Effectors of Lysine 4 Methylation of Histone H3 in *Saccharomyces cerevisiae* Are Negative Regulators of PHO5 and GAL1–10*

Christopher D. Carvin and Michael P. Kladde†

From the Department of Biochemistry & Biophysics, Texas A&M University, College Station, Texas 77843-2128

Post-translational modifications of histone amino-terminal tails are a key determinant in gene expression. Histone methylation plays a dual role in gene regulation. Methylation of lysine 9 of histone H3 in higher eukaryotes is associated with transcriptionally inactive heterochromatin, whereas H3 lysine 4 methylation correlates with active chromatin. Methylation of lysine 4 of H3 via Set1, a component of the *Saccharomyces cerevisiae* COMPASS complex, is regulated by the transcriptional elongation Paf1-Rtf1 and histone ubiquitination Rad6-Bre1 complexes, which are required for the expression of a subset of genes. This suggests that lysine 4 methylation of histone H3 may play an activating role in transcription; however, the mechanism of Set1 function remains unclear. We show here that H3 lysine 4 methylation also negatively regulated gene expression, as strains without Set1 showed enhanced expression of PHO5, wherein chromatin structure plays an important transcriptional regulatory role. Di- and trimethylation of H3 lysine 4 was detected at the PHO5 promoter, and a strain expressing a mutant version of histone H3 with lysine 4 changed to arginine, (which cannot be methylated) exhibited PHO5 derepression. Moreover, PHO5 was derepressed in strains that lacked components of either the Paf1-Rtf1 elongation or Rad6-Bre1 histone ubiquitination complexes. Lastly, PHO84 and GAL1–10 transcription was also increased in *set1Δ* cells. These results suggest that H3 methylation at lysine 4, in conjunction with transcriptional elongation, may function in a negative feedback pathway for basal transcription of some genes, although being a positive effector at others.

In eukaryotes, DNA is packaged with histone proteins to form nucleosomes that are further condensed into higher order chromatin structures. Generally, this compaction serves as a barrier for the binding of factors that elicit important cellular processes such as transcription and DNA replication. Thus, genes found in heavily condensed regions, such as heterochromatin, are transcriptionally silent. Expression of genes located in euchromatic regions, which are typically less compacted, is also regulated by chromatin structure.

Post-translational modifications of the amino-terminal tails of histone proteins are a key determinant in defining active and repressed chromatin. These modifications may alter chromatin structure directly by affecting histone-DNA and histone-histone interactions (1). They also allow for the recruitment of transcriptional activators or repressors. Acetylation of histone H3 at lysines 9 and 14 is strongly correlated with transcriptionally active and accessible chromatin. Histone methylation is associated with both active and repressed chromatin states. In eukaryotes other than budding yeast, heterochromatic silencing is marked by methylation of histone H3 at lysine 9. Conversely, euchromatic regions are associated with histone methylation of histone H3 at lysine 4 (H3 Lys-4) (2). Set1 is the catalytic subunit of a large complex named COMPASS (3), which is responsible for all H3 Lys-4 methylation observed in yeast (4). Set1 is required for full activation of a subset of euchromatic genes, including *RAM2, HAS1, INO1, PPH3*, and *MET16* (5, 6). Paradoxically, despite its presumed role in transcriptional activation, the absence of Set1 or other components of COMPASS leads to loss of ribosomal DNA (4, 7) and telomeric (8) silencing.

Set1-dependent methylation requires histone ubiquitination of lysine 123 of histone H2B via the ubiquitin-conjugating Rad6-Bre1 complex (9). Set1 is still recruited in the absence of Rad6; however, no resulting H3 Lys-4 methylation is observed (10). This is the first evidence that a modification of one histone regulates the trans-modification of another histone. Recent reports have also indicated that Set1 methylation is associated with transcriptional elongation (11). The Paf1-Rtf1 complex, which associates with RNA polymerase II, is required for H3 Lys-4 methylation as well as recruitment of the COMPASS complex (12). A *paf1* null strain shows no detectable histone ubiquitination; however, Rad6 is still recruited (13). As seen with *set1Δ* mutants, strains with deletions of *PAF1, RTF1*, or *RAD6* show loss of telomeric silencing (9, 12, 14).

In this report, we explored the role of Set1 in the transcriptional regulation of select genes of the phosphate-repressible PHO cluster (15). We found that loss of Set1 led to increased levels of expression of PHO5, coding for the repressible acid phosphatase (rAPase),1 under both repressed and active conditions. The expression of the high affinity phosphate transporter PHO84 is also higher in *set1Δ* than in *set1Δ* strains. Deletions of genes encoding critical components of the Rad6-Bre1 and Paf1-Rtf1 complexes, which are required for Set1-dependent methylation, also exhibited derepression of PHO5. Finally, we observed derepression of the GAL1–10 locus in strains lacking *SET1*. Our results suggest that methylation at Lys-4 of histone H3 may provide an activating signal at some genes although

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† To whom correspondence should be addressed: Dept. of Biochemistry & Biophysics, Texas A&M University, 2128 TAMU, College Station, TX 77843-2128. Tel.: 979-862-6677; Fax: 979-845-4946; E-mail: kladde@tamu.edu.

1 The abbreviations used are: rAPase, repressible acid phosphatase; ChIP, chromatin immunoprecipitation; COMPASS, complex proteins associated with Set1; Pi, inorganic phosphate; SAGA, Spt-Ada-Gcn5- acetyltransferase; YPD, yeast peptone-dextrose medium; YPG, yeast peptone-galactose medium; YPFD, yeast peptone-phosphate-dextrose medium.
displacement was confirmed by PCR, and the resulting diploid was sporulated as described elsewhere (17).

**TABLE I** Yeast strains

| Strain          | Genotype                        |
|-----------------|---------------------------------|
| CCY1467         | MATa leu2Δ lys2Δ ura3Δ pho3Δ::R  |
| CCY1468         | MATa leu2Δ lys2Δ ura3Δ pho3Δ::R  |
| CCY1471         | MATa leu2Δ lys2Δ ura3Δ pho3Δ::R  |
| CCY1472         | MATa leu2Δ lys2Δ ura3Δ pho3Δ::R  |
| YPH500ΔL        | MATa ade2Δ-101 his3Δ-200 leu2Δ-1 Δ1 trp1Δ-Δ3 lysozyme 2-Δ1 |
| WZY43           | MATa ade2Δ-101 his3Δ-200 leu2Δ-1 Δ1 trp1Δ-Δ3 lysozyme 2-Δ1 hht1Δ-Δ1::pWZ403-F4F10-HIS3, Ycp50-copyII (HHT2-HRP2) |
| JDY2            | MATa ade2Δ-101 his3Δ-200 leu2Δ-1 Δ1 trp1Δ-Δ3 lysozyme 2-Δ1 hht1Δ-Δ1::pWZ403-F4F10-HIS3 hht2Δ (K4R)-HHF2-TRP1 |
| MBB1198         | MATa his3Δ-200 ade2Δ-2 hisG leu2Δ ura3Δ met15ΔΔ trp1ΔΔ6 Tyh1his3Δ1-236 Tylnade2Δ1-515 cirΔ |
| MBB1217         | MATa his3Δ-200 ade2Δ-2 hisG leu2Δ ura3Δ met15ΔΔ trp1ΔΔ6 Tyh1his3Δ1-236 Tylnade2Δ1-515 cirΔ set1Δ::kanMX4 |
| BY4743          | MATa MATa MATa MATa his3Δ-200 ade2Δ-2 hisG leu2Δ ura3Δ met15ΔΔ trp1ΔΔ6 Tyh1his3Δ1-236 Tylnade2Δ1-515 cirΔ set1Δ::kanMX4 |
| CCY2895         | BY4743 set1Δ::kanMX4 set1Δ::kanMX4 31570 32773 33771 34425 34611 35727 |
| 32773           | BY4743 ade2Δ-2 his1Δ1-236 ade2Δ-2 leu2Δ-1 Δ1 hisG-1::pWZ403-F4F10-HIS3, Ycp50-copyII |
| 33771           | BY4743 bre1Δ::kanMX4 bre1Δ::kanMX4 |
| 34425           | BY4743 rad6Δ::kanMX4 rad6Δ::kanMX4 |
| 34611           | BY4743 rtf1Δ::kanMX4 rtf1::kanMX4 |
| 35727           | BY4743 paf1Δ::kanMX4 paf1::kanMX4 |
| CCY1467         | MATa leu2Δ lys2Δ ura3Δ pho3Δ::R  |
| CCY1468         | MATa leu2Δ lys2Δ ura3Δ pho3Δ::R  |
| CCY1471         | MATa leu2Δ lys2Δ ura3Δ pho3Δ::R  |
| CCY1472         | MATa leu2Δ lys2Δ ura3Δ pho3Δ::R  |
| YPH500ΔL        | MATa ade2Δ-101 his3Δ-200 leu2Δ-1 Δ1 trp1Δ-Δ3 lysozyme 2-Δ1 |
| WZY43           | MATa ade2Δ-101 his3Δ-200 leu2Δ-1 Δ1 trp1Δ-Δ3 lysozyme 2-Δ1 hht1Δ-Δ1::pWZ403-F4F10-HIS3, Ycp50-copyII (HHT2-HRP2) |
| JDY2            | MATa ade2Δ-101 his3Δ-200 leu2Δ-1 Δ1 trp1Δ-Δ3 lysozyme 2-Δ1 hht1Δ-Δ1::pWZ403-F4F10-HIS3 hht2Δ (K4R)-HHF2-TRP1 |
| MBB1198         | MATa his3Δ-200 ade2Δ-2 hisG leu2Δ ura3Δ met15ΔΔ trp1ΔΔ6 Tyh1his3Δ1-236 Tylnade2Δ1-515 cirΔ |
| MBB1217         | MATa his3Δ-200 ade2Δ-2 hisG leu2Δ ura3Δ met15ΔΔ trp1ΔΔ6 Tyh1his3Δ1-236 Tylnade2Δ1-515 cirΔ set1Δ::kanMX4 |
| BY4743          | MATa MATa MATa MATa his3Δ-200 ade2Δ-2 leu2Δ lys2Δ met15ΔΔ trp1ΔΔ6 Tyh1his3Δ1-236 Tylnade2Δ1-515 cirΔ set1Δ::kanMX4 |
| CCY2895         | BY4743 set1Δ::kanMX4 set1Δ::kanMX4 31570 32773 33771 34425 34611 35727 |
| 32773           | BY4743 ade2Δ-2 his1Δ1-236 ade2Δ-2 leu2Δ-1 Δ1 hisG-1::pWZ403-F4F10-HIS3, Ycp50-copyII |
| 33771           | BY4743 bre1Δ::kanMX4 bre1Δ::kanMX4 |
| 34425           | BY4743 rad6Δ::kanMX4 rad6Δ::kanMX4 |
| 34611           | BY4743 rtf1Δ::kanMX4 rtf1::kanMX4 |
| 35727           | BY4743 paf1Δ::kanMX4 paf1::kanMX4 |

**TABLE II** Primers used for generation of Northern hybridizations

| Probe    | Sequence                           | Primer name |
|----------|------------------------------------|-------------|
| ACT1     | GGCATGATCCCTTCTTACAAC              | DNO455      |
| ACT1     | CATGGTGACTGATAATGTTCC              | DNO456      |
| GAL1     | CTAGTCACAGAAGATGTTGAT              | CC0369      |
| GAL1     | AGCTGCGAACCCACTTTCC               | CC0370      |
| GAL10    | CTAGTTCAAAAGTGGAGAAGTA            | CC01135     |
| GAL10    | GCTAAGTGACCATATATAAGG             | CC01136     |
| PHO5     | TCTTTCCCTGGCGA                     | DNO425      |
| PHO5     | GCTACAAAGATGTTGTTG                | DNO426      |
| PHO8     | ATAGTTCCGCTAATAAGAT                | MK0628      |
| PHO8     | ATAGTTCCGCTAATAAGAT                | MK0629      |
| PPH3     | ATAGTTCCGCTAATAAGAT                | CC01135     |
| PPH3     | AAAGGAGTACCTGTTGATTGTT             | CC01139     |

*Primer contains a 5' tail with core T7 promoter sequence.

To analyze histone modification levels, antibodies specific for di- and trimethylated forms of histone H3 Lys-4 were used to immunoprecipitate formaldehyde cross-linked chromatin from strains MBY1198 and MBY1217 grown in YPD as described previously (17). Quantitative PCR amplification of input and immunoselected DNA was performed using primers A00236 and LFO740 as described elsewhere (22).

**RESULTS**

Deletion of SET1 Leads to Increased Levels of PHO5 Expression—To determine the role of histone H3 Lys-4 methylation at PHO5, we analyzed PHO5 expression levels in set1Δ strains under both repressive and activating conditions. To distinguish rAPase (Pho5) from constitutive acid phosphatase (Pho3) activity as well as to avoid potential cross-hybridization in Northern analyses, we used strains in which the entire coding sequence of PHO3 was deleted (18). Under the repressive conditions of minimal medium supplemented with P3, set1Δ strains reproducibly showed significantly higher levels of rAPase activity than set1Δ cells (Fig. 1A). This increased rAPase activity correlated with the higher PHO5 mRNA levels in set1Δ cells, suggesting that the derepression was because of increased transcription (Fig. 1B). We also observed enhanced PHO5 expression in fully activating conditions of minimal medium lacking P3 (Fig. 1C). Although the fold increase was lower, the increase by nearly 800 Miller units was substantial. Similarly, under no-P3 conditions, a modest but reproducible increase in PHO5 transcript was observed (Fig. 1D).

To better quantify the level of derepression due to the deletion of SET1, we grew cells under conditions of higher basal expression in rich medium supplemented with P3 (YPDP) at 23 °C. Under these conditions, rAPase activity was ~10-fold higher than when grown in minimal medium containing P3, at 30 °C (compare the levels observed for SET1Δ cells in Fig. 1A with those observed in Fig. 2A). Nevertheless, PHO5 expression was further derepressed in cells lacking Set1 (Fig. 2, A and B). Additionally, a strain containing a mutated version of histone H3 with Lys-4 replaced by arginine (K4R mutant), which can no longer be methylated, showed increased expression of PHO5 (Fig. 2C). It is important to note that the H3 Lys-4 strain, in which endogenous genes encoding histones H3 and H4 were deleted and complemented by a single copy episome containing histones H3 and H4, exhibited a significantly higher basal expression of PHO5 when compared with a congenic set1Δ strain. It is possible that this is because of the lower overall expression levels of these core histones, which have been shown previously to derepress PHO5 (23). Our results suggested that histone H3 Lys-4 methylation via Set1 plays a role in the repression of the euchromatic gene PHO5.

Methylation of Lys-4 of Histone H3 Is Present at the PHO5 Promoter—To see whether H3 Lys-4 methylation directly affects PHO5, we investigated the methylation state of histone H3 at the PHO5 promoter. ChIP analysis was performed using
examined the expression of PHO84, which codes for the high-affinity phosphate transporter. Like PHO5, PHO84 is only minimally expressed in high Pi conditions and is highly expressed in media where Pi is limiting. PHO84 mRNA levels were analyzed in SET1 and set1Δ cells grown in minimal high-Pi medium. As for PHO5 (Figs. 1 and 2), PHO84 expression is also derepressed in a set1 null strain, showing a marked 13-fold increase in transcription over the SET1 strain (Fig. 5A). Conversely, a slight reduction in the mRNA levels transcribed from the gene for the constitutive protein phosphatase PP5H3 is observed in set1Δ cells (Fig. 5B), as has been shown previously (6). These results demonstrate that Set1 may be a general repressor of PHO genes although it is required for full expression of some genes that do not respond to phosphate levels.

**GAL1–10 Is Also Negatively Regulated by Set1**—To determine whether Set1 is involved in the repression of other genes not under phosphate control, we examined the divergently transcribed GAL1–10 locus. SET1 and set1Δ strains were grown in repressed conditions in the presence of glucose (YPD) and semi-activating conditions (YPG + 0.5% glucose) prior to assaying for GAL1 and GAL10 mRNA accumulation. GAL1 and GAL10 transcripts are not detectable in YPD; however, more GAL1 and GAL10 mRNA accumulate in a set1Δ strain in YPG + 0.5% glucose (Fig. 6). These data are consistent with two previous microarray analyses that showed increased GAL1 transcript levels in a set1Δ deletion strain (27, 28). A recent study has also shown that, at early times of induction, GAL10 is expressed at higher levels in rad6Δ as well as set1Δ strains (29). Thus, Set1 may negatively regulate a myriad of genes with different functions and regulatory mechanisms.

**DISCUSSION**

Histone methylation at lysine 4 by Set1 via COMPASS is a prominent histone modification in yeast, with ~34% of the total histone H3 pool being methylated (30). Recent evidence has demonstrated that Set1-dependent methylation requires the monoubiquitination of histone H2B and the Pafl-Rtf1 complex, which has been implicated in transcriptional elongation through its interaction with the carboxyl-terminal domain of RNA polymerase II. The observation that H3 Lys-4 methylation is primarily associated with euchromatic genes although H3 Lys-9 methylation is correlated with heterochromatin in metazoan species suggests that each may play an integral role in the establishment of active versus inactive regions, respectively. Recent evidence has shown that Lys-9 methylation via the histone methyltransferase Suv39h leads to the recruitment of heterochromatin protein 1 (31, 32). Artificial targeting of histone methylation or heterochromatin protein 1 via chimeric fusion proteins to euchromatic regions also leads to local gene silencing (33, 34).

Although Set1-mediated Lys-4 methylation of histone H3 is associated with active chromatin, it is not known whether this modification leads to the recruitment of additional factors or serves another function. Furthermore, although this histone modification is associated with transcriptional elongation and appears to be prominent at core promoters and at the 5′ end of transcribed regions of euchromatic genes, it has been shown to be required for the full expression of only a few genes (5, 6). We presented evidence that Set1 is also involved in the repression of a subset of genes in active chromatin regions, showing that the loss of Set1 leads to higher levels of expression of PHO5 (Figs. 1, 2, and 4A), PHO84 (Fig. 5), and GAL1–10 (Fig. 6). This evidence indicated that, in addition to its previously characterized role in activation, H3 Lys-4 methylation has a repressive role in gene expression. General derepression of genes in our set1Δ mutant strain was not observed, because we confirmed
that PPH3 expression is down-regulated, as has been shown previously (6).

Deletions of genes coding components of complexes that regulate Set1 methylation also showed similar phenotypes as those observed in a set1 null strain (Fig. 4). Loss of Paf1, the most upstream regulator of H3 Lys-4 methylation, led to the largest derepression of PHO5. This suggests that other factors in addition to Set1 may be recruited by the Paf1-Rtf1 elongation complex. It was reported previously that a paf1 mutant causes both gene-specific increases or decreases in transcription, which demonstrates a dual role in gene regulation for transcriptional elongation (35). Interestingly, in this study, GAL10 and GAL7 were two of the genes that required Paf1 for full expression, suggesting further that Paf1-Rtf1 recruits additional proteins that affect gene expression positively or negatively. Similarly, loss of Ctk1, which phosphorylates the carboxyl-terminal domain repeat of RNA polymerase II, has both positive and negative effects on the transcription of various genes (36). More recently, the histone methyltransferase Set2, which methylates histone H3 at lysine 36, has also been associated with active chromatin and transcription elongation via the Paf1-Rtf1 complex and is required for full expression of a GAL1-1ac2 reporter (37). However, when the Set2 protein is tethered to a heterologous promoter via LexA, it serves as a repressor lowering transcription by more than 20-fold (38). Consistent with this observation, Set2 is responsible for the repression of the basal expression of GAL4 (39).

We also found that the Rad6-Bre1 complex, which monoubiquitinates histone H2B at lysine 123 as a prerequisite to H3 Lys-4 methylation by Set1, negatively regulates PHO5 (Fig. 4B). A previous report showed that ARG1 transcription is de-
repressed ~10-fold in the absence of Rad6 (40). Similarly, \( \text{GAL10} \) is expressed at much higher levels in a \( \text{rad6} \) null strain; however, the corresponding histone H2B lysine 123 to the arginine (K123R) mutant did not derepress \( \text{GAL10} \) transcription (29). This same histone mutant was also used in another study to show that loss of histone H2B ubiquitination at \( \text{GAL1} \) and \( \text{PHO5} \) delays transactivation (41). However, in this report, Rad6 was dispensable for \( \text{GAL1} \) activation. The reason for different phenotypes between \( \text{rad6} \Delta \) and histone H2B K123R mutant strains was unclear and may have resulted from strain differences or altered levels of expression of the episomal copy of the histone gene. It is also conceivable that histone H2B ubiquitination is required for basal repression as well as transcriptional activation as has been reported previously for the histone deacetylase Rpd3 (42).

Fig. 5. Set1 regulates other PHO-responsive genes. A, Northern analysis of \( \text{PHO84} \) expression of CCY1467 (\( \text{SET1}^+ \)) and CCY1471 (\( \text{set1} \)) strains grown in minimal high Pi medium. For quantification, \( \text{PHO84} \) transcript levels in each lane are normalized to the 18 S RNA. B, Northern analysis of \( \text{PPH3} \) expression in minimal medium normalized to the 18 S RNA.

A

\[ \text{SET1}^+ \text{ set1} \]

\( \text{PHO84} \)

1.0 13 Fold relative to \( \text{SET1}^+ \)

\( \text{18S} \)

B

\[ \text{SET1}^+ \text{ set1} \]

\( \text{PPH3} \)

1.0 0.7 Fold relative to \( \text{SET1}^+ \)


down-regulate distinct subsets of genes.

The mechanism for the opposing regulatory role at different loci remains unclear. We propose that Set1 regulates gene expression positively and negatively. Although Set1 methylation activity depends on the transcriptional elongation complex Pafl-Rtf1, our data also show that \( \text{PHO5} \) expression is derepressed in \( \text{set1} \) mutants that lack H3 lys-4 methylation. This suggests that H2B Lys-123 ubiquitination and H3 lys-4 methylation may establish a negative feedback loop on basal transcription. This view is consistent with the presence of a transcriptional elongation checkpoint in which Ctk1 phosphorylates serine 5 of the RNA polymerase carboxyl-terminal domain and recruits COMPASS that contains Set1 (16). At initial times of transcriptional initiation, transcriptional activators, such as Pho4 or Gal4, bind to their cognate DNA sites and recruit transcriptional coactivators, e.g., the histone acetyltransferase complex SAGA and the RNA polymerase machinery, including Pafl-Rtf1. During the transition to a stably elongating polymerase, Pafl-Rtf1 leads to increasing amounts of histone H2B ubiquitination and subsequent H3 lys-4 methylation, possibly ensuring assembly of the necessary RNA capping and processing factors (17). However, later in the activation process, recruitment of SAGA is increased, and the histone deubiquitinase Ubp8 of SAGA may remove H2B ubiquitination. This model is supported by data demonstrating a transient peak of histone H2B ubiquitination following transactivation of \( \text{GAL1} \) and \( \text{PHO5} \) (41, 44). Further studies are needed to elucidate the biochemical functions of histone methylation in transcription.

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REFERENCES
1. Hayes, J. J., and Hansen, J. C. (2001) Curr. Opin. Genet. Dev. 11, 124–129
2. Noma, K., Allis, C. D., and Grewal, S. I. (2001) Science 293, 1150–1155
3. Miller, T., Krogan, N. J., Dover, J., Erdjument-Bromage, H., Tempst, P., Johnston, M., Greenblatt, J. F., and Shi, K. A. (2001) Proc. Natl. Acad. Sci. U. S. A. 98, 12902–12907
4. Briggs, S. D., Bryk, M., Strahl, B. D., Cheung, W., Davie, J. K., Dent, S. Y., Johnston, M., Greenblatt, J. F., and Shi, K. A. (2001) Proc. Natl. Acad. Sci. U. S. A. 98, 12902–12907
5. Nislow, C., Ray, E., and Pillus, L. (1997) Mol. Cell. Biol. 17, 2431–2436
6. Santos-Rosa, H., Schneider, R., Bannister, A. J., Sherriff, J., Bernstein, B. E., Emre, N. C., Schreiber, S. L., Mellor, J., and Kouzarides, T. (2002) Nature 419, 407–411
7. Bryk, M., Briggs, S. D., Strahl, B. D., Curcio, M. J., Allis, C. D., and Winston, F. (2002) Curr. Biol. 12, 165–170
8. Krogan, N. J., Dover, J., Khorrami, S., Greenblatt, J. F., Schneider, J., Johnston, M., and Shi, K. A. (2002) J. Biol. Chem. 277, 10753–10755
9. Sun, Z. W., and Allis, C. D. (2002) Nature 418, 104–108
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