Ras-pathway has a dual role in yeast galactose metabolism

Mario G. Mirisola*, Alessia Gallo, Giacomo De Leo

Dipartimento di Biopatologia e Metodologie Biomediche, Via Divisi, 83, Università degli studi di Palermo, 90133 Palermo, Italy

Received 30 January 2007; revised 2 April 2007; accepted 2 April 2007
Available online 23 April 2007
Edited by Horst Feldmann

Abstract In the yeast Saccharomyces cerevisiae the genes involved in galactose metabolism (GAL1,7,10) are transcriptionally activated more than a 1000-fold in the presence of galactose as the sole carbon source in the culture media. In the present work, we monitored the activity of the GAL10 gene promoter in different Ras-cAMP genetic backgrounds. We demonstrate that overexpression of C-terminus of the nucleotide exchange factor Cdc25p stimulates GAL10 transcription in yeast strains carrying the contemporary deletion of both RAS genes. Moreover, the deletion of the chromosomal CDC25 gene provokes impaired growth on galactose based media in yeast strain lacking both RAS genes and adenylate cyclase (whose viability is assured by the presence of the Bcy1-11 allele). Surprisingly, reconstitution of the Ras-pathway inhibits GAL10-promoter activation. Activation of GAL10 gene promoter is indeed possible in the presence of Ras protein but only in strains with chromosomal deletion of adenylate cyclase. These results indicate a dual role of Ras-pathway on galactose metabolism and suggest that Cdc25p has a Ras-independent role in cellular metabolism.

© 2007 Federation of European Biochemical Societies. Published by Elsevier B.V. All rights reserved.

Keywords: Exchange factor; GTP-binding protein; Signal transduction; Galactose metabolism; Leloir pathway; Protein kinase A

1. Introduction

The Leloir pathway is the main enzymatic pathway for the conversion of galactose to glucose in organisms philogenetically distant as Escherichia coli and humans [1]. This conversion is mainly realized by three enzymes codified by genes collectively referred to as GAL genes in yeast: galactokinase (EC 2.7.1.6, GALK) corresponding to GAL1 in yeast, phosphorylates intracellular galactose to galactose-1-phosphate; galactose-1-phosphate uridytransferase (EC 2.7.7.12 GALT), corresponding to GAL7, transfers UMP from UDP-glucose to gal-1P forming UDP-gal, and, finally, UDP galactose 4'-epimerase (EC 5.1.3.2, GALE), whose yeast counterpart is GAL10, converts UDP-gal to UDP-glc, via a NAD+ dependent reaction [2].

Yeast cells respond to the presence of galactose as the sole carbon source with a several 1000-fold increase of the GAL genes expression [1–3]. These genes undergo a dual transcriptional regulation. They are repressed in the presence of glucose and activated in response to galactose [4]. Several experiments have demonstrated that activation and repression of the GAL genes act via independent pathways [5–7]. The major transcriptional activator of the GAL genes is the transcription factor Gal4p [8]. Gal4p is in turn subjected to two levels of regulation. It responds to the presence of intracellular galactose by 4-5-fold increase of its transcriptional level [6,8,9], and by post-translational modification of its interaction with the repressor Gal80p [10].

Many studies, in yeasts, have related the c-AMP-PKA pathway to diauxic shift [11–14]. Genetic manipulations of the Ras-cAMP pathway often result in galactose deficient phenotypes. Yeast strains expressing an hyperactivated RAS2 allele (RAS2G19V) show growth impairment on galactose-based media [15]. Furthermore, in strains with an activated allele of the adenylate cyclase (CYR1T1651I), contemporary deletions of both RAS genes or deletion of RAS1 combined with the presence of an attenuated RAS2 allele result in temperature-sensitive phenotype in galactose [16]. The Ras pathway has been demonstrated to be positively affected by two different nucleotide exchange factors: the essential Cdc25p and the non essential Sdc25p [17,18]. The overexpression of the former provokes growth inhibition in galactose [19] and enhanced transcription of the GAL4 gene [20]. Cdc25p has also been demonstrated to be essential for growth in galactose-based media [21]. We investigated the role of CDC25 and RAS2 gene products in galactose metabolism, monitoring the activity of the GAL10 gene promoter fused to human phenylalanine hydroxylase cDNA used as a reporter gene. This reporter was expressed in various yeast strains differing for the Cdc25p-Ras-cAMP pathway and the resulting activity of the GAL10 promoter measured.

2. Materials and methods

2.1. Media and yeast manipulation

YPD was used as rich medium (2% bacto peptone, 1% yeast extract and 2% glucose). Selective synthetic media were prepared with yeast nitrogen base without aminoacid at 0.67% final concentration, with the appropriate mixture of aminoacids and nucleic acid bases at the concentration indicated by Sherman [22], with glucose at 2% final concentration. Standard media containing carbon source different from glucose were obtained with 2% galactose in place of glucose. Genetic manipulation of yeasts were as described by Mortimer and Schild [23]. Yeasts transformations were carried out as described by Ito [24]. All components of media were from DIFCO (Becton Dickinson, CA, USA).

Abbreviations: PKA, protein kinase A; ATCC, American type culture collection; PAH, phenylalanine hydroxylase; RT-PCR, reverse transcriptase-polymerase chain reaction
Standard molecular biology methods have been performed as indicated by Sambrook et al. [25].

WOF6.1 (ras1Δras2Δcyr1::URA3 bcy1-11) strain was obtained transforming the ras1Δras2Δcyr1::HIS3 bcy1-11 (ABE2A, Verrotti et al., 1992) strain with the EcoRI/BamHI fragment of the pWOF6 vector (Fasano O. unpublished).

2.2. PAH reporter construction

The 1.8 kb Smal/HpaI fragment of the American type culture collection (ATCC) clone ATCC 61604, containing the entire coding region of the human phenylalanine hydroxylase (PAH) has been cloned into the unique SalI restriction site of the YEp51 yeast shuttle vector [26], after Klenow treatment to fill it in. The proper orientation of the insert has been verified by restriction analysis and joint ends have been verified by sequencing.

2.3. RNA preparation

The desired yeast strain was grown at 30°C, on the appropriate selective glucose-based medium, to OD600 = 0.8/1. Cells were collected by centrifugation and resuspended in the same medium, except for induced cultures, where galactose replaced glucose at the same concentration, and cultured at 30°C for additional 24 h. After centrifugation, the pellet, resuspended in acetate buffer (50 mM sodium acetate, 10 mM EDTA, pH 5), was vortexed for 5’ at 65°C in the presence of one volume of acid-washed glass beads (SIGMA G-1777, Milano, Italy) and one volume of phenol pH 5. The aqueous phase was extracted twice with chloroform and RNA was finally precipitated with 2.5 V of absolute ethanol, 0.3 M sodium acetate, pH 5.5. After centrifugation, the pellet was resuspended in TE 10:1. The RNA quality was verified evaluating the ribosomal RNA appearance after gel electrophoresis in denaturing conditions. Poly (A)⁺ RNA was obtained using a commercially available kit (QuickPrep™ Micro mRNA Purification Kit, Amersham, Milano, Italy), according to the manufacturer’s instruction.

2.4. RT-PCR

Poly (A)⁺ (1 μg) or total RNA, obtained as described above from the indicated yeast strain, was subjected to retro transcription in the presence of the RT primer indicated below in the presence of 1 μl of the Improm (Promega, Madison, WI, USA) reverse transcriptase at 42°C for 1 h, according to the manufacturer’s instructions. Different amounts of each cDNA were used for the subsequent PCR. The primers for the each PCR are indicated as For and Rev primers. PCR conditions for hPAH; GAL4; GAL50 were as follow: 94°C 30", 51°C 30", 72°C 45" for two cycles and 94°C 30", 60°C 30", 72°C 45" for additional 28 cycles. PCR conditions for CAP were 94°C 30", 51°C 30", 72°C 1’15" for 30 cycles. PCR conditions for CDC25 were 94°C 30", 58°C 30", 72°C 1’ for 30 cycles. PCR conditions for TYRI were 94°C 30", 54°C 30", 72°C 1’30" for 30 cycles.

2.5. Northern blot hybridisation

Total RNA (10 μg) were fractionated in a 1.0% agarose-formaldehyde gel and blotted onto nitrocellulose membrane (Schleicher & Schuell, PROTRAN BA 83, Dassel, Germany), via capillary action as described by Sambrook [25]. Filters were baked at 80°C for 2 h under vacuum. RNA blots were prehybridized with prehybridization buffer

<table>
<thead>
<tr>
<th>Primer name</th>
<th>DNA sequence 5’ → 3’</th>
</tr>
</thead>
<tbody>
<tr>
<td>hPAH-RT</td>
<td>gagggcaactgcaggatcc</td>
</tr>
<tr>
<td>hPAH Probe For</td>
<td>asacctgacccatagtatagacc</td>
</tr>
<tr>
<td>hPAH Probe Rev</td>
<td>tggcccatttttttcctcttc</td>
</tr>
<tr>
<td>GAL4-RT</td>
<td>cocctgtagacctcaaaag</td>
</tr>
<tr>
<td>GAL4-For</td>
<td>goggggctttcttgatctagca</td>
</tr>
<tr>
<td>GAL4-Rev</td>
<td>gssgcaacgctgaagatga</td>
</tr>
<tr>
<td>GAL80-For</td>
<td>toctgccggcagcggttac</td>
</tr>
<tr>
<td>GAL80-Rev</td>
<td>gcattcagaaaaaggaaat</td>
</tr>
<tr>
<td>GAL80-RT</td>
<td>gctgcacagaaaaaaggaaat</td>
</tr>
<tr>
<td>CAP-For</td>
<td>oggggtocatcatagtctgcagcttacca</td>
</tr>
<tr>
<td>CAP-Rev</td>
<td>eggggtcaggcttacagctaadtaacgatcagctaadacggatcagcatcactgtaaaacacctctctcagtcttgccagt</td>
</tr>
<tr>
<td>CAP-RT</td>
<td>tgggcattttttttgtctgctg</td>
</tr>
<tr>
<td>Cdc25-RT</td>
<td>tgaggcggcasacagggacatg</td>
</tr>
<tr>
<td>Cdc25-For</td>
<td>egctgcaggctcagcggcagctctca</td>
</tr>
<tr>
<td>Cdc25-Rev</td>
<td>gctaatatttttgaaacctagcattt</td>
</tr>
<tr>
<td>TYRI-RT</td>
<td>gggagaaagaggcagctcatc</td>
</tr>
<tr>
<td>TYRI-For</td>
<td>gctaatatttttgaaacctagcattt</td>
</tr>
</tbody>
</table>
(0.5 M Na₂HPO₄, pH 7.2, 7% SDS, 1 mM EDTA) at 65 °C for 2 h. The filters were then hybridized consecutively with random primer-labelled human PAH cDNA probes (Readyprime Kit, Amersham). After hybridisation, RNA filters were washed for 30 min with 50 ml of 40 mM Na₂HPO₄ pH 7.2, 1% SDS at 65 °C. The filters were blotted dry and exposed to X-ray film (X-OMAT, Eastman Kodak, Rochester, NY, USA) for 24–48 h at −80 °C.

2.6. Western blotting and immunodetection

Western blot of the human PAH protein has been performed as described by Mirisola et al. [27]. Western blot of Cdc25p has been performed using a 1:200 dilution of a commercially available anti Cdc25p antibody (Cdc25 (yC-19): described by Mirisola et al. [27]. Western blot of Ras2p has been done using a polyclonal antibody obtained as described by De Vendittis et al. [45] following the procedure previously described.

3. Results and discussion

3.1. Constructing the reporter plasmid

The coding sequence of the human phenylalanine hydroxylase gene (hPAH) has been cloned under the control of the GAL10 gene promoter of the shuttle vector YEp51 [26] to generate the reporter plasmid YEp51-PAH (for details, see Section 2).

The use of human PAH gene as a reporter has various advantages. PAH protein, normally expressed in mammalian liver cells, is a key enzyme in the production of tyrosine by means of phenylalanine hydroxylase [28]. Yeast cells produce tyrosine throughout a pathway that does not involve any hydroxylation reaction [29]. In addition, BLAST analysis, even querying with the otherwise conserved PAH catalytic domain alone revealed no significant homology between PAH sequence and the whole yeast genome. These two features guarantees minimal interference of reporter expression on phenotype analysis and virtually no cross-hybridisation effect in Northern or reverse transcriptase-polymerase chain reaction (RT-PCR) experiments.

Western blot using a commercial monoclonal antibody raised against PAH (PH8) of crude protein extracts confirmed the ability of the reporter to drive the expression of human PAH (Fig. 1). The in vivo neutrality of the PAH gene expression was confirmed in various genetic backgrounds (results not shown) and in different growth conditions.

3.2. Effect of the CDC25 gene overexpression on GAL10 promoter activity

A positive relationship between CDC25 gene overexpression and GAL genes transcriptional derepression has been previously reported [20,21]. We tested if Cdc25p acts on galactose metabolism via its well established role as nucleotide exchange factor (GEF) of the Ras proteins [30,17] or by an unknown metabolism via its well established role as nucleotide exchange factor [16]. Competent cells of this recipient yeast strain, expressing episcopal reporter PAH gene under the control of the yeast GAL10 gene promoter (YEp51-PAH) were transformed with CDC25 expression plasmids, either full length or C-terminus (pIND25-2H and pIND25-1H, respectively) or with the empty vector. Total RNA extracted from selected transformants grown on galactose, as described in Section 2, were analysed by RT-PCR, using PAH-specific oligonucleotides. We demonstrate that in the absence of both RAS genes, overexpression of the truncated form of Cdc25p is capable to activate the GAL10-dependent transcription of the PAH reporter gene (Fig. 2a) while full length Cdc25p has only a marginal effect. The different activity between full length and truncated version of Cdc25p can be explained by the different amount of the two proteins. Only the truncated form of Cdc25p can be efficiently overexpressed [20]. It has been demonstrated that full length Cdc25p, compared to its truncated version, has a reduced stability [34] probably caused by the presence of a cyclin disruption box in its N-terminus moiety [44].

To further confirm that C-terminus of Cdc25p is capable to activate GAL10-driven transcription we performed Northern blot analysis of poly (A)+ RNA extracted from the same yeast strains with or without the overexpression of the truncated Cdc25p. Radioactively labelled PAH coding sequence has been used as a probe in stringent hybridisation conditions (for details, see Section 2). A strong enhancement of the PAH-specific expression signal resulted in the presence of Cdc25 overexpression (Fig. 2b). In addition, whole protein extracts for details, see Section 2) from the same yeast strains were analysed by RT-PCR, using PAH-specific oligonucleotides. We confirmed (Fig. 2c) the ability of the C-terminus of Cdc25p nucleotide exchange factor to stimulate GAL10-dependent transcriptional activity. This result clearly indicates, for the first time, that Cdc25p has a Ras-independent role on galactose metabolism. Since GAL genes are normally activated by a 4–5-fold transcriptional increasing of GAL4 mRNA [6,8,9] we measured the mRNA level of GAL4 and GAL80 in the presence and in the absence of C-terminus Cdc25p. Total RNA from strains lacking both RAS genes and overexpressing
specific for GAL4 and GAL80 RNAs. From this experiment GAL4 transcript level results almost doubled in the presence of Cdc25p while GAL80-specific RNA appears unaffected (Fig. 3). This suggests that the Cdc25-dependent activation mechanism of GAL genes acts, directly or indirectly, enhancing the transcription and/or mRNA stability of the GAL4 gene. Van Aelst and coworkers have previously demonstrated that Cdc25p overexpression abolishes glucose repression of invertase activity in yeast cells [47]. Unfortunately, the plasmids we have used to overexpress Cdc25p are under the control of the GAL10 gene promoter limiting the possibility to observe the role of Cdc25p on glucose-based media. It would be interesting to overexpress Cdc25p under the control of a different gene promoter to see if Cdc25p is capable to relieve glucose repression of GAL genes expression both with and without the presence of RAS function.

The possibility of physical interaction of Cdc25p with proteins other than Ras has been suggested several times. Frascotti and colleagues [19] suggested a Cdc25-dependent stimulation of a GTPase, other than Ras proteins, with a role in galactose metabolism. Physical interaction and modulation between Cdc25p and chaperones has been detected [33] and a role of Cdc25p on stress response in a cAMP-independent pathway has been postulated [34]. In addition several CDC25-interactors have been identified by two hybrid screens. Further studies will be necessary to identify which protein of the galactose metabolism Cdc25p interacts to.

It must be noted that the truncated version of Cdc25p used in this study contains a domain (AA. 907–1589) of the Cdc25p, sufficient to enhance dissociation of the nucleotide bound to Ras protein [35]. For this reason, it is likely that this Ras-independent role of Cdc25p in galactose metabolism is due to its ability to enhance the nucleotide exchange of a different GTP binding protein rather than to an undiscovered biochemical function of the Cdc25p.

3.3. Phenotype of CDC25 gene deletion in strains lacking adenylate ciclase and/or both RAS genes

The chromosomal CDC25 gene disruption is normally lethal [30,36]. Herein, we evaluated the effect of the same gene deletion in strains lacking both RAS genes (AAT3B) or lacking both RAS genes and adenylate cyclase (ABH7C). The suppression of the lethality by an allele of the adenylate cyclase in the strain AAT3B is discussed in the previous paragraph. The lethality of the contemporary deletion of both RAS genes and/or adenylate cyclase (ABH7C) can be rescued by the presence of the bcy1-11 allele which allows sufficient kinase A activity, even in the absence of adenylate cyclase [37]. The AAT3B and ABH7C strain (for the relevant genotype, see Section 2) were engineered by replacing the CDC25 gene with a disrupted cdc25::LEU2 allele, using the disruption plasmid and procedure described by Baroni et al. [38], thus generating the AAT3BAl and ABH7CAl strains, respectively. Selected transformants were individually analysed by replica plating on different carbon sources at different temperatures of incubation. The results shown in Table 1 indicate that deletion of CDC25 in strain lacking both RAS genes (AAT3B) displays no phenotype while the same gene disruption in a strain (ABH7C) lacking both RAS genes and adenylate cyclase is always associated with an impaired growth on glycerol based media at 30 and 37 °C and on galactose based media at 37 °C for all colonies tested (Table 1 and Fig. 4). More exper-

---

The truncated form of Cdc25p or the corresponding empty vector have been subjected to RT-PCR using oligonucleotides...
ments would be necessary to discriminate if the different sensitivity of the two yeast strains to the CDC25 gene deletion is due to the presence/absence of the adenylate cyclase or to unidentified differences between the two yeast strains. However, the response to nutrients of yeast cells has been demonstrated to be modulated by Ras proteins and more recently by the Gα Gpa2 [39,40]. This latter protein has also been demonstrated to act in a Ras independent pathway [41] responding to extracellular nutrients [40]. Furthermore, in the fission yeast a direct interaction of Gpa2 with adenylate cyclase has been assessed [42,43]. It is therefore possible that the deletion of adenylate cyclase in the ABH7C strain abolishes both Ras dependent and Gpa2p dependent activation of adenylate cyclase resulting in the observed enhanced sensitivity to CDC25 gene deletion. It is interesting to note that while the phenotype resulting from the episomal expression of C-terminus Cdc25p may be due to non physiological interaction between the overexpressed Cdc25p and an unknown protein, the phenotype resulting from the chromosomal deletion of

![Cdc25p](image)

Fig. 3. Effect of Cdc25 overexpression on GAL4 and GAL80 mRNA level. Upper panel: RT-PCR of GAL4 mRNA (lanes 1–4) or GAL80 mRNA (lanes 5 and 6) were performed in the absence (lanes: 1, 2, and 5) or presence (lanes: 3, 4, and 6) of Cdc25p carboxy-terminus (AA. 907–1589) overexpression. Different dilution of cDNA were used for subsequent PCR: 1 μl (lanes: 1, 3, 5, and 6); 0.1 μl (lanes: 2 and 4). Lower panel: densitometric analysis of upper panel. The results are the average of three independent experiments.

| Phenotypes have been judged after three days of growth |
|-----------------|-----------------|-----------------|
|                 | YPD 30 °C | YPGly 30 °C | YPGal 30 °C |
|                 | 37 °C    | 37 °C     | 37 °C     |
| AAT3B           | +        | +         | +         |
| AAT3BA1         | +        | +         | –         |
| ABH7C           | +        | +         | +         |
| ABH7CA1         | +        | –         | +         |

<table>
<thead>
<tr>
<th>Temperature</th>
<th>CDC25 wt</th>
<th>cd25::LEU2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Glucose 30 °C</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Galactose 30 °C</td>
<td>+</td>
<td>+</td>
</tr>
</tbody>
</table>

![CDC25 deletion](image)

Fig. 4. Phenotypic effect of CDC25 deletion in a strain lacking both RAS genes. Replica plating of patches deriving from individual colonies of the ABH7C yeast strain carrying a wild type (first two patches) or a disrupted (the remaining 31 patches) allele of CDC25 (cdc25::LEU2, ABH7CA1) in glucose and galactose based media. Plates were incubated at 37 °C and analysed after 72 h.

CDC25 in a strain lacking both RAS genes and adenylate cyclase implies a physiological role of this exchange factor in galactose metabolism via a Ras-cAMP-independent pathway.

3.4. GAL10 promoter activity and RAS2 function

To further characterize the role of Ras pathway in galactose metabolism, wild type RAS2 or attenuated RAS2R80D81D alleles were re-introduced by homologous recombination [16] in a strain containing the PAH reporter plasmid and over-expressing the C-terminus of the Cdc25 protein. RT-PCR were performed using PAH-specific oligonucleotides in total RNA fractions extracted from glucose or galactose grown cells.
Surprisingly the \textit{RAS2} re-introduction completely abolishes the Cdc25-dependent activation of GAL10 promoter (result not shown). To shed a light on this Ras-dependent effect we measured the amount of exchange factor protein Cdc25p by immunoblot in different yeast strains. Whole protein extracts from strains expressing \textit{RAS2} wild type, \textit{RAS2}R80DN81D or the null allele in combination with C-terminus Cdc25p were subjected to SDS-PAGE and immunostained with a commercial anti-Cdc25p antibody (see Section 2 for details). The result shown in Fig. 5 indicates that the amount of Cdc25p strongly decreases in the presence of a wild type \textit{RAS2} allele compared to strains expressing a ras2 null allele or a ras2-attenuated allele (\textit{RAS2}R80DN81D). To discriminate if Ras2p exerts its action on the expression of the truncated form of Cdc25 at transcriptional or posttranscriptional level we performed RT-PCR using Cdc25-specific oligonucleotides on total RNA extracts from strains containing wild type, attenuated or null \textit{RAS2} alleles. \textit{CDC25} mRNA level, as judged by RT-PCR (Fig. 6), strongly decreases in the presence of active Ras2p while it is unaffected by the presence of attenuated Ras2p (\textit{Ras2R80DN81D}). Since the episomal expression of both \textit{PAH} and \textit{CDC25} (pIND25-1H) is under the control of the GAL10 gene promoter these results indicate that reintroduction of wild type \textit{RAS2} inhibits the transcription of \textit{GAL} genes while reintroduction of the attenuated allele of \textit{RAS2} (\textit{RAS2}R80DN81D) has no effect.

We further studied if the inhibitory role of Ras2p reintroduction on GAL10 promoter activity was due to the presence of Ras2p itself or to the activation of the adenylate cyclase. Yeast strain lacking both adenylate cyclase and \textit{RAS} genes (WOF6.1) was used as a recipient strain to express wild type and activated (G19V) Ras2 proteins under the control of the GAL10 gene promoter of the YEp51 high copy number shuttle vector (see Section 2 for details). Recombinant clones were transformed with an expression vector of the adenylate cyclase (YACW, \cite{46}) or with the corresponding empty vector. Total protein extracts from individual clones, after SDS-PAGE, were immunoblotted with a polyclonal anti-Ras antibody (see Section 2) confirming (Fig. 7) the possibility to overexpress both wild type and mutated forms of Ras2 protein. Adenylate cyclase reintroduction strongly diminished the amount of both wild type and activated Ras2 protein as judged
by immunoblot. These results indicate that reconstitution of the Ras pathway inhibits GAL10 driven transcription and that this inhibition is dependent upon activation of the Ras-cAMP-PKA pathway and not by the presence of Ras2 protein itself.

Acknowledgements: This work has been supported by the Italian Ministry of University and the Research (MIUR, ex 60%). We thank Italia Di Liegro and Riccardo Alessandro for critical reading of the manuscript.

References


gene CDC25 of *Saccharomyces cerevisiae*. EMBO J. 5 (9), 2363–2369.


