Unravelling glucan recognition systems by glycome microarrays using the designer approach and mass spectrometry

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Supplemental Results

Linkage analysis of gluco-heptasaccharides with linear sequences and homo-linkages by negative-ion ESI-CID-MS/MS

For ESI-CID-MS/MS analysis of the linear longer chain gluco-oligosaccharides, heptasaccharides (supplemental Table S3) were used as representatives. In the spectrum of α 1,2-linked Cyano-7 (Fig. 2*E*), the fragments observed were those with neutral losses of 18/78/120 Da arising from $[M-H]$ ⁻ and the respective C-ions, identifiable for three consecutive residues up to C_5 . These are the same fragmentation as those for the corresponding 1,2-linked disaccharide kojibiose (Fig. 2*A*), although the ^{0,4}A–h ions (*e.g.* m/z 1073, 911 and 749) were very weak. In the spectrum of the β1,3linked Lam-7 (Fig. 2F) only a full set C-ions, C₆ to C₁, were observed, with neutral losses of 162 Da, defining the linear sequence. The absence of A-type ions indicated 1,3-linkages as in nigerose (Fig. 2*B*). For the α 1,4-linked Malto-7, the spectrum (Fig. 2*G*) had features very similar to those of the 1,4-linked disaccharide maltobiose (Fig. 2*C*). The major ions were those with neutral losses of 60/78/120 Da from the [M-H]⁻ and the C-ions. These fragments are identifiable for four consecutive residues. Further product-ion scanning, using C_4 (m/z 665) as the precursor, revealed the fragmentation in the lower mass region (supplemental Fig. 2A). Similarly, the α 1,6-linked Dext-7 showed fragmentation features (Fig. $2H$) identical to that of the α 1,6-linked disaccharide isomaltose (Fig. 2*D*). The Dext-7 showed A-type fragmentation with neutral losses of 60/90/120 Da, apparent only for the first three consecutive residues. Further quasi-MS³ using fragment ions C_4 $(m/z 665)$ and $C₃(m/z 503)$ as precursors produced similar A-type fragment ions in the lower mass region, indicating 1,6-linkages (supplemental Fig. 2*B*).

Linkage analysis of a gluco-pentasaccharide isolated from the hydrolysate of barley βglucan by negative-ion ESI-CID-MS/MS.

A pentasaccharide, Barley-5a, was isolated from barley β-glucan hydrolysate obtained by digestion with a novel cellulase with high transglycosylation activity. The sequence was predicted to be Glcβ1,3Glcβ1,4Glcβ1,4Glcβ1,4Glc based on the literature knowledge of barley β-glucan and the specificity of the enzyme used for cleavage. The MS/MS spectrum (Fig. 4*A*) obtained agreed with the reducing and non-reducing terminal 1,4- and 1,3-linkages, respectively. However, a 1,6-linkage with A-type ion set -60/90/120 was identified for an internal linkage (Fig. 4A), which is clearly different from the 1,4-linkage with A-type ion set -60/78/120. Therefore the sequence for this pentasaccharide was assigned as Glcβ1,3Glcβ1,4Glcβ1,6Glcβ1,4Glc, different from the predicted three consecutive 4-linkages at the reducing side. The 2D TOCSY NMR spectrum (supplemental Table S4) of this oligosaccharide is consistent with the above mass spectrometric assignment and the expected β-configuration was corroborated. Six differentiated spin systems were clearly identified and attributable to the glucose residues; one α- and one β-reducing residue, a nonreducing terminal β-residue, and three internal residues characteristic of 3-linked-Glcβ, 4-linked-Glcβ, and 6-linked-Glcβ. The chemical shifts for H6 of the 6-linked glucose (in bold, supplemental Table S4) showed particularly clear glycosylation shifts.

Mixture analysis of *Poria cocos* **gluco-oligosaccharide fractions by ESI-CID-MS/MS and of derived NGLs by microarray**

Poria cocos polysaccharide was selected as a source of α 1,3-linear gluco-oligosaccharides(1). However, the ESI-CID-MS/MS product-ion spectrum of its heptasaccharide fraction Poria-7, obtained by gel filtration chromatography from the acid hydrolysate (BioGel P4 fraction), indicated the presence of 1,4-linked glucose as a minor (20-30 %) contaminant (Fig. 4*B*). This was revealed by the weak A-type ion set 60/78/120 (*e.g.* m/z 1091/1073/1031) unique for 4-linkage (Table 1*B*),

in addition to the major C-ions at m/z 989, 827, 665, 503, 341, consistent with dominant 1,3 linkage. These observations were in accord with our initial microarray binding data with NGLs of *Poria cocos* BioGel P4 oligosaccharide fractions with >DP-2 using *Tm*CBM41, which is known to recognize Glc α 1,4Glc-linked sequences (supplemental Fig. S6A). 1 H- and 13 C-NMR corroborated the presence of $α1,3$ -linked in addition to $α1,4$ -linked sequences (supplemental Table S5). Although the ¹H-NMR spectrum at 700 MHz was crowded (not shown), the relative peak heights of resolved resonances, such as those from H5 of the 3-linked Glc and H3 of the 4-linked glucose, indicated that the fraction contained at least 20% of α1,4-linked component. Therefore, the Poria fractions DP3 to DP13 were purified by preparative HPTLC to remove the α 1,4-linked contaminants (HPTLC fractions). HPTLC analysis of Poria-7, for example, showed that the contaminant was largely removed (supplemental Fig. 6*B*), and MALDI-MS analyses confirmed the heptasaccharide as the major component (supplemental Fig. 6*C*). The purified Poria-7 was analysed by ESI-MS/MS and the fragment ions from the 4-linked contaminant (m/z 1091/1073/1031) were largely removed (Fig. 4*B*). A series of NGL probes of Poria-DP3 to DP13 was generated (supplemental Table 6*A*) and microarray analysis corroborated purity as the binding signals by the 1,4-linkage-specific *Tm*CBM41 were largely disappeared, whereas strong binding signals were detected with the α1,3-linkage-specific MOPC104E (supplemental Fig. 6*A*).

Saturation Transfer Difference (STD)-NMR analyses of CBMs

STD NMR has been used to investigate the geometry and kinetics of protein-glycan complex formation(2). This technique involves NMR spectroscopy of a mixture of a protein with a ligand in solution. NMR spectra of the mixture are obtained with and without radiofrequency irradiation of the protein, and subtraction of one spectrum from the other. The difference spectrum contains only signals from parts of the ligand interacting with the protein, to which saturation has been transferred. It is therefore possible to use this method to determine binding epitopes on glycan ligands(3).

To complement the observations from microarray analyses the interaction of four β1,3 glucan-binding CBMs with 81.3-linked trisaccharide Lam-3 was analyzed in solution by STD-NMR. These were *Tm*CBM4-2, *Bh*CBM6, *Cm*CBM32 and *Cm*CBM6-2. The STD signals were detected with each of the four CBMs (supplemental Fig. 10A), indicating their ability to interact with Lam-3 under the solution phase NMR conditions. By comparing the STDs as percentages of the corresponding unperturbed signals, we were able to distinguish, at the atomic level, the modes of recognition by these CBMs in solution.

With *Tm*CBM4-2 (supplemental Fig. 10*B*), STDs were detected arising from all three glucose residues. The interactions with the H2 protons both of the reducing and the internal residue were particularly strong. These observation are in line with crystal structure evidence(4), in which the binding site is a groove that is long enough to accommodate a hexasaccharide. This can explain the lack of binding signals with Lam-2 and Lam-3 given by this CBM in the microarray analysis (Fig. 5*B*). Whereas, in solution, the trisaccharide tested here, Lam-3, may be completely included in the interior of the groove, neither the Lam-2 and Lam-3, gain adequate access to the binding groove when immobilised at their reducing end on the array surface.

With *Cm*CBM32-2, *Bh*CBM6 and *Cm*CBM6-2 (supplemental Fig. 10*C-E*), STDs were observed mainly from the non-reducing end residue of Lam-3, which implies that the non-reducing terminal makes the closest contacts with the three proteins, although with different contact protons. Literature data for *Cm*CBM32-2 are limited, but the data on *Bh*CBM-6 are in agreement with crystal structure, in which the binding site is described as a small, blocked-off groove(5). With *Cm*CBM6-2, STDs were observed strongly at the non-reducing residue and weakly at the internal and reducing residues. This CBM has a broad specificity and two glycan binding sites, one of which (cleft A) interacts with the NR residue, and the second of which (cleft B) accommodates at least a trimer(6); the STDs cannot distinguish between the two sites but the results might be

interpreted in terms of binding to both sites B and A; or possibly at site B alone. By way of validating the glucose linkage specificity in the STD experiments, we analyzed maltotriose (Glcα1,4Glcα1,4Glc) in the presence of *Tm*CBM4-2. In good agreement with the known specificity of the CBM and our observations in microarray analysis, no STD signals were observed (data not shown).

In sum, for the CBMs that bind more strongly to the non-reducing terminal of the trisaccharide ligand (*Cm*CBM32-2, *Bh*CBM6 and *Cm*CBM6-2) binding could be detected to oligosaccharides as short as DP-2; for *Tm*CBM4-2 which interacts with all the residues of the trisaccharide but most strongly with reducing and with internal residues, a chain length of DP-4 and longer was required on the array to detect binding.

Supplemental Discussion

Observations on Dectin-1 interactions with synthetic branched oligosaccharides by other methods using oligosaccharides in solution

Surface plasmon resonance (SPR) is another analysis system that has also been used in Dectin-1 studies with chemically synthesized oligosaccharides in solution as inhibitors of Dectin-1 binding to a glucan-phosphate-coated biosensor(7). We summarize the results in supplemental Table S8. Among the three branched analogs $HE-8^{B5}$, HE-9^{B6} and HE-10^{B7} and the linear HE-8, HE-9 and HE-10 (DP-8, DP-9 and DP-10, respectively) analyzed in the SPR inhibition system, the decasaccharide He-10^{B6}, with a DP-9 backbone and a single β 1,6 branch on the third residue at the non-reducing end was observed to be most potent inhibitor (IC_{50} 0.029 mM). The branched HE-8^{B5}, with a DP-7 backbone (IC₅₀ 0.13 mM) was recorded to be ten times more potent than the longer analog, HE-9^{B6}, with an DP-8 backbone (IC₅₀ 1.3 mM).

In another Dectin-1 study using chemically synthesized linear and branched glucooligosaccharides, ELISA inhibition assays were performed(8). Here the heptadecasaccharide (Structure 1 below), with a DP-16 backbone and a single β1,6 branch on the third residue at the non-reducing end, as in He-10 86 , and a linear DP-16 (Structure 2), were observed to be equally active as inhibitors of Dectin-1 binding to immobilized glucan polysaccharide.

Structure 1

Glcβ-3Glcβ-3Glcβ-3Glcβ-3Glcβ-3Glcβ-3Glcβ-3Glcβ-3Glcβ-3Glcβ-3Glcβ-3Glcβ-3Glcβ-3Glcβ-3Glcβ-3Glc

 │ Glcβ-6

Structure 2

Glcβ-3Glcβ-3Glcβ-3Glcβ-3Glcβ-3Glcβ-3Glcβ-3Glcβ-3Glcβ-3Glcβ-3Glcβ-3Glcβ-3Glcβ-3Glcβ-3Glcβ-3Glc

It is possible that the SPR inhibition system reveals effects of the β1,6 branch on oligosaccharides in solution with a particular backbone chain length. This phenomenon requires investigation. The HE-8 $B⁵⁵$ and HE-9^{B6} or a synthetic analog with a backbone chain longer than the nonassacharide that is required to detect binding in the microarrays are not currently available for conversion into NGLs for microarray analyses but will be the subject of future investigations.

Supplemental Methods

Proteins investigated. The proteins investigated and their reported oligosaccharide recognition with references are given in supplemental Table S2.

Lectins - Recombinant murine Dectin-1 extracellular carbohydrate recognition domain (CRD) fused to the Fc portion of human IgG at the *N*-terminus(9) was provided by Gordon Brown (University of Aberdeen, UK). Recombinant human Dectin-1 CRD with an *N*-terminal His₁₀-tag was purchased from R&D Systems (Minneapolis, MN); recombinant murine Dectin-1 CRD with an *N*terminal His₆-tag was a gift from Sino Biologicals (Beijing, China); recombinant human DC-SIGN CRD with the human Fc fused at *C*-terminus(10) was provided by Yvette van Kooyk (VU University Medical Center, Amsterdam) and by Alessandra Cambi (Radboud University Medical Center, The Netherlands); Concanavalin A (ConA) (biotinylated) was purchased from Vector Laboratories.

Monoclonal antibodies - Mouse myeloma antibody MOPC 104E-IgM was purchased from Sigma; the monoclonal anti-dextran antibodies m.3.4.1G6-IgG3 and m16.4.12E-IgA were from the Kabat collection of carbohydrate antigens and antibodies (currently housed at SRI International) and were prepared as biotinylated antibodies as described(11); vaccine induced anti-β-glucan antibodies 2G8-IgG and 1E12-IgM were prepared as described(12); 1H8-IgG was similarly produced (unpublished).

 CBMs - The CBMs were produced as recombinant proteins in *Escherichia coli*. Family 6 CBM from *Bacillus halodurans* (*Bh*CBM6), family 4 and family 41 CBMs from the marine hyperthermophile *Thermotoga maritima* (*Tm*CBM4-2 and *Tm*CBM41, respectively), were provided by Alisdair Boraston (University of Victoria, Canada); family 6 and family 32 CBM from the aerobic soil bacterium *Cellvibrio mixtus* (*Cm*CBM6-2 and *Cm*CBM32-2, respectively) were provided by Harry Gilbert (University of Newcastle, UK). Family 11 CBM from *Clostridium thermocellum* (*Ct*CBM11) was prepared as described previously. The recombinant *Bh*CBM6, *Tm*CBM4-2, *TmCBM41* and *CmCBM6-2* contain *N*- terminal His₆-tags, and *CmCBM32-2* and *CtCBM11* a *C*terminal His₆-tag (references are in supplemental Table S2).

Oligogluco-fructosides and glucan polysaccharides. *Cyanobacterium* gluco-oligosaccharide fructosides(13) were provided by Eckhard Loos (Regensburg, Germany). The polysaccharides used in this study are listed in supplemental Table S1. A glucan polysaccharide containing α 1.3linked sequence was isolated from *Poria cocos* mycelia(1); Dextran polysaccharide was from *Leuconostoc mesenteroides* (Sigma, Dorset, England); the cyclic β-glucan (CβG) was isolated from *Brucella* spp. as described(14); and pustulan was from *Umbilicaria papullosa* (Calbiochem, Nottingham, UK). Two glucan polysaccharides containing branched β 1,3- and β 1,6-linkages, grifolan and lentinan, were isolated from the barmy mycelium of *Grifola frondosa*(15) and from *Lentinus edodes*(16), respectively, as described.

Other gluco-oligosaccharides The disaccharides kojibiose (α 1,2), isomaltobiose (α 1,6), cellobiose (β1,4) and gentiobiose (β1,6) were purchased from Sigma, sophorose (β1,2) from Dextra Laboratories (Reading, England) and nigerose (α 1,3) from Wako Chemicals (Neuss, Germany). The α 1,4-linked malto-di- to heptasaccharides (Malto-2 to -7) were from Sigma. The β1,3-linked laminaribiose, triose and tetraose (Lam-2 to 4) were from Dextra Laboratories, laminaripentaose and -hexaose (Lam-5 and -6) were from Megazyme, and the laminariheptaose (Lam-7) was from Seikagaku (AMS Biotechnology, Abingdon, England). Gluco-oligosaccharides with mixed linkages were from the following sources: panose (Pano-3) and the gluco-tetraose with the sequence of $Glc_{\alpha}1.6Glc_{\alpha}1.4Glc_{\alpha}1.4Glc$ (Pullu-4) were from Sigma; isopanose (i-Pano-3) was provided by Takashi Tonozuka (Tokyo University of Agriculture and Technology). The following oligosaccharides were from Megazyme: barley glucotrioses (A) and (B), glucotetraoses (A), (B)

and (C) (Barley-3a and –b, Barley-4a, -b and -c, respectively), Barley penta- and hexasaccharides (Barley-5a and Barley-6a) and pullulan glucotetraose with the sequence of

 $Glc_{\alpha}1.6Glc_{\alpha}1.4Glc_{\alpha}1.4Glc$ and heptaose with the sequence of

Glc α 1,6Glc α 1,4Glc α 1,4Glc α 1,6Glc α 1,4Glc α 1,4Glc (Pullu-4 and –7, respectively). Linear β 1,3linked glucan octa-, nona, and decasaccharides HE-8, HE-9 and HE-10, and branched glucan nona-, deca- and undecasaccharides, HE-9^{B7} -10^{B2}, -10^{B3}, -10^{B5}, -10^{B7} and -11^{B2,6} were synthesized chemically, as described(17). The chemically synthesized hexasaccharide(18), $JG-6^{B1}$, was a generous gift from Jianxin Gu (Fudan University, Shanghai).

Fig. S1. Microarray analyses using microarrays of 12 soluble glucan polysaccharides to reveal their expression of ligands and antigens for the proteins investigated.

C Mammalian lectins of the immune system

The water-soluble polysaccharide samples (ID 1-12) are listed in supplemental Table S1. (*A*) murine monoclonal antibodies to α- or β-glucans; (*B*) microbial CBMs; (*C*) receptors of the innate immune system: murine Dectin-1 (His-tagged) and DC-SIGN (human Fc chimera). The binding scores are depicted as fluorescence intensities elicited with 30 and 150 pg polysaccharide per spot (blue and purple bar, respectively). The polysaccharides cyclic-β-glucan (ID 3) and laminarin (ID 5) are probably not efficiently retained on the nitrocellulose surface to elicit binding after a binding event due to their low molecular weights. The α1,3-glucose-containing *Poria cocos* polysaccharide (ID 13) is not water-soluble, therefore not included in the microarrays. This explains the lack of binding signals with the α1,3-glucan-specific MOPC-104E-IgM.

Fig. S2. Quasi-MS³ spectra of gluco-heptasaccharides with homo-linkages Malto-7 (α 1,4-linked) and Dext-7 (α1,6-linked).

A Malto-7 MS³ (quasi): fragment m/z 665 C_2 C_{3} $C₄$ 341 503 665 A_3 $B,$ -h $^{2,4}A_4$ $587^{0.2}A_4$ 161 $^{0,2}A_2$ $^{2,4}A_3$ 443 C, $-h$ 545 605 281 179 425 383 ڻڇ 675 700 725 760 125 150 175 200 225 275 300 375 625 650 $\overline{575}$ 600 625 650 75 100 ده. **AND** 425 475 600 B Dext-7 MS³ (quasi): fragment m/z 665 $^{0,4}A_4$ \mathbf{C}_3 503 545 100 $^{0,2}A_4$ C_a $^{0,2}A_3$ $^{0,3}A_4$ 605 665 C_{2} 443 575 341 enialista film alla m/z
700 725 750 $rac{1}{425}$ 450 $rac{1}{660}$ $rac{1}{675}$ 76 100 125 175 200 $\frac{1}{225}$ $\frac{1}{275}$ 350 375 475 600 600 650 675 MS³ (quasi): fragment m/z 503 \mathbf{C}_2 A_3 $^{0,2}A_3$ 341 \dot{a} 383 443 $^{0,3}A_3$ C_3 C_{1} 179 503 413 375 aoo 500 176 475

The fragment ions produced by cone voltage fragmentation were used as the precursors: (*A*) m/z 665 of Malto-7, (*B*) m/z 665 and m/z 503 of Dext-7.

Fig. S3. Negative-ion ES-CID-MS/MS product-ion spectrum of Pullu-7 with hetero-linkages.

Pullu-7 $(\alpha$ 1-6,4,4,6,4,4)

Fig. S4. Negative-ion ES-CID-MS/MS product-ion spectra of gluco-trisaccharides with mixed 1,4 and 1,6-linkages

Fig. S5. Negative-ion ES-CID-MS/MS product-ion spectra of 1,3-linked oligosaccharides with 1,6 branching.

(A) Single branched gluco-decasaccharide HE-10^{B7}; (B) Double branched gluco-undecasaccharide HE- $11^{B3,6}$

Fig. S6. Analyses of the α1,3-gluco-oligosaccharide rich Poria fractions, before and after removal of contaminating α1,4-gluco-oligosaccharides.

Lane 1: Malto-7; Lane 2: Poria-7

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(*A*) Microarray analyses using NGLs derived from Poria oligosaccharide fractions 3-13 (Bio-Gel P4 and HPTLC fractions), tested for binding by an α1,4-glucose specific CBM, *Tm*CBM41, and a α1,3-glucose specific antibody, MOPC 104-E; (*B*) Analytical HPTLC analysis of the Poria-7 oligosaccharide fraction before and after removal of the α1,3-glucose contaminant; Malto-7 was included as a reference; (*C*) MALDI-MS of the Bio-Gel P4 and HPTLC fractions of Poria-7.

Fig. S7. Carbohydrate microarray analyses of His-tagged murine and human Dectin-1.

Both recombinant proteins showed highly restricted binding to the higher oligomers of linear β1,3-linked glucose generated from curdlan polysaccharide. Please see legend to **Fig. 5** for details.

Fig. S8. 'On-array' inhibition of Dectin-1 and *Cm*CBM32-2 binding to immbobilized NGLs with β1,3-linked oligosaccharides

(A) Inhibition of the binding of murine Dectin-1 Fc chimera to immobilized β 1,3-linked Curd-13 NGL by 1,3-linked oligosaccharides Curd-11 and Curd-13 but not Lam-7; Curd-13 NGL was arrayed at 5 fmol/spot. The 'on-array' inhibition results thus corroborate the chain length requirement for Dectin-1 recognition observed in the microarrary analysis as there was a higher inhibitory activity of the curdlan oligosaccharide fraction with DP-13 over that with DP-11; and a lack of inhibition by the oligosaccharide with DP-7. (*B*) Inhibition of the binding of *CmCBM32-2* to immobilized β 1,3-linked Lam-5 NGL by β 1,3linked oligosaccharides Lam-3, Lam-5 and Lam-7; Lam-5 was arrayed at 5 fmol/spot. In contrast with Dectin-1, for *Cm*CBM32-2 the short β1,3 oligosaccharides showed high inhibitory activities of binding, thus corroborating the results of the microarray analysis.

The murine Dectin-1-Fc and *Cm*CBM32-2 were used at non-saturating concentrations of 5µg/ml. The final concentrations of the oligosaccharides used as inhibitors of binding are indicated on the Y axis. The results are expressed as percentage of inhibition of binding as follows: percentage inhibition= [(spot fluorescence intensity no inhibitor - spot fluorescence intensity with inhibitor)/(spot fluorescence intensity no inhibitor- spot fluorescence intensity negative control)] \times 100.

Fig. S9. Comparison of the binding of Dectin-1, 2G8-IgG, 1E12-IgM, *Tm*CBM4-2 and *Cm*CBM32-2 to natural linear β1,3-linked and synthetic branched β1,3/β1,6 oligosaccharides.

The results highlight different chain length-dependencies and the abilities of 2G8-IgG and 1E12-IgM antibodies, *Tm*CBM4-2 and *Cm*CBM32-2, but not Dectin-1, to bind branched β1,3/β1,6 oligosaccharides. The glucose linkages are symbolically indicated by diagrams in the top panel; for probe 157 the internal 1,3 linkage has an α-configuration. For probes 6, 8-13 glucose chain lengths of the major components are depicted.

Fig. S10: STD NMR analyses of CBMs with β1,3-linked trisaccharide Lam-3.

(*A*) Reference 1H NMR and STD spectra of Lam-3 in the presence of (*B*) *Tm*CBM4-2, (*C*) *Bh*CBM6-2, (*D*) *Cm*CBM32 and (*E*) *Cm*CBM6-2. Binding epitopes implied by the STD results are shown on the right for each CBM. All the experiments were performed at 30 ºC except for *Cm*CBM32-2 which was measured at 45 °C. The relative STD effects (highest STD signal normalized to 100%) are illustrated by dark, medium and light gray circles indicating strong (>80 %), medium (40–80%), and weak (<40%) STD effects, respectively. Overlapped STD signals that could not be clearly assigned are not shown on the structures. Asterisks indicate signals for which the STD is an approximate estimate due to partial overlap.

Table S1. Polysaccharides examined. Some of the glucan polysaccharides listed below were selected as sources of gluco-oligosaccharides after their partial depolymerization; reagents used for depolymerization are given. Those that were soluble, polysaccharides ID 1-12, were printed non-covalently onto nitrocellulose-coated slides and analyzed for binding with the proteins investigated as shown in supplemental Fig. S1.

¹Where known

2Curdlan polysaccharide was solubilized in an alkaline aqueous solution (50mM NaOH) prior printing.

Table S2. Glucan-recognizing proteins investigated and their reported oligosaccharide recognition.

Table S3. Gluco-oligosaccharides used for development of ESI-CID-MS/MS method.

¹Monosaccharide contents of oligosaccharides are given as Arab numerals.

	Chemical shifts in ppm						
	Glc β 1	$3Glc\beta1$	$4Glc\beta1$	$6Glc\beta$	$4Glc\alpha$	$4Glc\beta$	
H1	4.73	4.53	4.53	4.51	5.21	4.65	
H ₂	3.33	3.50	3.34	3.32	3.56	3.28	
H ₃	3.51	3.75	3.61	3.49	3.82	3.59	
H ₄	3.39	3.51	3.65	3.49	3.63	3.62	
H ₅	3.47	3.51	3.58	3.65	3.85	3.58	
H ₆	3.91	3.91	3.97	4.20	3.94	3.95	
H ₆	3.71	3.75	3.81	3.88	3.87	3.80	

Table S4.¹H NMR assignments for Barley-5a (Glcβ1,3Glcβ1,4Glcβ1,6Glcβ1,4Glc) in D₂O at 30 °C.

	Chemical shifts in ppm						
	α 1 \rightarrow 3 linked		α 1 \rightarrow 4 linked				
	13 _C	¹ Η	13 C	¹ Η			
C/H1	102.1	5.36	102.4	5.38			
C/H2	73.0	3.67	74.4	3.63			
C/H3	83.0	3.89	76.1	3.96			
C/H4	72.4	3.42	79.7	3.66			
C/H5	74.4	4.03	74.0	3.83			
C/H6	63.1	3.83	63.3	3.87			
		3.77		3.71			

Table S5. ¹H and ¹³C assignments for the Poriaco-7 fraction containing α 1,3-linked Glc with a minor component of α 1,4-linked glucan, in D₂O at 30 °C.

 1 Glucose units or degree of polymerization (DP) for the major components in each fraction;²Calculated masses for major components are given;³Positive-ion MALDI-MS was used for the analysis of AO-NGLS of cyano-, poriaco-, C β G-, cello- and pustulan-series and MNa⁺ were detected, whereas negative-ion MALDI-MS was used for the analysis of AO-NGLS of malto-, dextran- and curdian-series and [M-H]⁻ were detected;⁴Shown in brackets are assigned glucose units; and where multiple components were detected, relative intensities of ions greater 10% are given;⁵Nomenclature of the oligosacchide moieties correspond to the polysaccharide origins;⁶Disaccharides and malto- and curdlan oligosaccharides from commercial sources are asterisked; ⁷For the β1,6-linked pustulan series the major components of these fractions are oligomers with DP-15.

Table S6B. MALDI-MS analysis of NGLs derived from gluco-oligosaccharides or fractions with hetero-linkages.

 1 Glucose units or degree of polymerization (DP) for the major components in each fraction.
²Calculated masses for major components are given.
³Positive-ion MALDI-MS was used for the analysis and MNa⁺ was detected

4 Shown in brackets are assigned glucose units; and where multiple components were detected, relative intensities of ions greater 10% are given.

Table S6C. MALDI-MS analysis of NGLs prepared from additional commercial and chemically synthesized gluco-oligosaccharides.

 1 Positive-ion MALDI-MS was used for the analysis and MNa⁺ were detected. ²Shown in brackets are the assigned glucose compositions.

Table S7A. Oligosaccharide NGL probes included in the gluco-oligosaccharide microarrays, sorted by linkage type and degree of polymerization.

 1 ID, Probe position in the microarray matching the position in the binding-charts.

 2 Xyl, xylose; Man, mannose;

³Abbreviations for oligosaccharide moieties: Cyano-, from cyanobacterium gluco-fructosides; Poria-, from α 1,3-linked glucan polysaccharide isolated from Poria cocos mycelia; Malto-, from maltodextrins; Dext-, from dextran (MW 200 kDa); Pullu-, from Pullulan; CβG-, from cyclic β1,2-linked glucan isolated from *Brucella* spp; Lam-, laminarioligosaccharides; Curd-, from Curdlan; Cello-, from cellulose; Pust-, from pustulan; Barley-, from barley glucan; Grifo-, from branched glucan polysaccharide grifolan (95 kDa) isolated from the barmy mycelium of *Grifola frondosa*; Lenti- from branched glucan polysaccharide lentinan from *Lentinus edodes*; HE and Gu are synthetic oligosaccharides. The sequences of the gluco-oligosaccharide preparations highlighted in grey, representative of each series, were determined by ESI-CID-MS/MS. In the lentinan derived fractions a minor 1,4-linked glucose contaminant was detected which was corroborated by NMR (not shown). $\frac{1}{100}$ which was corroborated by NMR (not shown). $\frac{1}{100}$ and $\frac{1}{100}$ and $\frac{1}{100}$ and $\frac{1}{100}$ and $\frac{1}{100}$ integration with the cliquagaccharides by reduct

amino lipid, 1,2-dihexadecyl-sn-glycero-3-phosphoethanolamine (DHPE)(47); AO, NGLs prepared from reducing oligosaccharides by oxime ligation with an
aminooxy (AO) functionalized DHPE(48).

_aminooxy (AO) functionalized DHPE(48).
⁵An asterisk indicates the major component when multiple components are present (see supplemental Tables 6*A-*6C).

Table S7B. Fluorescence binding intensities elicited with all the proteins investigated. The numerical scores for the fluorescence binding signals are shown as means of duplicate spots at 5 fmol probe per spot (as in Fig.5 and 6 and supplemental Fig. 7) and are representative of at least 2 independent experiments.

¹ID, Probe position in the microarray matching the position in the binding-charts and in supplemental Table 7A.
²In the β1,6-linked pustulan series, fractions containing oligomers with >DP-8 as major components (prob contaminant containing ^α-linked mannose as detected by ConA binding. The weak binding detected to the NGLs of oligosaccharide fractions derived from branched β1,3/β1,6 lentinan (probes 142-151) was likely to the presence of an α1,4-linked glucose contaminant as corroborated by MS/MS (supplemental Table 7A, footnote 3) and NMR (not shown).
³ '-' refers to a fluorescence intensity < 500.

Table S8: Summary of Dectin-1 interactions with linear β1,3- and selected branched β1,3/β1,6-linked glucose sequences. SPR inhibition data taken from Adams et al 2008(7).

¹Position in the microarray; ²Surface plasmon resonance competition experiments using a glucan-phosphate-coated biosensor chip(7); ³Spot fluorescence intensity on the present study; ⁴Major components in factions; ⁵Not tested

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