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A broader role for AmyR in *Aspergillus niger*: Regulation of the utilisation of D-glucose or D-galactose containing oligo- and polysaccharides

Patricia A. vanKuyk^{1,2}, Jaques A.E. Benen¹, Han A.B. Wösten³, Jaap Visser^{1†} and Ronald P. de Vries^{3,4*}

¹ Molecular Genetics of Industrial Microorganisms, Wageningen University, Dreijenlaan 2, 6703 HA Wageningen, The Netherlands; ² Molecular Microbiology, Leiden University, Sylviusweg 72, 2333 BE Leiden, The Netherlands;

³ Microbiology & Kluyver Centre for Genomics of Industrial Fermentation, Utrecht University, Padualaan 8, 3584 CH Utrecht, The Netherlands; ⁴ CBS-KNAW Fungal Biodiversity Centre, Uppsalalaan 8, 3584 CT Utrecht, The Netherlands

*Corresponding author. E-mail r.devries@cbs.knaw.nl; Phone: +31 302122600; Fax +31 302512097.

Supplemental Data:

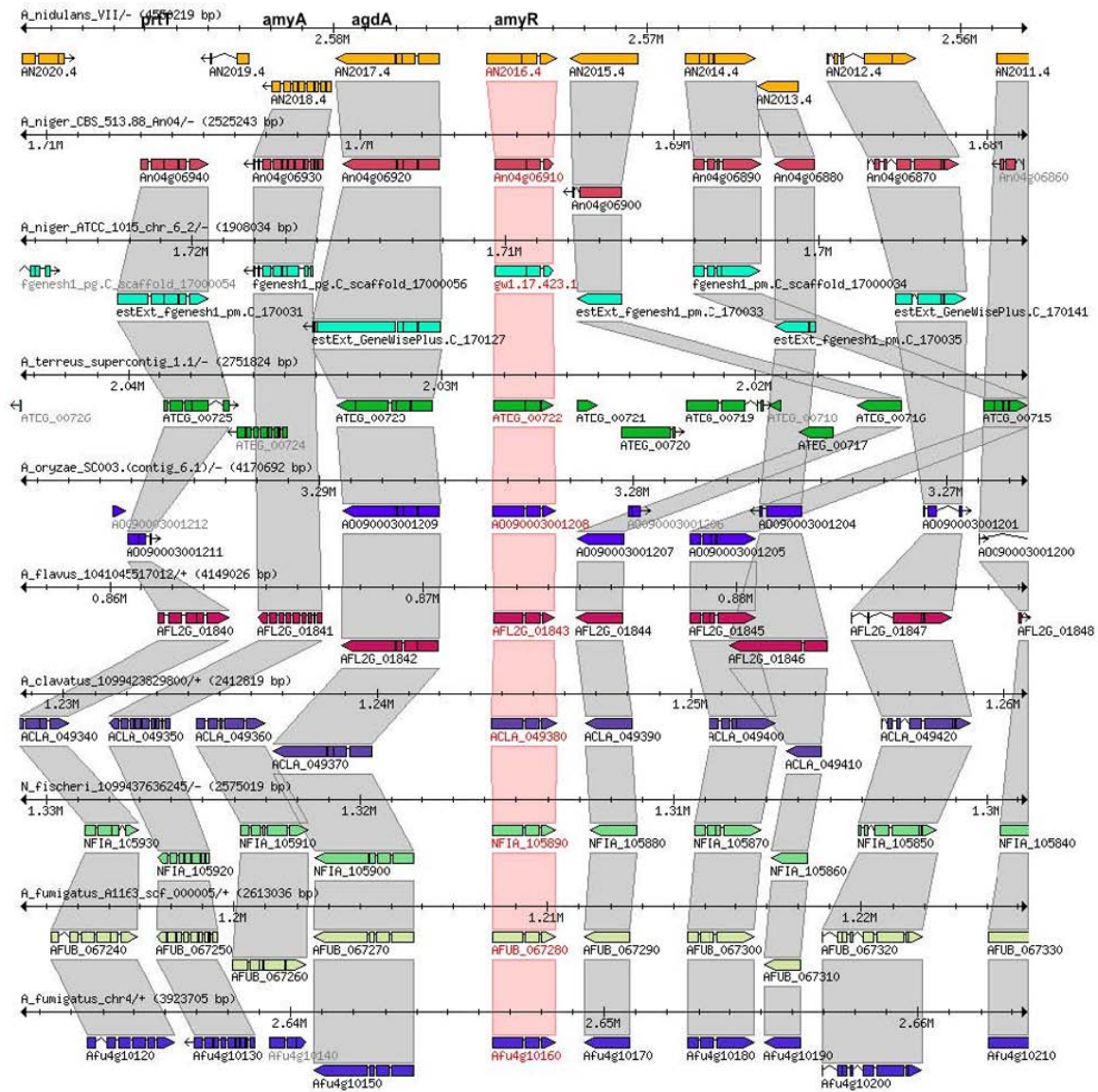
Supplemental Table 1: Micro array data of wild type (N402) and an amyR disruptant (dAmyR) after transfer to minimal medium containing 1% maltose.

Supplemental Figure 1: Synteny in 8 *Aspergilli* with respect to the amyR cluster.

Supplemental Figure 2: Synteny in 5 *Aspergilli* with respect to the *mal* cluster.

Supplemental Table 1: Micro array data of wild type (N402) and an amyR disruptant (dAmyR) after transfer to minimal medium containing 1% maltose.							
GH = glycoside hydrolase (www.cazy.org).							
BGL = β -glucosidase, AMY = α -amylase, AGD = α -glucosidase, GLA = glucoamylase, AGL = α -galactosidase, LAC = β -galactosidase							
Gene IDs in green are at least 2-fold higher in the wild type, gene IDs in yellow are at least 2-fold higher in the amyR disruptant. The data was obtained from Yuan et al (2008) and presented as the average of the duplicate datasets of that paper. The last column lists the number of putative AmyR binding sites in the promoter of the genes.							
*Only present in JGI niger genome, not in DSM genome.							
Gene id	Gene	Family	Function	N402 malt 2h	dAmyR malt, 2h	Fold change	AmyR binding sites
An01g04880		GH31	AGD	665.65	442.9	1.5	2
An01g10930		GH31	AGD	13516.65	891.3	15.2	2
An02g13240		GH13	AGD	388.6	222.55	1.7	1
An04g06920	<i>agdA/aglU</i>	GH31	AGD	11679.75	513.4	22.7	2
An09g05880		GH31	AGD	2706.85	2117.25	1.3	0
An13g03710		GH13	AGD	91.45	66.25	1.4	0
An18g05620		GH31	AGD	158.55	150.75	1.1	0
An01g01320		GH27	AGL	78.25	66.9	1.2	5
An02g11150	<i>aglB</i>	GH27	AGL	972	805.55	1.2	0
An04g02700		GH36	AGL	107.5	47.4	2.3	1*
An06g00170	<i>aglA</i>	GH27	AGL	93.05	16.15	5.8	4
An09g00260	<i>aglC</i>	GH36	AGL	1947.4	888.6	2.2	2
An09g00270	<i>aglC</i>	GH36	AGL	4310	1543.45	2.8	2
An11g06330		GH27	AGL	65.95	66.75	1.0	1
An14g01800		GH27	AGL	20.3	11.9	1.7	0
An01g13610		GH13	AMY	122.2	111.1	1.1	2
An04g06930	<i>amyA</i>	GH13	AMY	649.15	216.85	3.0	3
An05g02100		GH13	AMY	616.1	201.45	3.1	3
An09g03110		GH13	AMY	65.85	119.65	0.6	1
An11g03340		GH13	AMY	393.55	16.8	23.4	2
An12g06930		GH13	AMY	11.7	7.35	1.6	1
An12g06940		GH13	AMY	9.8	6.35	1.5	1
An02g08600		GH1	BGL	150.15	112.7	1.3	0
An03g03740		GH1	BGL	5500.25	3714.45	1.5	0
An03g05330		GH3	BGL	42.55	51	0.8	2
An04g03170		GH1	BGL	238.4	241.45	1.0	1
An06g02040		GH3	BGL	83.3	27.05	3.1	1
An07g09760		GH3	BGL	77.95	56.9	1.4	1
An08g08240		GH3	BGL	29.45	28.6	1.0	1
An11g00200		GH3	BGL	100.3	123.7	0.8	4
An11g02100		GH1	BGL	336.05	392.3	0.9	2
An11g06090		GH3	BGL	74.75	156.65	0.5	0
An14g01770		GH3	BGL	191.35	36.65	5.2	5
An15g01890		GH3	BGL	528.8	415.85	1.3	1
An15g04800		GH3	BGL	15.2	9.3	1.6	4
An17g00520		GH3	BGL	205.3	179.3	1.1	1
An18g03570	<i>bgl1</i>	GH3	BGL	17057.25	9408.25	1.8	0
An03g06550	<i>glaA</i>	GH15	GLA	16835.55	595.9	28.3	4
An12g03070		GH15	GLA	15.65	6.95	2.3	1
An01g10350		GH35	LAC	1375.35	1238.25	1.1	0
An01g12150	<i>lacA</i>	GH35	LAC	544.7	375.95	1.4	2
An06g00290		GH35	LAC	116.85	41	2.9	4
An07g04420		GH35	LAC	44.95	24.9	1.8	0
An14g05820		GH35	LAC	53.3	29.1	1.8	0
							2
An04g06910	<i>amyR</i>	Zn2Cys	regulator	1779.2	4.75	374.6	0
							0
An02g00590	<i>mstF</i>	MFS	sugar tran	13675.65	6724.65	2.0	3
An02g03540	<i>mstC</i>	MFS	sugar tran	241.75	269.85	0.9	1
An12g07450	<i>mstA</i>	MFS	sugar tran	21471.2	11371.85	1.9	3

Supplemental Figure 1. Synteny in 8 *Aspergilli* with respect to the *amyR* cluster. The *amyR*, *agdA*, *amyA* and *prtT* genes are indicated. Except for an insertion in *A. terreus* and the absence of *prtT* in *A. nidulans* this genomic region is highly conserved among the *Aspergilli*. Generated using the Sybil tool at the *Aspergillus* Genome Database (www.aspgd.org) (Crabtree et al. 2007).



Supplemental Figure 2: Synteny in 5 *Aspergilli* with respect to the *mal* cluster. The *malP* (maltose permease), *malT* (maltase) and *malR* (putative regulator) genes are indicated. Generated using the Sybil tool at the Aspergillus Genome Database (www.aspgd.org) (Crabtree et al. 2007).

