



## Review

Inorganic phosphate uptake in unicellular eukaryotes<sup>☆</sup>Claudia F. Dick<sup>a,\*</sup>, André L.A. Dos-Santos<sup>a</sup>, José R. Meyer-Fernandes<sup>b,c,\*\*</sup><sup>a</sup> Department of Molecular Microbiology and Immunology, Johns Hopkins University Bloomberg School of Public Health, Baltimore, MD, USA<sup>b</sup> Instituto de Bioquímica Médica Leopoldo de Meis, Universidade Federal do Rio de Janeiro, Rio de Janeiro, RJ, Brazil<sup>c</sup> Instituto Nacional de Ciência e Tecnologia em Biologia Estrutural e Bioimagem, Rio de Janeiro, RJ, Brazil

## ARTICLE INFO

## Article history:

Received 11 November 2013

Received in revised form 27 February 2014

Accepted 17 March 2014

Available online 25 March 2014

## Keywords:

P<sub>i</sub> transporter*Saccharomyces cerevisiae**Neurospora crassa**Trypanosoma cruzi**Trypanosoma rangeli**Plasmodium falciparum*

## ABSTRACT

**Background:** Inorganic phosphate (P<sub>i</sub>) is an essential nutrient for all organisms. The route of P<sub>i</sub> utilization begins with P<sub>i</sub> transport across the plasma membrane.**Scope of review:** Here, we analyzed the gene sequences and compared the biochemical profiles, including kinetic and modulator parameters, of P<sub>i</sub> transporters in unicellular eukaryotes. The objective of this review is to evaluate the recent findings regarding P<sub>i</sub> uptake mechanisms in microorganisms, such as the fungi *Neurospora crassa* and *Saccharomyces cerevisiae* and the parasite protozoans *Trypanosoma cruzi*, *Trypanosoma rangeli*, *Leishmania infantum* and *Plasmodium falciparum*.**Major conclusion:** P<sub>i</sub> uptake is the key step of P<sub>i</sub> homeostasis and in the subsequent signaling event in eukaryotic microorganisms.**General significance:** Biochemical and structural studies are important for clarifying mechanisms of P<sub>i</sub> homeostasis, as well as P<sub>i</sub> sensor and downstream pathways, and raise possibilities for future studies in this field.

© 2014 Elsevier B.V. All rights reserved.

## 1. Introduction

One important role for cellular transport systems is to allow the entry of all essential nutrients into the cytoplasmic compartment and, subsequently, into organelles, allowing for the metabolism of exogenous sources of carbon, nitrogen, sulfur, and phosphorus [1]. Monitoring the external environment is necessary for all living cells, particularly microorganisms [2]. The extra- or intracellular environment of unicellular parasites must adapt to changes. The transport of ions and organic solutes is an important modification that allows the parasite to react to modifications in the external conditions, such as the acquisition of nutrients, the elimination of metabolic waste products, and the regulation of cell volume [3].

Inorganic phosphate (P<sub>i</sub>) is an essential nutrient required for a large number of cellular functions. In addition, P<sub>i</sub> is involved in many biochemical reactions related to the transfer of phosphoryl groups [4–6]. Low availability of P<sub>i</sub> in the environment is a limiting compound for the growth of several organisms [7].

Active P<sub>i</sub> uptake by the plasma membrane is central for the maintenance of P<sub>i</sub> homeostasis and is the initial point for the utilization of this

anion [8,9]. Because of the negative electrochemical potential across the cell membrane, anionic P<sub>i</sub> cannot accumulate in the cytosol by simple diffusion. Therefore, P<sub>i</sub> uptake must be coupled to an inwardly directed Na<sup>+</sup> or H<sup>+</sup> gradient to facilitate the transport of P<sub>i</sub> against the gradient [10].

Two important P<sub>i</sub>-responsive P<sub>i</sub> transporter families in unicellular eukaryotes are (i) the inorganic phosphate transporter (PiT) family (TCDB# 2.A.20) and (ii) the H<sup>+</sup> symporter (PHS) family (TCDB# 2.A.1.9). The PiT family consists of functionally characterized P<sub>i</sub> transporters that catalyze P<sub>i</sub> either by H<sup>+</sup> or by Na<sup>+</sup> symport. Members of the PiT family have 354 to 681 amino acid residues and 10 to 12 transmembrane domains. The PHS family is part of the major facilitator superfamily (MFS, TCDB# 2.A.1) and comprises P<sub>i</sub>:H<sup>+</sup> symporters of 400–600 amino acid residues and 12 to 14 transmembrane domains [1].

This review provides a critical overview of the recent findings regarding P<sub>i</sub>-responsive P<sub>i</sub> uptake in eukaryotic microorganisms.

2. *Neurospora crassa*

The filamentous fungus *N. crassa*, which plays a crucial role in modern genetics, was the first microorganism in which the P<sub>i</sub> uptake mechanism was identified. It possesses two non-homologous, high-affinity phosphate permeases, PHO-4 and PHO-5 [11]. Similar to other transport systems that have been studied in *Neurospora*, the phosphate transport system appears to depend on metabolic energy [12].

In cells previously grown in P<sub>i</sub>-free medium, P<sub>i</sub> transport increased significantly, with an 8-fold increase over the original rate [13]. When

<sup>☆</sup> This work is dedicated to Adalberto Vieyra on his 70th birthday.

\* Corresponding author. Tel.: +1 443 287 1588.

\*\* Correspondence to: J.R. Meyer-Fernandes, Instituto de Bioquímica Médica, Universidade Federal do Rio de Janeiro, 21941-590 Rio de Janeiro, Brazil. Tel.: +55 21 2562 6781; fax: +55 21 2270 8647.

E-mail addresses: [cdick@jhsph.edu](mailto:cdick@jhsph.edu) (C.F. Dick), [meyer@bioqmed.ufrj.br](mailto:meyer@bioqmed.ufrj.br) (J.R. Meyer-Fernandes).

*N. crassa* is grown with an adequate supply of phosphorus, phosphate ions are brought into the cells by the phosphate transport system I (PTS I – cyclohexamide-insensitive). This constitutive system has a low affinity for phosphate. The affinity decreases further with increasing pH, and the system barely functions above pH 7 [12]. In contrast, when the organism is grown under conditions of limiting phosphorus, a number of derepressible proteins are synthesized that are necessary for scavenging phosphorus from the environment. These proteins include a high-affinity phosphate permease, which is part of a functional entity called the phosphate transport system II (PTS II – cyclohexamide-sensitive) [13].

For the PTS II, Mann et al. [14] identified an ORF of *PHO-4* that encodes a membrane carrier protein. *PHO-4p* is a large hydrophobic polypeptide of 590 aa, with 12 transmembrane domains, and a  $K_m$  for  $P_i$  of  $2.56 \pm 0.19 \mu\text{M}$  [11]. In addition, *PHO-5* encodes a high-affinity phosphate permease, with a  $K_m$  value of  $37.4 \pm 2.75 \mu\text{M}$  [11]. This permease is 569 aa in length with 12 transmembrane domains [15]; however, there is no similarity between *PHO-4* and *PHO-5* [11]. Strains of *N. crassa* containing null alleles of both  $\Delta\text{pho-4}$  and  $\Delta\text{pho-5}$  are unable to grow under restrictive conditions, indicating that both comprise the high-affinity phosphate transport system (PTS II) of *N. crassa* [15]. *PHO-5* is active at neutral pH, whereas *PHO-4* is active in alkaline pH, providing  $P_i$  during alkaline stress. Moreover, *PHO-4*  $P_i$  uptake is coupled to the  $\text{Na}^+$ -gradient, whereas *PHO-5* is a  $\text{H}^+$ -phosphate symporter, suggesting that *PHO-4* and *PHO-5* may use different mechanisms for phosphate transport [16,11].

Activation of PTS II is regulated by the phosphorus acquisition system, which includes four regulatory genes, *NUC-2*, *PREG*, *PGOV* and *NUC-1* [17]. *NUC-1* is a transcription factor that requires nuclear localization to activate the transcription of structural genes related to  $P_i$  acquisition [18]. Under high phosphate conditions, a cytoplasmic interaction occurs between *PREG* and *PGOV* (a cyclin-like protein and a mitogen-activated protein kinase, respectively), and the *PREG*–*PGOV* complex scavenges *NUC-1* in the cytosol [19]. However, under low phosphate conditions, an ankyrin repeat protein, *NUC-2*, inhibits the *PREG*–*PGOV* complex and *NUC-1* is translocated to the nucleus, thereby activating the transcription of  $P_i$  responsive genes [20].

Recently, it was shown that a MAPK activation cascade, the *MAK-2* signaling pathway, is also related to the activation of  $P_i$ -repressible genes. In *N. crassa*, the *MAK-2* signaling pathway includes at least two other MAPKs, *NRC1* and *MEK-2*, which are involved in the hierarchical activation of *MAK-2* [21]. During  $P_i$  shortage, the two MAPKs are functional and inactive under abundant  $P_i$  conditions. Moreover, the *nuc-2* mutant strain of *N. crassa* presents similar levels of MAPK transcription, which suggests that the MAPK transcription rate is dependent on *NUC-2* activity and indicates the complexity of the metabolic phosphorus-sensing network [22].

### 3. *Saccharomyces cerevisiae*

Because unicellular eukaryotes, such as yeast, interact directly with the environment, the regulation of  $P_i$  transport is maintained solely by the transduction of nutrient signals across the plasma membrane [9]. The phosphate signal transduction pathway (PHO

pathway) is responsible for regulating the expression of several genes responsive to  $P_i$  that are involved in the scavenging and specific uptake of  $P_i$  from extracellular sources in yeast [5].  $P_i$  response, mediated by the PHO pathway, is determined by the activity and localization of the transcription factor *PHO4*, a homolog of *NUC-1* in *N. crassa*. Its localization is controlled by the phosphorylation activity of the cyclin and cyclin dependent kinase (CDK) *PHO80*–*PHO85* complex, which is homologous to *PGOV*–*PREG* in *N. crassa*. During  $P_i$  starvation, the CDK inhibitor *PHO81* acts on the *PHO80*–*PHO85* complex to inactivate it. This allows dephosphorylated *PHO4* to localize to the nucleus and associate with other transcription factor, such as *PHO2*, thus inducing the expression of  $P_i$  responsive genes [23,24].  $P_i$  responsive genes codify high affinity transporters (*PHO84* and *PHO89*), secreted acid phosphatases (*PHO5*, *PHO11*, and *PHO12*) and other proteins related to  $P_i$  metabolism [25].

Two major types of transporters are responsible for  $P_i$  incorporation in *S. cerevisiae*, a high-affinity and a low-affinity transporter system. The low-affinity transporter system comprises *PHO87*, *PHO88* and *PHO90*, and has an apparent  $K_m$  for external phosphate of approximately 1 mM. It has also been proposed that this system is constitutively expressed system due to its insensitivity to  $P_i$  starvation conditions [26, 27].

The high-affinity transporter system consists of two  $P_i$  transporters, *PHO-84* and *PHO-89*. *PHO-84* has the highest affinity ( $K_m = 8.2 \mu\text{M}$ ), whereas *PHO-89* has a low  $K_m$  value ( $K_m = 770 \mu\text{M}$ ) [28]. *PHO-84* is a  $\text{H}^+$ : $P_i$  symporter with high activity under acidic conditions [29]. *PHO-89* is a  $\text{Na}^+$ : $P_i$  symporter that is active under alkaline conditions, having a strong preference for  $\text{Na}^+$  [30]. *PHO-84* expression and *PHO-89* expression are regulated by PHO system activation during  $P_i$  starvation [31].

*PHO-84* belongs to the phosphate: $\text{H}^+$  symporter (PHS) family (TC No. 2.A.1.9.1). The protein encoded by *PHO-84* ORF contains 596 amino acid residues and has a molecular size of 65 kDa, homologous to *PHO-5* in *N. crassa* [29]. This symporter is responsible for the largest amount of  $P_i$  uptake and is very sensitive to phosphate starvation conditions [32]. Wykoff et al. [33] showed that deletion of *PHO-84* causes the loss of almost all phosphate transport, indicating that low-affinity transport is down regulated in response to phosphate limitation. PKA activation is essential for down-regulation and *PHO-84* degradation. Moreover, inhibition of PKA decreases *PHO-84* clearance from the plasma membrane in response to exogenous  $P_i$  increases [34]. *PHO-84* is part of the  $P_i$  sensor machinery and involved in the cellular responses to the exogenous  $P_i$  concentration [25]. In addition, *PHO-84* acts as a transceptor, suggesting that it also has a nutrient sensor function. However, *PHO-84* uses the same phosphate-binding site for transport and signaling. Using a nontransported  $P_i$  agonist, it was possible to determine that signaling requires a specific conformational change that may be part of the conformational changes that occur during transport but does not require the complete transport cycle [35].

Moreover,  $\Delta\text{pho84}$  cells under high- $P_i$  conditions overexpress *PHO87*, *PHO90*, or *PHO91*, thereby increasing the  $P_i$ -uptake ability and suppressing constitutive *PHO5* phosphatase expression [33]. This is a major distinction from the *N. crassa* homolog *PHO-5*, which presents no compensatory effects in  $\Delta\text{pho-5}$  cells [15].

**Table 1**  
Kinetic parameters of  $P_i$  transport in trypanosomatid parasites.

	<i>T. rangeli</i>		<i>T. cruzi</i>		<i>L. infantum</i>	
	$\text{H}^+$ : $P_i$	$\text{Na}^+$ : $P_i$	$\text{H}^+$ : $P_i$	$\text{Na}^+$ : $P_i$	$\text{H}^+$ : $P_i$	$\text{Na}^+$ : $P_i$
$K_{0.5, \text{Na}}$ (mM)	–	1.2	–	4.5	–	nd
$K_{0.5, \text{P}_i}$ ( $\mu\text{M}$ )	45	58	73	9	16	nd
$V_{\text{max}}$ (*)	7	17	13	13	9.4	nd
$P_i$	$\text{H}_2\text{PO}_4^-$	$\text{H}_2\text{PO}_4^-$	$\text{H}_2\text{PO}_4^-$	$\text{H}_2\text{PO}_4^-/\text{HPO}_4^{2-}$	$\text{H}_2\text{PO}_4^-/\text{HPO}_4^{2-}$	nd
ATPase	$\text{H}^+$ -ATPase	$\text{Na}^+$ -ATPase	$(\text{H}^+ + \text{K}^+)$ ATPase	$\text{Na}^+$ -ATPase	$(\text{H}^+ + \text{K}^+)$ ATPase	nd

\* $\text{pmol } P_i \times \text{min}^{-1} \times (10^7 \text{ cells})^{-1}$ .

nd – not detected.

Download English Version:

<https://daneshyari.com/en/article/1947486>

Download Persian Version:

<https://daneshyari.com/article/1947486>

[Daneshyari.com](https://daneshyari.com)