

# A novel lectin from *Agrocybe aegerita* shows high binding selectivity for terminal N-acetylglucosamine

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A novel lectin was isolated from the mushroom *Agrocybe aegerita* (designated AAL-2) by affinity chromatography with GlcNAc (N-acetylglucosamine)-coupled Sepharose 6B after ammonium sulfate precipitation. The AAL-2 coding sequence (1224 bp) was identified by performing a homologous search of the five tryptic peptides identified by MS against the translated transcriptome of *A. aegerita*. The molecular mass of AAL-2 was calculated to be 43.175 kDa from MS, which was consistent with the data calculated from the amino acid sequence. To analyse the carbohydrate-binding properties of AAL-2, a glycan array composed of 465 glycan candidates was employed, and the result showed that AAL-2 bound with high selectivity to terminal non-reducing GlcNAc residues, and further analysis revealed that AAL-2 bound to terminal non-reducing GlcNAc

residues with higher affinity than previously well-known GlcNAc-binding lectins such as WGA (wheatgerm agglutinin) and GSL-II (*Griffonia simplicifolia* lectin-II). ITC (isothermal titration calorimetry) showed further that GlcNAc bound to AAL-2 in a sequential manner with moderate affinity. In the present study, we also evaluated the anti-tumour activity of AAL-2. The results showed that AAL-2 could bind to the surface of hepatoma cells, leading to induced cell apoptosis *in vitro*. Furthermore, AAL-2 exerted an anti-hepatoma effect via inhibition of tumour growth and prolongation of survival time of tumour-bearing mice *in vivo*.

**Key words:** *Agrocybe aegerita*, anti-hepatoma activity, fungal lectin, glycan-binding property, N-acetylglucosamine.

## INTRODUCTION

Changes in glycosylation patterns play important roles in embryonic development, metabolic homeostasis, pathogenic infections, immune surveillance and various diseases, including oncogenesis, diabetes and autoimmune disorders [1]. Therefore glycan analysis is of great importance for understanding the significance of glycan modifications. Lectins, with their diverse carbohydrate-binding properties, are potent tools for the study of glycan conjugates in various biological materials without glycan liberation. For example, lectins have been applied in the separation of cells at different stages, mitogenic activation of immune cells and identification of blood groups, as well as characterization of glycan alterations on the surface between normal and neoplastic cells [2–4].

The newly developed lectin array has been proved to be a powerful tool for the comprehensive analysis of glycans or glycoconjugates [5]. Much significant information has been obtained from use of lectin arrays.  $\alpha$ 1-2-Fucose-specific lectin (rBC2LCN) has been applied in the detection of undifferentiated induced pluripotent stem cells/embryonic stem cells, but not differentiated somatic cells [6], TKA (*Trichosanthes kirilowii* agglutinin) and PNA (peanut agglutinin) were used to distinguish the stem-like glioblastoma neurosphere cultured from a traditional adherent glioblastoma cell line [7], GNA (*Galanthus nivalis*

agglutinin), NPA (*Narcissus pseudonarcissus* agglutinin), PSA (*Pisum sativum* agglutinin), LcH (*Lens culinaris* lectin) and Con A (concanavalin A) have been used for the detection of high-mannose N-linked oligosaccharides on differentiated neutrophils in comparison with the promyelocytic leukaemia cell line HL-60 [8], DSL (*Datura stramonium* lectin), SLL [*Solanum lycopersicum* lectin; formerly LEL (*Lycopersicon esculentum* lectin)] and MAL (*Maackia amurensis* lectin) showed a binding preference for mouse laminin, whereas SNA (*Sambucus nigra* agglutinin), SSA (*Salvia sclarea* agglutinin) and TJA-I (*Trichosanthes japonica* agglutinin-I) showed strong binding to bovine transferrin [9]. More lectins with unambiguous and/or distinctive glycan-binding selectivity are needed to be studied and exploited for probes of glycan structures. Thus there is an urgent need to find powerful lectin candidates for glycan analysis.

Lectins are useful tools for tumour diagnosis, antiviral research and drug-delivery studies [10]. For example, MAL has been used in prostate cancer diagnosis because of its preferential binding to prostate-specific antigen [11], HPA (*Helix pomatia* agglutinin) recognizes the glycosylation changes of metastatic breast cancer [12], BCA (*Boodlea coacta* lectin) can potentially provide entry inhibition of HIV-1 and influenza viruses [13], microvirin has anti-HIV-1 activity with a high safety profile and low toxicity [14], and odorranalectin has been reported to be the smallest lectin so far and with potential for drug delivery and targeting

Abbreviations used: AAL-2, *Agrocybe aegerita* lectin 2; BLL, *Boletopsis leucomelas* lectin; GlcNAc, N-acetylglucosamine; GSL-II, *Griffonia simplicifolia* lectin-II; HPA, *Helix pomatia* agglutinin; IPTG, isopropyl  $\beta$ -D-thiogalactopyranoside; ITC, isothermal titration calorimetry; LacNAc, N-acetyl-lactosamine; MAL, *Maackia amurensis* lectin; MALDI, matrix-assisted laser-desorption ionization; MS/MS, tandem MS; nAAL-2, native AAL-2; ORF, open reading frame; PI, propidium iodide; PVL, *Psathyrella velutina* lectin; rAAL-2, recombinant AAL-2; RFU, relative fluorescence units; SLL, *Solanum lycopersicum* lectin; TBS, Tris-buffered saline; TOF, time-of-flight; WGA, wheatgerm agglutinin.

The nucleotide sequence data for *Agrocybe aegerita* lectin 2 will appear in the GenBank®, EMBL, DDBJ and GSDB Nucleotide Sequence Databases under accession number JN001164.

The glycan array data of AAL-2 were deposited in the Consortium for Functional Glycomics database with the labels primscreen\_3312–primscreen\_3315.

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[15]. An increasing number of lectins from plants and animals have been purified and characterized; however, the information on lectins isolated from fungal sources remains limited [16]. Fungal lectins are attractive because of their wide distribution, high content, varied carbohydrate-binding specificities and especially anti-tumour activities. *Agaricus bisporus* lectin was shown to possess anti-tumour activity against human colon cancer HT29 and breast cancer cell lines MCF-7 [17], *Russula lepida* lectin exhibited anti-proliferative activity in hepatoma HepG2 cells and human breast cancer MCF-7 cells [18], *Tricholoma mongolicum* lectin-1 and lectin-2 could inhibit the growth of sarcoma 180 cells [19], *Pleurotus citrinopileatus* lectin exerted potent anti-tumour activity in mice bearing sarcoma 180 [20], and *Grifola frondosa* lectin was shown to be cytotoxic to HeLa cells [21].

In the present paper, we report a novel fungal lectin AAL-2 (*Agrocybe aegerita* lectin 2) from the fruiting body of *A. aegerita*. A glycan array analysis showed that AAL-2 bound to non-reducing GlcNAc (*N*-acetylglucosamine) termini with high selectivity, even higher than the previously well-known GlcNAc-binding lectins WGA (wheatgerm agglutinin) and GSL-II (*Griffonia simplicifolia* lectin-II), which have been widely used in biochemical and biomedical research. Moreover, we showed that AAL-2 had anti-tumour activity not only for the induction of hepatoma cells apoptosis *in vitro*, but also for the inhibition of H22 hepatoma growth and prolongation of survival times of tumour-bearing mice *in vivo*. The cloning and prokaryotic/bacterial protein expression of AAL-2 provided clues to the deep investigation of the glycan-binding mechanism of AAL-2 and further application of AAL-2 in probing GlcNAc-related glycans or glycoconjugates.

## EXPERIMENTAL

### Chemicals and reagents

The edible mushroom *A. aegerita* was collected from the Sanming Institute of Fungi (Sanming, Fujian, P.R. China). GlcNAc was purchased from Sangon Biotech. Epoxy-activated Sepharose 6B was purchased from GE Healthcare.

### Cell lines and mice

A murine hepatoma cell line H22, and a human hepatoma cell line Huh7, were provided by the CCTCC (China Center for Type Culture Collection, Wuhan University). Male BALB/c mice (6–8-week-old) were purchased from the Hubei Experimental Animal Laboratory (Hubei, China) and maintained in a pathogen-free facility. Procedures were performed according to approved protocols and in accordance with recommendations for the proper care and use of laboratory animals.

### Preparation of GlcNAc-coupled Sepharose 6B matrix

GlcNAc-coupled Sepharose 6B was prepared according to the manufacturer's instructions (GE Healthcare). In brief, 2 g of epoxy-activated Sepharose 6B was washed twice with 200 ml of distilled water, mixed with GlcNAc at a final concentration of 200  $\mu$ mol/ml in distilled water (pH 13) at a temperature of 30°C for 15 h. Free remaining groups were blocked by incubating in 1 M ethanolamine, and the mixture was gently agitated at 45°C for 4 h. The Sepharose 6B-coupled GlcNAc matrix was washed extensively with TBS (Tris-buffered saline) (pH 7.2) and packed into an empty 100-mm-long glass column with a 10 mm inner diameter. The column was stored at 4°C until use.

### Purification of AAL-2 from mushroom *A. aegerita*

Dried *A. aegerita* fruiting bodies were crushed into a powder, and 50 g of the dried mass was dissolved and extracted three times with 1 litre of distilled water at 4°C. The extracts were pooled and centrifuged at 10000 g for 15 min. Solid ammonium sulfate was added to the supernatant to 40% saturation and centrifuged again at 10000 g for 15 min. Solid ammonium sulfate was then added to the supernatant to obtain 80% saturation, and the 40–80% precipitate was collected by centrifugation at 10000 g for 15 min. The precipitated protein was dissolved in 200 ml of distilled water and dialysed extensively against 50 mM TBS (pH 7.2) by changing the dialysis buffer three times at 4°C overnight. The sample was loaded on to an affinity column (GlcNAc-coupled Sepharose 6B matrix) pre-equilibrated with TBS (pH 7.2), and eluted with 0.2 M GlcNAc in 50 mM TBS (pH 7.2) after extensive washing with TBS. The enriched AAL-2 fraction was stored at –20°C.

SDS/PAGE was performed with a 15% acrylamide running gel and 5% stacking gel. Protein bands were identified by Coomassie Brilliant Blue R-250 staining.

### Preparation of tryptic peptides and peptide sequencing

The band corresponding to AAL-2 was excised from a Coomassie Brilliant Blue-stained SDS/polyacrylamide gel and tryptically digested according to standard protocols. The peptides were derivatized for the N-terminus with SPITC (4-sulfophenyl isothiocyanate) and desalted with ZipTip™. MALDI (matrix-assisted laser-desorption ionization)–MS was performed on a 4700-Proteomics Analyzer (Applied Biosystems) and PSD (power spectral density) spectra were collected with 3000 laser shots at 1 keV collision energy without CID (collision-induced dissociation). MS data were analysed by PMF (peptide mass fingerprinting) using MASCOT software.

### Molecular mass determination by MS

MALDI–TOF (time-of-flight) mass spectra were obtained using a Voyager-RP mass spectrometer (PerSeptive Biosystems) [22].

### cDNA cloning of AAL-2 and expression of rAAL-2 (recombinant AAL-2) in *Escherichia coli*

Total RNA was prepared from the fresh fruiting bodies of *A. aegerita* by grinding in liquid nitrogen followed by extraction with Plant RNA Isolation Reagent (BioTeke). Full-length cDNAs were synthesized from 1  $\mu$ g of total RNA using MMLV (Moloney murine leukaemia virus) reverse transcriptase (Promega) after RQ1 RNase-free DNase digestion (Promega) according to the manufacturer's instructions. Nested PCR was applied to amplify the AAL-2 coding sequence, and two pairs of primers were designed as follows: forward external primer *aal-2\_5'\_F1*, 5'-ATGAACGTGAACGTGGGAGG-3'; reverse external primer *aal-2\_3'\_R1*, 5'-CTAGTAATCCGTGCGAGTCCG-3'; forward ORF (open reading frame) primer *aal-2\_5'\_F2*, 5'-ATGACCAGCAACGTCATCAC-3'; reverse ORF primer *aal-2\_3'\_R2*, 5'-ATGCCTGCTGCTGTCCAAGT-3'. PCR was performed using Taq DNA polymerase (Promega) with the following temperature profile: 5 min at 95°C, 30 s at 94°C and 3 min at 72°C, for 35 cycles. The amplified product obtained with external primers was used as the template for a second round of amplification with the ORF primers. The purified PCR fragment was cloned into the pET-30a vector (Novagen) according to the manufacturer's instructions. The resulting plasmid containing rAAL-2 coding sequence was used

for transformation into *E. coli* BL21 cells (Novagen). Induction of protein expression was performed with 1 mM IPTG (isopropyl  $\beta$ -D-thiogalactopyranoside) at mid-exponential phase ( $D_{600}$  of 0.4–0.6), and the bacteria were grown for an additional 5 h at 37 °C with shaking at 220 rev./min. The bacteria were then harvested and lysed. The supernatant was loaded on to a GlcNAc–Sepharose 6B column, and rAAL-2 was purified by GlcNAc-coupled Sepharose 6B affinity chromatography as described above.

### Biotinylation of AAL-2

To biotinylate AAL-2, purified AAL-2 (200  $\mu$ g in 250  $\mu$ l of PBS) was mixed with 400  $\mu$ l of biotin ester solution (100  $\mu$ g of biotin ester/200  $\mu$ g of lectin) and left for 30 min at room temperature (24 °C). The biotin-labelled AAL-2 was collected using Sephadex G-250 and stored at –20 °C until use.

### Glycan array analysis

To determine the carbohydrate-binding specificity of AAL-2, glycan array analysis was performed by the Consortium for Functional Glycomics (Core H; <http://www.functionalglycomics.org/static/consortium/resources/resourcecoreh.shtml>). The printed glycan array (Mammalian Printed Array version 4.1) [23] was composed of 465 different natural and synthetic mammalian glycans. In the binding assay, array slides, containing six replicates per glycan or glycoconjugate, were incubated with different concentrations of biotinylated AAL-2 (0.1, 1, 50 and 200  $\mu$ g/ml). The slides were then washed, and bound lectin was detected using fluorescently labelled streptavidin. Array slides were subjected to imaging, and the fluorescence was measured as described previously [24]. Briefly, fluorescence intensity was detected using a ScanArray 5000 confocal scanner (PerkinElmer). ImaGene<sup>®</sup> image analysis software (BioDiscovery) was used to analyse the image. The relative binding for each glycan was expressed as mean RFU (relative fluorescence units) of four of the six replicates.

### ITC (isothermal titration calorimetry)

ITC experiments on the interaction of GlcNAc with AAL-2 were performed at 25 °C with a VP-ITC isothermal titration calorimeter (Microcal). Freshly purified AAL-2 was dialysed overnight in PBS (pH 7.2) at 4 °C. The protein concentration in the microcalorimeter cell (1.4478 ml volume) was 50  $\mu$ M. GlcNAc solution was made up to 7 mM in PBS and placed in the syringe. The first injection (4  $\mu$ l) was followed by 27 injections of 10  $\mu$ l, and the stirring rate was set at 300 rev./min. The dilution heat of the GlcNAc was measured by injecting GlcNAc solution into buffer alone and was subtracted from the experimental curves before data analysis. The experimental data were fitted to a theoretical titration curve using Microcal Origin software supplied with the instrument, and the standard molar enthalpy change for the binding,  $\Delta_b H_m^0$ , and the dissociation constant,  $K_d$ , were derived. The standard molar free energy change,  $\Delta_b G_m^0$ , and the standard molar entropy change,  $\Delta_b S_m^0$ , for the binding reaction were calculated by using the following thermodynamic equations:

$$\Delta_b G_m^0 = RT \cdot \ln K_d \quad (1)$$

$$\Delta_b S_m^0 = (\Delta_b H_m^0 - \Delta_b G_m^0) / T \quad (2)$$

### Haemagglutination assay

The haemagglutination activity of purified lectin was determined as described previously [25]. Briefly, the haemagglutination activity assay was performed on a microtitre plate, and the lectin sample (50  $\mu$ l, 1 mg/ml) was serially diluted with PBS and mixed with 50  $\mu$ l of a 2% suspension of chicken red blood cells at room temperature. Measurements were taken after 30 min when the control (no lectin added) was fully precipitated.

The effects of metal cations on the haemagglutination activity of AAL-2 were determined in the absence and presence of 10 mM  $\text{Ca}^{2+}$ ,  $\text{Zn}^{2+}$ ,  $\text{Mn}^{2+}$  or  $\text{Mg}^{2+}$  after dialysis against 20 mM EDTA. The effect of temperature on lectin stability was monitored over a temperature range by incubation with AAL-2 for 30 min at each temperature. The samples were then cooled rapidly and assayed for haemagglutination activity. The effect of pH on lectin stability was determined by incubating with AAL-2 with buffers of different pHs for 30 min, and haemagglutination activity was determined after neutralization.

### Preparation of a polyclonal anti-AAL-2 antibody

A rabbit polyclonal antibody against AAL-2 was prepared as reported previously [26]. Briefly, 500  $\mu$ g of nAAL-2 (native AAL-2) in 500  $\mu$ l of PBS was emulsified with 500  $\mu$ l of complete Freund's adjuvant (Sigma). The emulsion was injected into 6-month-old New Zealand White rabbits by multipoint subcutaneous implantation. The second and third inoculations were performed on days 24 and 36 with Freund's incomplete adjuvant (Sigma), and the fourth inoculation was performed on day 41 without any adjuvant. At 1 week after the final immunization, sera were separated from the collected blood samples and antibody against nAAL-2 was detected by ELISA.

### Cell culture

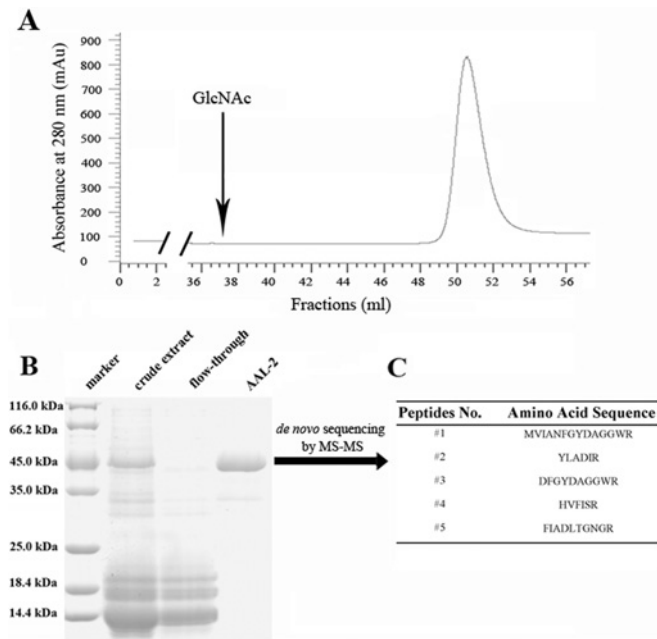
H22 cells and Huh7 cells were cultured in RPMI 1640 medium and DMEM (Dulbecco's modified Eagle's medium) respectively. Cell culture media were supplemented with 10% (v/v) heat-inactivated (56 °C, 30 min) FBS (fetal bovine serum), 5 units/ml penicillin and 50  $\mu$ g/ml streptomycin. All cells were maintained at 37 °C in a humidified atmosphere containing 5%  $\text{CO}_2$ . For all experiments, cells were plated 2 h before treatment to allow for adherence.

### Cell-adhesion assay, Annexin V/PI (propidium iodide) staining and FACS analysis

In the cell-adhesion assay, H22 and Huh7 cells were incubated with or without AAL-2, and then with polyclonal antibody against AAL-2 and FITC-conjugated goat anti-rabbit IgG. For Annexin V/PI staining, H22 and Huh7 cells were treated with AAL-2 at final concentrations of 0, 0.6, 1.2 or 2.4  $\mu$ M for 24 and 36 h respectively. The cells were collected, washed twice with ice-cold PBS (pH 7.4), and stained using an Annexin V/PI apoptosis kit (MultiScience Biotech). The samples were mixed gently and incubated in the dark. All samples were analysed by flow cytometry (Beckman, Epics Altra)

### Subcutaneous tumour models

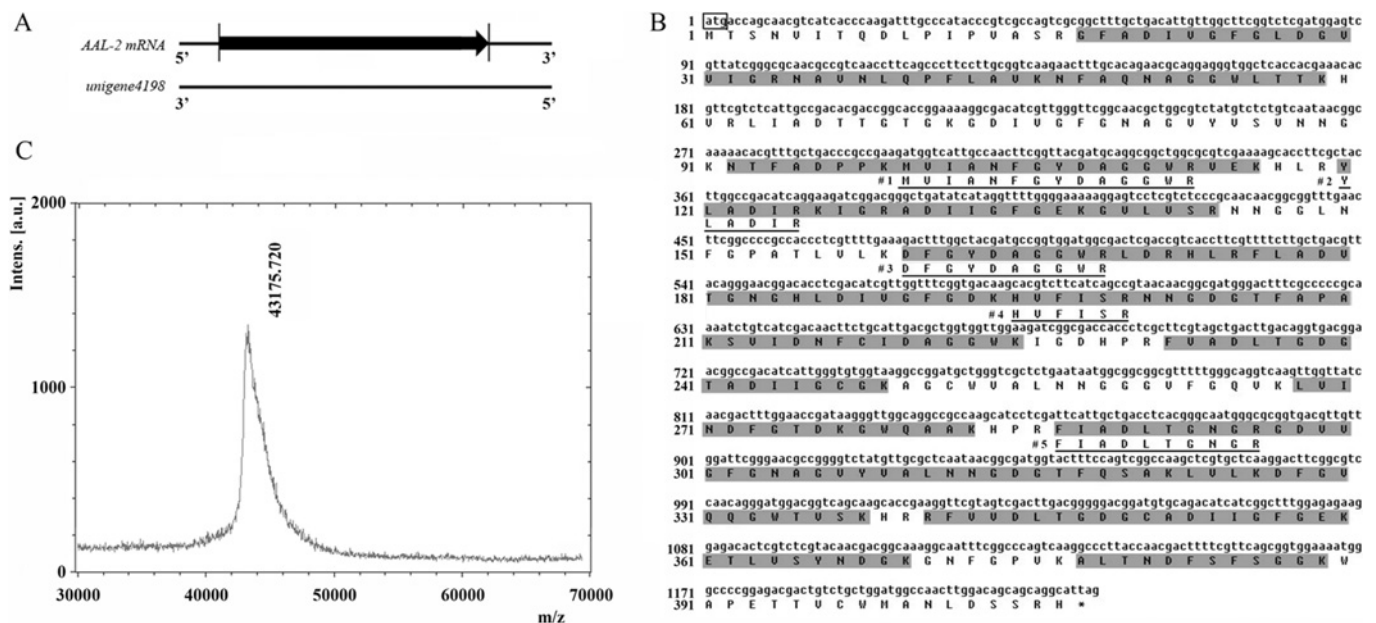
H22 cells ( $10^7$ ) in 100  $\mu$ l of PBS were subcutaneously injected into the right flank of BALB/c mice. At days 7, 9, 11, 13, 15, 17 and 19 after tumour inoculation, mice were injected at the tumour site with 5 mg of AAL-2/kg in 100  $\mu$ l of PBS or diluent control.



**Figure 1** Purification of AAL-2 and the amino acid sequences of tryptic peptides identified by MS

(A) Crude extract was applied to a GlcNAc monomer-coupled epoxy-activated Sepharose 6B column (1 cm × 10 cm) and equilibrated with TBS (pH 7.2). After washing with TBS, AAL-2 was eluted with TBS containing 0.2 M GlcNAc (indicated by the arrow). The plot was generated by ÄKTApriime (GE Healthcare). (B) SDS/polyacrylamide gel of AAL-2 was stained with Coomassie Brilliant Blue. Molecular masses are indicated in kDa. (C) Amino acid sequence data for AAL-2. The five tryptic peptides identified by MS/MS are shown.

Tumour volume (V) was determined by caliper measurements ( $V = L \times W^2/2$ ), where L is length and W is width.



**Figure 2** Identification of AAL-2 coding sequence

(A) The AAL-2 coding sequence is located on the complementary strand of UniGene 4198. (B) The AAL-2 coding sequence consists of 1224 bp, which is computationally translated into 407 amino acids. The deduced amino acid sequence is shown under the AAL-2 coding sequence, and the five tryptic peptides (underlined) of AAL-2 identified by MS are aligned under the deduced amino acid sequence. MALDI-TOF/TOF analysis revealed 69% sequence coverage of the full-length AAL-2 (grey box). The initiation codon ATG is boxed and the stop codon tag is marked with an asterisk. (C) Determination of AAL-2 molecular mass by MALDI-TOF-MS to be 43175.72 Da. Intens., intensity (in arbitrary units, a.u.).

## Statistical analysis

The two-sample Student's *t* test was used for comparisons between groups. Statistical analysis was performed with GraphPad Prism 5 software. Results are means ± S.E.M., and statistical significance was defined as  $P < 0.05$ .

## RESULTS

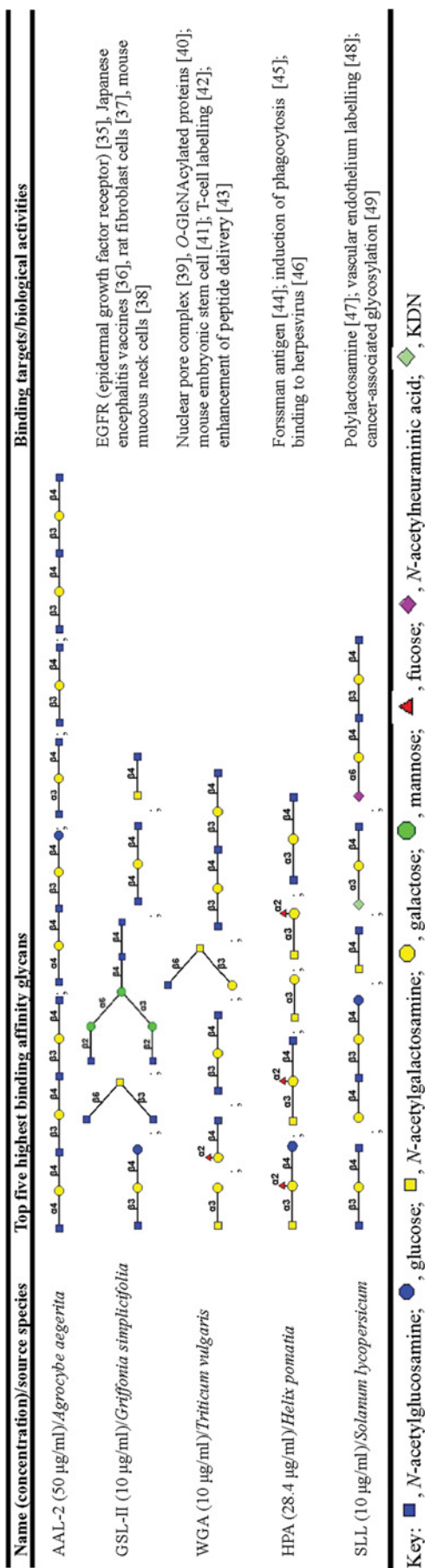
### Purification of AAL-2 and the determination of the amino acid sequences from AAL-2 tryptic peptides

Total crude proteins were extracted from dried *A. aegerita* fruiting bodies by water-extraction, 40–80% ammonium sulfate precipitation and dialysis against TBS. The total crude proteins were loaded on to the GlcNAc-coupled Sepharose 6B column and eluted with 0.2 M GlcNAc after extensive TBS washing (Figure 1A). A total fraction of 6 ml of eluate (48–54 ml) was collected. Representative purification fractions from the affinity chromatographic column were separated by SDS/PAGE in the presence of 2-mercaptoethanol. The eluate fraction yielded a single band (approximately 43 kDa) and was named AAL-2 (Figure 1B). AAL-2 was characterized further using *de novo* sequencing by MS/MS (tandem MS), and five tryptic peptides were identified (Figure 1C). The five peptide sequences were analysed further by BLASTP at NCBI (<http://www.ncbi.nlm.nih.gov/BLAST>), and only two peptides (labelled #1 and #3) showed homology with the GlcNAc-binding lectin PVL (*Psathyrella velutina* lectin) [27] (results not shown).

### Identification of the AAL-2 coding sequence

To determine the coding sequence of AAL-2, the *A. aegerita* transcriptome was sequenced. Raw Illumina sequencing data of the *A. aegerita* transcriptome was deposited in the Sequence





**Figure 5** Comparison of carbohydrate-binding specificity of AAL-2 with other GlcNAc-binding lectins

The lectin carbohydrate specificities are as summarized from the Consortium for Functional Glycomics (<http://functionalglycomics.org>). See also [35–49].

the glycan-binding profile of AAL-2, glycan array analysis was performed by testing the binding affinity of AAL-2 to 465 glycan candidates. The glycan array was performed at different concentrations (0.1, 1, 50 and 200 µg/ml) of AAL-2, and the binding glycans with more than 5000 RFU were listed according to the glycan-binding profile of AAL-2 at 200 µg/ml (Supplementary Table S1 at <http://www.BiochemJ.org/bj/443/bj4430369add.htm>). The results showed that the binding selectivity changed little with a wide concentration range (Figure 4A, lower panel). Almost all of the top 30 glycans in the binding profiles possessed terminal non-reducing GlcNAc (Figure 4A, upper panel, and Supplementary Figure S1 at <http://www.BiochemJ.org/bj/443/bj4430369add.htm>). In addition, Gal (galactose)–GlcNAc [LacNAc (*N*-acetyl-lactosamine)] linked behind would increase the binding affinity to the terminal GlcNAc, and the glycan GlcNAc-(LacNAc)<sub>3</sub> exhibited the highest binding affinity among the 465 glycan candidates (Figure 4A, upper panel). However, (LacNAc)<sub>3</sub>, with the absence of the terminal GlcNAc compared with GlcNAc-(LacNAc)<sub>3</sub>, showed significantly low binding affinity. In comparison with other GlcNAc-binding lectins (Figure 5), AAL-2 performed better than the well-known GlcNAc-binding lectins WGA and GSL-II, which have been used widely in glycan studies for their high GlcNAc-binding selectivity. Therefore AAL-2 can be defined as a lectin with high binding selectivity to glycans with non-reducing GlcNAc termini and has potential in GlcNAc-related glycan or glycoconjugate analysis.

ITC was also performed in order to thermodynamically characterize the GlcNAc and AAL-2 interactions. Figure 4(B) (upper panel) shows the raw ITC curve resulting from the injection of GlcNAc into a solution of AAL-2. The titration curve showed that GlcNAc binding to AAL-2 was exothermic, resulting in negative peaks in the plots of power against time. Figure 4(B) (lower panel) shows the plot of the heat evolved per mol of GlcNAc added, with the heat of GlcNAc dilution subtracted. Our calorimetric data were fitted to a sequential binding model, and the thermodynamic parameters for the binding of GlcNAc to AAL-2 are summarized in Table 1. The values of  $K_{d1}$  and  $K_{d2}$  are 195 and 459 µM respectively, which indicates that GlcNAc bound to AAL-2 with moderate binding affinity.

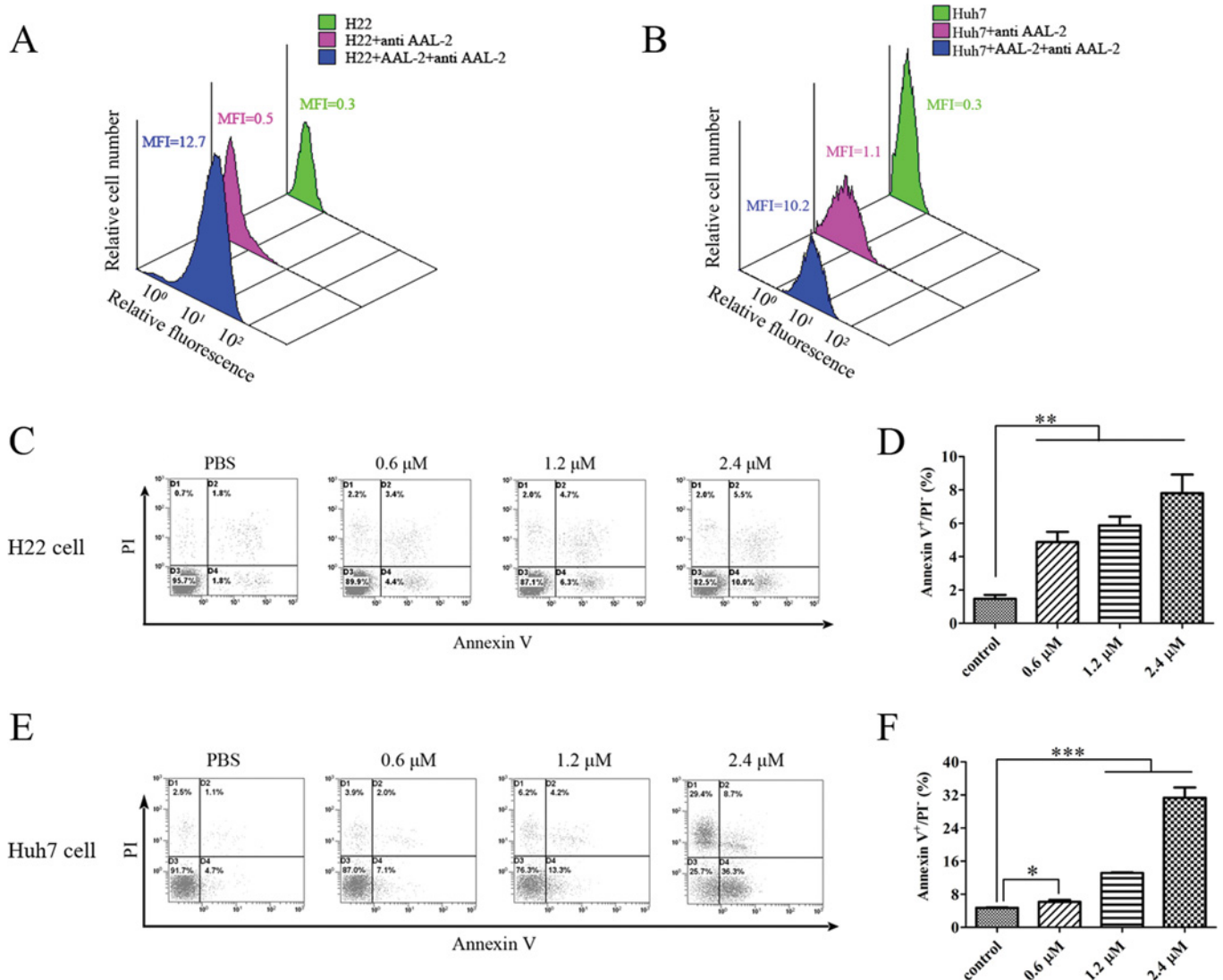
#### AAL-2 can induce apoptosis in hepatoma cells *in vitro*

AAL-2 could bind to H22 and Huh7 hepatoma cells (Figures 6A and 6B) and induce apoptosis of H22 cells and Huh7 cells *in vitro*.

**Table 1** Thermodynamic parameters for the binding of AAL-2 to GlcNAc as determined by ITC

Thermodynamic parameters,  $K_d$  and  $\Delta_b H_m^0$ , were determined by using the sequential binding sites model. The standard molar binding free energy ( $\Delta_b G_m^0$ ) and the standard molar binding entropy ( $\Delta_b S_m^0$ ) for the binding reaction were calculated using eqns (1) and (2) respectively. The buffer used in the assay was PBS (pH 7.2), ITC measurements was performed at 25 °C. Results are means  $\pm$  S.E.M. 1 cal = 4.184 J.

Thermodynamic parameter (unit)	Value
$K_{d1}$ ( $10^3$ M <sup>-1</sup> )	5.13 $\pm$ 0.36
$K_{d2}$ ( $10^3$ M <sup>-1</sup> )	2.18 $\pm$ 0.06
$K_{d1}$ (µM)	194.93 $\pm$ 70.16
$K_{d2}$ (µM)	458.72 $\pm$ 27.52
$\Delta_b H_{m1}^0$ (kcal · mol <sup>-1</sup> )	-32.22 $\pm$ 1.91
$\Delta_b H_{m2}^0$ (kcal · mol <sup>-1</sup> )	-31.69 $\pm$ 2.24
$\Delta_b G_{m1}^0$ (kcal · mol <sup>-1</sup> )	-5.06 $\pm$ 0.21
$\Delta_b G_{m2}^0$ (kcal · mol <sup>-1</sup> )	-4.56 $\pm$ 0.04
$\Delta_b S_{m1}^0$ (cal · mol <sup>-1</sup> · K <sup>-1</sup> )	-91.08 $\pm$ 1.92
$\Delta_b S_{m2}^0$ (cal · mol <sup>-1</sup> · K <sup>-1</sup> )	-91.01 $\pm$ 2.24



**Figure 6** AAL-2 induces apoptosis in hepatoma cells *in vitro*

AAL-2 could bind to H22 (A) and Huh7 (B) hepatoma cells. H22 cells and Huh7 cells were untreated (green histograms), incubated with the anti-AAL-2 antibody alone (pink histograms), or with both AAL-2 and anti-AAL-2 antibody (blue histograms), and analysed by flow cytometry. The mean fluorescence intensity (MFI) values of the different incubation conditions are indicated in each histogram. Apoptotic H22 (C) and Huh7 (E) cells were detected by Annexin V/PI staining after 24 and 36 h of incubation respectively with different concentrations of AAL-2. The percentages of pro-apoptotic H22 cells (D) and Huh7 cells (F) gated on Annexin V<sup>+</sup>/PI<sup>-</sup> were calculated. Results are means  $\pm$  S.E.M. ( $n = 3$ ); \* $P < 0.05$ , \*\* $P < 0.01$ , \*\*\* $P < 0.001$ .

The amount of apoptosis of H22 cells was 1.8% after 24 h of culture, and increased significantly to 4.4%, 6.3% and 10% at final concentrations of 0.6, 1.2 and 2.4  $\mu$ M respectively (Figures 6C and 6D). Similarly, the proportion of apoptotic Huh7 cells was 4.7%, and increased to 7.1%, 13.3% and 36.3% when treated with AAL-2 at final concentrations of 0.6, 1.2 and 2.4  $\mu$ M respectively for 36 h (Figures 6E and 6F). The results indicate that AAL-2 induced cell apoptosis in a concentration-dependent manner.

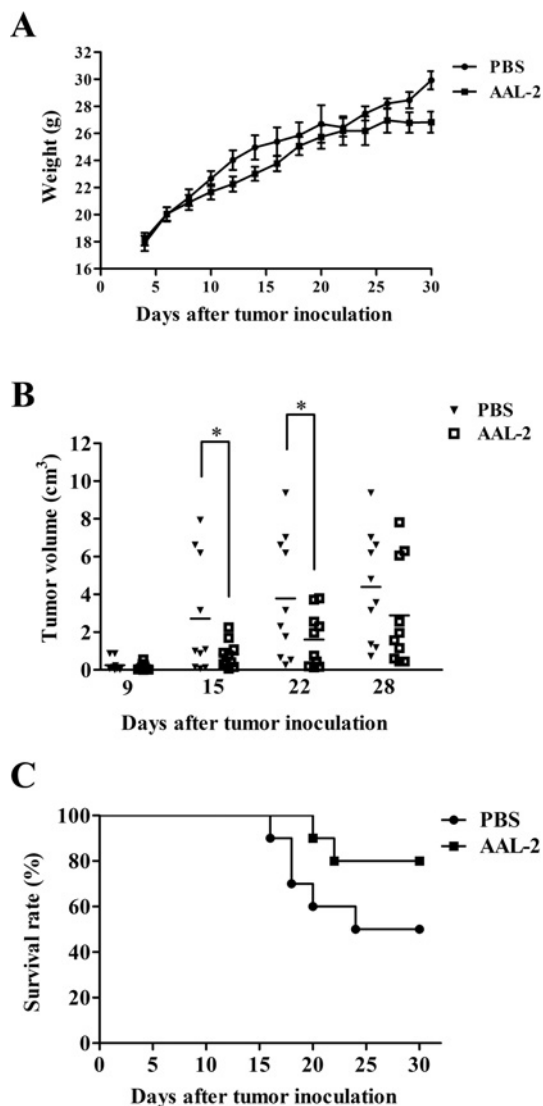
#### AAL-2 can inhibit hepatoma growth and extend the survival time of tumour-bearing mice *in vivo*

The anti-hepatoma activity of AAL-2 was investigated further by using a mouse model of H22 hepatocellular carcinoma. Mice treated with AAL-2 showed a significant reduction in tumour volume (Figure 7B), whereas body weight remained unaltered (Figure 7A) compared with control mice treated with PBS. In

addition, AAL-2 treatment was able to extend the survival time of tumour-bearing mice (Figure 7C). Overall, we conclude that AAL-2 has anti-hepatoma activity by inhibiting hepatocellular carcinoma growth and can extend survival times of tumour-bearing mice.

#### DISCUSSION

*A. aegerita* is one of the most cultivated mushrooms in China, and has been highly valued as a functional food for its anti-tumour and nutritional benefits [28]. We have previously purified AAL (*A. aegerita* lectin) from *A. aegerita*, which showed extensive anti-tumour activity owing to specific binding to the Thomsen-Friedenreich disaccharide tumour antigen and subsequently resulted in tumour cell apoptosis [29,30]. In the present study, a novel fungal lectin AAL-2 was purified from *A. aegerita* by using one-step affinity chromatography. AAL-2 showed high binding



**Figure 7** AAL-2 inhibits hepatocellular carcinoma growth and prolongs survival time of tumour-bearing mice *in vivo*

A total of  $10^7$  H22 cells were injected subcutaneously into the right flank of BALB/c mice. On days 7, 9, 11, 13, 15, 17 and 19 after tumour inoculation, mice were injected at the tumour site with 5 mg of AAL-2/kg in 100  $\mu$ l of PBS or diluent control. Tumour-bearing mice treated with AAL-2 and PBS were monitored for changes in body weight (**A**), tumour growth (**B**) and survival time (**C**). Results are means  $\pm$  S.D. ( $n=10$ ); \* $P < 0.05$ .

selectivity to glycans with a non-reducing GlcNAc terminus, and the binding affinity increased when one or more LacNAc disaccharides were linked to the terminal GlcNAc via  $\alpha$ 1-3,  $\alpha$ 1-4 or  $\beta$ 1-3,  $\beta$ 1-4 linkages to form a GlcNAc-(LacNAc)<sub>1-3</sub> structure, implying that the addition of a LacNAc could increase the binding affinity to terminal GlcNAc (Supplementary Table S1). The glycan GlcNAc-(LacNAc)<sub>3</sub> represented the highest binding affinity among the 465 candidates; however, the high binding affinity would be lost if the terminal GlcNAc was removed. In addition, the binding selectivity changed little at a wide concentration range of AAL-2, indicating that the glycan-binding activity of AAL-2 was highly selective, low noise and was not affected by the high concentration (200  $\mu$ g/ml) (Figure 4A, lower panel).

Our glycan array analysis revealed that AAL-2 bound to terminal GlcNAc with high selectivity. We then compared

further the glycan-binding specificity of AAL-2 with that of other GlcNAc-binding lectins: PVL, BLL (*Boletopsis leucomelas* lectin), GSL-II, WGA, HPA and SLL. The GlcNAc-binding specificity of PVL was determined by affinity chromatography, and PVL was shown to have preferential binding to oligosaccharides bearing non-reducing terminal  $\beta$ -GlcNAc linked 1-6 or 1-3, but poor affinity for 1-4 linkages [27], whereas AAL-2 bound preferentially to oligosaccharides bearing a non-reducing terminal  $\beta$ -GlcNAc linked via a 1-4 or 1-3, rather than a 1-6, linkage. The unique structure of carbohydrate-binding domains might contribute to the binding preference of AAL-2 to terminal  $\beta$ -GlcNAc-linked oligosaccharides; our future studies will focus on the analysis of the carbohydrate-lectin interactions via crystallization of the AAL-2 and GlcNAc complex. The GlcNAc-binding specificity of BLL was determined by frontal affinity chromatography, and BLL was shown to have high binding affinity for mono-, bi- and tri-antennary agalactosylated glycans [31], whereas AAL-2 showed high binding affinity for mono-terminal non-reducing GlcNAc residues. Other GlcNAc-binding lectins, i.e. GSL-II, WGA, HPA and SLL, with their top five highest binding glycans from the glycan array data are listed in Figure 5. The comparative analysis showed that AAL-2 and GSL-II had the highest binding selectivity for terminal GlcNAc, whereas AAL-2 showed even higher binding selectivity than did GSL-II, a well known and widely studied lectin for the recognition of terminal GlcNAc residues. Moreover, AAL-2 binds to glycans in a metal-ion-independent manner, whereas  $Ca^{2+}$  is required for GSL-II-binding activity (results not shown). The binding activity of AAL-2 was stable under 70°C and within the pH range 6.0–11.0 (Supplementary Figure S2 at <http://www.BiochemJ.org/bj/443/bj4430369add.htm>). We compared further the amino acid sequences of AAL-2, GSL-II, WGA and HPA. Surprisingly, amino acid sequences of these GlcNAc-binding lectins showed low similarity to each other, although they shared similar glycan-binding properties (Supplementary Figure S3 at <http://www.BiochemJ.org/bj/443/bj4430369add.htm>). AAL-2, although newly discovered, has the potential to be utilized as a molecular probe to detect terminal GlcNAc sugars with high binding selectivity in glycan analysis.

Polylectosamine has been reported to be present on the immune co-stimulatory molecules CD28 and CD19. In a previous study [32], B-cells, T-cells and macrophages in the absence of polylectosamines were found to be hypersensitive to stimulation, and SLL was used in the detection of the polylectosamines with at least three lactosamine unit repeats [(LacNAc)<sub>n>3</sub>] [32]. By using glycan arrays to detect the binding profile of lectins, SLL showed high binding selectivity for Neu5Ac (*N*-acetylneuraminic acid)/Fuc (fucose)-(LacNAc)<sub>3</sub> and (LacNAc)<sub>3</sub> (Consortium for Functional Glycomics database: [primscreen\\_PA\\_v2\\_711\\_09262005](http://primscreen_PA_v2_711_09262005)). In the present study, the glycan array data showed that AAL-2 bound to GlcNAc-(LacNAc)<sub>3</sub> with the highest affinity among the 465 glycan candidates, indicating that AAL-2 recognized polylectosamine (LacNAc)<sub>3</sub> with a terminal GlcNAc modification. Overall, the results imply that AAL-2 and SLL would form pairs of complementary probes to monitor changes and modifications of polylectosamine.

GlcNAc has been reported to be aberrantly expressed in several carcinomas, resulting in increased levels and abnormal types of GlcNAc on the cell surface [33,34]. The present study suggests that AAL-2, with high binding selectivity to GlcNAc, could bind to hepatoma cells and induce cell apoptosis. This binding property probably endowed AAL-2 with binding priority to those tumour cells, therefore leading to its potential applications for cancer diagnosis.



## AUTHOR CONTRIBUTION

Shuai Jiang, Yi Liang and Hui Sun designed the study. Yijie Chen, Man Wang, Yalin Yin, Yongfu Pan and Bianli Gu carried out the research. Guojun Yu and Yamu Li analysed data. Shuai Jiang, Barry Wong and Hui Sun wrote the paper.

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## SUPPLEMENTARY ONLINE DATA

# A novel lectin from *Agrocybe aegerita* shows high binding selectivity for terminal *N*-acetylglucosamine

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**Table S1 Carbohydrate-binding profiles of AAL-2 determined by glycan array analysis**

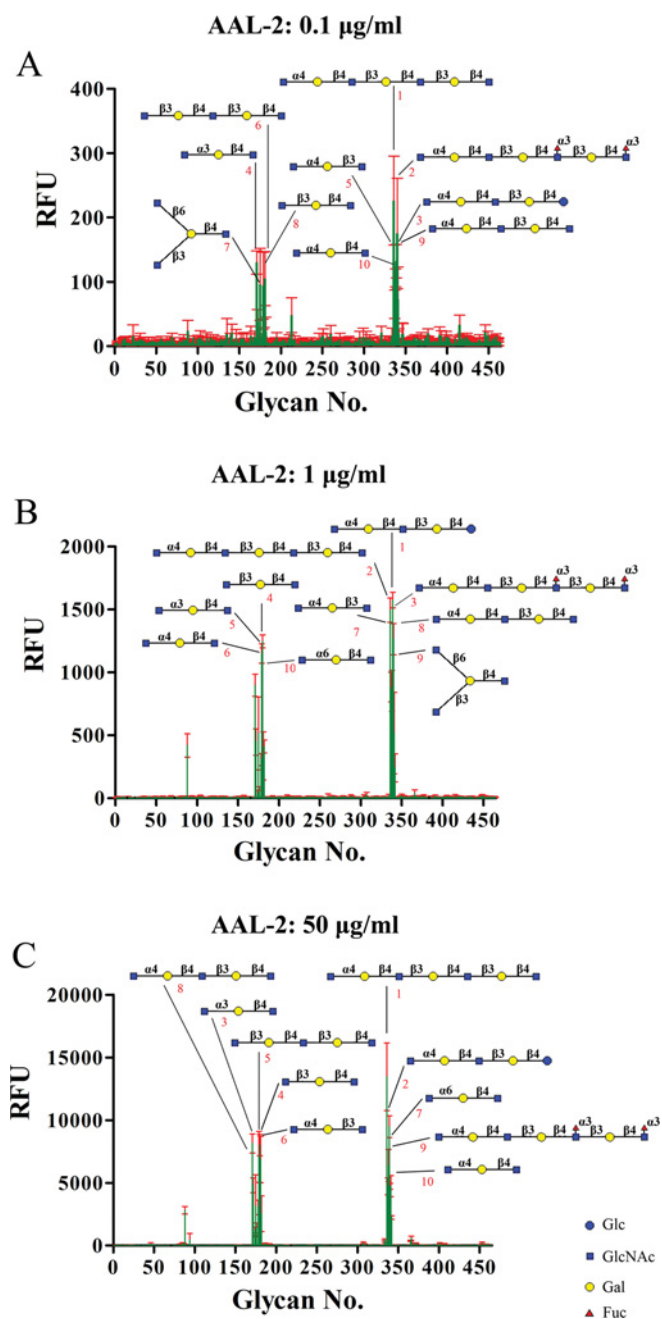
The Table lists the glycans present on the glycan array (Consortium for Functional Glycomics). The carbohydrate-binding profiles of AAL-2 at different concentrations (0.1, 1, 50 and 200  $\mu\text{g/ml}$ ) are shown. The glycans binding with more than 5000 RFU are listed according to the glycan-binding profile of AAL-2 at 200  $\mu\text{g/ml}$ . Average RFU represents the degree of binding of fluorescently labelled streptavidin to biotin-labelled AAL-2.

Order	Glycan number	Glycan structure	Average RFU for AAL-2 at			
			200 $\mu\text{g/ml}$	50 $\mu\text{g/ml}$	1 $\mu\text{g/ml}$	0.1 $\mu\text{g/ml}$
1	336	GlcNAc $\alpha$ 1-4Gal $\beta$ 1-4GlcNAc $\beta$ 1-3Gal $\beta$ 1-4GlcNAc $\beta$ 1-3Gal $\beta$ 1-4GlcNAc $\beta$ -Sp0	30519	13453	1496	226
2	171	GlcNAc $\alpha$ 1-3Gal $\beta$ 1-4GlcNAc $\beta$ -Sp8	24487	8139	898	130
3	175	GlcNAc $\beta$ 1-3(GlcNAc $\beta$ 1-6)Gal $\beta$ 1-4GlcNAc $\beta$ -Sp8	21115	3163	515	96
4	339	GlcNAc $\alpha$ 1-4Gal $\beta$ 1-4GlcNAc $\beta$ 1-3Gal $\beta$ 1-4Glc $\beta$ -Sp0	20868	9469	1575	132
5	179	GlcNAc $\beta$ 1-3Gal $\beta$ 1-4GlcNAc $\beta$ -Sp0	19530	7071	1151	94
6	172	GlcNAc $\alpha$ 1-6Gal $\beta$ 1-4GlcNAc $\beta$ -Sp8	19311	4796	447	38
7	337	GlcNAc $\alpha$ 1-4Gal $\beta$ 1-4GlcNAc $\beta$ -Sp0	19030	4716	883	65
8	181	GlcNAc $\beta$ 1-3Gal $\beta$ 1-4GlcNAc $\beta$ 1-3Gal $\beta$ 1-4GlcNAc $\beta$ -Sp0	18737	6858	336	105
9	180	GlcNAc $\beta$ 1-3Gal $\beta$ 1-4GlcNAc $\beta$ -Sp8	17289	8012	1247	20
10	338	GlcNAc $\alpha$ 1-4Gal $\beta$ 1-3GlcNAc $\beta$ -Sp0	16141	6376	853	106
11	341	GlcNAc $\alpha$ 1-4Gal $\beta$ 1-4GlcNAc $\beta$ 1-3Gal $\beta$ 1-4GlcNAc $\beta$ -Sp0	11672	4732	518	73
12	308	GlcNAc $\beta$ 1-4GlcNAc $\beta$ -Sp10	11572	93	6	5
13	94	GalNAc $\beta$ 1-3GalNAc $\alpha$ -Sp8	11198	450	11	5
14	340	GlcNAc $\alpha$ 1-4Gal $\beta$ 1-4GlcNAc $\beta$ 1-3Gal $\beta$ 1-4(Fuc $\alpha$ 1-3)GlcNAc $\beta$ 1-3Gal $\beta$ 1-4(Fuc $\alpha$ 1-3)GlcNAc $\beta$ -Sp0	8758	4730	1265	175
15	88	GlcNAc $\beta$ 1-3Gal $\beta$ 1-3GalNAc $\alpha$ -Sp8	8504	2809	420	24
16	182	GlcNAc $\beta$ 1-3Gal $\beta$ 1-4Glc $\beta$ -Sp0	8464	2539	411	23
17	178	GlcNAc $\beta$ 1-3Gal $\beta$ -Sp8	7339	3033	307	19
18	407	GlcNAc $\beta$ 1-6(GlcNAc $\beta$ 1-3)GalNAc $\alpha$ -Sp14	6992	108	9	4
19	309	GlcNAc $\beta$ 1-4GlcNAc $\beta$ -Sp12	6078	26	6	3
20	176	GlcNAc $\beta$ 1-3GalNAc $\alpha$ -Sp8	5896	1395	49	7
21	177	GlcNAc $\beta$ 1-3GalNAc $\alpha$ -Sp14	5782	7	7	8
22	190	GlcNAc $\beta$ 1-6GalNAc $\alpha$ -Sp8	5571	31	7	5
23	17	GlcNAc $\beta$ -Sp8	5331	11	4	5
24	174	GlcNAc $\beta$ 1-3(GlcNAc $\beta$ 1-6)GalNAc $\alpha$ -Sp8	5309	1136	36	10

The nucleotide sequence data for *Agrocybe aegerita* lectin 2 will appear in the GenBank®, EMBL, DDBJ and GSDB Nucleotide Sequence Databases under accession number JN001164.

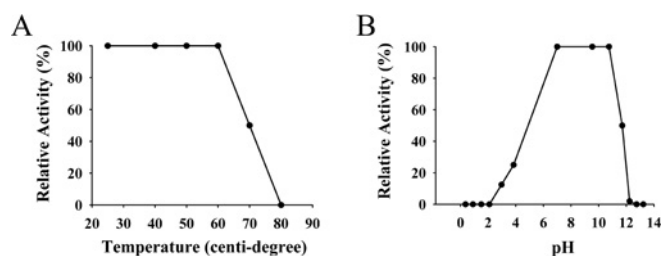
The glycan array data of AAL-2 were deposited in the Consortium for Functional Glycomics database with the labels primscreen\_3312–primscreen\_3315.

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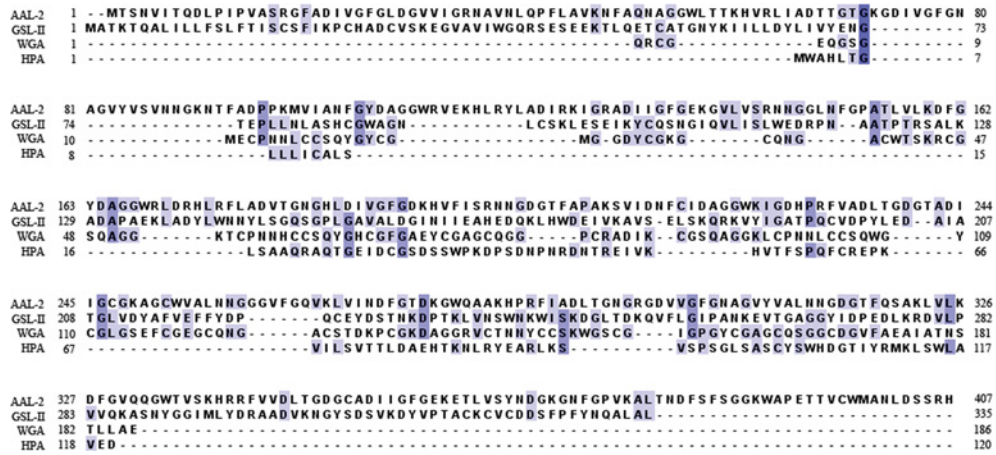
**Figure S1 Assessment of AAL-2-binding selectivity by glycan array**

A total of 465 glycans were assessed on the array (version 4.1 of the Consortium for Functional Glycomics), and our results showed the top ten binding specific glycans of AAL-2 at 0.1 (A), 1 (B) and 50 (C) µg/ml. Results are means  $\pm$  S.E.M. The entire glycan array version is available at <http://www.functionalglycomics.org/static/consortium/resources/resourcecoreh14.shtml>.



**Figure S2 Effects of temperature and pH on the haemagglutination activity of AAL-2**

The haemagglutination activity of AAL-2 was tested after treatment at different temperatures (A) (centi-degree = °C) and pH (B).



**Figure S3 Comparison of the AAL-2 amino acid sequence with other GlcNAc-binding lectins**

The AAL-2 amino acid sequence was aligned with GSL-II, WGA and HPA sequences. The background colour denotes similarity between the sequences, with the darker the shade meaning the stronger similarity.

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