Dss1 Is a 26S Proteasome Ubiquitin Receptor

Konstantinos Paraskevopoulos,1,5 Franziska Kriegenburg,2,6 Michael H. Tatham,3,5 Heike I. Rösner,2 Bethan Medina,1 Ida B. Larsen,2 Rikke Brandstrup,2 Kevin G. Hardwick,8 Ronald T. Hay,3 Birthe B. Kragelund,2 Rasmus Hartmann-Petersen,2,4,* and Colin Gordon1,*

1Medical Research Council Human Genetics Unit, Western General Hospital, Crewe Road, Edinburgh EH4 2XU, Scotland, UK
2Department of Biology, University of Copenhagen, Ole Maaløes Vej 5, 2200 Copenhagen N, Denmark
3Centre for Gene Regulation and Expression, College of Life Sciences, University of Dundee, Dundee DD1 5EH, Scotland, UK
4Wellcome Trust Centre for Cell Biology, University of Edinburgh, Edinburgh, EH9 3JR, Scotland, UK
5Co-first author
6Correspondence: rhpetersen@bio.ku.dk (R.H.-P.), colinbgordon@virginmedia.com (C.G.)

http://dx.doi.org/10.1016/j.molcel.2014.09.008
This is an open access article under the CC BY license (http://creativecommons.org/licenses/by/3.0/).

SUMMARY

The ubiquitin-proteasome system is the major pathway for protein degradation in eukaryotic cells. Proteins to be degraded are conjugated to ubiquitin chains that act as recognition signals for the 26S proteasome. The proteasome subunits Rpn10 and Rpn13 are known to bind ubiquitin, but genetic and biochemical data suggest the existence of at least one other substrate receptor. Here, we show that the phylogenetically conserved proteasome subunit Dss1 (Sem1) binds ubiquitin chains linked by K63 and K48. Atomic resolution data show that Dss1 is disordered and binds ubiquitin by binding sites characterized by acidic and hydrophobic residues. The complementary binding region in ubiquitin is composed of a hydrophobic patch formed by I13, I44, and L69 flanked by two basic regions. Mutations in the ubiquitin-binding site of Dss1 cause growth defects and accumulation of ubiquitylated proteins.

INTRODUCTION

The ubiquitin-proteasome system (UPS) is the major pathway for protein degradation in eukaryotic cells, regulating most cellular processes, including cell division, signal transduction, and development (Finley, 2009). Before degradation, proteins are conjugated to ubiquitin chains that act as recognition signals for the 26S proteasome, a large proteolytic complex that degrades substrate proteins (Finley, 2009).

Although proteasome function has been extensively studied, our knowledge of how this particle recognizes ubiquitylated substrates remains incomplete. Since the identification of the first intrinsic proteasomal ubiquitin receptor, Rpn10, studies have identified a group of so-called UBL-UBA domain proteins that act as transient, extrinsic proteasome substrate receptors (Deveraux et al., 1994; Seeger et al., 2003; Su and Lau, 2009; Wilkinson et al., 2001). More recently, an additional novel intrinsic receptor, Rpn13, was identified (Husnjak et al., 2008; Schreiner et al., 2008). However, budding yeast cells, deleted for the UBL-UBA domain proteins and mutated in both the Rpn10 and Rpn13 ubiquitin-interacting regions, are still viable (Husnjak et al., 2008). Moreover, ubiquitin conjugates still bind to 26S proteasomes lacking the ubiquitin-interacting regions of Rpn10 and Rpn13 (Peth et al., 2010). As proteasome function is essential, at least one additional ubiquitin receptor remains to be discovered (Saeki and Tanaka, 2008). Here, we present structural, biochemical, and genetic data that the disordered and multifunctional protein Dss1 (known as Sem1 in budding yeast), is another ubiquitin-binding subunit of the 26S proteasome.

RESULTS

Ubiquitin Binding to Rpn10 Is Not Essential for Viability

In fission yeast, substrate recognition by the 26S proteasome is accomplished by two intrinsic proteasome subunits, Rpn10 and Rpn13, and two extrinsic UBL-UBA domain proteasome cofactors, Rhp23 and Dph1 (Finley, 2009; Hartmann-Petersen et al., 2003; Sakata et al., 2012; Wilkinson et al., 2001) (Figure 1A). Studies have shown these receptors to be functionally redundant (Husnjak et al., 2008; Peth et al., 2010; Wilkinson et al., 2001). It was previously demonstrated, both in budding and fission yeast, that the gene for the UBL-UBA domain protein Rad23 (Rhp23 in fission yeast) functionally overlapped with the gene encoding the 26S proteasome ubiquitin receptor subunit Rpn10. Specifically, only a double deletion mutant (rpn10Δrhp23Δ) displayed severe growth defects (Wilkinson et al., 2001). In addition, Rhp23 variants unable to bind ubiquitin or the proteasome could not rescue the growth defects of the double mutant, implying that substrate recognition was at least partly responsible for the observed phenotypes (Wilkinson et al., 2001). Therefore, we asked whether lack of the ubiquitin- or proteasome-binding functions of Rpn10 contribute to the severe phenotype of the rpn10Δrhp23Δ double mutant. To this end, we cloned constructs of rpn10 that lacked the ubiquitin interaction motif (UIM), Rpn10ΔUIM, or the N-terminal proteasome-binding region, Rpn10ΔN82 (Figure 1B) (Seeger et al., 2003). The constructs were integrated into both rpn10Δ and rhp23Δ strains. These strains were then crossed, and the ability...
of the Rpn10 constructs to rescue the growth defects of the rpn10Δrhp23Δ double mutant were assayed by plating and selecting for the relevant spores. Surprisingly, this revealed that the Rpn10ΔUIM construct rescued the growth defects as efficiently as the full-length construct (Figure 1C; Figure S1A available online), while the Rpn10ΔN82 proteasome-binding mutant did not (Figure 1C). This implies that loss of Rpn10 ubiquitin binding does not contribute to the severe phenotype of the rpn10Δrhp23Δ double mutant.

The fact that the rhp23ΔΔrpn10ΔUIM mutant is viable is consistent with previous work, suggesting that the vWA domain has some unknown facilitator function in the UPS (Mayor et al., 2003), but not IUPred (Dosztányi et al., 2005), predicted with chemical shift perturbation analyses. Titration analyses with increasing amounts of ubiquitin disclosed the strongest binding to ubiquitin by binding site I (UBS-I), which is located with both K48 and K63 ubiquitin chains, while GST-Rhp23 was included as a positive control.

We performed an in vitro ubiquitin-binding assay using glutathione S-transferase (GST)-Dss1 and K48- and K63-linked ubiquitin chains. GST-Rhp23 was included as a positive control.

Scrutinizing the Dss1 sequence left us unable to identify any resemblance to known ubiquitin-binding sites (UBSs) or domains (Husnjak and Dikic, 2012). Structural prediction analyses of Dss1 suggested it to belong to the intrinsically disordered proteins (IDPs) (Figure 2C) (Uversky, 2011). PONDRe (Obradovic et al., 2003), but not IUPred (Dosztányi et al., 2005), predicted that a short stretch in the Dss1 C terminus is structured (Figure 2C). To probe this further, we analyzed Dss1 by heteronuclear nuclear magnetic resonance (NMR) spectroscopy. Assigned Cα chemical shifts relative to random coil shifts (Figure 2D) (Kjaergaard et al., 2011), combined with a low-dispersion 15N,1H-heteronuclear single quantum correlation (HSQC) spectrum (Figure 2E; Figure S2A), conclusively identified Dss1 as intrinsically disordered with a single, transiently populated α helix from F55 through K66. Successive addition of excess ubiquitin and analysis by NMR uncovered two distinct UBSs, identified from chemical shift perturbation analyses. Titration analyses with increasing amounts of ubiquitin disclosed the strongest binding to ubiquitin by binding site I (UBS-I), which is located at D38–D49 (dissociation constant, KD, = 50 ± 30 nM) and disclosed the second and weakest site, UBS-II, located at D16–N25 (apparent KD > 1 mM) (Figure 2F; Figures S2B and S2C).
These UBSs are conserved and located in the disordered region of Dss1 (Figure S3). Notably, both sites have a similar sequence, characterized by a series of hydrophobic residues flanked by acidic residues (Figure S3).

**Dss1 Binds a Hydrophobic and Positively Charged Area on Ubiquitin**

We subsequently mapped the corresponding interaction surface on ubiquitin by NMR, using 13C,15N-labeled ubiquitin (Figure 3). The perturbations of peak intensities of ubiquitin, imposed by addition of Dss1 (Figure 3A), mapped consistently to the surface-exposed common hydrophobic binding surface of ubiquitin involving the β sheet and the hydrophobic residues I13, L69, and I44 (Figures 3B–3D) but is also extended to the C terminus, resembling the binding site exploited by the E2 ubiquitin-conjugating enzyme Cdc34 (Arrigoni et al., 2012; Choi et al., 2010; Spratt and Shaw, 2011). Several positively charged residues located on the same surface were also significantly perturbed, whereas no perturbations were seen on the opposite face of ubiquitin (Figure 3C). A representation of the electrostatic surface of ubiquitin revealed a tripartite binding site of a hydrophobic patch flanked by two positively charged regions (Figures 3E and 3F). This directly mirrors the architecture of the UBSs identified in Dss1 (Figure S3). Moreover, the size of the interaction surface and the length of each UBS in Dss1 strongly suggest that the two UBSs bind independently to each their ubiquitin moiety. Of note, we observe that, depending on the linkages, there are unequal distances from the Dss1 binding site on ubiquitin to a second Dss1 binding site on a linked ubiquitin, suggesting that Dss1 may express a preference in the selection of different lysine-linked ubiquitin chains.

**Ubiquitin Binding Is Important for Dss1 Function**

As expected from the NMR data, mutation of either UBS-I (L40A, W41A, W45A) or UBS-II (F18A, F21A, W26A) clearly reduced binding to ubiquitin, and no ubiquitin binding was observed for Dss1 mutated at both sites (Figure 4A). Consistent with UBS-I being the stronger of the two binding sites, mutation of this site also had a greater effect on ubiquitin binding (Figure 4A).

For better understanding of the functional relevance of Dss1 and the importance of its ubiquitin-binding activity, a range of yeast mutants was created and tested in growth assays under various conditions. Expression of Dss1 or any of the Dss1 variants did not affect cell growth of wild-type cells (Figure S4A), whereas deletion of the dss1+ gene resulted in a growth defect that was especially pronounced at higher temperatures (Figure 4B). When introducing the Dss1 variants into the dss1Δ strain, we observed that cells expressing Dss1, mutated at both UBS-I and UBS-II, displayed a significant growth defect (Figure 4B), while each of the single UBS mutants or wild-type human Dss1 only partially restored growth (Figure 4B). Similar effects were observed on media containing canavanine (Figure S4B), a drug that inhibits protein folding and induces cell stress. Notably, these genetic effects correlated with the cellular accumulation of ubiquitin-protein conjugates. Thus, ubiquitin-protein conjugates accumulated in the dss1Δ strain, and this accumulation was not affected by ectopic expression of Dss1 mutated in both UBS-I and UBS-II (Figure 4C). Expression of either Dss1 UBS-I or Dss1 UBS-II mutants partially reduced the level of ubiquitin conjugates in the dss1Δ strain, while expression of wild-type S. pombe Dss1 or human Dss1 fully reduced ubiquitin-protein conjugates to wild-type levels (Figure 4C).

We next analyzed if any of the Dss1 mutants were also compromised in proteasome binding. We found that wild-type Dss1, as well as individual Dss1 UBS-I and Dss1 UBS-II mutants, all efficiently coprecipitated 26S proteasomes (Figure 4D). However, Dss1 mutated in both UBS-I and UBS-II failed to interact with 26S proteasomes (Figure 4D). Hence, the strong phenotype of Dss1 mutated in both UBS-I and UBS-II is likely caused by both loss of ubiquitin binding and loss of proteasome binding. In contrast, the intermediate phenotypes of Dss1 with single mutations in UBS-II or, in particular, in UBS-I can likely be attributed to a reduced ubiquitin binding since they still bind to the proteasome.

Recently, Dss1 was shown to function in proteasome assembly (Tomko and Hochstrasser, 2014). To assess the importance of Dss1 on overall proteasome integrity, we isolated 26S proteasomes from a dss1Δ strain and analyzed them biochemically. We found that proteasomes lacking Dss1 still efficiently interacted with polyubiquitlated proteins (Figure S4C) and were proteolytically active (Figure S4D). This suggests that, structurally, 26S proteasomes are not strongly affected by loss of Dss1 and that the contribution of Dss1 to the proteasomal substrate binding capacity in vitro is lower compared to the already known substrate receptors. This agrees with previous in vitro activity studies of purified proteasomes, lacking all known UBSs, which suggest the existence of an additional low-affinity substrate binding site (Peth et al., 2010). To further rule out that the observed phenotype of the dss1 null mutant was not caused by a general loss of 26S proteasome integrity, we performed label-free quantitative mass spectroscopy, comparing 26S proteasomes purified from wild-type, rpn10Δ, and dss1Δ cells (Figures S4E and S4F). In agreement with data from budding yeast (Bohn et al., 2013; Tomko and Hochstrasser, 2014), loss of Dss1 caused a modest reduction in 26S proteasome integrity (Figures S4E–S4G). Mutation of the Dss1 UBS-I only slightly reduced the amount of Rpn10 in the 26S proteasome (Figure S4H). Loss of Rpn10 was more disruptive, with the amounts of 26S proteasomes being reduced to around 10% of that found in wild-type cells (Figures S4E–S4G).

Collectively, these data imply that ubiquitin binding is important for the function of Dss1 in the 26S proteasome in vivo and that Dss1 could be responsible for the viability of the rhp23Δrpn10ΔUIM strain (Figure 1C). This being the case, then loss of Dss1 should impart growth defects in the rhp23Δrpn10ΔUIM strain. Indeed, spore viability of the dss1Δrhp23Δrpn10ΔUIM strain was reduced compared to cells expressing the full-length Rpn10 protein (Figures 4E and 4F). When introducing wild-type Dss1 and the Dss1 UBS-I and UBS-II mutants in the dss1Δrhp23Δrpn10ΔUIM strain, we found that neither the Dss1 UBS-I mutant nor the Dss1 UBS-II mutant was able to fully restore growth of the dss1Δrhp23Δrpn10ΔUIM strain (Figure 4F), suggesting that the ubiquitin-binding function of Dss1, described here, is important for proteasomal function and cell viability.
Figure 2. Dss1 Interacts Directly with Ubiquitin

(A) K48- and K63-linked ubiquitin chains (3 μg per assay) (input) were coprecipitated with GST-Dss1. GST and GST-Rhp23 proteins were included as negative and positive controls, respectively. The precipitated material was analyzed by SDS-PAGE and western blotting using antibodies to ubiquitin. Equal loading was checked by staining with Coomassie brilliant blue (CBB).

(B) I44A and wild-type (wt) monoubiquitin (10 μg) (input) were coprecipitated with GST-Dss1. GST and GST-Rhp23 proteins were included as negative and positive controls, respectively. The precipitated material was analyzed by SDS-PAGE and western blotting using antibodies to ubiquitin. Equal loading was checked by staining with CBB.

(legend continued on next page)
**DISCUSSION**

In this article, we demonstrate that Dss1 has a previously uncharacterized function as a ubiquitin-binding protein of the 26S proteasome: unlike other receptors, Dss1 interacts with ubiquitin via an unstructured UBS. Given the highly conserved nature of the UPS and the dss1+ gene itself (47% identity between fission yeast and human Dss1), and given that human Dss1 complements the phenotype of a fission yeast dss1D mutant, we propose that Dss1 acts as a ubiquitin receptor in all eukaryotes.

Most ubiquitin-binding proteins have well-defined and structured ubiquitin-binding domains or small motifs (Husnjak and Dikic, 2012). This is in sharp contrast to proteins interacting with the ubiquitin-like modifier SUMO that, in general, associate via short motifs located in intrinsically disordered regions (Vogt and Hofmann, 2012). The UBSs described here are both located in the disordered region of Dss1. We suspect that other ubiquitin-binding proteins may interact by a similar mechanism. In general, disordered proteins are not well conserved in sequence (Uversky, 2011), and by homology searches, we have not been able to identify other proteins containing any Dss1-like UBSs. However, we did note some similarity between the sites in Dss1 and the UBSs found in the E2-3R family of E2 ubiquitin-conjugating enzymes (Arrigoni et al., 2012) such as Cdc34 (Choi et al., 2010). Intriguingly, a recently described disordered region of Cdc34 binds an area on ubiquitin similar to the area we identified for Dss1 (Arrigoni et al., 2012; Choi et al., 2010; Spratt and Shaw, 2011), suggesting that these binding regions are required to be unstructured.

Previous studies in budding yeast have shown that cells lacking all known proteasomal UBSs still remain viable (Husnjak et al., 2008). The data presented here reveal that the same is

---

**Figure 3. Dss1 Exploits a Tripartite Binding Site on Ubiquitin**

(A) Changes in peak intensities of ubiquitin in response to Dss1 binding. The red dashed line marks residues where the intensity decreased to less than 35%, and the black solid line marks those residues where the intensities are less than 10% of the unbound. The red dots mark proline residues not visible in the spectra.

(B) and (C) Changes in peak intensities of ubiquitin by Dss1 addition mapped onto the 3D structure of ubiquitin (Protein Data Bank ID 1D3Z) (Cornilescu et al., 1998). The protein structure is shown in green. Light blue indicate residues with peak intensities decreased to less than 35%, and dark blue decreased to less than 10%. (B) is oriented as in (D) with the β sheet facing the viewer, and in (C), the opposite side is shown with the α helix facing the viewer.

(D) Ribbon representation of ubiquitin with the same color coding as in (B) and with specific residues labeled. Three lysine residues, K11, K48, and K63 of ubiquitin are shown in magenta sticks.

(E and F) Electrostatic surface representation of ubiquitin, calculated using PyMOL. Negative potentials are shown in red, positive potentials are shown in blue, and uncharged regions are shown in white. The tripartite Dss1 binding area is circled. (E) has the same orientation as in (B), and (F) has the same as in (C).

See also Figure S3.
Figure 4. UBSs in Dss1 Are Required for Proteasome Function
(A) K48-linked (left panel) and K63-linked (right panel) ubiquitin chains (input) (3 μg per assay) were coprecipitated with GST-Dss1, GST-Dss1 UBS-I mutant (L40A/W41A/W45A), GST-Dss1 UBS-II mutant (F18A/F21A/W26A), and GST-Dss1 UBS-I and UBS-II mutant (F18A/F21A/W26A/L40A/W41A/W45A). GST and GST-Rhp23 proteins were included as negative and positive controls, respectively. The precipitated material was analyzed by SDS-PAGE and western blotting using antibodies to ubiquitin. Equal loading was checked by staining with Ponceau S.

(legend continued on next page)
true for fission yeast, but this viability, at least in part, depends on Dss1. What happens to ubiquitylated substrates after reaching the 26S proteasome, but prior to or during degradation, is still an open question. For instance, we know little about the events taking place during the initial substrate capture by Rpn10 and Rpn13, localized at the tip of the regulatory particle, and the translocation to the central ATPase ring. It is possible that substrates are handed over from the outer receptors to an inner receptor more proximal to the ATPase ring. The localization of Dss1 near the ATPase pore and the deubiquitylating subunit Rpn11 (Bohn et al., 2013) would fit such a model. The disordered and flexible nature of Dss1 could then allow for interaction with substrates presented in various orientations. However, like most disordered proteins (Uversky, 2011), Dss1 is multifunctional, even within the 26S proteasome, where it appears to act both structurally and functionally. This complicates the interpretation of the dss1Δ phenotypes. Recently, budding yeast Sem1 was shown to play an important role in proteasome assembly (Tomko and Hochstrasser, 2014). Specifically, Sem1 catalyzes incorporation of subunits Rpn3 and Rpn7 into the 19S regulatory complex through sites that overlap with UBS-I and UBS-II in fission yeast Dss1. However, this function of Sem1 becomes dispensable at later stages of proteasome assembly. Although our proteomic analyses of dss1Δ 26S proteasomes do not indicate that the level of Rpn3 or Rpn7 is reduced compared to that of other subunits of the lid complex, we also noted that Dss1, mutated in both UBS-I and UBS-II, is not incorporated into 26S proteasomes. Notably, the Dss1 mutant in UBS-I alone was still incorporated into 26S proteasomes but continued to display the temperature-dependent growth defect and ubiquitin-conjugate stabilization. This suggests that the phenotypes connected with the Dss1 ubiquitin-binding activity is limited to that of the Dss1 UBS-I, which has a much greater affinity for ubiquitin compared to UBS-II. However, Dss1 also has proteasome-independent functions, including associating with DNA repair proteins (Yang et al., 2002) and the transcription-export complex (Ellisdon et al., 2012; Faza et al., 2009). We speculate that the ubiquitin-binding activity of Dss1 may also play a functional role for these cellular processes.

In conclusion, our studies suggest the intrinsically disordered protein Dss1 as a ubiquitin receptor for the 26S proteasome in fission yeast. Since Dss1 is phylogenetically conserved, we propose that Dss1 acts as a ubiquitin receptor in all eukaryotes.
The T7-tagged Sic1-PY was purified and in vitro ubiquitylated as described elsewhere (Kriegenburg et al., 2008).

NMR Samples and Recordings
Detailed methods are provided in the Supplemental Information.

SUPPLEMENTAL INFORMATION
Supplemental Information for this article includes four figures, one table, and Supplemental Experimental Procedures and can be found with this article online at http://dx.doi.org/10.1016/j.molcel.2014.09.008.

AUTHOR CONTRIBUTIONS

ACKNOWLEDGMENTS
We thank Dr. M. Seeger, Dr. K.B. Hendil, Dr. O. Nielsen, and Dr. J.R. Winther for discussions; and we thank A. Lauridsen, M. Wallace, M. Robertson, and D. Malmodin for technical assistance. This work has been supported financially by grants to C.G. and R.H.-P. from the Medical Research Council (UK), the Lundbeck Foundation, and the Danish Natural Science Research Council and to B.B.K. from the Carlsberg Foundation. M.H.T. is funded through a grant to C.G. and R.H.-P. from the Medical Research Council (UK), the Carlsberg Foundation, and the Danish Natural Science Research Council. Special thanks are due to Dr. M. Seeger, Dr. K.B. Hendil, Dr. O. Nielsen, and Dr. J.R. Winther for discussions; and we thank A. Lauridsen, M. Wallace, M. Robertson, and D. Malmodin for technical assistance. This work has been supported financially by grants to C.G. and R.H.-P. from the Medical Research Council (UK), the Lundbeck Foundation, and the Danish Natural Science Research Council and to B.B.K. from the Carlsberg Foundation. M.H.T. is funded through a CRUK programme grant (C434/A13067). R.T.H. holds a Welcome Trust Senior Investigator Award (098391/2/12/2). K.G.H. is supported by the Wellcome Trust (083610) and the Wellcome Trust Centre for Cell Biology core grant (090276). K.P. would like to thank Lea Harrington for salary support (084537).

REFERENCES


