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Michael P. Dux

Mehmet Inan

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# Identification and characterization of calcium and manganese transporting ATPase (*PMR1*) gene of *Pichia pastoris*

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## Abstract

A gene homologous to *Saccharomyces cerevisiae* *PMR1* has been cloned in the methylotrophic yeast *Pichia pastoris*. The entire *P. pastoris* *PMR1* gene (*PpPMR1*) codes a protein of 924 amino acids. Sequence analysis of the *PpPMR1* cDNA and the genomic DNA revealed that there is no intron in the coding region. The putative gene product contains all of the conserved regions observed in P-type ATPases and exhibits 66.2%, 60.3% and 50.6% identity to *Pichia angusta* (*Hansenula polymorpha*), *Saccharomyces cerevisiae* *PMR1* and human *ATP2C1* gene products, respectively. A *pmr1* null mutant strain of *P. pastoris* exhibited growth defects in media with the addition of EGTA, but with supplementation of  $\text{Ca}^{2+}$  to a calcium-deficient media reversed the growth defects of the mutant strain. Manganese reversed the growth defects of the mutant strain; however, the cell growth was not as profound as the  $\text{Ca}^{2+}$ -supplemented media. The results demonstrated that the *P. pastoris* gene encodes the functional homologue of the *S. cerevisiae* *PMR1* gene product, a P-type  $\text{Ca}^{2+}/\text{Mn}^{2+}$ -ATPase. The DNA sequence of the *P. pastoris* *PMR1* gene has been submitted to GenBank under Accession No. DQ239958.

**Keywords:** *Pichia pastoris*; *PpPMR1* ; ATPase; calcium; manganese

## Introduction

A number of ion-motive ATPases have been identified in a broad variety of organisms, from yeast to human. They have been grouped into four major classes, the F-, V-, P- and ABC-type ATPases (Pedersen, 2002). The P-type  $\text{Ca}^{2+}$  ATPases, having very distinct biochemical characterization from the other ATPases, includes secretory pathway  $\text{Ca}^{2+}$  ATPases (SPCA), sarco/endoplasmic reticulum  $\text{Ca}^{2+}$  ATPases (SERCA), and plasma-membrane  $\text{Ca}^{2+}$  pumps (PMCA) (Ton *et al.*, 2002). The secretory pathway  $\text{Ca}^{2+}$  ATPase (SPCA) or their yeast counterparts (*PMR1* pumps) have attracted attention recently when Hailey–Hailey disease was linked to a mutation in the human *ATP2C1* gene (Hu *et al.*, 2000; Sudbrak *et al.*, 2000).

The yeast *PMR1* gene product was localized only in later compartments of the secretory pathway (Antebi and Fink, 1992; Sorin *et al.*, 1997) whereas SERCA pumps are expressed both in the ER and in the Golgi complex (Wuytack *et al.*, 2003). The yeast *pmr1* mutants fail to concentrate  $\text{Ca}^{2+}$  and  $\text{Mn}^{2+}$  within the Golgi secretory pathway, leading to defective growth in media containing BAPTA or EGTA (Rudolph *et al.*, 1989; Wei *et al.*, 2000). Addition of extracellular  $\text{Ca}^{2+}$  reversed these defects in *pmr1* mutant yeast strains (Antebi and Fink, 1992). Given the central importance of  $\text{Ca}^{2+}$  as an intracellular messenger, it should not be surprising that complex mechanisms exist in cells to manage and control  $\text{Ca}^{2+}$ . Much of the  $\text{Ca}^{2+}$  accumulates in the endoplasmic reticulum and calciosomes.  $\text{Ca}^{2+}$  is released when messenger signals are generated. These signals are translated into desired intracellular responses by calcium-binding proteins, which in turn regulate many cellular processes, including secretion of proteins. Recently, it has been shown that, in addition to its role as  $\text{Ca}^{2+}$  and  $\text{Mn}^{2+}$  pumps, the *PMR1* gene product plays a central role with cellular functions, such as glycosylation, sorting (Rudolph *et al.*, 1989), endoplasmic reticulum-associated degradation (ERAD) (Durr *et al.*, 1998; Ramos-Castaneda *et al.*, 2005), salt tolerance (Park *et al.*, 2001), cell shape (Cortes *et al.*, 2004) and virulence (Bates *et al.*, 2005). The *pmr1* mutant strains were also evaluated for improved secretion of heterologous recombinant protein productions (Ko *et al.*, 2002; Sohn *et al.*, 1998).

*P. pastoris* has become an organism of interest for heterologous protein expression for industrial applications. This organism is also suitable for studying cellular processes such as peroxisome biogenesis and protein secretion (Johnson *et al.*, 1999; Mogelsvang *et al.*, 2003; Payne *et al.*, 2000). In this study, we report identification of the *Pichia pastoris* *PMR1* gene (*PpPMR1*), which codes for a *S. cerevisiae* *Pmr1p* homologue and phenotypic characterization of the *PpPMR1*-disrupted mutant strain.

## Materials and methods

### Strains, media and standard methods

The *P. pastoris* strain used in this study was GS115 (*hi4*). *Escherichia coli* *TOP10* cells and the plasmid pAO815 were purchased from Invitrogen (Carlsbad, CA). *S. cerevisiae* AAY247 (a gift from Audrey Atkin, University of Nebraska, Lincoln, NE) was used as a positive control for PCR. The medium used for cell growth was YSD (yeast extract 10 g/l, Soytone 10 g/l, dextrose 20 g/l) or minimal dextrose (MD: yeast nitrogen base with ammonium sulphate without amino acids 1.34 g/l, dextrose 10 g/l, biotin 0.0004 g/l). MDH medium consisted of MD with the addition of histidine (0.0004 g/l). Solid media were prepared with a 15 g/l agar addition. Synthetic  $\text{Ca}^{2+}$  deficient medium was prepared as MD medium with the omission of  $\text{CaCl}_2$ , as previously

described in Rudolph *et al.* (1989). The only calcium ions in this medium were from calcium salt of panthothenate (0.84  $\mu$ M). The cultures were grown at 30 °C in a stationary incubator on plates or with shaking at 225 rpm in a reciprocal shaker.

All DNA manipulations were performed using methods described by Sambrook *et al.* (1989). The DNA probes were labelled with digoxigenin, using a High Prime DNA Labeling and Detection Starter Kit from Roche Molecular Systems Inc. (Alameda, CA). Restriction enzymes and the Quick ligation kit were from New England Biolabs (Ipswich, MA). The SMART<sup>®</sup> RACE cDNA Amplification Kit was from BD Clontech (Palo Alto, CA). The primers were purchased from Eurogentec North America Inc. (San Diego, CA).

### ***Cloning of P. pastoris PMR1 gene***

To identify the *P. pastoris* *PMR1* gene, forward (5'GGTTGCTGCTATTCCAGAAGG-3') and reverse (5'-CCAACGGCGTAGTTGAACAT-3') primers were designed, based on the consensus sequence of the *PMR1* DNA sequence from *S. cerevisiae* (P13586), which were highly homologous to *P. angusta* (AAC68831) and *Yarrowia lipolytica* (O43108). The genomic DNA of *P. pastoris* GS115 strain was used as a template, along with the above primers to amplify the *PpPMR1* gene fragment. As a positive control, another PCR reaction was run using *S. cerevisiae* genomic DNA with the same primers. The expected ~1.6kb PCR product, based on the *S. cerevisiae* *PMR1* gene, was gel-purified from the PCR product of *P. pastoris* genomic DNA and subcloned into a pCRII-TOPO vector. The fragment was sequenced at the University of Nebraska Lincoln Genomics Core Research Facility (GCRF) by the dideoxy method.

Total RNA of *P. pastoris* GS115 was prepared from YSD-grown cells. The cells were broken with 0.5 mm Zirconia/silica beads in a Bead Beater (BioSpec Products Inc., Bartlesville, OK) with 1 min breaking time followed by a 5 min resting interval. Total RNA was extracted with TRI reagent (Molecular Research Center Inc., Cincinnati, OH). mRNA was purified from total RNA with Oligotex Spin Column Purification Kit (Qiagen Inc., Valencia, CA).

The entire DNA sequence of *PpPMR1* gene was obtained by the rapid amplification of cDNA ends (RACE) PCR method. The 5' and 3' RACE Ready cDNA was prepared following the instruction manual from the SMART RACE cDNA amplification kit (BD Biosciences, San Jose, CA). This cDNA was used as a template for 5' and 3' RACE PCR reactions, using a 5' RACE primer (CTGCATGGCATTCAATGGATTTGGCAGGTTG) and a 3' RACE primer (GCTGAAGGTATCGCCACTCCACTCACAG), respectively, in separate reactions. The PCR products were gel-purified and subcloned into a pGEM-T vector (Promega, Madison, WI). Insert fragments were sequenced and then assembled into one sequence. The entire *PMR1* gene sequence was amplified from 5' RACE Ready cDNA and GS115 total genomic DNA with forward (GGACAACCTGTTATTTGCTTCTTTCCTGG) and reverse (GCACATGAACTATATCTAATG) primers. The PCR products were then subcloned into the pCRIITOP vector and the insert fragments were sequenced, with 12 primers covering the entire sequence twice.

### ***Disruption of the PpPMR1 gene***

The *PpPMR1* gene was disrupted with a DNA fragment encoding the functional *HIS4* gene, which was excised from the plasmid pAO815 (Invitrogen) with *Bam*HI and *Bgl* II. The gel-purified fragment was inserted into the *Bgl*III site of the *PpPMR1* gene in the pCRIIPpPMR1 plasmid.

Then the plasmid was digested with *Afl*III and *Sac*I restriction enzymes. The 6.1 kb linear *pmr1* disruption fragment (Figure 3B) was gel-purified and transformed into *P. pastoris* GS115 electrocompetent cells prepared according to the method described by Wu and Letchworth (2004). The transformed cells were plated on MD + 10 mM CaCl<sub>2</sub> plates.

The single colonies grown on MD + Ca<sup>2+</sup> plates were inoculated in YSD broth and grown overnight at 30 °C. Chromosomal DNA from the yeast cells was prepared from the YSD culture using a Yeast Pure Chromosomal DNA kit (Epicentre, Madison, WI). Chromosomal DNA (3 µg) from the chosen clones was cut with *Eco*RI enzyme and then separated on a 0.8% agarose gel. The DNA fragments were transferred to a positively charged nylon membrane (BioRad, Hercules, CA). The 600 bp of *PMR1* gene (*Eco*RI and *Bgl*III) fragment was used as a probe for Southern blot analysis by following the instructions of a High Prime DNA Labeling and Detection Starter Kit from Roche Molecular Systems, Inc. (Alameda, CA).

## Results and discussion

### Cloning and sequence analysis of the *P. pastoris* *PMR1* gene

The *PMR1* genes of several yeasts, including *S. cerevisiae* (Rudolph *et al.*, 1989), *Y. lipolytica* (Park *et al.*, 1998), *H. polymorpha* (Kang *et al.*, 1998), *Neurospora crassa* (Benito *et al.*, 2000), *Aspergillus niger* (Yang *et al.*, 2001), *Schizosaccharomyces pombe* (Cortes *et al.*, 2004), *Candida albicans* (Bates *et al.*, 2005) and *Aspergillus fumigatus* (Soriani *et al.*, 2005) have been identified and characterized. The *pmr1* null mutants of these yeasts showed growth defects in media containing EGTA or BAPTA. The addition of Ca<sup>2+</sup> reversed the growth defects of these mutants.

In order to clone the *PpPMR1* gene, a PCR experiment was carried out with two primers which were specific to the *S. cerevisiae* *PMR1* gene. The *S. cerevisiae* *PMR1* gene-specific primers were used rather than degenerate primers, due to high homology of the DNA sequences of conserved regions from *S. cerevisiae*, *P. angusta* and *Y. lipolytica* *pmr1* proteins. A 1.6 kb PCR product was obtained both from *S. cerevisiae* AAY247 and *P. pastoris* GS115 genomic DNA with the same primers. The sequence of the DNA fragment of *P. pastoris* revealed 65% homology to the *S. cerevisiae* *PMR1* gene. This fragment was likely a product of the *PpPMR1* gene. Specific RACE PCR primers were designed, based on the DNA sequence of the 1.6 kb fragment. The entire *PMR1* gene was obtained by RACE PCR. The 5' and 3' RACE PCR products were sequenced and assembled to one sequence. Finally, a full-length sequence encoding the entire *PpPMR1* gene was amplified, using first-strand cDNA and genomic DNA as templates with two specific primers. The sequences of the cDNA and genomic DNA products were identical, suggesting that the *PpPMR1* gene does not contain any intron.

The DNA sequence of *PpPMR1* and deduced amino acid sequence revealed that the coding region was 2772 bp, encoding 924 amino acids with a calculated molecular mass of 101 000 Da (Figure 1). The *pmr1* protein contained all of the 10 highly conserved regions (a–j) of P-type ATPases (Serrano *et al.*, 1986) (Figure 2). Comparison of amino acid sequences with secretory pathway ATPases revealed 66.2% and 60.3% identity with

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1 GGGACAAC TGTATTGCTTCTTTCCTGGTGGATTGAATTTGTAAGTCTCTGTAACCTTATTCTACTAGAGAGCTATTGGATTGAACAG
91 ATTTGGGCATTTAGTGAAC TCAAGATGACAGCTAATGAAAACTCTTTTGAGATGAGCTGACAGGATCTCTGGAATCTGCCGCCCTGCA
1 MTANENPFENELELTGSSSESAPPA
181 TTGGAATCGAAGACTGGAGAGTCTCTTAAGTATTGCAATATACCGTGGATCAGGTCATAGAAGAGTTTCAAACGGATGGTCTCAAAGGA
23 LE S K T G E S L K Y C K Y T V D Q V I E E F Q T D G L K G
271 TTGTGCAATCCAGGACATCGTATATCGGAGTCTTTCATGGCCAAATGAAATGGAAGTCGAAGAGGAAGAGTCTTTTTCGAAA
53 LCNSQD I V Y R R S V H G P N E M E V E E E E S L F S K
361 TTCITGTCAAGTTCTACAGCGATCCATTGATCTGTACTGATGGGTTCCGCTGTGATTAGCTTTTGTATGCTAACATTGATGATGCG
83 F L S S F Y S D P L L L L L M G S A V I S F L M S N I D D A
451 ATATCTACTACTGCAATTACGATCGTTGTACAGATTGGATTGTTCAGAGTATCGATCCGAGAAATCATTGGAGCATGAACAGG
113 I S I T M A I T I V T V T V G F V Q E Y R S E K S L E A L N K
541 TTAGTCCCTGCCGAAGCTCATCTAACTAGGAATGGGAACACTGAAACTGTCTTGTGCGCAACCTAGTCCCAGGAGACTTGGTGGATT
143 LVPAEAE AHL TRNGNTE T V L A A N L V P G D L V D F
631 TCGGTTGGTGACAGAATCCGGCTGATGTGAGAATTATTCACGCTTCCACTGAGTATCGACGAGAGCAACTTGGTGAATGAA
173 SVGDRIPADVRIIHASHLS IDE SN L T G E N E
721 CCAGTTTCTAAAGACAGCAAACTGTGAAAGTGTACCCAAACATCCCTTGACAGCCGTTTATGTATTGGGTATATGGGCATTTA
203 P V S K D S K P V E S D D P N I P L N S R S C I G Y M G T L
811 GTCTGTGATGGTAATGGCAAGGTATGTCTATCGGAACAGCAAAAACAGCTTTTGGCTCTGTTTTGGAAATGATGAGCTCTATTGAG
233 VR D G N G K G I V I G T A K N T A F G S V F E M M S S I E
901 AAACCAAGACTCCTCTCAACAGGCTATGGATAAACTTGGTAAGGATTTGCTGCTTTTCCCTGCGAATCATGGGCATCGGCTTG
263 K P K T P L Q Q A M D K L G K D L S A F S F G I I G L I C L
991 GTTGTTGTTTTCAAGGTAGACCTTGGTAAATGTTCCAGACTCTGTATTCTGGGCTGTGTCTATCCAGAAAGTCTTCTCTATT
293 V G V F Q G R P W L E M F Q I S V F W A V A A I P E G L P I
1081 ATTGTACTGTACTCTTCTCTGGTGTGTGCGTATGGTAAACAGAGGGCCATCGTCAAAAGACTGCCTAGTGTGAACTTTGGGA
323 I V T V T L A L G V L R M A K Q R A I V K R L P S V E T L G
1171 TCCGTCATGTTATCTGTAGTGATAAGACGGGAACATTGACCCAAAATCATATGACCGTAAACAGATTATGGACTGTGGATATGGCGGAT
353 S V N V I C S D K T G T L T Q N H M T V N R L W L T V D M G D
1261 GAAATCTTGAATTAACAAGGGGATCCATGCAAACTTACTCAAACCCGATACGCTAAAGTTCTGCAAACTGTGATATGATCAAC
383 E F L K I E Q G E S Y A N Y L K P D T L K V L Q T G N I V N
1351 AATGCCAAATATCAATGAAAAGGAAAAATACCTCGGAACCCAACTGTATGTCAATATTGAACTTTAGAAAAATTTGATTTGAG
413 N A K Y S N E K E K Y L E N G N T D I A I I E S L E K F D L Q
1441 GACATTAGAGCAACAAGGAAAGAAATGTTGAGATTCCATTTCTCGTCCAAGAAATATCAGGCGTCACTGTTCACCTGTGAGACAAA
443 D I R A T K E R M L E I P F S S K K Y Q A V S V H S G D K
1531 AGCAAATCTGAAATTTTGTAAAGCCCTCTGAACAAAGTTTGGAAAGATGTTCAAGATATTACAAGTCTGCAAGTATCGCCACTCA
473 S K S E I F V K G A L N K V L E R C S R Y Y N A E G I A T P
1621 CTCACAGATGAAATAGAAAGAAATCCTTGCAATGGCCGATAGCTAGCATCTCAGGATTGAGAATACTGCTGTTTGTCTACGACAAA
503 L T D E I R R K S L Q M A D T L A S S G L R I L S F F A Y D K
1711 GGCNAFTTGAAGAATCGGCGATGGACCATCGGATATGATCTTTGTGGTCTTTTAGGTATGAACGATCCCTCTAGACACTCTGTAAT
533 Q N F E E T G D G P S D M I E F C G L L G M N D P P R P S V S
1801 AAATCAATTTGAAATTCATGAGAGGTGGGTTACATATTATGATTACAGGAGATTCAGAATCCACGGCGTAGCCGTTGCCAAACAG
563 K S I L K F M R G G V H I M I T G D S E S T A V A V A K Q
1891 GTCGGAATGTAATGACAATCAAATATGCTGTCTTCCAGTGGAGACGATATAGATGCTATGAGTACAGACACTGCTCTAGGCGATC
593 V G M V I D N S K Y A V L S G D D I D A M S T E Q L S Q A I
1981 TCACATGTTCTGATTGCCCCGACTACTCCAAAACATAAGGTGTCATTTGAAGAGCACTACAGGCCAGGAGATATTGTTCAATG
623 S H C S T F A R T T P K H K V S I V R A L E V S F A D I V A M
2071 ACTGGTGACGGTGTCAATGATGCCCGACTTAAACTGGCCGACATCGGAATGGCATGGGTAATATGGGGACCGATGTTGCCAAAGAG
653 T G D G V N D A P A L K L A D I G I A M G N M G T D V A K E
2161 GCAGCCGACATGGTTTTGACTGTATGACTTTTCTACAACCTTATCTGCAATCCAGGAGGGTAAAGGTATTGTTTCAACAATCCAGAAC
683 A A D M V L T D D D F S T I L S A I Q E G K G I F Y N I Q N
2251 TTTTAAAGTCCAACCTTCTACTCAATTTGCTGCTTCTTGCTIAATGCTCTGAGTACTGCTTCAACTGCCAAATCCATGAATGCC
713 P L L T F Q L S T S I A A L S I A L S T A F N P N P L N A
2341 ATGCAGATTTGTGGATCAATATTATCTGGATGGACCTCCAGCTCAGCTTTGGGTTGTGAGCCAGTGTGATAAGCTGTGATGAAACAAA
743 M Q I L W I N I I M D G P P A Q S L G V E P V D K A V M N K
2431 CCACCAAGAAGCGAATGATAAAATCTGACAGTAAGGTGATTCAAAGGTAAGTACAAAGTAGTTTATCATCTGTTGTGGTACTCTG
753 P P R K R N D K I L T G K V I Q R V V Q S S F F I I V C G T L
2521 TACGTATACATGATGAGATCAAAGTATGATGAGTACAGCAGCAAGAGACACTACGATGACCTTTACATGCTTTGATCTTGGATCTGACATGTT
803 Y V Y M H E I K D N E V T A R D T T M T F T C F V F F D M F
2611 AACGCATTAACGACAAAGACCACTTCAAAGTATTGCAGAACTGGATGGAATAAATACTATGTTCAACTTTTCCGTTGCAGCTTCTATT
833 N A L T T R H E S K S I A E L G W N N T M F N F S V A A S I
2701 TTGGGTCACTAGGAGCTATTACATTTTTCAGCTCTATTTCCAGACTGAACCTCTGAGCTCAAAGATTGGTCCATTATTG
863 L G Q L G A Y I P F L Q S I F L T E P L S L K D L V H L L
2791 TTGTTATCGAGTTGAGTATGGATTGAGACAGCTTCGAAAACCTACTGCTCAGGAGACGTGACGATCCCCATACAATGGATACAGCATG
893 L L S S S V W I V D E L R K L Y V R R R R D A S P Y N G Y S M
2881 GCTGTTGATATAGATTTTAACTTAGAATCATTAGATATAGTTTTCATGTGCAAAAAAAAAAAAAAAAAAAAAAAAAA
923 A V *
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**Figure 1.** Nucleotide sequence and predicted amino acid sequence of *P. pastoris* PMR1 gene (GeneBank Accession No. DQ239958). The amino acid sequences corresponding to regions a-j of ATPases are underlined (Serrano, 1988)

those of *P. angusta* and *S. cerevisie* pmr1, respec-(regions a-j), the following putative functional. Relatively high sequence identity was found regions were detected: residues E318,N749 and with the human ATP2C1 (50.6%), human ATP2C2 D753 are predicted to be involved in binding of (47.2%) and mouse ATP2C1 (51.2%) gene prod-calcium ions, whereas Q<sub>758</sub> is predicted to be ucts. Other than those highly conserved domains involved in manganese ion binding (Wei *et al.*,

<p>Region a</p> <p>QEQYRSEKSLAENKLVPAEHLTR  QEQYRSEKSLAENKLVPELAHLTR  QEQYRSEKSLAENKLVPAECHLMR  QEQYRSEKSLAENKLVPEAHLIR  QEQYRSEKSLAENKLVPECHCVR  QEQYRSEKSLAENKLVPECHCVR  QEQYRSEKSLAENKLVPECHCVR  QEQYRSEKSLAENKLVPECHCVR  QEQYRSEKSLAENKLVPECHCVR  QEQYRSEKSLAENKLVPECHCVR</p>	<p>Region b</p> <p>VLAANLVPGDLVDFSVGDRIPADVR  VMASTLVPGDLVHFQVGDRIADVR  VLAATLVPGDLVHFQVGDRIADVR  VLAATLVPGDLVHFQVGDRIADVR  VLAATLVPGDLVHFQVGDRIADVR  VLAATLVPGDLVHFQVGDRIADVR  VLAATLVPGDLVHFQVGDRIADVR  VLAATLVPGDLVHFQVGDRIADVR  VLAATLVPGDLVHFQVGDRIADVR  VLAATLVPGDLVHFQVGDRIADVR  VLAATLVPGDLVHFQVGDRIADVR</p>	<p>Region c</p> <p>IDENSLTGENEPVSK  IDESNLTGETNPI SK  IDESNLTGENEPVHK  IDESNLTGETTPVTK  VDESSTGETAPCSK  IDESNLTGETTPCSK  VDESSTGETAPCSK  IDESNLTGETTPCSK  IDESNLTGETTPCSK  IDESNLTGETTPCSK</p>	
<p>Region d</p> <p>YMGTLVRDGNKGVIGTAKNTAFG  FMGTLVRDGHGSGVIVATSHKTAIG  YMGTLVKBGHGKGVIVGTGNTSPF  YMGTLVRDGNKGVIVGTGNTSPF  SMGTLVRCGKAGKGVIVGTGENSEFG  FMGTLVRCGKAGKGVIVGTGENSEFG  FMGTLVRCGKAGKGVIVGTGENSEFG  FMGTLVRCGKAGKGVIVGTGENSEFG  FMGTLVRCGKAGKGVIVGTGENSEFG  FMGTLVRCGKAGKGVIVGTGENSEFG  FMGTLVRCGKAGKGVIVGTGENSEFG</p>	<p>Region e</p> <p>FQISVFWAAVAIPEGLPIIVT  FQISVCLAVAAIPEGLPIIVA  FQISVSLAVAAIPEGLPIIVT  FTIGVSLAVAAIPEGLPIIVT  FTISVSLAVAAIPEGLPIIVT  FTISVSLAVAAIPEGLPIIVT  FTISVSLAVAAIPEGLPIIVT  FTISVSLAVAAIPEGLPIIVT  FTISVSLAVAAIPEGLPIIVT  FTISVSLAVAAIPEGLPIIVT  FTISVSLAVAAIPEGLPIIVT</p>	<p>Region f</p> <p>MAKQRAIVKRLPSVETLGSVNVICSDRTGTLTON  MAKQRAIVKRLPSVETLGSVNVICSDRTGTLTON  MAKQRAIVKRLPSVETLGSVNVICSDRTGTLTON  MAKQRAIVKRLPSVETLGSVNVICSDRTGTLTON  MAKQRAIVKRLPSVETLGSVNVICSDRTGTLTON  MAKQRAIVKRLPSVETLGSVNVICSDRTGTLTON  MAKQRAIVKRLPSVETLGSVNVICSDRTGTLTON  MAKQRAIVKRLPSVETLGSVNVICSDRTGTLTON  MAKQRAIVKRLPSVETLGSVNVICSDRTGTLTON  MAKQRAIVKRLPSVETLGSVNVICSDRTGTLTON  MAKQRAIVKRLPSVETLGSVNVICSDRTGTLTON</p>	
<p>Region g</p> <p>VKGAL  AKGAI  VKGAF  VKGAG  MKGAY  MKGAY  MKGAL  IRGAL  MKGAL</p>	<p>Region h</p> <p>FCGLLGMNDPPRPVSVKSIKLFMRGGVHIIMITGDESTAVAVAKQVGMV  FCGLLGMNDPPRPVSVKSIKLFMRGGVHIIMITGDESTAVAVAKQVGMV  FTGLLGMNDPPRPVSVKSIKLFMRGGVHIIMITGDESTAVAVAKQVGMV  FAGLMGLYDPPRPVSVKSIKLFMRGGVHIIMITGDESTAVAVAKQVGMV  FLGLVGIIDPPRPVSVKSIKLFMRGGVHIIMITGDESTAVAVAKQVGMV  FLGLVGIIDPPRPVSVKSIKLFMRGGVHIIMITGDESTAVAVAKQVGMV  FLGLVGIIDPPRPVSVKSIKLFMRGGVHIIMITGDESTAVAVAKQVGMV  FLGLVGIIDPPRPVSVKSIKLFMRGGVHIIMITGDESTAVAVAKQVGMV  FLGLVGIIDPPRPVSVKSIKLFMRGGVHIIMITGDESTAVAVAKQVGMV  FLGLVGIIDPPRPVSVKSIKLFMRGGVHIIMITGDESTAVAVAKQVGMV  FLGLVGIIDPPRPVSVKSIKLFMRGGVHIIMITGDESTAVAVAKQVGMV</p>	<p>Region i</p> <p>FARTTPRHKVSIVRALQARGDIVAMTGDGVNDAPALKLADIGIAM  FARTTPEHRVSIVRALQMRGDIVAMTGDGVNDAPALKLADIGIAM  FARATPEHKLNIVRALRKRKGVVAMTGDGVNDAPALKLADIGIAM  FARTSPEDMKMKIKVGFQRRGDVVAMTGDGVNDAPALKLADIGIAM  FYRASPRHKMKIKVGFQRRGDVVAMTGDGVNDAPALKLADIGIAM  FYRASPRHKMKIKVGFQRRGDVVAMTGDGVNDAPALKLADIGIAM  FFRTSPRHKMKIKVGFQRRGDVVAMTGDGVNDAPALKLADIGIAM  FYRASPRHKMKIKVGFQRRGDVVAMTGDGVNDAPALKLADIGIAM  FARTSPRHKMKIKVGFQRRGDVVAMTGDGVNDAPALKLADIGIAM  FARTSPRHKMKIKVGFQRRGDVVAMTGDGVNDAPALKLADIGIAM</p>	<p>Region j</p> <p>MGTDVAKEAADMLTDDDFSTILSAIEEGKGI <i>P. pastoris</i> (100%)  NGTDVAKEAADMLTDDDFSTILHAIREGKGI <i>P. angusta</i> (66.2%)  IGTDVAKEAADMLTDDDFSTILTAIEEGKGI <i>S. cerevisiae</i> (60.3%)  GGTDVAKEAADMLTDDDFATILSAIEEGKGI <i>Y. lipolytica</i> (56.3%)  TGTDVCKEAADMLTDDDFQTIMSAIEEGKGI <i>M. musculus</i> (51.2%)  TGTDVCKEAADMLTDDDFQTIMSAIEEGKGI <i>H. sapiens</i> ATP2C1 (50.6%)  TGTDVCKEAADMLTDDDFQTIMSAIEEGKGI <i>H. sapiens</i> ATP2C2 (47.4%)  CGTDVCKEAADMLTDDDFSTMTAAIEEGKAI <i>C. elegans</i> (47.9%)  GTDVAKEAADMLTDDDFSTILSAIEEGKGI Consensus</p>

**Figure 2.** Amino acid sequence alignment of with conserved domains (regions a–j) of homologous *PMR1* genes of *P. pastoris* (ABB70815), *P. angusta* (AAC68831), *S. cerevisiae* (P13586), *Y. lipolytica* (O43108), *M. musculus* (CAD82864), *C. elegans* (CAC19896), *H. sapiens* ATP2C1 (AAH28139) and *H. sapiens* ATP2C2 (NP 055676). GeneBank protein Accession Nos are given in parentheses following each organism name

2000; Mandal *et al.*, 2000). These analysis results demonstrate that the *PMR1* gene product is probably a Ca<sup>2+</sup>/Mn<sup>2+</sup> ATPase pump.

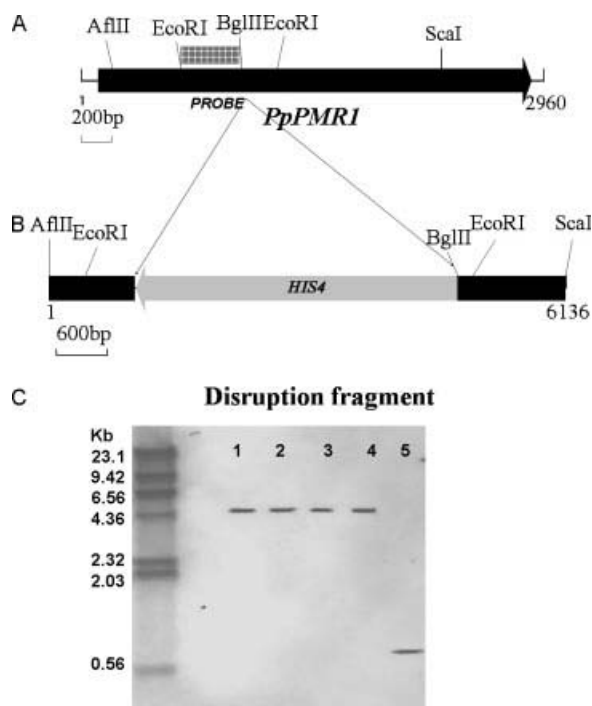
### **Disruption of *PpPMR1* and gene characterization of a null mutant**

To disrupt the *PpPMR1* gene, a 4 kb *Bgl*III/*Bam*HI fragment harbouring the functional *HIS4* gene of

*P. pastoris* from the pAO815 plasmid was inserted at the internal *Bgl*III site of the *PpPMR1* gene in the plasmid pCRII-*PMR1* (Figure 3A, B). The 6.1 kb *Af*II–*Sca*I fragment was gel-purified and transformed into the GS115 (*his4*<sup>−</sup>) strain. The colonies were screened for growth on MD plates with 10 mM CaCl<sub>2</sub>. Four colonies were further characterized by Southern blot analysis, using the DIG-labelled *Eco*RI/*Bgl*III (400 bp) fragment as a probe (Figure 3C). As expected, the mutant strains had a 4.5 kb band, while the host strain, GS115, had a 617 bp band with an expected intact *PMR1* gene. This result proves that the 6.1 kb fragment disrupted the *PpPMR1* gene, since the genomic DNA digested with *Eco*RI enzyme in Figure 3C shows the different band patterns.

After confirming that the *PpPMR1* gene was disrupted, clone #2 was chosen for further characterization experiments. To show that mutation in the *PMR1* gene of *P. pastoris* was

consistent with the previous *PMR1* mutations in different yeasts,

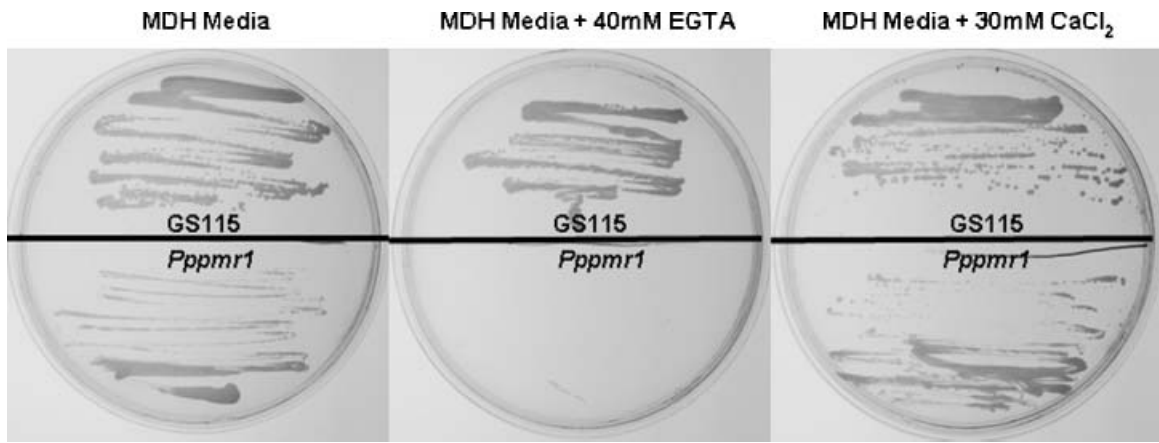


**Figure 3.** Disruption strategy of the *PpPMR1* gene. (A) Diagram of the coding region of the *PpPMR1* gene. The 400 bp *EcoRI*–*BglIII* fragment of *PpPMR1* was DIG-labelled and used as a probe for Southern blot analysis. Only relevant restriction enzymes are shown. (B) *PMR1* disruption fragment. A 4 kb *BamHI*–*BglIII* fragment encoding the *HIS4* gene is inserted at the *BglIII* site of the *PpPMR1* gene. The 6.1 kb *AflIII*–*ScaI* fragment was transformed into *P. pastoris* GS115 strain. (C) Southern blot analysis of *P. pastoris* chromosomal DNA. Lanes 1–4, *Pppmr1* mutant strains; lane 5, GS115. The molecular size of the DIG-labelled marker is also shown

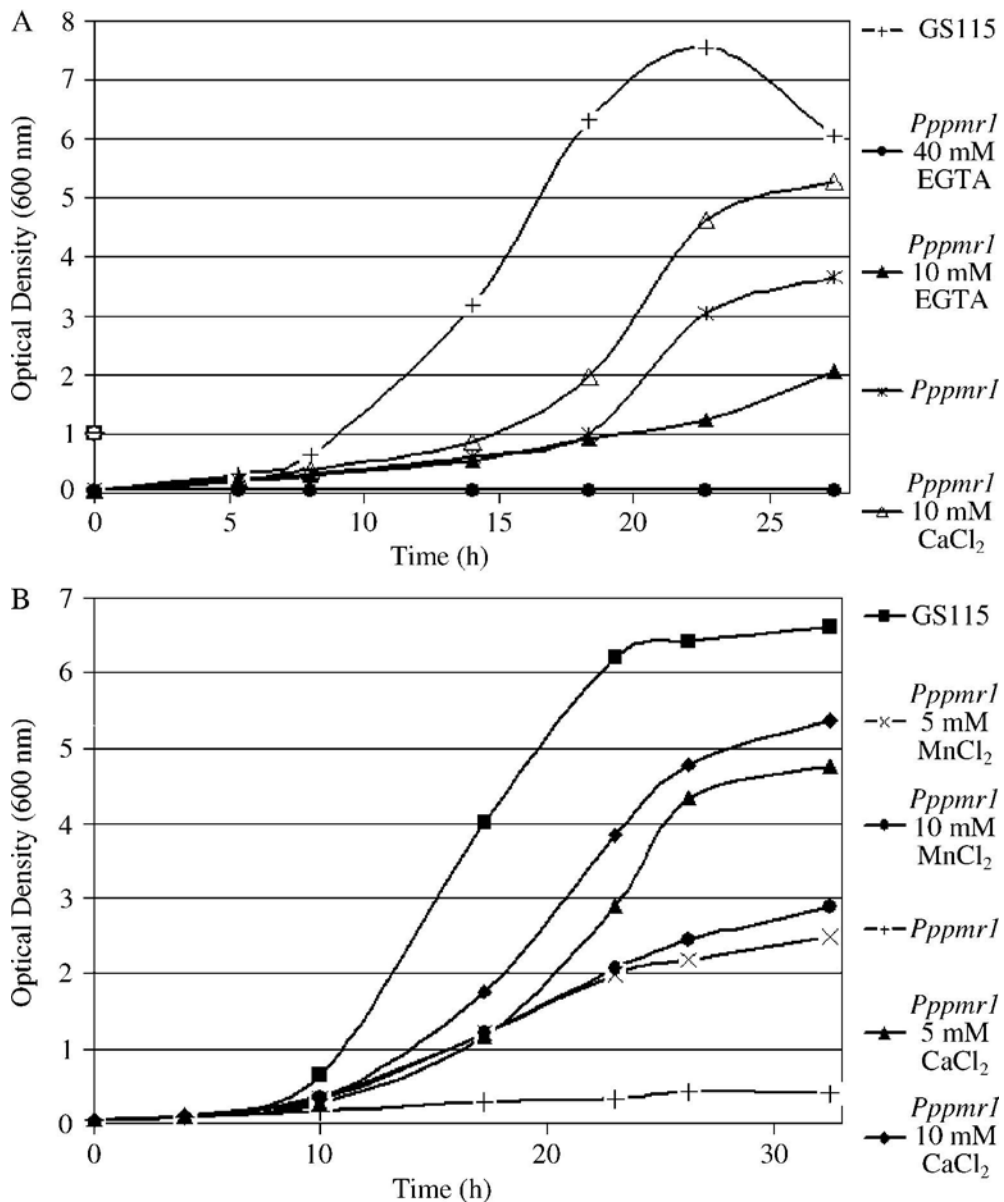
the GS115 wild-type strain and the mutant *Pppmr1* strain were plated on MDH plates, and MDH plates with the addition of either 40 mM EGTA or 30 mM  $\text{CaCl}_2$ . As shown in Figure 4, the *pmr1* mutant did not grow on minimal media containing EGTA, and the growth was reduced on MDH plates which had low  $\text{Ca}^{2+}$  concentration, but with the addition of 30 mM  $\text{CaCl}_2$  the *Pppmr1* strain growth recovered and was identical as the GS115 wild-type strain. The addition of 40 mM EGTA and 30 mM  $\text{CaCl}_2$  did not affect the growth of the GS115 strain on the plates.

The mutant strains' growth characteristics were evaluated further in liquid media. Figure 5A shows growth curves of GS115 in MDH and *Pppmr1* mutant in MD. It is clear from Figure 5A that the mutant had a longer lag time than GS115. The addition of 10 mM calcium to the medium slightly shortened the lag time by about 5 h. alternatively, the addition of EGTA (10 mM) prolonged the lag time and 40 mM EGTA stopped growth completely. These observations were in agreement with the report for other *pmr1* mutant yeast strains (Kang *et al.*, 1998; Park *et al.*, 1998; Rudolph *et al.*, 1989). Similar results were observed with  $\text{Ca}^{2+}$ -deficient media. The only calcium source in this medium was from the calcium salt of panthothenate, which was not enough to support the growth of the *Pppmr1* mutant, while GS115 growth was not affected (Figure 5B). The mutant strain did not grow during the 25 h of analysis on the  $\text{Ca}^{2+}$ -deficient media. Again, the



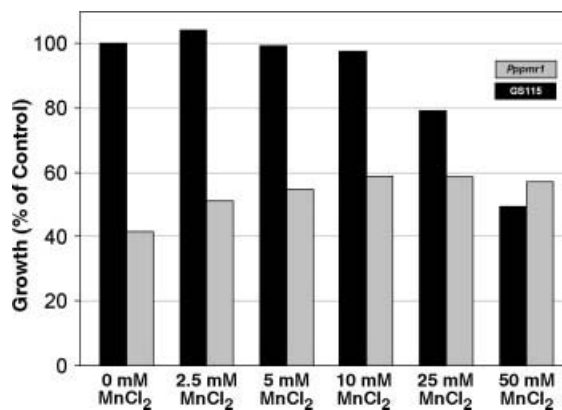


**Figure 4.** Growth characteristics of *P. pastoris* *Pppmr1* and GS115 on solid media. The indicated strains were grown for 2 days in YSD medium, then streaked on MDH, MDH + 40 mM EGTA, and MDH + 30 mM CaCl<sub>2</sub> plates. The plates were incubated for 3 days at 30 °C



**Figure 5.** Growth characteristics of *P. pastoris Pppmr1* and GS115 on defined media. (A) MD media. Growth of GS115 wild-type in MDH and the *Pppmr1* mutant in MD, MD + 10 mM CaCl<sub>2</sub>, MD + 10 mM EGTA, and MD + 40 mM EGTA. The results are an average of two separate experiments run in duplicate. (B) Calcium-deficient media. Growth (A600) of GS115 wild-type in calcium-deficient medium + histidine and the *Pppmr1* mutant in calcium-deficient medium, calcium-deficient medium + 5 and 10 mM CaCl<sub>2</sub>, and calcium-deficient medium + 5 and 10 mM MnCl<sub>2</sub>. The results are an average of two separate experiments run in duplicate

addition of 5 and 10 mM Ca<sup>2+</sup> did partially recover pathway Ca<sup>2+</sup>/Mn<sup>2+</sup>-ATPase, which acts as a growth. The addition of 5 and 10 mM MnCl<sub>2</sub> was Ca<sup>2+</sup>/Mn<sup>2+</sup> pump. able to promote the growth of the *pmr1* mutant, We have tested the *Pppmr1* mutant for man-but was not as significantly as Ca<sup>2+</sup>-containing ganese sensitivity, as reported in *S. cerevisiae* media. These results demonstrate that the *Pppmr1* by Wei *et al.* (2000). Interestingly, the *P. pas*-mutant strain is defective in a P-type secretion *toris Pppmr1* mutant did not show sensitivity to



**Figure 6.** Effect of MnCl<sub>2</sub> on growth of GS115 and *Pppmr1*. Growth of GS115 wild-type in MDH and the *Pppmr1* mutant in MD medium with varying concentrations of MnCl<sub>2</sub> (2.5–50 mM MnCl<sub>2</sub>), was measured after 48 h and is plotted as a percentage of growth of the control GS115 culture. The results are an average of two separate experiments run in duplicate

manganese concentrations up to 50 mM in MD medium (Figure 6). Regardless of the amount of manganese in MD medium containing about 1 mM CaCl<sub>2</sub>, *Pppmr1* showed 40–60% of growth of the GS115 strain, which was grown in MD medium without manganese supplementation. The GS115 strain showed about a 50% reduction in growth at the 50 mM MnCl<sub>2</sub> concentration, but not *Pppmr1*. This was contrary to *S. cerevisiae pmr1* mutants, which were shown to be hypersensitive to higher concentrations of manganese (>2mM) due to a loss of Mn<sup>2+</sup> transport outside the cell through the secretory pathway. (Lapinskas *et al.*, 1995; Wei *et al.*, 2000). However, this is not surprising, since manganese toxicity was also not observed in the *C. albicans pmr1* mutant (Bates *et al.*, 2005). Further investigation is needed to truly understand the differences between the *Pppmr1* mutant and the mutants shown by Lapinskas *et al.* (1995) and Wei *et al.* (2000).

Future research will also be focused on the effect of *Pppmr1* mutations on the secretion and processing of recombinant proteins. Mutations in the *PMR1* gene in different types of yeast have been shown to reduce outer chain glycosylation of secreted proteins (Ko *et al.*, 2002; Sohn *et al.*,

1998). *P. pastoris* has shown to be a very useful host system and this mutant strain should increase the usefulness in future of recombinant protein production.

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