Identification of a 31 kDa Protein in *Saccharomyces cerevisiae* Whose Phosphorylation is Controlled Negatively by the *CDC25* Gene Product

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(Received 5 February 1988; revised 13 May 1988)

Phosphoprotein patterns in two mutants of *Saccharomyces cerevisiae*, *cdc25-20* (ts) and *cdc25-20* (ts) *bey l*, were analysed by two-dimensional polyacrylamide gel electrophoresis. Comparison with the phosphoprotein patterns of the mutants *cyrl-2* (ts) and *bey l*, analysed in a previous study, demonstrated not only that the *CDC25* gene product is a positive element in the regulation of adenylyl cyclase activity, as suggested by recent studies, but that it is also a negative element in the phosphorylation of a 31 kDa protein (p31c and p31d), a protein whose phosphorylation is correlated with cell cycle arrest, and dephosphorylation with cell cycle initiation, respectively. Moreover, the phosphorylation phenotype of p31c and p31d suggests that the activity of the *CDC25* protein is subject to feedback regulation by cAMP-dependent protein kinase, and that the *CDC25* protein is a key element in an ammonium (NH₄⁺) signal-response system.

**INTRODUCTION**

Recent genetic and biochemical studies have provided evidence that the adenylyl cyclase/cAMP pathway in *Saccharomyces cerevisiae* exerts a positive control on cell cycle initiation and vegetative growth, and simultaneously a negative control over sporulation (for a review see Matsumoto *et al.*, 1985), although the second conclusion has been challenged (Olempska-Beer & Freese, 1987). Since the transition between vegetative growth and sporulation is normally controlled by nutritional signals, we might expect adenylyl cyclase to be the effector system to which one or more nutritional sensing systems are coupled. We have presented evidence consistent with this possibility in a recent study that showed that response to NH₄⁺ is mediated by adenylyl cyclase (Tripp *et al.*, 1986). This conclusion was based on the striking similarity in the two-dimensional gel electrophoretic pattern of phosphoproteins from NH₄⁺-starved cells and in a mutant expressing a thermosensitive adenylyl cyclase, *cyr l-2* (ts) (Matsumoto *et al.*, 1984), arrested at the restrictive temperature. This analysis led us to identify several proteins whose phosphorylation was controlled positively or negatively by the cAMP pathway. Those proteins whose phosphorylation was controlled positively were found in proliferating cells, while the negatively controlled phosphoproteins appeared during cell cycle arrest, brought about by either NH₄⁺ starvation or inactivation of adenylyl cyclase.

In this report we describe an extension of this type of analysis to the class II start gene, *CDC25* (Reed, 1980). *CDC25* is of special interest since mutants that express a temperature-sensitive *CDC25* gene product are also derepressed for sporulation (Shilo *et al.*, 1978), a phenotype similar to that of *cyr l-2* (ts) (Matsumoto *et al.*, 1983). This result suggested that the *CDC25* gene product was involved in regulating the cAMP pathway (Tripp & Piñon, 1986). Recent complementation studies in vivo (Camonis *et al.*, 1986; Broek *et al.*, 1987; Robinson *et al.*, 1987) and analysis of adenylyl cyclase activity in vitro (Daniel *et al.*, 1987) have shown that the *CDC25* gene product, and more particularly its carboxy-terminal domain, is required for the RAS-dependent (Toda *et al.*, 1985) regulation of adenylyl cyclase activity.

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Farrell (1975). Approximately equal amounts of protein were loaded on each gel. For all

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Yeast strains. Strains CR15-S22H [MATα cdc25-20(ts) ura3-52 trpl-289] and CR41-S2 [MATα cdc25-20(ts) bcy1 ade2 his71] were used in this study. The origin and phenotype of CR15-S22H and CR41-S2 are described in Tripp & Piñon (1986). CR15-S22H does not complement other cdc25(ts) strains; the allele number of the mutation in CDC25 in CR15-S22H is unknown, and we denote it arbitrarily as cdc25-20. CR41-S2 is a segregant of a cross between cdc25 and bcy1 mutants and is considered to be a cdc25-20(ts) bcy1 double mutant by the following criteria: (a) when crossed to a cdc25(ts) strain, the resulting diploid is temperature sensitive, and sporulates at 34 °C; (b) when crossed to a bcy1 strain, the resulting diploid is not temperature sensitive and does not sporulate.

Media and labelling conditions. Cells were grown in the low phosphate medium CM with 1% (w/v) glucose (Tripp et al., 1986), and supplemented with uracil, adenine, tryptophan or histidine (40 μg ml⁻¹ of each) as required. Non-cycling medium (NCM) is CM without NH₄Cl. Labelling with radioactive ³²P₀²⁻ (from ICN) was done in CM or glucose-induced activation of adenylyl cyclase was normal at the restrictive temperature (Portillo & Mazón, 1986), while, in contrast, no activation of adenylyl cyclase was seen in a strain with RASI and RAS2 inactivated (M. J. Mazón & R. Piñon, unpublished results). In addition, although the CDC25 product was specifically required for the glucose-induced activation of the yeast plasma membrane H⁺-ATPase (Portillo & Mazón, 1986), the adenylyl cyclase/cAMP pathway was not (M. J. Mazón & R. Piñon, unpublished results).

These various observations suggest that the CDC25 gene product may have at least two functions—first, positive control over adenylyl cyclase, and secondly, positive control over cell cycle initiation by a mechanism independent of the cAMP pathway. Our objective in this study was to identify and distinguish between the different phosphoprotein pathways in which the CDC25 gene product might participate by an analysis of the phosphoprotein pattern in the mutants cdc25-20(ts) and cdc25-20(ts) bcy1. Consistent with other studies, we have found that CDC25 is a positive element in the regulation of adenylyl cyclase activity. However, we have also found that CDC25 is a negative element in the phosphorylation of a 31 kDa protein (p31c and p31d), identified previously (Tripp et al., 1986) as a protein whose phosphorylation and dephosphorylation is associated with cell cycle arrest and initiation, respectively. The phosphorylation phenotypes of p31c and p31d in different mutants and under different nutritional conditions are consistent with a model in which the activity of the CDC25 protein is subject to feedback regulation by the cAMP pathway. Our analysis also suggests that a NH₃ nutritional sensory system is coupled to the cell division cycle regulatory mechanism via CDC25 and cAMP-dependent and cAMP-independent phosphorylation pathways.

METHODS

Nonetheless, other observations hint at a more complex role for CDC25. In contrast to the low cAMP levels of one temperature-sensitive cAMP mutant, cdc25-5 (Camonis et al., 1986), cAMP levels were normal in another mutant, cdc25-1 (Martegani et al., 1986; Portillo & Mazón, 1986), which nevertheless remained temperature sensitive. Consistent with this phenotypic difference was the observation that although only the carboxy-terminal portion of the cloned CDC25 gene was required for complementation of the cdc25-5 mutation (Camonis et al., 1986), it was not required for the complementation of the cdc25-1 allele (Lisziewicz et al., 1987). Moreover, although the bcy1 mutation can bypass the RAS1 and RAS2 requirement (Kataoka et al., 1984), it did not suppress the cdc25-20 mutant (Tripp & Piñon, 1986). In cdc25-1 cells, the glucose-induced activation of adenylyl cyclase was normal at the restrictive temperature (Portillo & Mazón, 1986), while, in contrast, no activation of adenylyl cyclase was seen in a strain with RASI and RAS2 inactivated (M. J. Mazón & R. Piñon, unpublished results). In addition, although the CDC25 product was specifically required for the glucose-induced activation of the yeast plasma membrane H⁺-ATPase (Portillo & Mazón, 1986), the adenylyl cyclase/cAMP pathway was not (M. J. Mazón & R. Piñon, unpublished results).

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Yeast phosphoprotein controlled by CDC25

RESULTS

Comparison of cdc25-20(ts) and cyrl-2(ts) phosphoprotein patterns

The phosphoprotein profile of cdc25-20(ts) cells labelled with [32P]orthophosphate at the permissive (26 °C) and restrictive temperature (36 °C) is shown in Fig. 1. In this experiment cells were labelled at 26 °C for 2 h during exponential-phase growth, while at 37 °C, cells were labelled between 2 and 4 h after the temperature shift. Cells labelled between 0 and 2 h, or between 0 and 4 h, had similar phosphoprotein patterns. By 4 h after a shift to 36 °C, more than 90% of the cdc25-20(ts) cells were unbudded. Several differences in the phosphoprotein patterns between permissive and restrictive conditions are evident in Fig. 1. The majority of these differences are strikingly similar to those observed in our previous study of the mutant cyrl-1-2(ts) (Tripp et al., 1986) in a comparison study of proliferating and temperature-arrested cyrl-2(ts) cells. Phosphoprotein a (pp31a) was found to be a major phosphoprotein in proliferating cells, but was not detected at the restrictive temperature for cyrl-1-2(ts) cells. Its presence in bcyl cells under all conditions tested led us to conclude that the phosphorylation of p31a is regulated positively by cAMP-dependent protein kinase. The presence of pp31a in cdc25-20(ts) cells at the permissive, but not at the restrictive temperature shows that the phosphorylation of p31a is also regulated positively by the CDC25 gene product. Phosphoprotein b (pp31b), like pp31a, is phosphorylated on serine residues, and on acid hydrolysis has a phosphopeptide pattern very similar to that of pp31a, suggesting that pp31a and pp31b may be different phosphorylated forms of the same protein. The phosphorylation/dephosphorylation of both appears to be regulated coordinately (Tripp et al., 1986), but the level of phosphorylation of pp31b is always less than that of pp31a. As a result, in some autoradiographic exposures pp31b is not visualized. In some gels, small variations in the focusing range of the first electrophoretic dimension resulted in pp31a, the most basic of the phosphoproteins of interest, being excluded from the gel, and not appearing in the autoradiogram (e.g. Fig. 2B). In all such cases, repetition of the experiment or running a second gel showed that pp31a was present in vegetative medium (CM) under proliferation conditions, and in bcyl cells under CM and NCM conditions.

Other phosphoproteins, for example c, d, s and z, which were detected easily at the restrictive temperature (Fig. 1B), were, however, also major phosphoproteins in cyrl-1-2(ts) cells at 37 °C (Tripp et al., 1986). These proteins belong to the group of proteins whose phosphorylation is normally correlated with cell cycle arrest (Tripp et al., 1986).

Labelling time-course studies (not shown) indicated that some of the changes observed in Fig. 1, for example the disappearance of pp31a or appearance of pp31c and pp31d, took place within 15 min after the temperature shift, a period which is short compared to the time required for the culture as a whole to arrest. This relatively rapid response suggests that these changes in phosphorylation may be one of the early signals leading to cell cycle arrest. These phosphorylation differences do not appear to be the result of a heat shock response, since as shown previously pp31a is readily detected in wild-type and bcyl cells after a shift to the restrictive temperature, whereas phosphoproteins c, d, s and z are not readily detected under the same conditions (Tripp et al., 1986).

It is important to note that in a number of cases (e.g. phosphoproteins s, o, p and q) the changes in phosphorylation intensity after the shift to the restrictive temperature are not as great in cdc25-20(ts) as were seen in cyrl-1-2(ts) cells (Tripp et al., 1986). Possibly the difference in phosphorylation intensity of a given protein spot between the two strains may be influenced by their respective genetic backgrounds, or by differential effects of CYR1 and CDC25 gene product inactivation. Nevertheless, the changes are in the same direction: for example temperature shift to the restrictive temperature resulted in increased phosphorylation of s, o, p and q. The important result is that the major changes, disappearance of phosphoprotein a and the appearance of c and d, are the same in cdc25-20(ts) (Fig. 1) and cyrl-1-2(ts) (Tripp et al., 1986) upon shift to 36 °C. These data taken together suggest that inactivation of the CDC25 gene
Fig. 1. Two-dimensional gel electrophoretic analysis of phosphoproteins from \textit{cdc25-20} (ts) cells (strain CR15-S22H). A, Phosphoprotein pattern of exponentially growing cells at 26 °C; B, phosphoprotein pattern at 36 °C. Strain CR15-S22H was grown in CM + 1% glucose at 26 °C to a cell density of $5 \times 10^6$ cells ml$^{-1}$. The culture was then split into two equal parts, one part remaining at 26 °C, and the other shifted to 36 °C. The 26 °C culture was labelled with $[^{32}\text{P}]$orthophosphate (200 $\mu$Ci ml$^{-1}$; 7.4 MBq ml$^{-1}$) for 2 h while the 36 °C culture was labelled with the same amount of $[^{32}\text{P}]$orthophosphate between 2 and 4 h after the temperature shift. The cells were harvested and broken as described in Methods, and total cell proteins were extracted and resolved by two-dimensional gel electrophoresis. Approximately equal amounts of protein were loaded on each starting gel. Isoelectric focusing in the first dimension is from left (basic, pH 7-4) to right (acidic, pH 5-4). Autoradiography was done with an intensifying screen (A, 8 h exposure; B, 4 h exposure).
Yeast phosphoprotein controlled by CDC25

We reported previously that the cdc25-20(ts) bcyl double mutant is temperature sensitive even though cAMP-dependent protein kinase activity is presumably constitutive in this mutant (Tripp & Pignon, 1986). A phosphoprotein analysis of the double mutant would allow us to test this hypothesis more specifically, and to probe also for other cell-cycle-specific functions of CDC25. We did two types of experiment with the double mutant cdc25-20(ts) bcyl, a simple temperature upshift as described in Fig. 1, and a temperature upshift combined with a nutritional downshift, i.e. a CM to NCM shift. The phosphoprotein patterns in CM and NCM at the permissive and restrictive temperature for cdc25-20(ts) bcyl cells are shown in Figs 2 and 3, respectively. At a temperature permissive for cdc25-20(ts), pp3la and pp3lb were readily detected in the double mutant, while pp3lc and pp3ld, although detectable, were significantly less prominent, a phenotype characteristic of NH2-depleted bcyl cells (Tripp et al., 1986). The presence of pp3la in the double mutant in NCM at both temperatures (Fig. 3A, B) indicates that the nitrogen starvation signal is being suppressed by bcyl as shown previously (Tripp et al., 1986), and biochemically confirms the bcyl genotype in strain CR41-S2. Moreover, this result indicates that the phosphorylation of p31a is regulated by CAMP-dependent protein kinase, rather than directly by the CDC25 gene product. Hence, the disappearance of pp3la in cdc25-20(ts) cells at 36 °C (Fig. 1B), but not in cells of the double mutant cdc25-20(ts) bcyl, confirms that inactivation of the CDC25 gene product normally leads to the inactivation of adenylyl cyclase.

In our previous analysis (Tripp et al., 1986) we concluded that the phosphorylation of p31c and p31d was controlled negatively by CAMP-dependent protein kinase, since pp3lc and pp3ld appeared following the inactivation of adenylyl cyclase, and were not seen in bcyl cells. However, as seen in Figs 2 and 3, the appearance of pp3lc and pp3ld in cdc25-20(ts) bcyl cells only at the restrictive temperature for cdc25-20(ts) argues that the phosphorylation of p31c and p31d is also controlled negatively by the CDC25 gene product itself.

Other phosphoprotein differences between CM and NCM conditions in the double mutant are apparent. For example, proteins α and β are prominent in CR41-S2 (Fig. 2), while only β is seen clearly in strain S22H (Fig. 1), a difference due perhaps to the presence of bcyl in strain CR41-S2. Both of them respond strongly to the temperature shift in CR41-S2 in CM (Fig. 2), while β in S22H does not respond as strongly. However, both α and β clearly respond to the NCM shift (Figs 2A and 3A). Hence, the phosphorylation of α and β appears to depend to different extents on CAMP-dependent protein kinase, CDC25 and an NH3+-responsive system. Phosphoprotein γ, on the other hand, does not respond strongly to CDC25 inactivation (Fig. 1), and is more prominent in CR41-S2 (Fig. 2), but does respond strongly to NH3+ depletion. Similarly, phosphoprotein δ appears to be regulated by NH3+, but not by the CDC25 gene product. These differences are consistent with our previous findings that not all phosphoprotein changes seen after a CM to NCM shift can be attributed to the adenylyl cyclase/cAMP system (Tripp et al., 1986).

DISCUSSION

Our first result (Fig. 1) shows that inactivation of the CDC25 product leads to a set of phosphoprotein changes that are similar to those which occur when adenylyl cyclase is inactivated, or when cells are starved of NH3+ (Tripp et al., 1986), and which appear to be correlated with proliferation and cell cycle arrest. For example, pp3la was identified previously as a substrate of CAMP-dependent protein kinase based on the observation that pp3la disappears when adenylyl cyclase is inactivated, and that it is always present in bcyl cells. Similarly, pp3la disappears when cdc25-20(ts) cells are shifted to the restrictive temperature (Fig. 1B). In addition, as in cyrl-2(ts) cells (Tripp et al., 1986), when cdc25-20(ts) cells are shifted to the restrictive temperature, two new major phosphoproteins, pp31c and pp31d, appear (Fig.
Fig. 2. Phosphoproteins from cdc25-20(ts) beyl cells (strain CR41-S2) in vegetative medium (CM). A, phosphoprotein pattern at 26 °C; B, phosphoprotein pattern at 36 °C. Stain CR41-S2 was grown and labelled as described in the legend to Fig. 1 (A, 6 h exposure; B, 4 h exposure).
Fig. 3. Phosphoproteins from NH₄-starved cdc25-20(ts) bcyl1 cells (strain CR41-S2). A, Phosphoprotein pattern at 26 °C; B, phosphoprotein pattern at 36 °C. Strain CR41-S2 was grown as described in the legend to Fig. 1. At a cell concentration of 5-6 x 10⁶ cells ml⁻¹ the culture was divided into two equal parts, both were shifted to NCM, one incubated at 26 °C and the other at 36 °C. After 4 h in NCM, the cells were labelled for 2 h with [³²P]orthophosphate (120 μCi ml⁻¹; 4.44 MBq ml⁻¹) (A, 6 h exposure; B, 2 h exposure).
Table 1. Summary of phosphorylation phenotype of p31a, p31c and p31d

Data are from this study and from Tripp et al. (1986). + indicates the presence of the phosphorylated form. CM and NCM are defined in Methods. Labelling conditions are as described in this study and in Tripp et al. (1986).

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Temperature</th>
<th>Medium</th>
<th>pp31c and pp31d</th>
<th>pp31a</th>
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<tr>
<td>Wild-type</td>
<td>26 °C</td>
<td>CM</td>
<td>-</td>
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<tr>
<td></td>
<td>26 °C</td>
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<td>36 °C</td>
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<td></td>
<td>36 °C</td>
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<tr>
<td>cyr1-2(ts)</td>
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<td>CM</td>
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<td>bcyl</td>
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<tr>
<td>cdc25-20(ts)</td>
<td>26 °C</td>
<td>CM</td>
<td>-</td>
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1B). These same phosphoprotein pattern changes – loss of pp31a and appearance of pp31c and pp31d – were also observed in wild-type cells arrested by NH4+ starvation (Tripp et al., 1986). Conversely, bcyl cells, which do not undergo a regulated cell cycle arrest when subjected to NH4+ starvation, did not show this change in phosphoprotein pattern in response to NH4+ starvation (Tripp et al., 1986). Taken together, these data show that conditions which lead to a regulated cell cycle arrest, such as inactivation of the CDC25 or CYR1 gene products, or NH4+ starvation, are correlated with changes in specific phosphoproteins. More specifically, these results suggest that the inactivation of the CDC25 product leads to the inactivation of adenylyl cyclase. With respect to pp31a, the phenotype of cdc25-20(ts) bcyl at the permissive temperature is the same as that of bcyl (i.e. pp31a is present under all conditions studied; Tripp et al., 1986), demonstrating that under conditions in which cAMP-dependent protein kinase is not regulated by cAMP, the phosphorylation of p31a is not directly dependent on the function of CDC25.

The summary of phosphorylation phenotypes (Table 1) also makes clear that although the phosphorylation and dephosphorylation of p31a appears to be correlated with proliferation and cell cycle arrest, respectively, nevertheless the dephosphorylation of pp31a is not necessary for a regulated cell cycle arrest [e.g. cdc25-20(ts) bcyl cells at the restrictive temperature; Fig. 3B]. This suggests that the conversions between p31a and pp31a may be secondary consequences of the mechanism that controls the transition between proliferation and cell cycle arrest. Alternatively, since pp31a is not present in sporulating cells (unpublished observations), the dephosphorylation of pp31a may be required for sporulation [bcyl and cdc25-20(ts) bcyl cells do not sporulate].

The second result is that the phosphorylation of p31c and p31d is controlled negatively by the CDC25 gene product. The appearance of pp31c and pp31d in the double mutant cdc25-20(ts) bcyl, at the restrictive but not the permissive temperature, indicates that the phosphorylation of p31c and p31d is also controlled by the CDC25 protein. The correlation between cell cycle arrest and the phosphorylation of p31c and p31d (Table 1) suggests that the dephosphorylation of pp31c and pp31d is required for cell cycle initiation. We propose that this event may define one cell-cycle-specific function controlled by the CDC25 gene product that is independent of CDC25-mediated regulation of adenylyl cyclase activity. Additional evidence in support of this possibility comes from a recent analysis of a suppressor of CDC25 mutants, SPR25, isolated and cloned in our laboratory, which shows that SPR25-mediated suppression of the cdc25-20 temperature-sensitive phenotype (i.e., resumption of growth at 36 °C) is accompanied by dephosphorylation of pp31c and pp31d (M. L. Tripp, R. Bouchard & R. Piñon, unpublished results). We do not yet know if this event is related to another CDC25-mediated process, the activation of the plasma membrane H+-ATPase (Portillo & Mazon, 1986). In addition, we do not know if p31c and p31d are different proteins, although the similarity in their
Yeast phosphoprotein controlled by CDC2

Nutritional signals

\[ CDC25 \]

Adenylyl cyclase

pp3lc and pp3ld

+ Proliferation

- Sporulation

Model 1: Independent regulation of pp3lc and pp3ld by CDC25 and cAMP-dependent protein kinase

pp3lc and pp3ld

+ Proliferation

- Sporulation

Model 2: Regulation of pp3lc and pp3ld by CDC25 and feedback regulation of CDC25 by cAMP-dependent protein kinase

Fig. 4. Schematic diagram of the two models discussed in the text describing the elements involved in the regulation of pp3lc and pp3ld phosphorylation. In model 1 cAMP-dependent protein kinase and the CDC25 gene product are independently required to regulate the phosphorylation of pp3lc and pp3ld. In version 2 of model 2, pp3lc and pp3ld are regulated by the CDC25 product, and the activity of the CDC25 product is regulated by cAMP-dependent protein kinase. A causal relationship between dephosphorylation of pp3lc and pp3ld and cell proliferation has not yet been demonstrated.

phosphopeptide patterns after acid hydrolysis suggests that pp3lc and pp3ld may be the same protein. Since both pp3lc and pp3ld contain phosphoserine and phosphothreonine (Tripp et al., 1986), inactivation of the CDC25 protein results (presumably indirectly) in the activation of a serine–threonine-specific protein kinase, or alternatively, in the inactivation of a serine–threonine-specific protein phosphatase.

The phosphorylation phenotypes of pp3lc and pp3ld (see Table 1) also suggest two other conclusions. In the preceding paragraph, we have argued that the phosphorylation of pp3lc and pp3ld is controlled negatively by the CDC25 product. However, pp3lc and pp3ld also appear when adenylyl cyclase is inactivated, i.e. cyrl-2(ts) at 36 °C, and are not seen in bcy1 cells under any condition (Table 1). This suggests that the phosphorylation of pp3lc and pp3ld is regulated negatively by both the CDC25 product and cAMP-dependent protein kinase. Two different models can be proposed (see Fig. 4 for a schematic diagram).

Model 1: regulation by the two elements is independent, for example, the phosphorylation of pp3lc and pp3ld might be controlled by two different protein kinases, one regulated negatively by cAMP-dependent protein kinase and the other also regulated negatively by the CDC25 protein. Since the CDC25 gene does not appear to encode a protein kinase (Broek et al., 1987), two different mechanisms would have to be postulated to regulate the two putative protein kinases. The essential feature of this model would be that inactivation of only one element (either the CDC25 product or cAMP-dependent protein kinase) would be sufficient to permit pp3lc and pp3ld to be phosphorylated.

Model 2: regulation is not independent, in which case inactivation of both elements would be required. Two different versions of this model are possible. In the first (version 1), for example, the CDC25 product might independently regulate a protein kinase that is itself also controlled by cAMP-dependent protein kinase. Alternatively, the activity of the CDC25 gene product itself might be under positive feedback regulation by cAMP-dependent protein kinase (version 2). Version 1 of model 2 is incompatible with the phenotype of cyrl-2(ts) cells, that is there is no
reason to suppose that inactivation of adenyl cyclase would also lead to the inactivation of the CDC25 product. On the other hand, in the context of the known relationships between CDC25 and adenyl cyclase, the feedback version of model 2 would predict that inactivation of the CDC25 product would be a consequence of adenyl cyclase inactivation. Version 2 of model 2 can easily account for the phenotype of cyrl-2(ts) and bcyl as follows. In cyrl-2(ts) cells, inactivation of adenyl cyclase would lead to the inactivation of cAMP-dependent protein kinase, which in turn would lead to the inactivation of the CDC25 protein. In bcyl cells, on the other hand, activity of cAMP-dependent protein kinase is constitutive, thereby maintaining the CDC25 protein in an active state, and preventing the appearance of pp31c and pp31d. In the cdc25-20(ts) bcyl double mutant, pp31c and pp31d would appear only at the restrictive temperature, since inactivation of this function of the CDC25 product can occur only at the restrictive temperature.

The p31c and p31d phenotype in NH₄⁺-depleted cells places another constraint on the possible models, the result of which favours the feedback version of model 2 over that of model 1. The appearance of pp31c and pp31d in NH₄⁺-depleted wild-type cells and also in NH₄⁺-depleted cdc25-20(ts) bcyl cells only at the restrictive temperature, indicates that at least with respect to the phosphorylation of p31c and p31d, the response to NH₄⁺-starvation is mediated by the CDC25 gene product. There are two implications to this conclusion. The first is that the CDC25 gene product is either a sensor for the NH₄⁺ signal or is functionally coupled to it, and that its ability to respond to the NH₄⁺ signal depends on its state of activation. The second implication is that since depletion of NH₄⁺ in wild type cells also leads to the appearance of pp31c and pp31d, NH₄⁺-starvation probably normally leads to the inactivation of the CDC25 protein. However, since pp31c and pp31d are not seen under NH₄⁺-depletion conditions at the permissive temperature in the cdc25-20(ts) bcyl double mutant, the appearance of pp31c and pp31d (presumably due to the inactivation of the CDC25 product) in the normal case requires concomitant inactivation of cAMP-dependent protein kinase. This suggests that the CDC25 product and cAMP-dependent protein kinase do not act independently in the phosphorylation of p31c and p31d. This circumstance is most easily accommodated in the feedback version of model 2. Since the CDC25 protein contains more than one consensus sequence for cAMP-dependent protein kinase phosphorylation (Camonis et al., 1986; Broek et al., 1987), this requirement might mean that the CDC25 protein is a direct substrate of cAMP-dependent protein kinase, or alternatively that the activity of the CDC25 protein (that is, its ability to respond to the NH₄⁺ signal) is modulated indirectly by cAMP-dependent protein kinase. The possibility of a feedback control system involving the CDC25 protein and cAMP-dependent protein kinase has recently been suggested independently in a study of the control of cAMP levels in S. cerevisiae (Nikawa et al., 1987). Such a system of control would not be unusual since feedback regulation of elements of signalling systems by protein phosphorylation is well documented (Sibley et al., 1987).

Hence, if the CDC25 gene product were the sensor for the NH₄⁺ signal or were functionally coupled to it, then (since CDC25 is a positive effector of adenyl cyclase) the absence of NH₄⁺ would lead to the inactivation of adenyl cyclase (one function of CDC25), and this in turn would lead to the inactivation of the CDC25 product via the cAMP-dependent protein kinase feedback loop, and finally the appearance of pp31c and pp31d (the second function of CDC25). As a consequence, pp31a, pp31c and pp31d would be maintained in the proper phosphorylation equilibrium in response to NH₄⁺ availability. A feedback system of this type may provide an efficient way for the cell to modulate and fine-tune the activity and responsiveness of the nutritional signal response system.

We thank M. Hopkins for technical help with some of these experiments and Jeanne Lopez for help in strain construction. This work was supported by Public Health Service grant AI20388 from the National Institutes of Health, and MBRS Program grant SO6RR08135.
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