified by PCR both truncated and complete NHA1 ORFs encoding proteins of 888 and 985 amino acid residues, respectively. The two DNA fragments were cloned with the NHA1’s own putative promoter region (0.7 kb) in the multicopy vector YEp352 (see Methods, plasmids pCSemyc and pCSMEmyc). Both plasmids were transformed into the Na⁺-sensitive B31 strain (enA1-Δ nha1Δ). As expected, overexpression of Nha1 proteins in B31 brought about a significant decrease in Na⁺ sensitivity.

Next, the DNA fragment corresponding to the complete NHA1 ORF was cloned in a series of vectors differing in promoters and/or copy number. Table 1 summarizes the Na⁺ tolerances of the B31 strain transformed with different plasmids harbouring the complete NHA1 ORF. Expression of the NHA1 gene behind strong promoters (PGKI, ADH1, GPD1) did not cause higher Na⁺ tolerance than that observed for NHA1 expression behind its own promoter, even though the amount of NHA1 mRNA in cells transformed with pMAADH426 was very high (Fig. 2a, lane 4). In the case of pMAGPD426, a plasmid with a very strong promoter (GPD1), the Na⁺ tolerance was only slightly higher but the growth of transformed cells was very slow, even in media without NaCl. Such an effect could result from overloading of the secretory pathway. A similar effect was observed during overexpression of the CAN1 gene (encoding a plasma membrane permease for basic amino acids), where the cells were full of mislocalized Can1p but their growth and transport activity were very low (H. Sychrová, unpublished data). In conclusion, the highest Na⁺ tolerance was observed in a strain transformed with a multicopy vector harbouring the truncated version of the NHA1 gene behind its own promoter.

Transcription of NHA1

NHA1 transcripts were visualized on Northern blots with a [32P]-riboprobe since our previous attempts using a DNA probe were unsuccessful. Fig. 2a) shows the levels of mRNA corresponding to the NHA1 gene, prepared from exponentially growing cells. As expected, no significant mRNA signal was detected in B31 in which the NHA1 allele had been deleted (lane 2). In all other strains (lanes 1, 3 and 4), NHA1 transcripts with an approximate size of 3.5 kb were detected. The expression of the NHA1 gene under the control of its own promoter was insensitive to the addition of NaCl to the culture medium (data not shown).

Western blot analyses

To visualize the product of NHA1 in Sacch. cerevisiae, we tagged Nha1p with the c-myc epitope. In plasmids pCSEmyc and pCSMEmyc, the sequence encoding the epitope (EQKLISEEDLN) was attached to the 3’ end of the gene behind the last codon of truncated (888 aa) and complete (985 aa) versions of NHA1, respectively. The attachment of the epitope did not influence the protein function: the expression of tagged NHA1 versions in Sacch. cerevisiae resulted in the same level of salt tolerance as in cells transformed with plasmids con-
Table 1. NaCl tolerance on YNB plates of Sacch. cerevisiae B31 transformed with different plasmids containing the complete NHAl ORF

At the concentrations reported, no appreciable growth was observed.

<table>
<thead>
<tr>
<th>Plasmid</th>
<th>Copy number*</th>
<th>Promoter</th>
<th>Terminator</th>
<th>NaCl tolerance (mM)</th>
</tr>
</thead>
<tbody>
<tr>
<td>YEp352 MC</td>
<td>MC</td>
<td>-</td>
<td>-</td>
<td>&lt;400</td>
</tr>
<tr>
<td>pCSMCY MC</td>
<td>MC</td>
<td>NHAl</td>
<td>CYCl</td>
<td>1000</td>
</tr>
<tr>
<td>pMA52 MC</td>
<td>MC</td>
<td>PGK1</td>
<td>PGK1</td>
<td>600</td>
</tr>
<tr>
<td>pMAADH426 MC</td>
<td>MC</td>
<td>ADH1</td>
<td>CYCl</td>
<td>900</td>
</tr>
<tr>
<td>pMAGPD426 MC</td>
<td>MC</td>
<td>GPD1</td>
<td>CYCl</td>
<td>400</td>
</tr>
<tr>
<td>pBS2 SC</td>
<td>SC</td>
<td>NHAl</td>
<td>CYCl</td>
<td>700</td>
</tr>
</tbody>
</table>

* MC, multicity; SC, single copy.

Fig. 2. Northern blot analysis of the NHAl transcripts in Sacch. cerevisiae with a 32P-labelled riboprobe. Total RNA was extracted from exponentially growing cells of wild-type W303.1A (lane 1), and the B31 strain (enal-46 nhalA) transformed with YEp352 (lane 2), pCSCY (lane 3) or pMA426ADH (lane 4). (a) RNA samples (60 µg in lanes 1, 2 and 3, 20 µg in lane 4) were run in agarose/formaldehyde gel, transferred to nitrocellulose membrane and hybridized with the NHAl probe. The probe corresponding to the last 2000 nt of the gene was obtained by in vitro run-off transcription from NHAl cloned in pBluescript and linearized by Hpal. The positions of the 3.5 and 1.8 kb rRNAs are indicated. (b) Ethidium-bromide-stained rRNAs on the membrane were visualized by UV light as a control.

Fig. 3. Immunodetection of c-myc-tagged complete Nha1p (lane 1), truncated Nha1p (lane 2) and Can1p (lane 3). (a) Total cell extracts (10 µg per lane); (b) isolated plasma membranes (10 µg total protein per lane).

taining original, non-tagged NHAl genes (data not shown).

The amount of complete and truncated c-myc-tagged Nha1 transporters in the cells was estimated using Western blots. Immunoreactive signals were first detected in total protein extracts of G19 strain containing either pCSEmyc, pCSMEmyc or 'empty' YEpmyc181. As a control, protein extracts from G19 cells transformed with the pCAMyc181 plasmid (Matejcková & Sychrova, 1997) containing a c-myc epitope-tagged version of the plasma membrane amino-acid permease CAN1 were also prepared. Fig. 3(a) shows that both tagged Nha1 proteins have an apparent molecular mass corresponding approximately to those calculated from deduced primary structures (109 and 98 kDa, respectively). No immunoreactive signal was detected in extracts from G19 cells transformed with 'empty' YEpmyc181 vector (data not shown). The amount of both truncated and complete Nha1 proteins in total cell extracts was much smaller than the amount of Can1p expressed in the same vector. If Western blot analysis was performed with purified plasma membranes, immunoreactive signals with similar relative intensities were detected (Fig. 3b), indicating that at least an important part of protein was localized in the plasma membrane. The smaller quantity of Nha1 protein in comparison with Can1p is probably due to the rather weak NHAl promoter, resulting in low expression. Moreover, on both types of Western blots, the signal corresponding to truncated protein was much weaker than the signal of the complete Nha1p, which suggests lower stability of the truncated version.

Role of the NHAl gene in Na+ and K+ tolerance

To assess the benefits of the NHAl gene for alkali cation tolerance, the growth of W303.1A-derived strains with different combinations of alleles enal-4/ENA1-4 and nha1Δ/NHAl was tested on plates of YPD medium at
Table 2. Na⁺ and K⁺ tolerance of Sacch. cerevisiae strains on YPD plates at different pH values

At the concentrations reported, no appreciable growth was observed.

<table>
<thead>
<tr>
<th>Strain</th>
<th>NaCl (mM)</th>
<th>KCl (mM)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>pH...</td>
<td>3:6</td>
</tr>
<tr>
<td>W303.1A (ENA1-4 NHA1)</td>
<td></td>
<td>500</td>
</tr>
<tr>
<td>C25 (ENA1-4 nha1Δ)</td>
<td></td>
<td>400</td>
</tr>
<tr>
<td>G19 (ena1-Δ NHA1)</td>
<td></td>
<td>350</td>
</tr>
<tr>
<td>B31 (ena1-Δ nha1Δ)</td>
<td></td>
<td>200</td>
</tr>
<tr>
<td>B31(pCSMCY)</td>
<td></td>
<td>700</td>
</tr>
<tr>
<td>B31(pCSCY)</td>
<td></td>
<td>900</td>
</tr>
<tr>
<td>B31(pGB34)</td>
<td></td>
<td>400</td>
</tr>
</tbody>
</table>

Fig. 4. Growth of strains expressing different combinations of NHA1 and ENA genes in the presence of KCl at different pH values. Serial 10-fold dilutions of saturated cultures were spotted onto YPD medium at pH 5.5, 6.6 or 7.0 supplemented with KCl as indicated.

different pH values and increasing concentrations of NaCl and KCl. These strains were also transformed with plasmids containing either complete NHA1 (pCSMCY), or truncated NHA1 (pCSCY) or ENA1 (pGB34).

Regarding the function of NHA1 in Na⁺ tolerance, at pH 7.0 NHA1 showed a very slight effect, which was only observed in the absence of the ENA genes. Overexpression of Nha1p did not show a significant effect at this pH [B31(pCSMCY) and B31(pCSCY) in Table 2]. At pH 5.5, the increase in tolerance caused by the presence of NHA1 was very clear in the absence of ENA genes, which encode a more effective system at this pH. Overexpression of Nha1p increased the Na⁺ tolerance above the level observed for the chromosomal NHA1 copy [Table 2, B31(pCSMCY) vs G19]. At pH 3.6, the results were similar to those described for pH 5.5, except that the lower activity of Ena ATPases, probably reflecting the loss of expression of ENA1 (Garcia-de-Blas et al., 1993), left a major role to Nha1p. At this pH the Na⁺ tolerance of the strain lacking the NHA1 gene (C25) was lower than the wild-type (400 mM and 500 mM NaCl, respectively, Table 2) and overexpression of NHA1 (either complete or truncated) increased the tolerance of the ENA1-4 nha1Δ strain over the limit of the wild-type. Interestingly, the truncated version of NHA1 conferred on cells higher Na⁺ tolerance than the complete gene (700 and 900 mM NaCl, respectively, Table 2).

Unlike the findings for Na⁺ tolerance, where the role of Nha1p seemed to be less important compared to that of Ena ATPases, K⁺ tolerance showed a distinctive function of Nha1p (Table 2). At pH 7.0, the effect of NHA1 presence was negligible, thus confirming that Nha1p as an electroneutral cation/proton antiporter does not function at this pH. Conversely, at pH 5.5, and especially at pH 3.6, the function of Nha1p in K⁺ tolerance was evident. At both acidic pH values, Ena ATPases had no effect in the presence of Nha1p (W303.1A vs G19) and the absence of the NHA1 gene decreased considerably the K⁺ tolerance, both in the presence (C25) or in the absence (B31) of ENA genes (Table 2). Interestingly, contrary to Na⁺ tolerance, overexpression of Nha1p did not improve K⁺ tolerance above the level of the wild-type, suggesting that factors other than K⁺ were already limiting growth when NHA1 was normally expressed. Comparing in more detail the effects of NHA1 and ENA genes at pH values ranging from 5.5 to 7.0, Fig. 4 shows
that Nha1p had a greater effect on K⁺ tolerance up to pH 6.6, but at higher pH values, Ena ATPases were more important (see ENA1 nha1 vs ena1 NHA1).

In summary, the results demonstrate the complementary functions of Ena ATPases and the Nha1 antiporter both for Na⁺ and especially K⁺ tolerances in cells growing at different pH values. The Ena ATPases are effective at moderately acidic or alkaline pH values, whereas at acidic pH values ionic homeostasis depends mainly on the activity of Nha1p.

### Intracellular K⁺/Na⁺ ratio

As it is likely that the positive role of Nha1p in Na⁺ tolerance is associated with maintenance of low intracellular concentrations of Na⁺, we estimated the influence of external Na⁺ concentration on the K⁺/Na⁺ ratio in cells of strains with deleted or overexpressed NHA1 and with the ena1-4Δ background to avoid the Na⁺ efflux mediated by Na⁺ ATPases. In the absence of NaCl in the growth medium, the internal concentration of K⁺ ions was almost constant in all strains tested including 'K⁺-sensitive' B31, independent of the external concentration of KCl ranging in our experiments from 1 mM to 0.5 M (data not shown). To measure changes in the K⁺/Na⁺ ratio, cells were grown in liquid AP media pH 5.5 containing a constant low concentration of K⁺ (1 mM) and increasing concentrations of sodium (0–100 mM).

If the cells were grown in the presence of NaCl, the total intracellular concentration of Na⁺ plus K⁺ was similar to the internal concentration of K⁺ in the absence of NaCl (Fig. 5). With increasing Na⁺ concentration in the media, a progressively larger part of the internal K⁺ was replaced by Na⁺ (Fig. 5). The K⁺/Na⁺ ratio in the cells depended not only on external Na⁺ concentration but also on the presence of Nha1p. Strains overexpressing NHA1 could preserve higher K⁺/Na⁺ ratios in the presence of higher concentrations of external Na⁺ than strains B31 and G19, and again, an advantageous difference for the truncated allele was observed [cf. Fig. 5, B31(pCSCY) vs B31(pCSCMY)]. We conclude that the function of Nha1p influences the intracellular K⁺/Na⁺ ratio, which in turn plays a very important role in Na⁺ tolerance. In our conditions, similar to that shown by Camacho et al. (1981), the K⁺/Na⁺ ratio must be higher than 1:2 to guarantee normal growth of cells in the presence of Na⁺.

### Nha1p mediates Na⁺ efflux

The high intracellular concentrations of Na⁺ in the B31 mutant accompanied by its defective growth suggested that Nha1p might mediate an efflux of Na⁺, similar to that observed for the homologous Sod2p in Schiz. pombe. To test this possibility we measured Na⁺ loss in strains with an ena1-4A background (to avoid the Na⁺ efflux mediated by Na⁺ ATPases) harbouring either a chromosomal copy of NHA1 (G19) or multicopy vectors with truncated [B31(pCSCY)] and complete [B31(pCSCMY)] NHA1 versions, respectively. As a negative control, the B31 strain lacking NHA1 was used.

To preload the cells of these four strains with equivalent amounts of intracellular Na⁺, cells were grown in the presence of different NaCl concentrations [20 mM for B31; 40 mM for G19; 60 mM for B31(pCSCMY); 90 mM for B31(pCSCCY)] to obtain an initial intracellular K⁺/Na⁺ ratio of about 1:1 (approx. 300 nmol mg⁻¹ of each). Na⁺-preloaded cells were resuspended in a Na⁺-free incubation buffer containing 50 mM KCl to prevent Na⁺ uptake and the loss of Na⁺ was followed over 20 min (Fig. 6). In accordance with observed differences in Na⁺ tolerance, B31 strains overexpressing NHA1 genes showed higher Na⁺ efflux than the G19 strain harbouring only one copy of NHA1. In the strain lacking both ENA1-4 and NHA1 (B31), no significant loss of Na⁺ was observed (Fig. 6). We also detected a difference in the initial rate of efflux mediated by truncated and complete Nha1 proteins, respectively. Slightly higher initial Na⁺ loss observed in cells with truncated Nha1 protein could explain their increased Na⁺ tolerance.

Further, we found that the initial rate of Na⁺ efflux in strains overexpressing NHA1 genes decreased with time and the efflux almost stopped at a certain intracellular Na⁺ concentration (approx. 120 nmol mg⁻¹). This could be due to an accumulation of a portion of the intracellular Na⁺ in vacuoles via the recently described Na⁺/H⁺ exchanger Nhx1p (Nass et al., 1997). To eliminate the possible distortion of our results brought about by intracellular sequestration of Na⁺, we loaded the cells very rapidly (incubation with NaCl for 10 min), transferred them to a Na⁺-free incubation buffer and the Na⁺ loss was measured. Under these conditions, the Na⁺
K⁺/H⁺ and Na⁺/H⁺ antiporter in Sacch. cereuisiae

K⁺/H⁺ and Na⁺/H⁺ antiporter in Sacch. cereuisiae

**K⁺/H⁺ and Na⁺/H⁺ antiporter in Sacch. cereuisiae**

**efflux from cells overexpressing Nhalp was continuous, leaving almost no Na⁺ ions in the cells within 20 min (data not shown).**

The tests described above were performed in the absence of external Na⁺, thus leaving unanswered the question of whether Nhalp can mediate Na⁺ efflux against a concentration gradient. To address this question, we measured the net Na⁺ loss in B31(pCSMCY) cells suspended in a buffer pH 5.5 containing a Na⁺ concentration similar to the initial internal Na⁺ concentration and a significant Na⁺ loss at an initial rate of about 5 nmol mg⁻¹ min⁻¹ was found (data not shown). This observation is in accordance with the putative Na⁺/H⁺ antiporter mechanism, in which Na⁺ efflux is driven by ΔpH.

**Nha1p mediates K⁺ efflux**

In addition to Na⁺ extrusion, K⁺ extrusion is also an important component of ionic homeostasis in cells. In Sacch. cereuisiae, two-thirds of the K⁺ taken up by growing cells is returned to the external medium (Rodriguez-Navarro & Ramos, 1984; Ortega & Rodriguez-Navarro, 1985). Several reports suggested that K⁺ efflux could be mediated by a K⁺/H⁺ antiporter (Ortega & Rodriguez-Navarro, 1985; Peña & Ramirez, 1991; Camarasa et al., 1996; Ramirez et al., 1996). Consistent with this notion and with the defective growth of NHA1-deficient strains (C25 and B31) in the presence of high concentrations of KCl, we studied the K⁺ loss from strains containing either no NHA1 (B31) or the chromosomal NHA1 gene (G19) to confirm the role of Nha1p in K⁺ efflux. Cells of both strains were grown at pH 5.5 in the presence of 3 mM KCl, harvested, resuspended in incubation buffer containing 200 mM RbCl, and the K⁺ loss from cells followed. Cells harbouring functional Nha1p (strain G19) lost K⁺ at an initial rate of about 2 nmol mg⁻¹ min⁻¹, whereas cells lacking the NHA1 gene did not show any appreciable K⁺ loss.

In cells grown in a medium containing NaCl and with approximately the same initial intracellular K⁺ and Na⁺
content (approx. 300 nmol mg⁻¹ of each), simultaneous measurements of the loss of both cations at pH 5.5 (in the presence of 20 mM RbCl to inhibit Na⁺ and K⁺ influx) showed (Fig. 7a) that the Na⁺ loss was only slightly higher than the K⁺ loss, indicating that Nhalp is able to mediate at acidic pH the efflux of both cations with comparable affinity.

As the efflux of Na⁺ is inhibited by permeable organic acids, which decrease the internal pH (Rodriguez-Navarro et al., 1981), the Nhalp function could be limited by the concomitant intracellular pH decrease, and similarly its activity could also be influenced by an increase in the cytosolic pH. In a first experiment, we measured Na⁺ and K⁺ losses in an alkaline incubation buffer (pH 8.0), and found that the increase in the external pH activated the effluxes, which were almost identical for both cations (Fig. 7b) (it is worth mentioning that these experiments were performed in the absence of external Na⁺ and K⁺, so the ΔpH was not necessary to drive the process). In a second experiment, we measured the Na⁺ and K⁺ loss from cells resuspended in an alkaline buffer containing 20 mM NH₄Cl (to increase the intracellular pH). Interestingly, as shown in Fig. 7(c), the alkalinization of the intracellular pH resulted in a very high efflux of both ions in the strain overexpressing NHA1. These conditions might also permit detection of another marginal system involved in K⁺ loss as the internal K⁺ concentration decreased very slowly in the strain lacking NHA1 (B31, Fig. 7c).

Based on these results, we conclude that not only is the product of the Sacch. cerevisiae NHA1 gene involved in Na⁺ efflux as predicted from its deduced primary sequence, but also that it plays an important role in K⁺ loss from cells.

**DISCUSSION**

The major goal of the present work was to characterize the function(s) of the product of the Sacch. cerevisiae NHA1 gene. Our present results show that the product of NHA1 is located in the plasma membrane and probably exchanges cytoplasmic K⁺ and Na⁺ with external H⁺.

The phenotype of increased salt tolerance obtained upon cloning the gene was enhanced by a truncation of the NHA1 ORF (Prior et al., 1996). The ability of a C-terminal truncation to increase protein activity has already been observed for other plasma membrane proteins (Grauslund et al., 1995). In the case of Nhalp, the truncation of 97 amino acids at 446 aa from the last putative transmembrane stretch, lowers the amount of protein present in the cells as indicated by Western blot analysis, perhaps as a consequence of elimination of some stabilizing region(s). Regarding these results, we are at present trying to characterize the function of the Nhalp C-terminal region in more detail.

Detection of tagged Nhalp in the isolated plasma membranes, together with measurements of K⁺ and Na⁺ losses from cells with functional Nha1p, suggest that Nha1p is located in the plasma membrane of Sacch. cerevisiae.

Although Nhalp has high amino acid sequence similarity with a Na⁺/H⁺ antiporter of Schiz. pombe, our results indicate that its role is more complex. Nhalp is not only involved in NaCl tolerance by mediating the efflux of Na⁺ like its Schiz. pombe homologue, but also plays an important part in K⁺ efflux and KCl tolerance at acidic pH values. Comparing the effects of the lack and overexpression of Nhalp on NaCl and KCl tolerance (Table 2), it can be proposed that the function of this protein is more important for K⁺ tolerance than Na⁺ tolerance. Because high KCl is not a natural stress, it can be deduced that the major function of Nhalp is related to K⁺ homeostasis, by maintaining the steady-state level of K⁺. Through this activity, Nhalp could participate in regulation of intracellular pH, cell volume and osmo-regulation. The finding of an antiport system mediating exchange of both K⁺ and Na⁺ with H⁺ is new in the physiology of yeasts. In Schiz. pombe, a role of Sod2p in K⁺ efflux has never been shown and the only systems characterized in yeasts as mediating K⁺ efflux are the Tok1p channel of Sacch. cerevisiae (Ketchum et al., 1995) and the Ena2 alkali-cation ATPase of Schwanniomyces occidentalis (Bañuelos & Rodriguez-Navarro, 1998).

As we observed that Na⁺ and K⁺ effluxes mediated by Nhalp are activated when the internal pH increases, we regard it as likely that the NHA1 antiporter has dual functions. At acid external pH, Nhalp participates in regulation of the internal concentrations of alkali cations using the high gradient of protons across the plasma membrane as a driving force to eliminate (when necessary) toxic amounts of Na⁺ or an excess of K⁺ from cells. When cytoplasmic pH increases, possibly when the external pH is in the upper limit for the growth of Sacch. cerevisiae, Nhalp could act as a short-term safety valve to contribute to the buffering of cytosolic pH by using the outward gradient of K⁺ (or Na⁺) which can drive in some protons.

The function of Nhalp cannot be considered redundant with the function of the Ena ATPases, which probably also exchange Na⁺ and K⁺ for H⁺ (Benito et al., 1997), but complementary. The requirement for two different systems (an alkali-cation/proton antiporter and an alkali-cation ATPase) for regulation of cellular alkali cation concentration may be connected with the natural environment of Sacch. cerevisiae cells in which acid pH values prevail, although growth at near neutral pH is also possible. In the fission yeast Schiz. pombe, which grows more strictly at acid pH, only a proton antiport mechanism for Na⁺ efflux has been demonstrated (Jia et al., 1992) (nothing being known about K⁺ homeostasis and efflux in this yeast). On the other hand, Schwan. occidentalis is able to grow at alkaline pH and it possesses two different types of alkaline-pH-inducible Na⁺ ATPases, mediating efflux of both Na⁺ and K⁺. In Schwan. occidentalis a Na⁺/H⁺ antiporter probably does not exist as no efflux of Na⁺ was detected in a strain...
with an *enaΔ* background at acid pH values (Bañuelos & Rodríguez-Navarro, 1998).

In *Sacch. cerevisiae*, the Nha1p function can be co-ordinated not only with *Ena1p* but also with the function of a Na⁺/H⁺ exchanger (encoded by the NHX1 gene) which mediates the active sequestration of Na⁺ in cells, probably in vacuoles (Nass et al., 1997). As was shown, this Na⁺ sequestration is enhanced when the intracellular pH decreases. Hence it would be interesting to study whether, upon exposure to NaCl, the toxic high concentration of Na⁺ is eliminated from the cytoplasm by cooperation of three systems, two of which are associated with the plasma membrane, a Na⁺ ATPase (Enap) and a Na⁺/H⁺ antiporter (Nha1p), and the third one located in the vacuole (Nhx1p). The action of Nha1p would import protons, resulting in a drop in intracellular pH which could trigger the sequestration activity of Nhx1p. The decrease in intracellular pH caused by the alkali cation/proton antiport activity of Nha1p could also play an important role in triggering other processes, for example response to osmotic shock and/or cell volume control. Thus our future studies will be focused on the general role of Nha1p in cell physiology.

The existence of at least two different mechanisms involved in yeast salt tolerance and their distribution in different yeast species according to their special needs during environmental stress may be an important feature of adaptation to salt stress. Therefore, the characterization of yeast Na⁺ and K⁺ transporting systems may be significant for the urgent biotechnological challenge of equipping crop plants with the capacity to grow in the world’s increasing areas of acid and salted soils (Serrano et al., 1997).

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