Recombinant *Aspergillus* β -galactosidases as a robust glycomic and biotechnological tool

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Supplemental Tables

Supplemental Table S1. Influence of galactose and glucose on enzymatic activity.

Activity of recombinant *Aspergillus* galactosidases and non-recombinant *A. oryzae* galactosidase (*) in the presence of different concentrations of galactose and glucose. For each enzyme, the activities at various conditions are shown in relation to the maximal activity measured for that enzyme. Average values (% activity) +/- standard error are shown.

galactose [mM]	A. niger rlacA	A. nidulans rlacA	A. nidulans rlacB	A.oryzae*	
0	<u>100 +/- 0.0</u>	58.9 +/- 0.1	<u>100 +/- 0.5</u>	<u>100 +/- 2.6</u>	
0.95	90.3 +/- 1.5	<u>100 +/- 0.1</u>	71.9 +/- 4.2	30.4 +/- 5.4	
4.75	65.8 +/- 1.7	92.2 +/- 3.4	33.7 +/- 2.7	23.8 +/- 1.2	
9.5	47.9 +/- 0.3	39.7 +/- 4.8	24.8 +/- 2.7	23.4 +/- 4.6	
47.5	15.9 +/- 0.2	34.6 +/- 5.9	4.6 +/-0.7	12.5 +/- 3.0	
95	5.1 +/- 0.2	16.6 +/- 0.2	2.6 +/-0.3	8.9 +/- 1.7 2.5 +/- 1.4	
475	2.5 +/- 0.1	4.14 +/- 0.0	0.2 +/- 0.1		
950	1.0 +/- 0.3	1.72 +/- 0.3	0.2 +/- 0.5	0.3 +/- 0.0	
glucose [mM]	A. niger rlacA	A. nidulans rlacA	A. nidulans rlacB	A.oryzae*	
glucose [mM] 0	A. niger rlacA 82.2 +/- 7.3	A. nidulans rlacA 45.3 +/- 1.7	A. nidulans rlacB 79.6 +/- 5.9	A.oryzae* 62.6 +/- 5.3	
glucose [mM] 0 9.5	A. niger rlacA 82.2 +/- 7.3 90.2 +/- 5.2	A. nidulans rlacA 45.3 +/- 1.7 51.7 +/- 1.0	A. nidulans rlacB 79.6 +/- 5.9 80.1 +/- 0.3	A.oryzae* 62.6 +/- 5.3 67.5 +/- 2.9	
glucose [mM] 0 9.5 23.75	A. niger rlacA 82.2 +/- 7.3 90.2 +/- 5.2 96.5 +/-5.3	A. nidulans rlacA 45.3 +/- 1.7 51.7 +/- 1.0 51.2 +/- 3.4	<i>A. nidulans</i> rlacB 79.6 +/- 5.9 80.1 +/- 0.3 97.1 +/- 10.4	A.oryzae* 62.6 +/- 5.3 67.5 +/- 2.9 70.0 +/- 5.5	
glucose [mM] 0 9.5 23.75 47.5	A. niger rlacA 82.2 +/- 7.3 90.2 +/- 5.2 96.5 +/-5.3 91.6 +/- 3.1	A. nidulans rlacA 45.3 +/- 1.7 51.7 +/- 1.0 51.2 +/- 3.4 57.3 +/- 1.8	A. nidulans rlacB 79.6 +/- 5.9 80.1 +/- 0.3 97.1 +/- 10.4 97.7 +/- 3.1	A.oryzae* 62.6 +/- 5.3 67.5 +/- 2.9 70.0 +/- 5.5 77.7 +/- 1.5	
glucose [mM] 0 9.5 23.75 47.5 95	A. niger rlacA 82.2 +/- 7.3 90.2 +/- 5.2 96.5 +/-5.3 91.6 +/- 3.1 99.2 +/- 0.5	A. nidulans rlacA 45.3 +/- 1.7 51.7 +/- 1.0 51.2 +/- 3.4 57.3 +/- 1.8 71.4 +/- 3.4	<i>A. nidulans</i> rlacB 79.6 +/- 5.9 80.1 +/- 0.3 97.1 +/- 10.4 97.7 +/- 3.1 99.1 +/- 13.3	A.oryzae* 62.6 +/- 5.3 67.5 +/- 2.9 70.0 +/- 5.5 77.7 +/- 1.5 86.9 +/- 5.1	
glucose [mM] 0 9.5 23.75 47.5 95 190	A. niger rlacA 82.2 +/- 7.3 90.2 +/- 5.2 96.5 +/-5.3 91.6 +/- 3.1 99.2 +/- 0.5 100.0 +/- 1.3	A. nidulans rlacA 45.3 +/- 1.7 51.7 +/- 1.0 51.2 +/- 3.4 57.3 +/- 1.8 71.4 +/- 3.4 93.0 +/- 2.8	A. nidulans rlacB 79.6 +/- 5.9 80.1 +/- 0.3 97.1 +/- 10.4 97.7 +/- 3.1 99.1 +/- 13.3 100.0 +/- 8.5	A.oryzae* 62.6 +/- 5.3 67.5 +/- 2.9 70.0 +/- 5.5 77.7 +/- 1.5 86.9 +/- 5.1 100.0 +/- 10.1	
glucose [mM] 0 9.5 23.75 47.5 95 190 950	A. niger rlacA 82.2 +/- 7.3 90.2 +/- 5.2 96.5 +/-5.3 91.6 +/- 3.1 99.2 +/- 0.5 <u>100.0 +/- 1.3</u> 90.8 +/- 3.2	A. nidulans rlacA 45.3 +/- 1.7 51.7 +/- 1.0 51.2 +/- 3.4 57.3 +/- 1.8 71.4 +/- 3.4 93.0 +/- 2.8 100 +/- 6.6	<i>A. nidulans</i> rlacB 79.6 +/- 5.9 80.1 +/- 0.3 97.1 +/- 10.4 97.7 +/- 3.1 99.1 +/- 13.3 <u>100.0 +/- 8.5</u> 82.2 +/- 8.2	A.oryzae* 62.6 +/- 5.3 67.5 +/- 2.9 70.0 +/- 5.5 77.7 +/- 1.5 86.9 +/- 5.1 <u>100.0 +/- 10.1</u> 88.1 +/- 13.0	

Supplemental Table S2. β -1,3 activity using lacto-*N*-tetraose as substrate.

Ratio of β -1,3 activity and β -1,4 activity after 2, 24 and 48h is shown. For *A. niger* and *A. nidulans* rlacA, values after 24 and 48h (marked with an asterisk) overestimate the activity as almost complete conversion of lacto-*N*-neotetraose (β -1,4 substrate) already occurred after 2h (see Figure 4 in the main manuscript).

Ratio of β -1,3 activity vs β -1,4 activity after [h] of incubation	2	24	48	
A. niger rlacA	0.027	0.242*	0.616* 0.979*	
A. nidulans rlacA	0.043	0.429*		
A. nidulans rlacB	0.005	0.195	0.280	
A. oryzae galactosidase	0.019	0.081	0.429	

Supplemental Figures



Supplemental Fig. S1 Sequence alignment of the three recombinant galactosidases

The sequences used in the current study are depicted. Conserved sequence motifs (yellow, green, orange, grey, light blue) and C-terminal myc (red) and HIS tags (dark blue) are highlighted.

A A. niger rlacA

	1	F TWI	SRPSRI	GTASIK	HRIN	GFTL TEHSDP	AKRELLQKY	7 TWDDKSLFIN	GERIMIFSGE	FHPFRLPVKE	LQLDIFQKVK
	81	ALGI	NCVSFY	VDWALVI	EGKP	GEYRADGIFD	LEPFFDAASH	E AGIYLLARPG	PYINAESSGG	GFPGWLQRVN	GTLRSSDKAY
	161	LDA	rdnyvsh	VAATIA	K YQI	TNGGPIILYC	PENEYTSGCO	C GVEFPDPVYM	QYVEDQAR <mark>NA</mark>	GVVIPLINND	ASASGNNAPG
	241	TGK	AVDIYG	HDSYPL	GFDC .	A <mark>NP T</mark> VWP SGD	LPTNFRTLHI	. EQSPTTPYAI	VEFQGGSYDP	WGGPGFAACS	$\texttt{Ellnnefe}_{\underline{R}}\texttt{V}$
	321	FYKI	NDFSFQI	AIMNLY	MIFG	GTNWGNLGYF	NGYTSYDYG	5 AVTES <mark>RNIT</mark> R	EKYSELKLLG	NFAKVSPGYL	TASPG <mark>NLT</mark> TS
	401	GYAI	TTDLTV	TPLLG <mark>N</mark>	<mark>ST</mark> GS	FFVV <u>R</u> HSD¥S	SEESTSYKLI	LPTSAGSVTI	PQLGGTLTLN	GR DSKIHVTD	Y <mark>NVS</mark> GTNIIY
	481	STAI	EVFTW <u>K</u> K	FADGEVI	LVLY	GGAGEHHELA	ISTKSNVTV:	I EGSESGISS <u>k</u>	QTSSSVVVGW	DVSTTRRIIQ	VGDLKILLLD
	561	RNS.	AANAMAb	QLATDG	TSPG	FSTPEKVASS	IIVKAGYLVI	R TAYLKGSGLY	LTADF <mark>NAT</mark> TS	VEVIGVPSTA	KNLFINGDKT
	641	SHT	D <u>K</u> NGIW	SATVDY	NAPD	ISLPSLKDLD	WEYVDTLPE	C QSSYDDSLWP	AADLKQTKNT	LRSLTTPTSL	YSSDYGFHTG
	721	YLL	RGHFTA	. TG <mark>NES</mark> TI	FAID	TQGGSAFGSS	VWL <mark>NGT</mark> YLG:	5 WTGLYANSDY	NATYNLPQLQ	AGKTYVITVV	IDNMGLEE <mark>NW</mark>
	801	TVGI	EDLMKTP	RGILNFI	LLAG	RPSSAISWK	TGNLGGEDYI	DKVRGPLNEG	GLYAERQGFH	ÖDEDD 2 ÖNM K	SSSPLEGLSE
	881	AGIO	GFYSASF	DLDLPK	GWDV	PLFLNIG <mark>NST</mark>	TPSPYRVQV	A ANGAÔAWKAI	SNIGPQTSFP	VPEGILNYRG	TNWLAVTLWA
	961	LDS	ICCKLES	LELSYT	TPVL	TALGEVESVD	QPKYKKRKG	A YAAASFLEQK	LISEEDLNSA	VDHHHHHH	
B	A	. n	idulai	ns rla	cА						
	1	ĘV	al th <u>k</u> ln	IG FTITER	HPDAE	KR ellQk yv	r wod <u>k</u> slfin	G ER <mark>IMIFGAEI</mark>	HPWRLPVPSL	WRDILQKVKA	LGFNCVSFYV
	81	DW	ALLEGKP	G EYRAE	GSFAU	EPFFDAASD	L GIYLIARPG	P YINAEASGGG	FPGWLQR <mark>LNG</mark>	TIRSSDQSYL	DATENYVSHI
	16	1 GG	L TAK YQI	T NGGPV:	ILYQP	DNEYSGGCC	G QEFPNPDYF	Q YVIDQA <mark>RRAG</mark>	IVVPTISNDA	WPGGHNAPGT	<mark>GK</mark> GEVDIYGH
	24	1 DN	YPPSTPY	A LVEYQ	VGAFD	PWGGPGFEQ	C AALTGYEFE	R VFHKNTFSFG	VGILSLYMTF	GGTNWGNLGH	PGGYTSYDYG
	32	1 SP	IKETREI	T REKYSE	e <mark>lk</mark> ll	GNFIKSSPG	Y LLATPGKLT	N TTYTNTADLT	VTPLLG <mark>NGT</mark> G	SFFVLRHSDY	SSQASTPYKL
	40	1 <u>R</u> L	PTSAGQL	T IPQLG	GSLVL	. NGRDSKVHL	V DYDVAGT <mark>K</mark> I	L YSTAEVFTWK	KEHD GKALAL	XCCPCENHEL	AVSSKAKVKV
	48	1 VE	GLGSGIS	S KQIRGA	AVVVA	WDVEPARR I	V QIGDL <u>KIFL</u>	L DRNSAYNYWV	PQLGTETSIP	YATEKAVAAS	VIV<u>k</u>agylv<u>r</u>
	56	1 TA	<u>YVKGR</u> DL	H LTADF	NAT TP	VEVIGAP <u>K</u> T.	A ENLFING <u>KK</u> .	A HHTVDKNGIW	STEVGYSPPK	IVLPVLEDLK	WESIDTLPEI
	64	1 QP	SYDDSPW	P DANLP	FKNTI	YPLRTPTSL	Y ASDYGFHTG	Y LLF <u>R</u> GHFTAN	GRESNESIQT	QGGQAFGSSV	WLSGTYLGSW
	72	1 TG	DNDYQDY	N ATYTLI	PSLKA	GKEYVFTVV	7 DNMGLNENW	I VGQDEM <u>K</u> KP <u>R</u>	GILNYELSGH	EASDITWELT	GNFGGEDYVD
	80	1 KV	RGPLNEG	G LYAERI	нвхнџ	PYPPTKSKD	* KSSTPLTGL:	S KPGISFYTAS	FDLDIKSGWD	VPIYFEFGNS	TPAPAYRVŲ
	00	1 1 1 1	A A AGET E	VI TOPI	EDI MG	AVDUUUUUU	GINWVAVI.	L WALFGSGART	DSPKLVHGIP	VEIALDVEGV	ELP <u>RIUSKK</u> G
	90	1 1 1	AAAST <mark>BE</mark>	<u>Antoni</u> O'	CD BIAD	XVD IIIIIIIII					
С	A	. ni	dular	ns rlad	сΒ						
	1	FQ <mark>N</mark>	SQSEWP	IHDNGLS	s kaa	QWDHYSFYIN	GQR IFLFSGE	: FHYW <u>R</u> IPVPA	LWRDILEKIK	AIGFTGFAFY	SSWAYHAPN <mark>N</mark>
	81	QTVI	FSTGA <u>R</u>	DITPIYI	DLAK	ELGMYIIVRP	GPYVNAEAS!	GGFPLWLTTG	AYGSTRNDDP	RYTAAWEPYF	AEVSEITSKY
	161	QVTI	GHYTLC	YQIENEY	YGQQ .	WIGDPRDRNP	NQTALAYMEI	. LQASARENGI	TVPLTGNDPN	MNTKSWGSDW	SDAGGNLDTV
	241	GLDS	SYPSCWS	CDVSVC	TGTN	GEYVPYKVLD	YYDYFQEVQF	TMPFFMPEFQ	GGSYNPWDGP	EGGCTEDTGA	DF ANLF YRWN
	321	ICÔI	VSAMSL	YMMFGGT	TNUG	GIAAPVTASS	YDYSAPISEI	RSIGSKYYET	KLLALFTRCA	KDL TMTDRLG	<mark>NGT</mark> QYTDNEA
	401	VIAS	SELRNPD	TNAAFY	VTTH	LDTTVGTDES	FKLHVNTSK	ALTIPRHGGT	IRLNGHHSKI	IVTDFNFGSE	TLLYSTAEVL
	481	TYAN	FD <u>R</u> KPT	LVLWVP1	TGES	GEFAIKGAKS	GSVAKCSGCS	NIKFHEDSGS	LTVAFTQGEG	ISAFÖFDNCA	RVVLLDRQKA
	561	YTF	APAL TD	NPLVPE	GESV	LVSGPYLVRT	ARLARSTLTI	. RGDSKGETLE	IFAPRKIKKV	TWNGKAVEAT	RTSYGSLKAI

641 LAKPPSVELP TLNGWKYSDS LPERFPTYDD SGAAWVDANH MTTPNPNKPA TLPVLYADEY GFHNGVRLUR GYFNSSASGV 721 YLNIQGGAAF GWSAWLNGHF LGSHLGSASI QQANGTLDFP ANTLNTEGTP NVLLVVHDDT GHDQTTGVLN PRGILEARLL 801 SEASDNNDDD SPGFTHWRVA GTAGGESDLD PYRGYYNEDG LYAERVGWHL PGFDDSKWAT VNGTSLSFTG ATVRFFRTVI 881 PPLSIPENTD VSISFVFSTP NVNNTSAGNT SAFRAQLFVN GYQYGRYNPY VGNQVVYPVP PGILDYNGEN TIGVAVWAQT 961 EAGARLNLDW RVNYVLGSSL DAGRLDVSGL RPGWNEERER FAAAASFLEQ KLISEEDLNS AVDHHHHHH

Supplemental Fig. S2 Protein identity verification by mass fingerprint analysis

Purified (A) *A. niger* rlacA (B) *A. nidulans* rlacA and (C) *A. nidulans* rlacB were subjected to digestion with trypsin and subsequently analyzed by MALDI-TOF/TOF MS. Amino acid sequences in red font represent protein sequence covered by tryptic peptides whereas underlined positions indicate trypsin cleavage sites. Sequences underlined in grey represent amino acid sequences that were attached to the native protein during cloning. Sequences highlighted in red and blue indicate recombinant c-myc and His-tag and amino acid triplets highlighted in green indicate potential N-glycosylation sites.



Supplemental Fig. S3 Divalent metal ion susceptibility of recombinant galactosidases.

PNPG Reactions were supplemented with (A) 10 mM and (B) 1 mM of the respective metal salts. Black bars - *A. niger* rlacA, light grey bars - *A. nidulans* rlacA and grey bars - *A. nidulans* rlacB. Values represent averages +/- standard error. % relative activity compared with standard reactions without ion supplementation (= 100 %) is shown.



Supplemental Fig. S4 Temperature stability of *Aspergillus* β -galactosidases.

The β -galactosidases were incubated at indicated temperatures for 2 hours and remaining activity was determined by standard PNPG assay. Black squares represent incubations without BSA and open circles represent incubations supplemented with BSA. % activity +/- standard error is shown.



Supplemental Fig. S5 MS/MS data of PA labeled N-glycan structure containing Gal β 1,4Fuc used a substrate for recombinant β -galactosidases.

The parent ions of the major structures observed in the experiments described in Figure 5 were subject to MS/MS analyses to verify the removal of the galactose residue. (A) no enzyme control (parent ion m/z equals 1500.5 is substrate (hydrogen adduct)) (B) *A. nidulans* rlacB (parent ion m/z equals 1338.5 for processed and 1500.5 for unprocessed substrate (both as hydrogen adducts)). The data show that the 162 Da loss from the substrate is due to galactose removed from the core fucose (m/z 446 rather than 608) and not due to mannose cleavage. Comparable results were obtained for *A. niger* rlacA and *A. nidulans* rlacA (data not shown). The glycans are depicted following the nomenclature of the Consortium for Functional Glycomics (http://www.functionalglycomics.org).



Supplemental Fig. S6 Analysis of potential mannosidase activity of the enzyme preparations.

2-aminopyridine-labeled Man9 glycan was incubated with both native and recombinant enzymes at optimal pH for fungal galactosidases (pH 4.5 or pH 5.0) and optimal pH for typical a1,2-mannosidases (pH 6.9). (A) dextran standard (B) Man9-PA control (C) A. oryzae galactosidase pH 4 (D) A. oryzae galactosidase pH 6.9 (E) A. niger rlacA at pH 4.5 (F) A. niger rlacA at pH 6.9 (G) A. nidulans rlacA at pH 5.0 (H) A. nidulans rlacA at pH 6.9 (I) A. nidulans rlacB at pH 5.0 (J) A. nidulans rlacB at pH 6.9 and (K) positive control reaction at pH 6.9 using a recombinant mannosidase I derived from P. pastoris producing Man8B. Lower case letters above peaks in panel C represent (a) Man8A (b,c) Man 6 and 7 isomers (d) Man5 and (e) Man6. The glycans are depicted following the glycan of the Consortium Functional Glycomics nomenclature for (http://www.functionalglycomics.org).



Supplemental Fig. S7 Recombinant Aspergillus galactosidases process lactose.

4 μ g of either heat inactivated or functional *A. niger* rlacA, *A. nidulans* rlacA and *A. nidulans* rlacB were used per reaction in a total volume of 50 μ L containing 20% w/v lactose. Incubations were analyzed after 4 h (A) and 24 h (B). The high efficiency of *A. niger* rlacA leads to production of GOS in the first phase of incubation. GOS and lactose are mostly digested into glucose and galactose after 24 hours. The low conversion of lactose when using *A. nidulans* rlacB stems from the low efficiency of this enzyme. Retention times of lactose, galactose, glucose and galacto-oligosaccharides (GOS) are indicated in (A).



Supplemental Fig. S8 Influence of organic solvents on activity of analyzed β -galactosidases.

Reactions were performed with PNPG as substrate at 37°C with different concentrations of various solvents: (A) acetonitrile, (B) acetone, (C) isopropanol, (D) ethanol, (E) methanol and (F) water at different concentrations. Values represent averages +/- standard error.



Supplemental Fig. S9 Stability of analyzed β -galactosidases subjected to freeze/thaw cycles.

 β -galactosidase activity after several freeze/thaw cycles of the respective enzymes at a concentration of 100 µg mL⁻¹. Data without BSA (black squares, solid trendline) and with BSA (1 mg mL⁻¹) supplementation (open circles, dashed trendline) are shown. Values represent averages +/- standard error.



Supplemental Fig. S10 Summary of bioreactor cultivation of *P. pastoris* X-33 expressing *A. niger* and *A. nidulans* rlacA.

Cultivations were performed essentially as described previously (Gasser, *et al.*, 2010). Figures show the time-course for the production of *A. niger* rlacA (A) and *A. nidulans* rlacA (B). Red lines indicate pH, whereas black lines indicate the temperature throughout the cultivation. Yeast dry mass (YDM) and growth rate (μ) are indicated by green and blue squares, respectively. Black squares indicate β -galactosidase activity in culture supernatant. Total protein samples from culture supernatants were analyzed by SDS-PAGE (on the right in A and B) at the time points indicated in the diagrams. B - batch samples, FB - fed-batch samples. Gels were stained with Coomassie Brilliant Blue.