A Conserved Non-Canonical Docking Mechanism Regulates the Binding of Dual Specificity Phosphatases to Cell Integrity Mitogen-Activated Protein Kinases (MAPKs) in Budding and Fission Yeasts

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Abstract

Dual-specificity MAPK phosphatases (MKPs) are essential for the negative regulation of MAPK pathways. Similar to other MAPK-interacting proteins, most MKPs bind MAPKs through specific docking domains known as D-motifs. However, we found that the Saccharomyces cerevisiae MAPK Msg5 binds the MAPK Slt2 within the cell wall integrity (CWI) pathway through a distinct motif (IYT). Here, we demonstrate that the IYT motif mediates binding of the Msg5 paralogue Sdp1 to Slt2 as well as of the MKP Pmp1 to its CWI MAPK counterpart Pmk1 in the evolutionarily distant yeast Schizosaccharomyces pombe. As a consequence, removal of the IYT site in Msg5, Sdp1 and Pmp1 reduces MAPK trapping caused by the overexpression of catalytically inactive versions of these phosphatases. Accordingly, an intact IYT site is necessary for inactive Sdp1 to prevent nuclear accumulation of Slt2. We also show that both Ile and Tyr but not Thr are essential for the functionality of the IYT motif. These results provide mechanistic insight into MKP-MAPK interplay and stress the relevance of this conserved non-canonical docking site in the regulation of the CWI pathway in fungi.

Introduction

Among the most ancient signalling routes are the mitogen-activated protein kinase (MAPK) pathways that transduce extracellular stimuli into appropriate cellular responses. MAPKs contain a highly conserved TXY motif in the kinase activation loop in which both Thr and Tyr residues must be phosphorylated to achieve kinase activation [1]. Their main negative regulators are therefore protein phosphatases. Prominent among these is a subfamily of dual-specificity phosphatases (DSPs) that specifically dephosphorylate both Thr and Tyr residues in target MAPKs. These enzymes are designated as dual-specificity MAPK phosphatases (MKPs) and play an essential role in the regulation of MAPK signalling [2,3]. This MKP-mediated dephosphorylation event not only requires a transient enzyme-substrate interaction involving the active site of these enzymes, but also the formation of a complex through specific docking interactions between conserved regions within both MKPs and MAPKs [4]. Such docking sites are located outside the catalytic domains of these proteins and promote binding specificity and high affinity interactions. One of the best characterised docking motifs found in MAPK phosphatases and other MAPK-interacting proteins is the D-domain, which is also known as the kinase interaction motif (KIM). D-domains comprise a cluster of basic residues followed by a hydrophobic sub-motif containing Leu, Ile or Val separated by one residue (Lys/Arg-X2–6-Y-X-Q) [5],[6]. A second type of MAPK-docking site named the DEF motif (for docking site for ERK FXFP) is also present in the MAPK phosphatase MKP-1 [7]. Whereas D-motifs interact with acidic residues in the common docking (CD) domain of MAPKs, DEF motifs bind to a hydrophobic pocket that is only exposed upon MAPK activation [8].

All eukaryotic cells possess multiple MAPK pathways, which coordinate many physiological processes. Saccharomyces cerevisiae has five MAPK signalling pathways involved in mating, pseudohyphal/invasive growth, osmoregulation, ascospore formation and cell wall integrity (CWI) [9]. The CWI pathway is mediated by the MAPK Slt2 and is responsible for orchestrating changes in the cell wall through the cell cycle and in response to various forms of stress, especially cell wall insults, to ensure cell survival [10]. Therefore, this pathway is tremendously important for yeast physiology, and consequently it is conserved among fungal species [11]. Then, MAPKs orthologous to S. cerevisiae Slt2 operate in other fungi, like Pmk1 in Schizosaccharomyces pombe, Not
only MAPKs but many other components participating in fungal CWI pathways are conserved [11]. MKPs orthologous to S. cerevisiae Msg5 and its parologue Sdp1, both of which dephosphorylate the MAPK Slt2 [12–14], are also broadly present in other fungi. In S. pombe, the MKP Pmp1 is responsible for dephosphorylating the CWI MAPK Pmk1 [15].

The MKP Msg5 is not only regulating the CWI but also the mating pathway in S. cerevisiae. We have recently shown that, whereas the interaction with the CD domains of the mating MAPKs Fus3 and Kss1 involves a canonical Msg5 D-domain, a novel motif [102Y105T106] in Msg5 is mediating binding to the CWI MAPK Slt2 and its pseudokinase parologue Mpl1 [16]. To build on these findings and broaden the work beyond S. cerevisiae Msg5, we have studied the relevance of this motif for other yeast MKPs. Here we show that the IYT site is also involved in the interaction of Sdp1 to Slt2, and in Pmp1 binding to its partner MAPK Pmk1 [17]. We have recently shown that, the IYT site is underlined). PCR products were sub-cloned into pEG-KG (2 μm, GALI–10CAS-CYC) [21].

To express Sdp1-Myc in S. cerevisiae, the plasmid YCplac22SDP1m was sub-cloned into pYES2 (2 μm, GALI) [22]. The YCplac22SDP1m plasmid was obtained by site-directed mutagenesis of YCplac22SDP1m and pYES2SDP1myc and pYES2SDP1 C140Amyc, respectively, following the method previously described [12] using the oligonucleotides FSDP1 5'-GGAATTCATCCATGAGCCATGGCCATGAACATATACGCATCACC-3' and RDP3 5'-GAGCTCCGGTACTTTTCTATAACTGTTGGC-3'.

Conservation of a CWI MAPK-Binding Motif in MKPs

Materials and Methods

Yeast strains and culture conditions

The S. cerevisiae strains used in this work were DD1-2D (MATa ura3 his3-112 leu2-3,112 ade2-101 trp1-63 leu2-1 ura3-52 his3-) and BY4741 (MATa, his3Δ1 leu2Δ2 met15Δ0 ura3A0) and Y00897 (BY4741 isogenic, gas1Δ:KanMX4) from Euroscarf (Frankfurt, Germany). Yeast cultures were performed as reported previously [18]. When necessary, Congo red (Sigma) was added at the indicated concentrations.

DNA manipulation and plasmids

General DNA methods were performed using standard techniques. In order to express Mpl1 fused to GST in S. cerevisiae cells, pEG(KG)-Mpl1 was constructed by PCR amplifying the corresponding Mpl1 region using pET15b-Mpl1 [16] as a template and the primers FMLP1 5'-TCGCCGATCCATGAGCCATGGCCATGAACATATACGCATCACC-3' (BamHI site is underlined) and 5'-TCGCCGATCCATGGCCATGAACATATACGCATCACC-3' or 5'-CATGCCGATCCATGGCCATGAACATATACGCATCACC-3' (BamHI site is underlined). PCR products were sub-cloned into pEG-KG (2 μm, GALI–10CAS-CYC) [21].

To express Sdp1-Myc in S. cerevisiae, the plasmid YCplac22SDP1m was sub-cloned into pYES2 (2 μm, GALI) by cloning the GST-Sdp1 plasmid into YEp352 [23]. To this end, Sdp1 and Sdp1IAYATA plasmids were amplified with upstream primers 5'-CATGCCGATCCATGGCCATGAACATATACGCATCACC-3' and 5'-CATGCCGATCCATGGCCATGAACATATACGCATCACC-3' (BamHI site is underlined). The Sdp1 and Sdp1IAYATA plasmids were used as templates for pET15b and then the Sdp1IAYATA-GST fusion was obtained by cloning the Sdp1IAYATA-GST plasmid into pET15b [16].

The YEp352GST plasmid was obtained by cloning the GST-encoding EcoRI-SalI fragment from pEG(KG) into YEp352 [25]. Plasmids YEplac22MSG5GST and YEplac22MSG5 C140Amyc expressing Msg5-GST and Msg5 C140Amyc-GST, respectively, were generated in two steps. Firstly, the BamHI fragment carrying the promoter and the corresponding ORF of MSG5 from YCplac22MSG5m or YCplac22MSG5 C140Amyc [12] were sub-cloned into YEplac22. Secondly, the SalI fragment from YEplac22MSG5 bearing GST was sequentially cloned in the SalI site. The YEplac22MSG5 C140Amyc-GST plasmid was obtained by site-directed mutagenesis on YEplac22MSG5 C140Amyc using the mutagenic primers 5'-AGCGAGGCCTCTCGAGCTCTTCACACTCTTTTCTAAACACTTTGCGG-3' and 5'-AGAGATGTTGTAGCCGATCCATGGCCATGAACATATACGCATCACC-3'.

In order to determine MLP1 transcriptional induction, the episomic vector YEplac352, bearing an MLP1-GFP fusion [pMLP1-GFP] [24], or pMLP1-LacZ, carrying the transcriptional fusion of the MLP1 promoter to the lacZ gene [25], were used. For Slt2
localisation studies, cells were transformed with the plasmid pRS425-SLT2-GFP [13].

To construct the integrative plasmid pIL-pmp1-GST, the pmp1 ORF plus regulatory sequences were amplified by PCR using S. pombe genomic DNA as a template, employing the 5′-oligonucleotide Pmp1X-F (TATATTTAGATCCAGCATCAGTCCTTTCTTCTCTCT), which hybridises at a position ~700 bp upstream of the pmp1 ATG start codon and contains an XbaI site (underlined), and the 3′-oligonucleotide Pmp1B-R (TATATGGATCCAGAACATATTACCTTATAGCCGC), which hybridises at the 3′ end of pmp1 ORF (except the stop codon) and incorporates a BamHI site. The resulting PCR fragment was digested with XbaI and BamHI and cloned into the integrative plasmid pIL-GST [19].

The integrative plasmid pIL-pmp1(C158S):GST was obtained by site-directed mutagenesis employing pIL-pmp1:GST as template and the mutagenic oligonucleotides Pmp1C158S-F (GTTTTAATTAATAGCTCAAATGGGCA) and Pmp1C158-R (TGCCCATTTGACCTAAATTAAAC). To construct the plasmid pIL-pmp1(I10A Y11A T12A):GST, the mutagenic oligonucleotides used were Pmp1AA-A (ATGTCTCAAAAAGCTACCTCTCTTAAGTCGCGCCTCCGAACCTTTCCCTGGTTTC) and Pmp1AAA-R (GAACCCAGGGGAGATTTG-GAGGGGCACGTCTTTAAGGGAGGTAGTTTTTGAGAC-AT). The integrative plasmid pIL-pmp1(I10A Y11A T12A C158S):GST was prepared using pIL-pmp1(I10A Y11A T12A C158S):GST as the template and the mutagenic oligonucleotides Pmp1C158S-F and Pmp1C158-R. In all cases, the mutated pmp1 ORFs plus regulatory sequences were amplified by PCR with the oligonucleotides Pmp1X-F and Pmp1B-R, digested with XbaI and BamHI, and cloned into pIL-GST, as above. Finally, the resulting plasmids were digested at the unique NotI site within leu1, and the linear fragments were transformed into strain MI212. Transformants leu1 were obtained and the correct integration of the fusions was verified by both PCR and Western blot analysis.

Preparation of bacteria and yeast extracts

Recombinant GST- or His-tagged proteins were expressed in the E. coli strain Rosetta DE3 (Novagen). Cells were collected and lysed by sonication in PBS buffer containing 2 mM PMSF, 1 mM DTT, 1 mM EDTA, and 1 mg/ml Lysozyme in the presence of a protease-inhibitor cocktail (Roche). Extracts were clarified by centrifugation and then stored at −80°C. Budding and fission yeast extracts were obtained as previously described in [18] and [19], respectively.

Binding assays

For in vivo binding assays, cells were collected and lysed as above in lysis buffer lacking SDS and NP40. Yeast lysates were incubated with glutathione-Sepharose beads (GE Healthcare) for two hours. Beads were washed extensively with the same buffer, resuspended in SDS loading buffer, and proteins were analysed by SDS-PAGE and immunoblotting as described [12]. In vitro binding assays were performed by mixing E. coli extracts containing GST or GST-fused proteins with E. coli extracts bearing the corresponding His-tagged proteins, and then processed as above.

Purification of Pmk1-HA6H and Pmp1-GST fusions was performed with Ni2+--NTA-agarose beads (Qiagen) and glutathione-Sepharose beads (GE Healthcare), respectively, as described previously [20].

Immunoblotting analysis

In experiments carried out with budding yeast, immunodetection of Glucose-6-phosphate dehydrogenase (G6PDH) and Myc-tagged proteins was carried out using polyclonal anti-G6PDH (Sigma) and monoclonal 4A6 (Millipore) or 9E10 (Santa Cruz Biotechnology) antibodies, respectively. Polyclonal anti-phospho-p44/p42 MAPK (Thr202/Tyr204) (Cell Signaling), anti-GST (Santa Cruz Biotechnology) and anti-His antibodies (Sigma) were also used as described previously [18]. The primary antibodies were detected using a fluorescein-conjugated secondary antibody with an Odyssey Infrared Imaging System (LI-COR Biosciences).

In experiments performed with fission yeast, dual phosphorylation in Pmk1 was detected with polyclonal anti-phospho-p42/p44 as above, whereas total Pmk1 was detected after incubation with mouse monoclonal anti-HA antibody (12CA5, Roche Molecular Biochemicals). The immunoreactive bands were revealed with an anti-mouse-HRP-conjugated secondary antibody (Sigma) and the ECL system (GE Healthcare). GST fusions were detected with a goat anti-GST-HRP conjugated polyclonal antibody (GE Healthcare).

β-Galactosidase activity assays

β-Galactosidase activity was determined according to [26]. Values are averages of at least three independent transformants assayed in duplicate.

Flow cytometry assays

For Mpl1-GFP analysis, cells were collected, washed twice with PBS, and then analysed by flow cytometry in a Guava easyCyte flow cytometer, acquiring green fluorescence through a 488 excitation laser and a 525/30 BP emission filter (BFP). The marker was set using yeasts that do not express GFP.

Fluorescence microscopy

For the visualisation of GFP on live yeast cells containing pRS425-SLT2-GFP, exponentially growing cultures were centrifuged at 3000 r.p.m., washed once with water and observed. Cells were examined under an eclipse TE2000U microscope (Nikon) and digital images were acquired with an Orca C4742-95-12ER charge-coupled-device camera (Hamamatsu Photonics) and Aquacosmos Imaging Systems software.

Results

The IYT motif of S. cerevisiae Sdp1 mediates binding to the CWI MAPK Slt2

Our BLAST search to know the conservation of the IYT motif among fungi showed the existence of a significant number of yeast Mgs5 orthologues bearing this motif (Figure 1A). A detailed analysis of the amino acid sequence of the region surrounding this site in these proteins revealed some interesting features. For instance, the frequent presence of basic and acidic residues previous to the IYT signature, the invariant Ile and Tyr and the existence of either Thr or Ser as the third residue within the motif (Figures 1B and 1C). Among the MKPs carrying this motif are phylogenetically distant from S. cerevisiae Mgs5, as observed in the dendrogram shown in Fig. 1A. We first addressed the functional conservation of this motif by analysing its importance in the interaction of Sdp1 with its target MAPK.
Sdp1 does not contain any classical D-domain, suggesting that the IYT motif present in its sequence could mediate the interaction with Slt2. In contrast to other yeast Msg5 orthologues, the IYT motif in Sdp1 is located close to the N-terminus (at position +2 from the initial Met) (Figure 1B). In order to investigate the involvement of the Sdp1 IYT motif in Slt2 binding, residues Ile3, Tyr4 and Thr5 were changed to alanine, and the interaction of this mutant version of Sdp1 (Sdp1IAYATA) with Slt2 was assayed by both in vivo and in vitro co-purification experiments. As shown in Figure 2A, GST-Slt2 pulled down the Myc-tagged form of wild type Sdp1 but not the mutated version Sdp1IAYATA-Myc in experiments carried out with yeast extracts containing these proteins. In agreement with this, the mutated GST-Sdp1IAYATA protein produced in E. coli did not interact in vitro with the E. coli-produced Shl2-His (Figure 2B). In parallel experiments we also found that the Shl2 pseudokinase parologue Mpl1 interacted both in vivo and in vitro with wild type Sdp1 but not with Sdp1IAYATA (Figures 2C and 2D). These results indicate that the IYT motif of Sdp1 is involved in the interaction with both Shl2 and Mpl1.

Mutation of the IYT motif reduces the ability of wild type Sdp1 to down-regulate the CWI pathway and of inactive Sdp1 to act as a substrate trap for Shl2

Previous studies of cells lacking Sdp1 revealed no evident phenotype except for a slight increase of Shl2 phosphorylation in response to heat shock [13]. Our analysis of several sdp1Δ mutant strains from different cellular backgrounds showed that these mutants presented no sensitivity to cell wall perturbing agents and high temperature. Likewise, they also showed no alteration of Shl2 phosphorylation under these conditions in comparison to wild type cells (data not shown). Therefore, in order to analyse the relevance of the IYT motif for Sdp1 function, we studied the effect caused by the expression of high doses of Sdp1 and Sdp1IAYATA in S. cerevisiae. To this end, we overproduced the Myc-tagged versions of the corresponding SDP1 alleles from the GAL1 promoter. Overexpression of a catalytically inactive form of Sdp1 has been shown to result in the accumulation of phosphorylated Shl2 [14]. Therefore, we also included in the study the phosphatase-dead version Sdp1C140A-IAYATA, which bears a mutation at the conserved cysteine that is known to abolish the catalytic activity within all PTPs, and the double mutant Sdp1C140A-IAYATA that is also
affected in the IYT site. To easily analyse their down-regulatory impact on CWI signalling, the overexpression experiments were carried out in a gas1Δ mutant strain, which presents a constitutively activated CWI pathway due to the lack of beta-1,3-glucanosyltransferase activity, which is required for cell wall assembly [27]. As readouts of the effect of the different Sdp1 versions on Slt2 function, we analysed both Slt2 phosphorylation and the transcriptional activity mediated by the main Slt2 substrate, the transcriptional factor RLM1. To this end, a reporter transcription assay based on the expression of lacZ under the control of the cell wall damage-inducible Rlm1-dependent MLP1 promoter was used [25]. As can be seen in Figures 3A and 3B, the overexpression of Sdp1 significantly reduced the amount of phospho-Slt2 and the level of Rlm1-driven transcription in the gas1Δ mutant. Mutation of the IYT motif within Sdp1 did not result in any apparent differences with wild type Sdp1 regarding the level of phosphorylated Slt2. In contrast, MLP1 expression was significantly higher in comparison with that of cells expressing wild type Sdp1, indicating a reduced function of the mutant Sdp1IAYATA version on Slt2 activity. As expected, expression of Sdp1C140A caused an accumulation of phosphorylated Slt2 (Figure 3A), probably due to the formation of a stable complex of this inactive DSP form with Slt2, a phenomenon known as substrate trapping that occurs in other tyrosine phosphatases [28]. This stable association of inactive Sdp1C140A with Slt2 seems to impede downstream signalling, since although leading to high phospho-Slt2 levels, a significant decrease in MLP1-driven beta-galactosidase activity was observed (Figure 3B). Of interest, removal of the IYT motif from catalytically inactive Sdp1 reduced the amount of phosphorylated Slt2 and increased Rlm1-dependent transcriptional activation (Figure 3, A and B), suggesting reduced binding of the double Sdp1C140A-IAYATA mutant to Slt2. As seen in gas1Δ cells, this mutant version of Sdp1 also lost the ability to act as a substrate trap for Slt2 compared with Sdp1 C140A when overexpressed in wild type cells (Figure 3C).

It is known that Slt2 concentrates in the nucleus, although it is also located at the cytoplasm [13,29]. As shown in Figure 3D, the overexpression of inactive Sdp1C140A significantly reduced the nuclear localisation of this MAPK, suggesting that the trapping effect prevents the translocation of Slt2 to the nucleus. The IYT motif was necessary for Sdp1C140A to promote this effect, as cells overexpressing Sdp1 C140A-IAYATA showed nuclear accumulation of Slt2 (Figure 3D). Collectively these experiments support the notion that this motif indeed mediates the interaction between Sdp1 and Slt2.

In order to determine the relevance of each residue within the IYT motif, we generated versions of Sdp1C140A in which Ile3, Tyr4 and Thr5 were individually changed to Ala and the effect on Slt2 trapping was analysed. As can be observed in Figure 3E, mutation of any of the two first amino acids in the motif led to a failure of inactive Sdp1 to trap Slt2. However, mutation of the third residue did not preclude trapping of the MAPK, indicating that binding is
not disrupted by this mutation. In summary, only the invariant amino acids, namely Ile and Tyr (Figure 1C), are indispensable for this motif to act as a MAPK docking site.

Mutation of the IYT motif of Msg5 reduces Slt2 but not Fus3 trapping

We next studied whether mutation of the IYT motif also reduced the substrate trapping ability of inactive Msg5 on Slt2. To this end, we analysed, as above, the amount of phosphorylated Slt2 and MLP1-driven lacZ expression in wild type cells overexpressing Msg5 C319A, which carries an inactivating mutation at the catalytic site [17], and Msg5 C319A-IAYATA that additionally lacks the IYT motif. As shown in Figure 4A, the overexpression of Msg5 C319A from a multicopy plasmid under its own promoter resulted in increased levels of phosphorylated Slt2 relative to cells carrying the empty vector or overexpressing wild type Msg5, both in the absence or the presence of Congo red, which is an agent that affects the cell wall, therefore leading to CWI pathway activation [30]. The accumulation of phosphorylated Slt2, due to the substrate trapping activity of the inactive Msg5 version, was significantly reduced in cells bearing Msg5 C319A-IAYATA, suggesting a reduced interaction of this version of Msg5 with Slt2. Remarkably, Msg5 C319A also led to Fus3 trapping (Figure 4A), but
the accumulation of phosphorylated Fus3 was not reduced by removal of the IYT motif of inactive Msg5D. This result confirms that this site does not mediate the interaction of Msg5 with the mating MAPK, as previously reported [16]. Similarly to that occurring in Sdp1C140A-expressing cells, the increased Slt2 phosphorylation promoted by Msg5C1319D does not lead to an increased pathway output, but, on the contrary, to a reduction of MLP1 transcription compared to control cells, as revealed by β-galactosidase activity assays (Figure 4C). Removal of the IYT site in the inactive Msg5 led to an increase in Rlm1 transcriptional activity, indicating a significant reduction of the trapping effect.

We further analysed the functionality of Msg5 versions by monitoring their effect on the Congo red sensitivity displayed by an msg5Δ strain. This phenotype is indicative of an affected cell wall, likely derived from an altered Slt2-mediated response in this mutant [12]. As expected, expression of wild type Msg5 complemented the Congo red-sensitivity phenotype of cells lacking this phosphatase (Figure 4C). Of interest, the inactive Msg5C1319D version also rescued the Congo red sensitivity of the msg5Δ strain, probably owing to its substrate trapping effect, which leads to a diminished signalling output by antagonising the interaction of Slt2 with Rlm1. In contrast, the msg5Δ phenotype could not be rescued by Msg5C1319A, suggesting the inability of this variant to reduce the CWI pathway response due to a lack of the docking site in the trapping inactive mutant.

The IYT motif mediates binding of MKP Pmp1 to Pmk1 in fission yeast

We next investigated the functional relevance of the IYT motif in the interaction between the MKP Pmp1 and the MAPK Pmk1 of the CWI pathway in S. pombe [15],[31]. The N-terminal end of Pmp1 contains a perfectly conserved IYT motif at positions 10–12 (Figure 1A). As previously reported [15], basal Pmk1 phosphorylation of a mutant lacking Pmp1 phosphatase is increased in comparison to control cells (Figure 5A). The Pmk1 hyperactivation displayed by this mutant has a dramatic effect on chloride homeostasis in fission yeast and consequently leads to strong sensitivity to this anion (Figure 5B; [15]). Expression in pmp1Δ cells of genomic C-terminal GST-tagged versions of either wild type Pmp1 or the mutant Pmp1IAYATA version, in which the I10Y11T12 motif was substituted by three consecutive alanines, reduced Pmk1 phosphorylation to a similar extent (Figure 5A). However, Pmp1IAYATA was shown to be less effective than wild type Pmp1 with regard to suppressing the chloride sensitivity phenotype of pmp1Δ (Figure 5B), indicating that this motif is biologically relevant for Pmp1 function. Indeed, co-purification experiments performed with strains expressing C-terminal epitope tagged genomic copies of Pmp1 and Pmk1 to GST and HA6H, respectively, revealed the importance of the IYT motif of Pmp1 for the interaction with Pmk1. As observed in Figure 5C, the in vivo binding of a catalytically inactive version of Pmp1 (Pmp1C158S) to Pmk1 resulted in abrogated function when the inactive phosphorylation version also lacked the IYT motif (Pmp1C158S-UAYATA). Similar to the results obtained with both Msg5 and Sdp1 in budding yeast, expression of inactive Pmp1C158S induced a strong raise in the quantity of phosphorylated Fus3 in the same transformants (additionally carrying antibody (middle panel) and anti-G6PDH antibodies (lower panel), detected with anti-phospho-p42/44 (two upper panels), anti-GST (Slt2, Kss1 and Fus3), Msg5-GST and G6PDH (as a loading control) were prepared and phosphorylated MAPKs (Msg5C319A-IAYATA) plasmids. Cells were grown to mid-log phase at 24°C and a 10-fold dilution series of this culture was spotted onto YPD agar medium in the absence (no stress) or presence of Congo Red (75 μg/ml) and incubated for 2 days at 24°C. Similar results were obtained in three different experiments and selected images correspond to representative blots.

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Figure 4. Effect of the lack of the IYT motif of inactive Msg5 on MAPK trapping. (A) Western blotting analysis of the wild type strain YPH499 bearing YEp352GST (vector), YEp352MSG5GST (Msg5), YEp352MSG5C319AGST (Msg5C319A) or YEp352MSG5C319A-AAYATAAGST (Msg5C319A-IAYATA) plasmids. Cells were grown to mid-log phase at 24°C and then aliquots were treated or not with Congo red (30 μg/ml) for 180 min. Protein extracts were prepared and phosphorylated MAPKs (Slt2, Kss1 and Fus3), Msg5-GST and G6PDH (as a loading control) were detected with anti-phospho-p42/44 (two upper panels), anti-GST antibody (middle panel) and anti-G6PDH antibodies (lower panel), respectively. (B) Expression of MLP1-GFP was examined by determining GFP signal in the same transformants (additionally carrying pMLP1-GFP plasmid) and growth conditions as in Figure 4A. Data shown are the average of three independent experiments performed in duplicate. Error bars indicate standard deviations. (C) Upper panel: Western blotting analysis of the msg5Δ mutant strain DDI-2D, carrying the same plasmids as in Figure 4A. Lower panels: sensitivity to Congo red of the same transformants as above. Cells were grown in liquid selective medium at 24°C, and a 10-fold dilution series of this culture was spotted onto YPD agar medium in the absence (no stress) or presence of Congo Red (75 μg/ml) and incubated for 2 days at 24°C. Similar results were obtained in three different experiments and selected images correspond to representative blots.

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level of phosphorylated Pmk1 (Figure 5E). Notably, this high Pmk1 phosphorylation was greatly reduced in cells expressing Pmp1C158S-IAYATA (Figure 5E), confirming the role of the IYT motif of Pmp1 in binding and trapping Pmk1.

Discussion

It is well accepted that the specificity and efficiency of action of MAPK phosphatases (MKPs) on their cognate MAPKs are controlled by docking interactions. We found in a previous work that the interaction of the S. cerevisiae dual-specificity phosphatase Msg5 with MAPKs of different signalling pathways, namely mating and CWI MAPKs, was mediated by distinct docking mechanisms. Particularly, this MPK uses a conventional D-domain to interact with the CD domain of Fus3 and Kss1, whereas a novel motif (IYT) was responsible for binding to Slt2 and its parologue Mlp1 in a CD-independent manner [16]. Here, we present evidence that the IYT motif acts as an efficient and specific docking site on other fungal Msg5 orthologues. Several results obtained in the present study support this conclusion. First, removal of the IYT motif in both Sdp1 from S. cerevisiae and Pmp1 from S. pombe precludes interaction with Slt2 and Mlp1, and with Pmk1, respectively. Second, substrate-trapping inactive versions of ScMsg5, ScSdp1 and SpPmp1 lacking this motif have a reduced ability to trap their target CWI MAPKs. Third, whereas inactive Sdp1 prevents Slt2 from concentrating in the yeast nucleus, this Sdp1 version lacking the IYT motif does not significantly alter Slt2 localisation. Fourth, the IYT sequence is present in the non-catalytic region of many fungal Msg5 orthologues. Although most of them belong to genera close to Saccharomyces, this motif is also born by the MKP Pmp1 of the evolutionarily distant yeast S. pombe. This suggests that this docking motif was present in ancestral MKPs and has probably been maintained through evolution in some MKPs for a specific purpose, namely the regulation of CWI MAPKs.

In contrast to other fungal species, S. cerevisiae possesses two MKPs [11], Msg5 and Sdp1, likely generated from the ancient whole genome duplication that occurred in this yeast [32]. However, whereas Msg5 is able to inactivate mating and CWI MAPKs, Sdp1 displays a selective action on Slt2, reflecting functional divergence along evolution. The presence in Msg5 of a large N-terminal non-catalytic region carrying both the characteristic D-domain of most MKPs and the IYT docking motif...
explains why this phosphatase regulates both types of MAPKs. Pmk1 is the only reported MAPK regulated by the S. pombe MKP Pmp1. The short N-terminal regulatory region containing an IYT motif but lacking the typical D-domain in Pmp1 is the most likely reason for its exclusive targeting to the CWI-MAPK Pmk1. Although the crystal structure of Sdp1 has been previously determined [33], it corresponds to a truncated version lacking 16 residues from the amino-terminus, and thus the IYT motif. Therefore, the structural basis underlying the binding mechanism involving this docking site cannot be readily predicted. Analysis of the region upstream the IYT motif in fungal Msg5 orthologues revealed other residues that were relatively conserved, such as a negatively-charged amino acid at position −3 and two basic residues at position −5. However, the absence of this region in Sdp1 together with the reported dispensability of the two arginines at positions 96 and 97 in S. cerevisiae Msg5 for binding to both Slt2 and Mlp1 [16] suggest that interaction through the IYT motif does not require these previous residues. Moreover, mutational analysis of each of the residues composing the IYT motif in Sdp1 showed that only the invariant amino acids Ile and Tyr are essential for binding. Of interest, we have found that atypical human DSPs DSP18 and DSP21, which lack any known specific MAPK targeting motif, carry an IYE sequence at their unique C-terminal extension [34]. The fact that the third residue seems to be dispensable in fungal MKPs for MAPK binding suggests that this IYE sequence could be also acting as a docking site in these human DSPs. This opens up the possibility that this motif has been shaped through evolution in these atypical phosphatases to mediate interactions with target MAPKs in higher eukaryotes.

Mutations that reduce the catalytic activity of protein phosphatases without affecting their substrate affinity have been named “substrate-trapping”, due to their ability to form a stable enzyme-substrate complex [28]. In the case of MKPs, the formation of such complexes with the MAPK may antagonise binding between the MAPK and its downstream substrates impeding signalling transmission. This is indeed what we observed when catalytically inactive versions of Msg5, Sdp1 and Pmp1, mutated in the conserved essential Cys at the active site, are overexpressed in yeast cells. The lack of phosphatase activity of these substrate-trapping mutant versions led to phosphorylation of the corresponding MAPK in the complexes. However, these phosphorylated and therefore active MKPs are paradoxically unable to activate their targets. Elimination of the IYT docking motif in such inactive MKPs released the partner MAPK, namely Slt2 in S. cerevisiae or Pmk1 in S. pombe, from the trapping complex, allowing signal propagation. In view of these results, the analysis of MAPK phosphorylation and specific transcriptional induction upon overexpression of a catalytically inactive MKP is a powerful approach for identification of target MAPKs of such MKP. This strategy can be especially useful for MKPs whose deletion or overexpression does not give rise to an evident phenotype, like Sdp1. Msg5 has proven to be a more potent phosphatase than Sdp1, controlling Slt2 phosphorylation both under basal and stimulating conditions [18,35], whereas Sdp1 seems to dephosphorylate Slt2 only upon heat stress activation [13]. However, we could not detect increased phosphorylation of Slt2 at high temperature in any sdp1Δ mutant strain analysed (data not shown). Moreover, recent large-scale analysis in S. cerevisiae comparing the impact of every single phosphatase gene deletion on either the global expression profile or the phosphoproteome also showed that the absence of Sdp1 affects gene transcription and protein phosphorylation to a much lesser extent than Msg5 [36,37]. This is consistent with the lack of an apparent phenotype of sdp1Δ mutants under cell wall stress conditions (data not shown), while an msg5Δ mutant is hypersensitive to this stress [12]. The fact that the inactive Msg5 trapping mutant, which interferes with signalling from Slt2 to downstream effectors, suppressed the Congo red hypersensitivity of msg5Δ cells supports the idea that this phenotype is due to an up-regulated CWI pathway response.

In summary, our work provides evidence on the conservation of an interaction motif in MKPs for selective binding to CWI MAPKs. Furthermore, we unravel the essential residues within this MKP motif for binding to MAPKs. Since various MKPs can be regulated by the same MKP and, conversely, several MKPs are able to dephosphorylate a particular MAPK, the existence of different mechanisms mediating binding of these proteins ensures accurate signal transduction. Our findings reveal the high flexibility of these proteins to differentially regulate structurally similar MAPKs.

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Author Contributions
Conceived and designed the experiments: JC HM M. Molina. Performed the experiments: ASR M. Molina. Analyzed the data: ASR M. Madrid JC HM M. Molina. Contributed reagents/materials/analysis tools: ASR M. Madrid. Wrote the paper: JC HM M. Molina.

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