Interactions of Surfactant Proteins A and D with
Saccharomyces cerevisiae and Aspergillus fumigatus

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Surfactant proteins A (SP-A) and D (SP-D) are members of the collectin family of calcium-dependent lectins and are important pulmonary host defense molecules. Human SP-A and SP-D and rat SP-D bind to Aspergillus fumigatus conidia, but the ligand remains unidentified. To identify a fungal ligand for SP-A and/or SP-D, we examined the interactions of the proteins with Saccharomyces cerevisiae. SP-D but not SP-A bound yeast cells, and EDTA inhibited the binding. SP-D also aggregated yeast cells and isolated yeast cell walls. Treating yeast cells to remove cell wall mannanprotein did not reduce SP-D binding, and SP-D failed to aggregate chitin. However, SP-D aggregated yeast glucan before and after treatment with a β(1→3)-glucanase, suggesting a specific interaction between the collectin and β(1→6)-glucan. In support of this idea, SP-D-induced yeast aggregation was strongly inhibited by pustulan [α(1→6)-linked glucosyl homopolymer] but was not inhibited by laminarin [α(1→3)-linked glucosyl homopolymer]. Additionally, pustulan but not laminarin strongly inhibited SP-D binding to A. fumigatus. The pustulan concentration for 50% inhibition of SP-D binding to A. fumigatus is 1.0 ± 0.3 μM glucose equivalents. Finally, SP-D showed reduced binding to the β(1→6)-glucan-deficient kre6 yeast mutant. Taken together, these observations demonstrate that β(1→6)-glucan is an important fungal ligand for SP-D and that glycosidic bond patterns alone can determine if an extended carbohydrate polymer is recognized by SP-D.

Pulmonary surfactant is a complex mixture of lipids and proteins. It is well known that surfactant lowers the surface tension at the air-liquid interface in the lung. Recent studies also support a host defense role for surfactant and particularly for pulmonary surfactant proteins A (SP-A) and D (SP-D).

SP-A and SP-D are produced by type II cells and Clara cells in the lung and are members of the C-type lectin protein superfamily. SP-A and SP-D share many structural features. Both proteins are composed of a short N-terminal region involved in covalent cross-linking, followed by a collagen-like domain, a neck region, and a C-terminal carbohydrate recognition domain (CRD) that binds carbohydrates in a calcium-dependent manner (9, 18, 29). Both proteins form higher-order structures but differ in the organization of these structures. SP-D predominantly forms a cruciform-like dodecamer, whereas SP-A forms a bouquet-like octadecamer (18). Although the proteins are very similar, important functional differences exist. For example, SP-A but not SP-D specifically binds phosphatidylcholine and dipalmitoylphosphatidylcholine, whereas SP-D but not SP-A binds phosphatidylinositol (17, 26).

SP-A and SP-D are thought to be important components of the innate immune system (5, 24, 30, 36), and recent animal studies have demonstrated host defense roles for these proteins. For example, SP-A-deficient mice are more susceptible to intratracheally instilled group B streptococci (20), Pseudomonas aeruginosa (22), and respiratory syncytial virus (21) than wild-type animals. Moreover, intranasally administered SP-D reduced respiratory syncytial virus replication in the lungs of infected mice (12). In many cases it is thought that SP-A and SP-D mediate their host defense roles by binding carbohydrates on the surface of pathogenic microorganisms, but the precise polysaccharide structures recognized by the proteins have not been determined. Additionally, although the monosaccharide specificity of SP-A and SP-D has been examined in detail (11, 29), very little is known about how the proteins interact with other carbohydrates such as long-chain polysaccharides present on the surface of many microorganisms.

Recent work has shown that human SP-A and SP-D and rat SP-D bind Aspergillus fumigatus conidia (1, 23). Inhibitor studies and use of mutant surfactant proteins led to the conclusion that the proteins bind to surface carbohydrate structures on the conidia, but the surfactant protein ligand(s) was not identified. The purpose of the present study was to identify SP-A and/or SP-D fungal ligands. This is important since elucidation of the ligand structures recognized by these proteins is critical to our understanding of their in vivo host defense functions. Additionally, these investigations will broaden our understanding of carbohydrate recognition by SP-A and SP-D.

Since A. fumigatus conidia are difficult to disrupt and the organism is not well defined genetically, we used Saccharomyces cerevisiae as a model fungus. This yeast is well characterized genetically and biochemically and is easily manipulated in the laboratory. Since cell wall composition is common in many fungi including S. cerevisiae (3, 6, 8, 15), we feel that the knowledge gained from this work will be directly applicable to other fungi, including important pulmonary pathogens.
For a given experiment, the difference in starting $A_{500}$ of all samples analyzed was generally less than 3%. SP-D or buffer was added to the appropriate samples after 5 min. The final volume for all samples tested was 800 µl. The $A_{500}$ of the samples was measured every minute for 2 h after protein addition (except for glucan aggregation analysis, in which case the measurements were only recorded for 18 min after protein addition). Aggregation is indicated by a drop in $A_{500}$ greater than the negative control (without added protein) as the aggregated material sediments to the bottom of the assay tube. Following analysis, the starting $A_{500}$ was normalized to the negative control tube for ease of data interpretation.

Preparation of pustulan and laminarin. Pustulan stock solutions were prepared by boiling the 20 mM glucose equivalents in water for 5 min. The stock solution was then diluted to the desired concentration in CBB. Laminarin solutions were prepared by directly dissolving solid laminarin in CBB at room temperature.

Zymolyase treatment of yeast glucan. Yeast glucan (10 mg) was suspended in 10 mM Tris (pH 7.4) and digested with 8 mg of zymolyase [a β-(1→3)-glucan digesting enzyme] for 16 h at 37°C. The total reaction volume was 3 ml. The digested material was dialyzed against H$_2$O, washed with CBB, and subjected to aggregation analysis as described above.

**RESULTS**

**S. cerevisiae binding and aggregation.** As an initial step toward identifying a fungal ligand for SP-A and/or SP-D, we first examined if either protein bound the well-characterized yeast *S. cerevisiae*. We performed binding experiments using proteins from various sources (Fig. 1). As can be seen, SP-D but not SP-A bound the cells and EDTA inhibited the binding. Since SP-D is known to aggregate microorganisms including *Escherichia coli* (16) and *A. fumigatus* (23), we also tested for SP-D-induced *S. cerevisiae* aggregation by measuring changes in $A_{500}$ (Fig. 2). As shown, SP-D aggregated the cells and EDTA inhibited the aggregation. Similar results were seen when SP-D was tested for its ability to aggregate yeast cell walls (Fig. 3), suggesting that a SP-D ligand was cell wall associated. This provided a convenient method for rapidly evaluating the interaction of SP-D with the cells under a variety of conditions and to determine if the protein recognized insoluble cell wall material such as chitin or glucan (see below).

Mannan is a major constituent of the yeast cell wall and is a known inhibitor of SP-D binding to carbohydrate structures (12). We therefore considered it a likely target for SP-D binding to *S. cerevisiae*. To test this idea, we treated the cells with HF to remove the cell wall mannoprotein (15) and PNGase F to remove mannann attached to cell wall proteins. If SP-D bound only yeast mannan, we expected that these treatments would reduce or eliminate the observed binding. These treatments, however, did not reduce binding by SP-D (not shown). This finding demonstrates that SP-D ligands other than mannan are present on the yeast cell but does not exclude the possibility that SP-D recognizes mannan on the yeast cell surface.

**Interactions with chitin and glucan.** In addition to mannoprotein, the yeast cell wall also contains chitin and glucan (3, 15). Chitin is a polymer of β-(1→4)-linked N-acetylglucosamine subunits. When tested directly, SP-D failed to aggregate chitin...
Glucan is a glucose polymer with subunits connected by the β(1→3)- and β(1→6)-glycosidic bonds that should mimic yeast β(1→6)-glucan. Laminarin is a soluble glucose homopolymer linked via β(1→3) glycosidic bonds that should mimic yeast β(1→3)-glucan. For comparison we also tested maltose, a known carbohydrate-based SP-D inhibitor, for its ability to inhibit aggregation (Fig. 6). We have reported the inhibitor concentrations as glucose equivalents because the polymorphic nature of the long-chain carbohydrates makes direct molar comparisons less accurate. As expected, maltose inhibited SP-D induced yeast aggregation in a concentration-
dependent manner (Fig. 6a). Essentially no inhibition was seen at 20 mM glucose equivalents, but complete inhibition was seen at 200 mM. By comparison, pustulan was a very strong inhibitor of the aggregation. Figure 6b shows that 0.5 mM glucose equivalents of pustulan partially inhibited yeast aggregation and 2 mM glucose equivalents almost completely inhibited the aggregation. Clearly, pustulan is a much more powerful inhibitor of SP-D-induced yeast aggregation than maltose. Finally, we tested laminarin for its ability to inhibit yeast aggregation. As shown in Fig. 6c, laminarin failed to inhibit aggregation at 20 mM glucose equivalents. Due to the experimental design and the limited solubility of laminarin, higher concentrations of this polysaccharide could not be tested in this assay. It is also noteworthy that in separate experiments we demonstrated that these carbohydrate inhibitors did not alter the sedimentation of yeast cells in the absence of SP-D (not shown).

We next wanted to determine the 50% inhibitory concentrations (IC50s) for pustulan and laminarin. We first attempted to use these carbohydrates to inhibit SP-D binding to S. cerevisiae. We found that laminarin failed to inhibit SP-D binding to S. cerevisiae even when used at 100 mM glucose equivalents (not shown). However, although nearly 50% inhibition of SP-D binding to S. cerevisiae was seen at 10 μM glucose equivalents of pustulan, we were unable to determine the IC50 using our detection system. The most likely explanation for this observation lies in the fact that lectins are known to cause aggregation and precipitation of multivalent carbohydrate ligands (28). Thus, if SP-D bound and caused precipitation of pustulan, the aggregated material would be intensely stained for the lectin in our assay. These aggregates either could be mistaken for yeast cells when analyzed by flow cytometry or could adhere to the yeast cell surface. In either case, these stained aggregates could prevent accurate IC50 determinations. Indeed, small, intensely stained, amorphous aggregates were seen when yeast cells that had been subjected to pustulan IC50 determinations were examined microscopically (not shown). These aggregates were seen both free in solution and adhering to the yeast cell surface, and their numbers increased with increasing pustulan concentration. Thus, we conclude that SP-D aggregates pustulan. These aggregates prevented us from determining the IC50 for pustulan inhibition of yeast binding by SP-D.

We also tested pustulan and laminarin for the ability to inhibit SP-D binding to A. fumigatus. Although pustulan aggregates were also seen in these samples, they did not prevent IC50 determinations (Fig. 7) probably because the aggregates do not adhere as well to the A. fumigatus conidia as to the yeast surface. Pustulan was found to be an extremely powerful inhibitor of SP-D binding to A. fumigatus, with an IC50 of (1 ± 3) × 10−3 mM glucose equivalents. In contrast, maltose inhibited the binding weakly (IC50 of [1.9 ± 0.2] × 101 mM) and laminarin failed to inhibit binding (IC50 of >1.0 × 102 mM).

The inhibition of aggregation and binding data presented above clearly demonstrate that SP-D specifically recognized the glucose polymer linked via β(1→6) glycosidic bonds but failed to recognize the β(1→3)-linked polymer. This finding supports our hypothesis that SP-D binds β(1→6)-glucan on the yeast cell surface.

FIG. 3. S. cerevisiae cell wall aggregation by SP-D. Yeast cell walls were suspended in calcium-containing buffer with or without 10 mM EDTA at room temperature. After 5 min, recombinant human SP-D was added to a final concentration of 5 μg/ml. Buffer was added to the negative control sample. The A700 of the suspensions was monitored every minute for 2 h after protein addition. For the graphs shown, the starting A700 for all samples was normalized to the buffer control for ease of interpretation. The graph shows representative data from duplicate experiments.

FIG. 4. Glucan aggregation by SP-D. Glucan powder was suspended in calcium-containing buffer with or without 10 mM EDTA at room temperature. After 5 min, recombinant human SP-D was added to a final concentration of 10 μg/ml. Buffer was added to the negative control sample. The A700 of the suspensions was monitored every minute for 18 min after protein addition. For the graphs shown, the starting A700 for all samples was normalized to the buffer control for ease of interpretation. The graph shows representative data from duplicate experiments.
Further investigate our hypothesis that to cause a 50% reduction in the amount of our binding assay. Deletion of the A negative control sample. The was added to a final concentrations of 10 mM EDTA at room temperature. After 5 min, recombinant human SP-D was suspended in calcium-containing buffer with or without 10 mM EDTA. For the graphs shown, the starting A₃₅₀ for all samples was normalized to the buffer control for ease of interpretation. The graph shows representative data from duplicate experiments.

SP-D binding to β(1→6)-glucan-deficient yeast mutants. To further investigate our hypothesis that β(1→6)-glucan is a ligand for SP-D, we tested the kre6 (2, 31, 32) yeast mutant in our binding assay. Deletion of the KRE6 gene has been shown to cause a 50% reduction in the amount of β(1→6)-glucan in yeast cell walls without alterations in the size or structure of the polymer (31). Additional analysis has shown that deletion of the KRE6 gene does not alter the amount of cell wall mannoprotein (31), chitin (31), or β(1→3)-glucan (32), making it an ideal mutant to test in our binding assay. If SP-D bound β(1→6)-glucan on intact yeast cells, we expected to see reduced binding to this mutant. As shown in Fig. 8, SP-D showed reduced binding to the kre6 mutant yeast compared to the wild-type parent strain. The observed 35% reduction is consistent with the conclusion that SP-D binds yeast β(1→6)-glucan. We also tested kreg sknl and kreg mutant yeast for SP-D binding. These mutants have essentially no β(1→6)-glucan in their cell walls (25, 32). SP-D bound these cells, but significantly less aggregation was seen for the mutants than the wild-type parents (not shown), suggesting a defective interaction between the lectin and the mutant yeast cells.

DISCUSSION

SP-A and SP-D are important pulmonary host defense molecules. Human SP-A and SP-D and rat SP-D have been shown to bind the fungus A. fumigatus (1, 23). These studies indicated that the fungal ligand was likely carbohydrate based, but the specific target molecule was not identified. More recently, van Rozendaal et al. (34) have demonstrated that SP-D binds Can-
dida albicans and inhibits cell growth by aggregating the organism. C. albicans binding by SP-D was inhibited by EDTA and competing sugars, suggesting that SP-D recognizes carbohydrate structures on these cells as well. To study fungal recognition by SP-A and SP-D further, we examined the interactions of the proteins with the well-characterized yeast S. cerevisiae. Human SP-D but not SP-A bound yeast cells in a manner that was inhibited by EDTA. In the present study, we used 20 μg of SP-A and SP-D per ml for our binding studies. Similar concentrations were used in a previous study examining binding to A. fumigatus (1). Estimates of the in vivo SP-D concentration in rats range from 36 to 216 μg/ml (36). SP-A concentrations are approximately 10 times that of SP-D, but most of the SP-A is lipid associated (36). We feel that the conditions tested are relevant to the physiologic surfactant protein concentrations that may be encountered in the lung.

SP-D also aggregated yeast cells. Since functional differences have been noted between human and rat SP-A (1), we also tested rat SP-A and SP-D for yeast binding (not shown). The results were similar to those shown for the human proteins; no functional differences were seen between human and rat SP-A or SP-D in interactions with S. cerevisiae.

We were originally surprised that SP-A failed to bind S. cerevisiae since the protein is known to bind yeast mannann (11), a component of the yeast cell wall. We speculate that charge repulsion may contribute to the failure of SP-A to bind the yeast cells. Yeast cells are known to carry a negative charge due to phosphate groups present in their cell wall mannann (13, 14), and SP-A would also carry a negative charge under test conditions (pH 7.4). Alternatively, the specific mannann conformation on the yeast cell surface may not allow SP-A binding, whereas different polysaccharide conformations present in the isolated mannann allow binding. No charge repulsion problem exists for SP-D. In fact, Håkansson et al. (10) have noted that SP-D carries a local positive charge in the cavity formed at the junction of its CRDs, and they have proposed that this may assist in recognition of negatively charged ligands.

After noting that SP-D also aggregated yeast cell walls (Fig. 3), we focused our ligand identification efforts on this cellular component. The cell wall is the outermost part of the cell and would therefore be more accessible to SP-D than underlying structures. The yeast cell wall is composed of mannoprotein, chitin, β(1→3)-glucan and β(1→6)-glucan (3, 15). Since yeast mannan is known to inhibit SP-D recognition of carbohydrate structures (12), it seemed likely that mannoproteins were ligands for SP-D. To test this idea, we treated the cells with HF to remove cell wall mannoproteins and PNGase F to remove cell wall mannann. Unexpectedly, these treatments did not reduce SP-D binding (not shown). While these data do not exclude the possibility that SP-D binds mannoprotein structures on the yeast cell wall, they do demonstrate that mannan is not the only SP-D ligand present.

Since SP-D failed to aggregate chitin, we next determined if SP-D interacted with glucan. Figure 4 shows that SP-D aggregated yeast glucan and EDTA inhibited the aggregation. Yeast glucan is a mixture of β(1→6-) and β(1→3)-linked glucose subunits. The fact that SP-D aggregated glucan demonstrated that the protein recognized this cell wall component. However, since both β(1→3) and β(1→6)-linked polymers were present
in the glucan preparation tested, we continued our investigations into SP-D ligand specificity. We next treated glucan with the β(1→3)-glucan-digesting enzyme zymolyase. SP-D aggregated zymolyase-treated glucan (Fig. 5), which suggested a direct interaction between the protein and β(1→6)-glucan.

To further confirm β(1→6)-glucan-specific recognition by SP-D, we tested pustulan and laminarin for the ability to inhibit SP-D-induced S. cerevisiae aggregation and A. fumigatus binding. If SP-D specifically recognized glucose polymers linked by β(1→6) glycosidic bonds, we expected that pustulan but not laminarin would strongly inhibit aggregation and binding. The data presented in Fig. 6 and 7 in Results confirm our expectations. Although it cannot be formally excluded that minor contaminants in the commercial pustulan preparation contribute to the observed inhibition, we consider this possibility highly unlikely. First, the pustulan conforms to the expected structure by nuclear magnetic resonance analysis (from the supplier), and second, dialyzed pustulan inhibited SP-D-induced yeast aggregation to the same extent as pustulan that was not dialyzed (not shown). For the experiment shown in Fig. 7, significant inhibition was found at concentrations as low as 0.1 μM glucose equivalents. Thus, any minor contaminant would have to be extraordinarily potent to be effective at such concentrations. We feel the most reasonable explanation for the collective data is that pustulan but not laminarin is a powerful SP-D inhibitor.

The fact that laminarin failed to inhibit SP-D-induced aggregation, while pustulan strongly inhibited the aggregation, is not unexpected considering existing structural knowledge: SP-D and mannose-binding protein A (MBP-A) are both C-type lectins and are highly homologous (the CRDs of human SP-D and rat MBP-A are 45% identical). The structures of rat MBP-A CRD in a complex with a carbohydrate (35) and SP-D (10) are known, and the structures of the CRDs of these two proteins are very similar. When the αC atoms of the SP-D CRD are superimposed with the MBP-A CRD, the root mean square deviation is 0.7 to 0.8 Å (10). Closer examination reveals that the region defining the carbohydrate-binding pocket in MBP-A is very similar to the corresponding region in SP-D (amino acids Glu 185 to Asp206 for MBP-A and amino acids Glu321 to Asp342 in SP-D). SP-D and MBP-A share 15 of 22 amino acids in this region, including all residues identified as critical for carbohydrate and calcium binding (Glu 185, Asn187, Glu 193, Asn205, and Asp206, using the MBP-A numbering scheme). The MBP-A and SP-D structures are also very similar in this region. The structure of MBP-A complexed with a carbohydrate revealed that the protein binds polysaccharides via interactions with hydroxyl groups at the 3 and 4 positions on the sugar ring and explained why the protein bound mannose and glucose but failed to bind galactose (35). A parallel

FIG. 6. Inhibition of SP-D-induced yeast aggregation. Yeast cells were suspended in calcium-containing buffer with or without carbohydrate inhibitor at room temperature. After 5 min, recombinant human SP-D was added to all samples except the negative control (final SP-D concentration was 5 μg/ml). Buffer was added to the negative control sample. The A700 of the suspensions was monitored every minute for 2 h after protein addition. For the graphs shown, the starting A700 for all samples was normalized to the buffer control for ease of interpretation. Maltose, pustulan, and laminarin concentrations are reported as glucose equivalents (Glc eq.). The graph shows representative data from duplicate experiments.
mutagenesis study confirmed that by changing amino acids Glu 185 and Asn 187 to Gln and Asp respectively, the protein's monosaccharide affinity could be changed from mannose/galactose to galactose (7). Analogous mutagenesis work has been done with SP-D, which also shows higher affinity for glucose than for galactose (29), with similar results (27). Together, the carbohydrate recognition specificity, mutagenesis results, and structural similarity strongly suggests that SP-D binds carbohydrates by a mechanism similar to that used by MBP-A.

As stated above, MBP-A binds saccharides via interactions with the hydroxyl groups at positions 3 and 4 on the sugar. Assuming that SP-D interacts with the same positions on the sugar unit, the protein would be expected to only bind the nonreducing terminal glucose unit of a β(1→3)-linked glucosyl polysaccharide. This is because the 3 position on all other glucose units is involved in a glycosidic bond and is not available for interaction with the protein (Fig. 9 is presented for reference). This would be the case for laminarin and explains why this polysaccharide failed to inhibit SP-D-induced yeast aggregation or binding to A. fumigatus. However, in a β(1→6)-linked glucosyl polysaccharide, the hydroxyl groups at the 3 and 4 positions are available for interactions with the protein on every sugar unit (Fig. 9). This would be the case for pustulan and explains why this carbohydrate strongly inhibited SP-D-induced yeast aggregation and binding to A. fumigatus.

The preceding observations not only explain the inhibition by laminarin and pustulan but also support our conclusion that β(1→6)-glucan is a fungal ligand for SP-D. SP-D does not bind β(1→3)-glucan since the 3 position on all glucose units is unavailable for interactions with the protein. Similarly, SP-D does not bind chitin since the 4 position is unavailable for interactions with the protein in that polymer. However, both the 3 and 4 positions are available for interactions with SP-D on all glucose subunits on β(1→6)-glucan. Therefore, based on structural and experimental considerations, we feel that β(1→6)-glucan is an ideal ligand for SP-D. However, as stated previously, we cannot exclude the possibility that SP-D also binds mannoprotein structures on the yeast cell surface.

To provide additional support for our hypothesis that β(1→6)-glucan is a fungal ligand for SP-D, we tested the kre6 yeast mutant in our binding assay (Fig. 8). The cell wall of this
mutant has approximately 50% less β(1→6)-glucan than the wild-type cell wall without alterations in mannoprotein or chitin (31). Additionally, no alteration in the amount of β(1→3)-glucan was found in the wall of this mutant (32). As expected, SP-D showed reduced binding to the kre6 mutant compared to the wild type, leading us to conclude that β(1→6)-glucan is a fungal ligand for SP-D. The fact that SP-D bound the kre6 skn1 and kreb5 mutants (not shown) suggests that other SP-D ligands are present on the surface of these cells. These ligands may include yeast mannan. Additionally, it is possible that the mutants incorporate into their walls polymers not found in wild-type cells that also serve as ligands for SP-D.

In summary, we have shown that SP-D but not SP-A binds S. cerevisiae and that β(1→6)-glucan is a fungal ligand for SP-D. Since many fungi have similar cell wall compositions, we expect that these observations will be general to SP-D interactions with other fungi including Candida and Aspergillus. Additionally, our inhibitor data for putastulan and laminarin demonstrate that only certain carbohydrate conformers are recognized by SP-D and that bond patterns alone, regardless of subunit composition, can determine if a polysaccharide is recognized by SP-D. We are currently using computational modeling to explore this area further.

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