A conserved protein interaction network involving the yeast MAP kinases Fus3 and Kss1

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The Saccharomyces cerevisiae mitogen-activated protein kinases (MAPKs) Fus3 and Kss1 bind to multiple regulators and substrates. We show that mutations in a conserved docking site in these MAPKs (the CD/7m region) disrupt binding to an important subset of their binding partners, including the Ste7 MAPK kinase, the Ste5 adaptor/scaffold protein, and the Dig1 and Dig2 transcriptional repressors. Supporting the possibility that Ste5 and Ste7 bind to the same region of the MAPKs, they partially competed for Fus3 binding. In vivo, some of the MAPK mutants displayed reduced Ste7-dependent phosphorylation, and all of them exhibited multiple defects in mating and pheromone response. The Kss1 mutants were also defective in Kss1-imposed repression of Ste12. We conclude that MAPKs contain a structurally and functionally conserved docking site that mediates an overall positively acting network of interactions with cognate docking sites on their regulators and substrates. Key features of this interaction network appear to have been conserved from yeast to humans.

Introduction

The components of intracellular signaling pathways are dynamically interconnected into complex networks, where the proteins correspond to the nodes of the network and the protein–protein and enzyme–substrate interactions are the links between them. The links are a key to understanding not only the overall flow of information, but also systems level questions of why particular network structures have evolved, and how network structure contributes to function (Vespignani, 2003). In addition, the links are potential drug targets that might yield highly specific therapeutic effects. For example, it would be beneficial to be able to block the ability of a kinase to phosphorylate some of its substrates while not interfering with its ability to phosphorylate others.

The mating pheromone response pathway of the yeast Saccharomyces cerevisiae provides an advantageous model system for exploring these issues because it is one of the best characterized multilevel signaling pathways in eukaryotes (for review see Dohlman and Thorner, 2001). Mating is initiated when peptide pheromone secreted by a cell of one mating type binds to a receptor on the surface of a cell of the opposite mating type. Receptor occupancy activates a heterotrimeric G protein, and the Gα subunit then transmits the mating signal to downstream components, leading to the activation of a MAPK cascade.

The MAPK cascade module consists of three sequentially acting protein kinases. The last in the sequence is the MAPK (also termed extracellular signal–regulated kinase; ERK) that is phosphorylated and thereby activated by a MAPK/ERK kinase (MEK, or MKK). MEK activity is regulated, in turn, via phosphorylation by the first member of the module, a MEK kinase (MEKK). In the yeast mating pathway, the MEKK is Ste11, which activates the MEK Ste7, which then activates two MAPKs, Kss1, and Fus3. The Ste5 adaptor/scaffold protein binds to all three tiers of this module, first enabling Ste11 activation, and then assisting signal transmission from MEKK to MEK to MAPK (Elion, 2001).

The downstream targets of the active MAPKs include the Ste12 transcription factor and its associated repressors Dig1 and Dig2 (Elion et al., 1993; Cook et al., 1996; Tedford et al., 1997). MAPK-mediated phosphorylation of Ste12, Dig1, and Dig2 is thought to underlie the transcriptional induction of a battery of over 200 genes (Roberts et al.,...
Results

Sevenmaker-region mutants of Kss1 and Fus3

To determine the region(s) of the MAPKs required for interaction with the D-site in Ste7MEK, site-directed mutagenesis was used to introduce amino acid substitutions into candidate regions of Fus3MAPK and Kss1MAPK. The D-site of Ste7 is contained within its first 19 residues; within this region, two dibasic submotifs (R4 K5 and R9 R10), and a hydrophobic submotif (L15 L17), are involved in MAPK interaction (Bardwell et al., 2001). Because basic submotifs are a prominent feature of the D-site of Ste7, and of other D-sites, acidic patches on the surface of the MAPKs were prioritized for mutagenesis; one such patch was the CD/7m region, a cluster of negatively charged surface residues on the back side of the kinase, opposite the catalytic cleft. We found that the Ste7–MAPK interaction was essentially abolished by mutations in this region.

Figure 1. Yeast MAPK protein interactions and the CD/sevenmaker region. (A and B) Subset of the protein interactions in which the yeast MAPKs Kss1 and Fus3 participate. (C) Sequences of D. melanogaster rolled (GenBank/EMBL/DDJB accession no. P40417), H. sapiens ERK2 (NP_620407), and S. cerevisiae Kss1 and Fus3 proteins (P14681 and S28548) in the CD/7m region. The COOH-terminal–most residue shown is indicated on the right. The site of the sevenmaker mutation in rolled (D334N) is underlined. Residues identical in all four proteins are denoted at the bottom by an asterisk. (D) Altered amino acids in the CD/7m-region mutants of Kss1 and Fus3 are underlined.
binding, with the binding of the wild-type set at 100. The percent of the input of wild-type Fus3 bound to Ste7, Ste5, and Dig1 was 14.0, 12.6, and 0.6, respectively. For Kss1: 9.0, 3.7, and 1.3, respectively. (C) Dissociation constants (K_d) for MAPK interactions with GST-Ste7 and GST-Ste5. The mean K_d (in micromolar) is shown, as well as the SEM (s.e.) and the number of experiments performed to determine the mean (N). (D) The Ste7 D-site competes with Ste5241-336 for Fus3 binding. 35S-labeled, wild-type Fus3 protein (~1 pmole) was incubated with 6 μg of purified GST or GST-Ste5241-336 prebound to glutathione-Sepharose beads, and with either no peptide, 25 or 100 μM of Ste72-22 peptide (Ste7ds) or 25 or 100 μM of a scrambled control for this peptide (scram7; (Bardwell et al., 2001)). Other details as in B, above. The bar graph shows the quantification of relative binding, as determined using a phosphorimager. After subtracting the nonspecific background adsorption to GST alone, 19.7% of the input Fus3 bound to wild-type GST-Ste5 in the absence of peptide. Results were normalized by setting this value as 100%. Data show the mean ± SD of two experiments.

The CD/7m alleles constructed for this paper are shown in Fig. 1; most consist of single or multiple substitutions of charged residues with alanines; the exception is Fus3-7m2, which contains a D317N substitution, mimicking the original sevenmaker allele of Drosophila rolled. A description of our mutants in other regions of the MAPKs, and their effects on MAPK protein–protein interactions will appear separately (unpublished data).

The mutations diminish binding to Ste7 and Ste5

The CD/7m mutants of Kss1MAPK and Fus3MAPK were tested for in vitro binding to Ste7MEK, Ste5, and Dig1 (Fig. 2). The MAPK-interacting domains of these proteins were fused to S. japonicum GST, and the resulting fusion proteins were expressed in bacteria and purified by adsorption to glutathione-agarose beads. These fusions (or GST alone as a control) were then incubated with Kss1 or Fus3 (or mutants thereof) that had been produced in radiolabeled form by in vitro translation, and partially purified by ammonium sulfate precipitation. Bead-bound complexes were collected by sedimentation and analyzed by SDS-PAGE and autoradiography. The minimal MAPK-binding domain of Ste5 is contained within residues 241–336, as determined by a two-hybrid screen (residues 213–452) bound to wild-type Fus3 and Kss1 (Fig. 2 B). Unexpectedly, the CD/7m-region mutants to Ste7 and Ste5 manifested significant binding to Ste5, whereas the binding of the double and triple Kss1 mutants, like all three Fus3 mutants, were more substantially impaired. Dig1 and Dig2 were initially identified in a two-hybrid screen using Kss1 as bait (Cook et al., 1996). A GST fusion protein containing this region bound to wild-type Fus3 and Kss1 (Fig. 2 B). In contrast to the results seen when MAPK binding to Ste7 and Ste5 was examined, MAPK binding to GST-Dig1213-452 was not significantly impaired by the CD/7m-region mutations (Fig. 2 B). Hence, the mutations compromise some, but not all, of the protein–protein interactions in which the MAPKs participate. In support of this conclusion, the Kss1-7m1, 7m2, and 7m3 mutants, like wild-type Kss1 protein (Printen and Sprague, 1994), exhibited a robust interaction with full-length Ste11MEK in the two-hybrid assay (unpublished data). Subsequent experiments revealed that the MAPKs also bind to another region of Dig1 (see below).

We quantified formation of the Ste7 and Ste5 complexes using a method described previously (Fig. 2 C; Bardwell et
al., 1996; Ho et al., 2003). Both Kss1 and Fus3 bound to GST-Ste7 with high affinity ($K_d \approx 0.1 \mu M$). Mutations in the CD/7m region decreased the Ste7–MAPK binding affinity by $>500$-fold. Compared with the Ste7–Fus3 interaction, the Ste5–Fus3 interaction was weaker ($K_d \approx 1 \mu M$), and was less severely impaired by the CD/7m-region mutations ($\sim12$-fold decrease in binding affinity). Interestingly, the Ste5–Kss1 interaction ($K_d \approx 6.5 \mu M$) was weaker than the Ste5–Fus3 interaction. The affinity of the Ste5–Kss1 interaction was decreased approximately sixfold by the CD/7m-region mutations.

Ste5 and Ste7 partially compete for docking to Fus3

The observation that the CD/7m-region mutations reduced MAPK binding to both Ste7$^{\text{MEK}}$ and Ste5 suggested that these two proteins might compete for MAPK docking. Consistent with this possibility, a peptide version of the Ste7 docking site (residues 2–22) inhibited the binding of wild-type Fus3 protein to GST-Ste5$_{241-336}$ by almost 80% (Fig. 2 D). A control peptide consisting of residues 2–22 of Ste7 in a scrambled order was not inhibitory.

The CD/7m mutations abolish MEK–MAPK complex formation in cell extracts

To assess the effects of the CD/7m-regions mutations on protein stability in vivo, the wild-type and mutant coding sequences were subcloned into a low copy (CEN) expression vector, driven by their endogenous promoter, and expressed in a strain lacking endogenous Kss1 and Fus3 (i.e., a kss$\Delta fuc3\Delta$ strain), All four of the Kss1 mutant proteins were produced at levels comparable to wild type (not depicted and see Fig. 4 A). The Fus3-7m1 and 7m2 mutant proteins, however, were produced at only $\sim40\%$ of the wild-type level and the Fus3-7m3 protein could not be detected (not depicted and see Fig. 4 D). The pheromone response pathway positively regulates $FUS3$ expression; however, decreased levels of Fus3-7m mutants was also observed in a $KSS1+$ strain (unpublished data), suggesting that a signaling defect is not the underlying cause. Hence, the mutations appear to destabilize Fus3 protein to a variable extent depending on the precise mutation.

Wild-type Kss1 and Fus3 proteins are found in complexes with full-length Ste7$^{\text{MEK}}$ protein in yeast cell extracts (Bardwell et al., 1996). When assessed in this assay, both of the Kss1 mutants tested (7m2 and 7m3), and both of the Fus3 mutants tested (7m1 and 7m2), were unable to form complexes with Ste7 (Fig. 3), consistent with the results obtained using in vitro–translated and bacterially expressed proteins (Fig. 2).

Phosphorylation of the Kss1-7m3 mutant is reduced

Ste7$^{\text{MEK}}$ phosphorylates the Fus3 and Kss1 MAPKs on a threonine and tyrosine residue located in a surface loop (the activation loop) situated near the MAPK active site. The reduced ability of the CD/7m-region mutants of the MAPKs to bind to Ste7 and Ste5 suggested that they might also have a defect in their ability to be phosphorylated, and thereby activated, in response to pheromone stimulation. To examine this, the wild-type and mutant Kss1 alleles were expressed at endogenous levels in a strain lacking Fus3. As assessed using an antibody that specifically recognizes the dually phosphorylated MAPKs (Sabbagh et al., 2001), wild-type Kss1 protein was hyperphosphorylated after a 5-min treatment with 500 nM pheromone (Fig. 4 A). Phosphorylation of the Kss1-7m1 mutant, which exhibited a moderate defect in binding to Ste7 in vitro and only a modest defect in binding to Ste5 (Fig. 2), was undiminished relative to wild-type Kss1. In contrast, phosphorylation of the Kss1-7m3 mutant, which exhibited a substantial defect in binding to Ste7 and Ste5 in vitro (Fig. 2), was significantly reduced relative to wild type (Fig. 4 A).

In parallel, as a marker for pheromone-induced transcription, the pheromone-stimulated expression of a $FUS1$-lacZ reporter gene was monitored. $FUS1$ is representative of a battery of genes that is induced after exposure to mating pheromone (Roberts et al., 2000). As shown in Fig. 4 B, the Kss1-7m1 mutants had a substantially reduced ability to drive the expression of the reporter gene. Surprisingly, this was even somewhat true of the Kss1-7m1 mutant, which was phosphorylated normally (Fig. 4 A).

Similarly, the ability of the Fus3-7m mutants to support pheromone-induced transcription was assessed. We compensated for the somewhat reduced stability of the Fus3-7m mutants by expressing them from two different low copy plasmids (each with a different selectable marker) in the same strain. Using this procedure, it was possible to produce the mutants at a level that was 80% of that obtained when wild-type Fus3 was expressed from either selectable plasmid (not depicted and Fig. 4 D). Such strains were used for all
bioassays. When expressed in this manner in a strain lacking Kss1, both Fus3-7m1 and Fus3-7m2 showed dramatic defects in their ability to drive FUS1-lacZ expression in pheromone-stimulated cells (Fig. 4 C). In contrast, these mutants were dually phosphorylated to a level comparable to wildtype Fus3 (Fig. 4 D), despite their inability to dock with Ste7Mpk and reduced binding to Ste5 (Figs. 2 and 3).

Kss1 is phosphorylated and activated during mating in a wild-type cell, where it acts with Fus3 to promote pheromone-induced transcription (Sabbagh et al., 2001); moreover, Kss1 can partially support pheromone-induced transcription in the absence of functional Fus3 (Roberts et al., 2000). Indeed, pheromone-induced reporter gene expression was ~50% of wild-type in the fus3-7m1 KSS1 strain (Fig. 4 C). In addition, Kss1 was hyperphosphorylated in this strain (Fig. 4 D, compare lane 1 with lane 3). When three independent experiments like that shown in Fig. 4 D were averaged, Kss1 phosphorylation was 3.1 (± 0.6)-fold higher in the fus3-7m1 KSS1+ strain relative to wild-type. Active Fus3 initiates a feedback loop that limits the magnitude and duration of Kss1 phosphorylation (as well as its own phosphorylation; Sabbagh et al., 2001). Fus3-7m1 is apparently unable to initiate this feedback loop.

The mutants have pheromone response defects

To further determine the net effect of protein–protein interactions mediated by the CD/7m region of Kss1 and Fus3 on the transmission of the mating pheromone signal, selected mutants of Kss1 and Fus3 were tested in several different measures of the mating pheromone response. The Fus3-7m1 and Kss1-7m3 mutants were the focus of this analysis, because they exhibited a clear binding defect to Ste7 and Ste5 (Fig. 2), and because they contained equivalent amino acid substitutions (Fig. 1 D).

First, as a measure of the long-term effects of pheromone action, pheromone-imposed cell-cycle arrest and recovery from arrest were monitored using the standard halo bioassay. As shown in Fig. 5 A, compared with wild type, the fus3-7m1 kss1Δ strain exhibited smaller and much more turbid haloes, indicating a marked reduction in the initial strength of pheromone-imposed arrest and/or a substantially accelerated rate of recovery.

Second, to assess pheromone-regulated morphogenesis, the formation of a mating projection (shmoo formation) was monitored 4 h after initial exposure to pheromone. This treatment induced wild-type cells to form substantial mating projections (Fig. 5 B, compare a with b); in contrast, cells lacking both MAPKs did not form projections as expected (Fig. 5 B, c). Cells lacking Fus3 underwent some pheromone-induced shape changes but did not form obvious projections (Fig. 5 B, d), whereas cells lacking Kss1 formed projections that were smaller than wild type (Fig. 5 B, e). These controls confirm that both MAPKs are required for normal pheromone-induced morphogenesis, with Fus3 playing a primary role, in agreement with the work of the Elion lab (Farley et al., 1999). In cells lacking Kss1, the Fus3-7m1 mutant was unable to support any morphogenesis, so that the cells resembled those lacking both MAPKs (Fig. 5 B, f). In contrast, the cells containing Fus3-7m1 and wild-type Kss1 were able to undergo substantial morphogenesis, although not with wild-type efficiency (Fig. 5 B, g). Hence, Kss1 was able to almost completely suppress the morphogenesis defect of the fus3-7m1 strain, but not of the fus3Δ strain.

Finally, to assess the role of CD/7m-mediated interactions in overall mating proficiency, mating assays were performed (Fig. 5 C). In a quantitative mating assay, cells lacking Kss1 (but containing Fus3) mated with essentially wild-type efficiency (96%), whereas cells lacking Fus3 (but containing Kss1) mated with reduced efficiency (9%), and cells lacking both MAPKs were unable to mate (<0.02%), as has been extensively documented elsewhere (Farley et al., 1999). In cells lacking Fus3, replacing wild-type Kss1 with Kss1-7m3 resulted in an 18-fold drop in mating efficiency. Kss1-7m2 was equally defective in mating, whereas Kss1-7m1 was only twofold down (unpublished data). Similarly,
in cells lacking Kss1, replacing wild-type Fus3 with Fus3-7m1 resulted in a 12-fold decrease in mating; Fus3-7m2 was less severely compromised (fourfold decrease). Thus, the double-substitution mutants of the CD/7m-region of the MAPKs have significantly diminished functionality relative to wild type.

As was seen in the analyses of pheromone-regulated morphogenesis (see above), the mating defect of Fus3-7m1 was substantially enhanced when Kss1 was absent, such that the fus3-7m1 kss1Δ strain mated much worse than the fus3-7m1 KSS1+ strain (Fig. 5 C). Conversely, Fus3-7m1 substantially suppressed the mating defect of the fus3Δ KSS1+ strain. This striking mutual suppression was even more evident when mating was performed at 37°C (unpublished data). The presence of Kss1 also partially suppressed (or the absence of Kss1 enhanced) the cell-cycle arrest defect of Fus3-7m1 (unpublished data). These data suggest that Fus3-7m1 is defective in a function that Kss1 can provide (most likely, pheromone-induced transcription; Fig. 4 C), but is still able (to some extent) to execute cell-cycle arrest and morphogenesis functions that Kss1 cannot provide, perhaps because the CD/7m region of Fus3 is not involved in its ability to bind the relevant substrates.

The mutants are also defective in downstream interactions

The previous results demonstrate that several of the CD/7m mutants are phosphorylated (and presumably activated) to near wild-type levels, but are unable to support Ste12-driven expression of mating genes. This suggested that the CD/7m mutants must also be defective in interacting with some of their downstream substrates. We focused on the transcriptional regulators Ste12, Dig1, and Dig2. All three proteins are known substrates of the MAPKs, although the target residues critical for regulation are undetermined.

First, the Kss1–Ste12 interaction was scrutinized (the Fus3–Ste12 interaction is much weaker, and hence was not examined). In an in vitro binding assay (Fig. 6 A), unphosphorylated Kss1 bound to GST-Ste12 with reasonably high affinity (Ki ≈ 2 μM). The Kss1-7m3 mutant bound with a somewhat reduced affinity (Ki ≈ 8 μM), but still exhibited clearly detectable binding to Ste12. It is unclear whether this modest drop in binding affinity has a significant functional consequence in vivo.

Second, the interaction of Kss1 with Ste12, Dig1, and Dig2 was evaluated in the two-hybrid assay. A fusion of wild-type Kss1, or the Kss1-7m3 mutant, to the Gal4 DNA-binding domain (GDB) was tested against fusions of Ste12, Dig1, or Dig2 to the Gal4 transcriptional activation domain (GAD). In this assay, wild-type Kss1-GDB displayed a minimal background activation of the two-hybrid reporter gene, and the interaction with Ste12, Dig1, or Dig2 was 4–, 3–, and 23-fold above this background, respectively, consistent with our previous reports (Cook et al., 1996; Bardwell et al., 1998a). For reasons that are unclear, the background level of expression driven by Kss1-7m3-GDB was substantially higher than that driven by wild-type Kss1-GDB. Coexpression of Kss1-7m3-GDB with full-length Dig1-GAD or Dig2-GAD did not increase reporter gene expression above this already high background level, whereas coexpression of Kss1-7m3-GDB with Ste12-GAD resulted in a further about sixfold increase in signal (unpublished data). These results suggest that Kss1-7m3 has a defect in binding to full-length Dig1 or Dig2 but is still able to bind to Ste12.

The observations that Kss1-7m3 was compromised in its ability to bind to full-length Dig1 or Dig2 in the two-hybrid assay, but was able to bind to Dig1313-452 (Fig. 2), appeared to be contradictory. Although DIG1(213-452) was the shortest DIG1 coding sequence to be isolated from the two-
Figure 6. The mutants are defective in binding to D-sites in Dig1 and Dig2. (A) Binding of ~1 pmole 35S-labeled Kss1 or Kss1-7m3 to 2 μg of GST or 1 μg of GST-Ste12. Experimental design as in Fig. 2. The bottom panel shows a representative loading control for the GST fusion proteins, stained with Coomassie blue. (B) Sequences of the peptides covalently attached to cellulose membrane for peptide array experiment. Conserved residues of the D-site or FXFP-site are underlined. The peptides correspond to the following portions of the full-length proteins, where the NH2-terminal methionine is considered to be residue 1: Ste7D, residues 2–23; Dig1D, 92–113; Dig2D, 95–116; Dig1F, 402–423; Dig2F, 288–309. (C) Autoradiogram of representative peptide spots bound to 35S-labeled Fus3. (D) Graphical representation of relative peptide binding, as quantified on a phosphorimager. The average fold above background binding to the Ste7 peptide was set to 100, and the other peptides were normalized relative to it. Data obtained with Fus3 and Kss1 were pooled. Four experiments were normalized relative to Fus3. (E) Binding of Fus3–Dig1D, 92–113; Fus3–Dig2D, 98–114; Kss1 and Kss1-7m3, to GST-Dig193–111 and GST-Dig298–114. Grey bars represent the 5% input control for the GST fusion proteins, stained with Coomassie blue. The mutants are defective in binding to D-sites in Dig1 and Dig2. The binding of radiolabeled Fus3 or Kss1, and the Fus3–Dig2 peptide, to GST-Dig193–111 and GST-Dig298–114 was measured. Wild type Fus3 and Kss1 bound with high affinity to these fusion proteins, whereas the CD/7m-region mutants did not (Fig. 6E). The strongest interaction (Fus3–Dig2) had a Kd of roughly 1 μM. Two other interesting observations emerged from the quantification of this experiment. First, Fus3 bound to both the Dig1 and Dig2 D-site peptides, but not to the corresponding mutant peptides. In addition, both MAPKs bound to the Dig1 FXFP-containing peptide, but not to the corresponding mutant peptide. Finally, both MAPKs did not appreciably bind to the Dig2 FXF-containing peptide; moreover, what little binding there was to this peptide was not lessened by mutation of the two phenylalanine residues. Thus, the putative D-sites in Dig1 and Dig2 can bind to Kss1 and Fus3, as can the putative FXFP site in Dig1.

To determine if the CD/7m-region mutations impaired the binding of the MAPKs to the D-sites in Dig1 and Dig2, the binding of radiolabeled Kss1 and Fus3, and the Fus3-7m1 and Kss1-7m3 mutants, to GST-Dig193–111 and GST-Dig298–114 was measured. Wild type Fus3 and Kss1 bound with high affinity to these fusion proteins, whereas the CD/7m-region mutants did not (Fig. 6E). The strongest interaction (Fus3–Dig2) had a Kd of roughly 1 μM. Two other interesting observations emerged from the quantification of this experiment. First, Fus3 bound to both the Dig1 and Dig2 D-site peptides, but not to the corresponding mutant peptides. In addition, both MAPKs bound to the Dig1 FXFP-containing peptide, but not to the corresponding mutant peptide. Finally, both MAPKs did not appreciably bind to the Dig2 FXF-containing peptide; moreover, what little binding there was to this peptide was not lessened by mutation of the two phenylalanine residues. Thus, the putative D-sites in Dig1 and Dig2 can bind to Kss1 and Fus3, as can the putative FXFP site in Dig1.

CD/7m mutants of Kss1 are defective in Kss1-imposed repression of Ste12

Unphosphorylated Kss1 binds to Ste12 and potently represses the transcription of filamentation genes (Madhani...
et al., 1997; Bardwell et al., 1998a). Unphosphorylated Kss1 also represses the basal expression of pheromone-responsive genes (Bardwell et al., 1998b). This Kss1-imposed repression requires Kss1-Ste12 binding, because both Kss1-imposed repression and Kss1-Ste12 binding are reduced by a point mutation (Y231C) in Kss1 (Bardwell et al., 1998a), as well as by mutations in a different region of Kss1 known as the MAPK-insertion region (Madhani et al., 1997; unpublished data). Kss1-imposed repression also requires the Dig1 and Dig2 repressors, and we have proposed that Kss1, by virtue of its ability to bind to both Ste12 and Dig1/2, stabilizes the Ste12-Dig complex, thereby potentiating Dig-dependent repression of Ste12 (Bardwell et al., 1998b). Kss1-imposed repression of Ste12 does not require that Kss1 be activated. In fact, activation-loop phosphorylation of Kss1 weakens Kss1-Ste12 binding and thereby relieves repression (Bardwell et al., 1998a). Hence it is possible to completely separate Kss1-imposed repression from upstream signaling. The model of Kss1-imposed repression is shown in Fig. 7 A.

Because Kss1-7m3 was deficient in Dig1 and Dig2 binding (Fig. 6), we reasoned that if Kss1-Dig binding is required for Kss1-imposed repression, then Kss1-7m3 should be defective in repression. To test this hypothesis, the Kss1-7m mutants were expressed in place of wild-type Kss1 in a filamentation-competent strain; Ste12-dependent transcription of filamentation genes was then monitored in a quantitative assay, using a reporter gene driven by a filamentation response element (FRE; Madhani and Fink, 1997). This experiment was performed in a strain lacking Ste7MEK, so as to separate any potential repression defect of Kss1-7m3 from the effects of its reduced phosphorylation by Ste7 (Fig. 4). As shown in Fig. 7 B, in both haploids and diploids, FRE-driven transcription was low in a ste7Δ kss1+ strain, as Ste12 protein was constitutively repressed by Kss1 protein that was locked in its repressive (i.e., unphosphorylated) state. Removal of Kss1 (ste7Δ kss1Δ) resulted in a substantial (>10-fold) derepression of FRE-driven transcription as described previously (Cook et al., 1997; Madhani et al., 1997). Replacement of Kss1 with Kss1-7m2 or Kss1-7m3 also depressed FRE-driven transcription, to a level that was ~60% of that obtained in the absence of Kss1; Kss1-7m1 had only a slight repression defect. A bioassay of haploid invasive growth supported the conclusions drawn from the reporter gene data (unpublished data). In summary, the CD/7m-region mutants of Kss1 are defective in Kss1-imposed repression, likely due to decreased Dig binding.

Discussion

Common D-sites in MAPK-interacting proteins

Here, we found that mutations in an evolutionarily conserved surface patch of the MAPKs, the CD/7m region, compromised the binding of the yeast MAPKs Fus3 and Kss1 to multiple partners, including the Ste7 MEK, the Ste5 scaffold protein, and the Dig1 and Dig2 transcriptional repressors. Significantly, however, only some of the protein–protein interactions that the MAPKs participate in were impaired. Of those that were, most (the exception being Ste5) were mediated a common docking site on the MAPK-interacting partner, the D-site, that has the rough consensus (K/R)1-3-X1-6-ψ-X-ψ where ψ represents a hydrophobic residue, typically L or I. The basic and hydrophobic submotifs of the D-site apparently bind to the MAPK in a highly cooperative fashion, as mutation of either can dramatically diminish binding (Zúñiga et al., 1999; Bardwell et al., 2001). It is likely that the basic submotif of the D-site interacts directly with the acidic residues of the CD/7m region (Tanoue et al., 2000). The MAPK-binding domain of Ste5 (Ste5241-336) does not contain a clear consensus D-site. However, it does contain two dibasic submotifs. Furthermore, a Ste5318-339 peptide, which contains both of these submotifs, binds to Fus3 in an array assay (unpublished data).

That the same region of MAPKs is required for binding to many MAPK-interacting proteins suggests that these proteins may compete with each other for binding to their cognate MAPKs, binding in a competitive and perhaps mutually exclusive fashion (Bardwell et al., 2003). Indeed, we showed here that the Ste7 D-site competed with Ste5 for binding to Fus3MAPK (Fig. 2 D). This result suggests that, in a Ste5–Ste7–MAPK complex, the MAPK can bind with high affinity either to Ste5 or Ste7, but not to both simultaneously. Similarly, mammalian c-Jun N-terminal kinase (JNK) MAPKs bind to D-sites in scaffolds such as JIP1-3 and β-arrestin 2 (Enslen et al., 2000; Sharrocks et al., 2000), and also bind to a D-site in the MKK4 (Ho et al., 2003). The competitive binding of MEKs and scaffolds to MAPKs may influence the dynamics of scaffold-assisted MAPK activation in a manner that is not presently understood.
Binding to Ste7

The interaction between the Ste7 MEK and its cognate MAPKs Kss1 and Fus3 has the highest affinity of any MEK–MAPK interaction yet measured in any organism (Kd ≈ 5–100 nM, depending on the assay; Bardwell et al., 1996, 2001). This affinity was decreased more than 500-fold by the CD/7m region mutations (Fig. 2). In cells, this is predicted to decrease the fraction of Ste7 bound to the MAPKs at any instant in time from greater than 90% to less than 5%. Consistent with this prediction, the Kss1-7m mutant was inefficiently phosphorylated by Ste7 in vivo (Fig. 4). On the other hand, there was no obvious decrease in the phosphorylation of the Fus3 mutants, perhaps because other protein interactions compensated for the loss of Ste7-dependent docking (Bardwell et al., 2001). In addition, any defects in MAPK activation caused by the CD/7m-region mutations may have been counterbalanced by defects in negative regulatory mechanisms, for example, decreased binding of the mutants to MAPK phosphatases, or the defect in the Fus3-dependent feedback circuit.

Binding to Dig1 and Dig2

We found that the CD/7m mutants of Kss1 and Fus3 exhibited reduced binding to full-length Dig1 and Dig2 in the two-hybrid assay. Accordingly, these MAPK mutants also lost the ability to bind to isolated versions of putative D-sites found in the NH2-terminal halves of Dig1 and Dig2 (Fig. 6). Binding of the mutants to the COOH-terminal half of Dig1, perhaps to an FXFP-type docking site located there, was undiminished. Collectively, these data indicate that the interaction of the MAPKs with Dig1 and Dig2 is bimodal, with the D-site playing a major role in stable complex formation. The importance of both the D-site and the FXFP-like site for Dig1 function in vivo has been delineated recently by Thorner’s lab (J.X. Zhu-Shimoni and J. Thorner, personal communication).

What is the cellular function of the CD/7m-region–mediated interactions of the MAPKs with Dig1 and Dig2? Our data indicate that the CD/7m mutants are defective in both positive and negative components of MAPK-regulated transcription. The defect in positive regulation was exemplified by the Fus3-7m1 and 7m2 mutants, which were significantly compromised in their ability to support pheromone-induced transcription (Fig. 4). The MAPKs are thought to positively regulate transcription by phosphorylating Ste12 and/or Dig1 and Dig2, thereby destabilizing the Ste12–Dig complex. It is likely that the CD/7m-region–mediated docking of Fus3 and Kss1 to this complex potentiates these phosphorylation events. This model is consistent with a series of studies showing that the docking of animal MAPKs to transcription factors potentiates the phosphorylation of nearby target residues (Sharrocks et al., 2000).

The MAPKs, particularly Kss1, negatively regulate gene expression by a mechanism termed “MAPK-imposed repression” (Fig. 7A). We proposed a model for this process in which Kss1 stabilizes the interaction of the Dig repressors with their target, Ste12, by virtue of its ability to bind to all three proteins (Bardwell et al., 1998b). This model was supported by the finding that two mutants of Kss1, Y231C and ∆loop, that had reduced binding to Ste12 (but undimin-ished binding to Dig1 and Dig2) were partially deficient in repression (Bardwell et al., 1998a). This paper provides important support for another key tenet of this model. The Kss1-7m3 mutant, deficient in binding Dig1 and Dig2, but still able to bind Ste12 (Fig. 6), was defective in Kss1-imposed repression (Fig. 7). Hence, Kss1-Dig binding is indeed required for repression, as proposed.

A caveat to the above interpretation is that Kss1-7m3 was partially compromised in its ability to bind to Ste12298–473 in vitro (Fig. 6). We discount the significance of this modest effect on Ste12 binding, because Kss1-Y231C and Kss1-∆loop both bind to Ste12 much worse than Kss1-7m3, but support Kss1-imposed repression better than Kss1-7m3 (Bardwell et al., 1998a; unpublished data).

CD/7m-region–mediated interactions have an overall positive role

Most of the previous genetic and cell-based studies of 7m-region mutants of MAPKs emphasized a hyperactive, gain of function phenotype that was attributed to a decreased interaction with negative regulators such as deactivating phosphatases (Bott et al., 1994; Brunner et al., 1994; Chu et al., 1996; Hall et al., 1996; Karim and Rubin, 1999; Zhan and Guan, 1999). These findings are not entirely consistent with subsequent evidence, here extended to yeast, that the CD/7m region also mediates interactions with positively acting upstream regulators and downstream substrates (Tanoue et al., 2000). Hence, heretofore, genetic studies of the consequences of mutating the MAPK sevenmaker region contradicted the far-reaching implications of the biochemical studies.

Hall et al. (1996) isolated a 7m-region mutant, Fus3D317G, that protected overproduced Fus3 from repression by the HOG–MAPK pathway. We did not specifically examine this phenotype. In contrast to our results, however, Hall et al. (1996) did not find that their allele had a signaling defect, perhaps due to the particular allele they used. Zhan and Guan (1999) observed that Fus3D317N and Fus3D317G conferred a slightly hyperactive phenotype when expressed in wild-type cells; they did not examine the phenotype of these mutants in fus3Δ cells. The tissue culture studies of ERK2D319N also were based on expression of the mutant in cells containing endogenous ERK2 (Bott et al., 1994; Chu et al., 1996). There is also some evidence that the ERK2D319N mutant may compromise the interaction with phosphatases more so than it does with other targets (Yung et al., 2001; unpublished data); perhaps the same is true of Drosophila rolledD324N. Differences in expression levels might also account for some of the above discrepancies, because we found that multi-copy expression of the Fus3-7m mutants suppressed their signaling defect (unpublished data).

Here, we showed that, when expressed at near-endogenous levels in a fus3Δ kss1Δ strain, the Fus3 and Kss1 CD/7m-region mutants exhibited deficiencies in multiple mating end points (Figs. 4 and 5). These observations provide important genetic evidence that the network of interactions mediated by the MAPK CD/7m region has overall a positive role in signal transmission. Our results are in agreement with those of Farley et al. (1999), who isolated and studied a series of Fus3 reduced-function alleles, two of which had mutations in the CD/7m region.
Conclusions

It is apparent that an interaction network involving MAPKs and multiple binding partners has been structurally and functionally conserved from yeast to humans (Fig. 8). Indeed, it seems that the network architecture has been conserved to a greater degree than the component nodes, as no homologues of Ste5, Dig1, or Dig2 can be recognized in any animal genome. Thus, the links in the MAPK network have apparently been preserved, even though some of the component nodes have changed completely, replaced by scaffolds and transcription factors that may be partial analogs of Ste5 and Ste12/Dig1/Dig2, but are clearly not orthologues. Evidently, the network itself is more evolutionarily stable than the nodes that constitute it.

Materials and methods

Yeast strains used in this paper are described in Table S1. Standard yeast media and culture conditions, and bioassays for pheromone response were prepared as described previously (Bardwell et al., 1996). Two-hybrid analysis was performed as described previously (Bardwell et al., 1999a). Plasmids used in this work are described in Tables S2–S8.

Oligonucleotide-directed, PCR-based mutagenesis was performed using the Quickchange kit (Stratagene), and confirmed by sequencing. In vitro transcription and translation were performed in a coupled system (SPT3) purchased from Novagen; 35S)methionine was used to label the translation products. Partial purification of translation products, and determination of dissociation constants from binding assay results were performed as described previously (Bardwell et al., 1996, 2001). GST fusion proteins were produced in bacteria as described previously (Cook et al., 1996; Bardwell et al., 2001), except GST-Ste12p as-gly, which was produced in yeast (Bardwell et al., 1998a). The peptide array binding assay was performed as described previously (Ho et al., 2003). GST coedimentation assays (Cook et al., 1996; Bardwell et al., 2001), coinmunoprecipitation from yeast cell extracts and quantification of reporter gene expression (Bardwell et al., 1996), and analysis of Kss1 and Fus3 phosphorylation levels in vivo (Sabbagh et al., 2001), were also performed as described previously. Binding assay results were quantified using a Phosphorlmager (Molecular Dynamics, Inc.). Immunoblots were quantified using an Odyssey infrared imaging system (LI-COR Inc.).

Microscopy

For Fig. 5 B, formalin-fixed cells were mounted under a standard coverslip and visualized using a microscope (model Axioskop 2 MOT; Carl Zeiss MicroImaging, Inc.) equipped with a 100× oil-immersion objective, NA 1.4, at RT. The images were acquired using a camera (model Axiocam HRc; Carl Zeiss MicroImaging, Inc.) and Axiovision V3.04E software.

Online supplemental material

Yeast strains used in this paper are described in Table S1. Plasmids used here are described in Tables S2–S8. All supplemental tables are available at http://www.jcb.org/cgi/content/full/jcb.200310021/DC1.

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