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Erratum

Erratum: Ntana, F., et al. Aspergillus: A Powerful Protein Production Platform. *Catalysts* 2020, *10*, 1064

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The author wishes to make the following erratum to this paper [1]: Update due to some reporting errors in Tables 2, 8, 10 and 12.

Due to typographical errors concerning reference [47] and [51,52], replace:

Table 2. Approaches for improving recombinant protein production through promoter engineering.

Process	Modification	Performance	Improvement Factor	Reference
Promoters	Use of several promoters (P) in *A. awamori*	PB2 from *Acremonium chrysogenum*: 0.25–2 mg/L thaumatin	-	[46]
		PpcbC from *Penicillium chrysogenum*: 0.25–2 mg/L thaumatin		
		PgdhA from *A. awamori*: 1–9 mg/L thaumatin		
		PgpdA from *A. nidulans*: 0.75–11 mg/L thaumatin		
	Insertion of multiple copies of an activator protein-binding site from the *cis*-regulatory region of *A. niger glaA* to the new promoter in *A. niger*	396.0 ± 51.5 mg/L of *Vitreoscilla* hemoglobin compared to 19.7 ± 4.8 mg/L from the strain with 1 copy	20	[45]
	Use of hybrid promoters (combination of a human hERa-activated promoter (pERE), *S. cerevisiae URA3* promoter and *A. nidulans nirA* promoter) in *A. nidulans*	pERE-URA-nirA + *lacZ*: 25 U of β-galactosidase activity/mg of protein	-	[47]
		pERE-URA-RS (random stuffer-link) + *lacZ*: 100 U of β-galactosidase activity/mg of protein	4	
		pERE-RS-nirA + *lacZ*: 1400 U of β-galactosidase activity/mg of protein [1 pM inducer (DES)]	56	
	Use of a hemolysin-like protein promoter (Phyl) for heterologous production in *A. oryzae*	Reporter gene: Endoglucanase Cel B Pamy: 24.1 ± 5.5 U/mL, Phyl: 57.9 ± 17.4 U/mL	2.4	[48]
		Reporter gene: *Trichoderma* endoglucanase I Pamy: 7.7 ± 3.9 U/mL, Phyl: 27.8 ± 1.3 U/mL	3.6	
		Reporter gene: *Trichoderma* endoglucanase III Pamy:4.0 ± 0.6 U/mL, hyl:31.7 ± 3.3 U/mL	7.9	
	Regulatory elements (TerR and PterA) from *A. terreus* terrain gene cluster for *E. coli lacZ* expression in *A. niger*	Promoter activity ~5000 mU/mg when TerR under PgpdA (No activity when TerR under the native promoter)	-	[49]
		Promoter activity ~10,000 mU/mg (when TerR under PgpdA in 2 copies)	2	
		Promoter activity ~15,000 mU/mg (when TerR under PamyB)	3	

Table 2. *Cont.*

Process	Modification		Performance	Improvement Factor	Reference
	A. niger α-glucosyltransferase produced under the *A. niger* pyruvate kinase promoter		2000 U/mL total activity of α-glucosyltransferase compared to 600 U/mL in the wild type	3.3	[50]
	Overexpression of the transcription factor RsmA, while the aflR promoter was inserted in front of the *pslcc* in *A. nidulans*		60,000 U/mL of *Pycnoporus sanguineus* laccase compared to 4000 U/mL in the control strain	15	[51,52]
	A novel promoter from *Talaromyces emersonii* (Pglucan1200) for expressing *glaA* in *A. niger*		6000 U/mL of GlaA, enzyme activity increased by about 25% compared to 5000 U/mL in the strain with the PglaA	1.2	[53]
	The constitutive promoter of *ecm33* (Pecm33) from *A. niger* in *A. niger*	Maltose:	Pecm33 activity induced by 1.7 compared to PglaA activity that induced by 2.7	-	[54]
		Glucose:	Pecm33 activity induced by 1.1 compared to PglaA activity that induced by 1.8		
		Xylose:	Pecm33 activity induced by 2 compared to PglaA activity that induced by 1.3 Increased Pecm33 activity at 37 °C		

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Promoters	Use of several promoters (P) in *A. awamori*	PB2 from *Acremonium chrysogenum*: 0.25–2 mg/L thaumatin	-	[46]
		PpcbC from *Penicillium chrysogenum*: 0.25–2 mg/L thaumatin		
		PgdhA from *A. awamori*: 1–9 mg/L thaumatin		
		PgpdA from *A. nidulans*: 0.75–11 mg/L thaumatin		
	Insertion of multiple copies of an activator protein-binding site from the *cis*-regulatory region of *A. niger glaA* to the new promoter in *A. niger*	396.0 ± 51.5 mg/L of *Vitreoscilla* hemoglobin compared to 19.7 ± 4.8 mg/L from the strain with 1 copy	20	[45]
	Use of hybrid promoters (combination of a human hERa-activated promoter (pERE), *S. cerevisiae URA3* promoter and *A. nidulans nirA* promoter) in *A. nidulans*	pERE-RS-nirA+ *lacZ*: 25 U of β-galactosidase activity/mg of protein	-	[47]
		pERE-URA-nirA+ *lacZ*: 100 U of β-galactosidase activity/mg of protein	4	
		pERE-URA-RS + *lacZ*: 1400 U of β-galactosidase activity/mg of protein [1 pM inducer (DES)]	56	
	Use of a hemolysin-like protein promoter (Phyl) for heterologous production in *A. oryzae*	Reporter gene: Endoglucanase Cel B Pamy: 24.1 ± 5.5 U/mL, Phyl: 57.9 ± 17.4 U/mL	2.4	[48]
		Reporter gene: *Trichoderma* endoglucanase I Pamy: 7.7 ± 3.9 U/mL, Phyl: 27.8 ± 1.3 U/mL	3.6	
		Reporter gene: *Trichoderma* endoglucanase III Pamy:4.0 ± 0.6 U/mL, hyl:31.7 ± 3.3 U/mL	7.9	
	Regulatory elements (TerR and PterA) from *A. terreus* terrain gene cluster for *E. coli lacZ* expression in *A. niger*	Promoter activity ~5000 mU/mg when TerR under PgpdA (No activity when TerR under the native promoter)	-	[49]
		Promoter activity ~10,000 mU/mg (when TerR under PgpdA in 2 copies)	2	
		Promoter activity ~15,000 mU/mg (when TerR under PamyB)	3	

Table 2. *Cont.*

Process	Modification		Performance	Improvement Factor	Reference
	A. niger α-glucosyltransferase produced under the *A. niger* pyruvate kinase promoter		2000 U/mL total activity of α-glucosyltransferase compared to 600 U/mL in the wild type	3.3	[50]
	Overexpression of the transcription factor RsmA, while the aflR promoter was inserted in front of the *pslcc* in *A. nidulans*		0.06 U/mL of *Pycnoporus sanguineus* laccase compared to 0.004 U/mL in the control strain	15	[51,52]
	A novel promoter from *Talaromyces emersonii* (Pglucan1200) for expressing *glaA* in *A. niger*		6000 U/mL of GlaA compared to 5000 U/mL in the strain with the PglaA	1.2	[53]
	The constitutive promoter of *ecm33* (Pecm33) from *A. niger* in *A. niger*	Maltose:	Pecm33 activity induced by 1.7 compared to PglaA activity that induced by 2.7	-	[54]
		Glucose:	Pecm33 activity induced by 1.1 compared to PglaA activity that induced by 1.8		
		Xylose:	Pecm33 activity induced by 2 compared to PglaA activity that induced by 1.3 Increased Pecm33 activity at 37 °C		

Due to a typographical error concerning reference [109], replace:

Table 8. Approaches for improving recombinant protein production through engineering protein degradation pathways.

Process	Modification	Performance	Improvement Factor	Reference
Protein degradation pathways— ERAD and Vacuole	Deletion of *derA* and *derB* in *A. niger*	ΔderA: 80% decrease in *Trametes* laccase production	0.2	[99]
	-	ΔderB: 15.7% increase in *Trametes* laccase	1.15	
	Deletion of *doaA* and overexpression of *sttC* in *A. niger*	Higher GUS activity compared to parental strain (no quantitative data available)	-	[106]
	Disruption of *Aovps10* in *A. oryzae*	83.1 and 70.3 mg/L chymosin compared to 28.7 mg/L in parental strain	3–2.5	[108]
		22.6 and 24.6 mg/L human lysozyme compared to 11.1 mg/L in parental strain	2–2.2	
	Deletion of ERAD key genes (*derA*, *doaA*, *hrdC*, *mifA* and *mnsA*) in *A. niger*	ΔderA and ΔhrdC: 2-fold increase compared to parental strain (single-copy)	2	[107]
		ΔderA: 6-fold increase compared to parental strain (multi-copy) Relative amount of intracellular GlaGus (β-glucuronidase levels) fusion protein detected in total protein extracts of strains with impaired ERAD and respective parental strain	6	

Table 8. *Cont.*

Process	Modification	Performance	Improvement Factor	Reference
	Disruption of genes involved in autophagy in *A. oryzae*	ΔAoatg1: 60 mg/L chymosin	2.3	[109]
		ΔAoatg13: 37 mg/L chymosin	1.4	
		ΔAoatg4: 80 mg/L chymosin	3.1	
		ΔAoatg8: 66 mg/L chymosin	2.5	
		ΔAoatg15: Not detectable	-	
		Control: 26 mg/L chymosin	-	

with

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	-	ΔderB: 15.7% increase in *Trametе* laccase	1.15	
	Deletion of *doaA* and overexpression of *sttC* in *A. niger*	Higher GUS activity compared to parental strain (no quantitative data available)	-	[106]
	Disruption of *Aovps10* in *A. oryzae*	83.1 and 70.3 mg/L chymosin compared to 28.7 mg/L in parental strain	3–2.5	[108]
		22.6 and 24.6 mg/L human lysozyme compared to 11.1 mg/L in parental strain	2–2.2	
	Deletion of ERAD key genes (*derA*, *doaA*, *hrdC*, *mifA* and *mnsA*) in *A. niger*	ΔderA and ΔhrdC: 2-fold increase compared to parental strain (single-copy)	2	[107]
		ΔderA: 6-fold increase compared to parental strain (multi-copy) Relative amount of intracellular GlaGus (β-glucuronidase levels) fusion protein detected in total protein extracts of strains with impaired ERAD and respective parental strain	6	
	Disruption of genes involved in autophagy in *A. oryzae*	ΔAoatg1: 60 mg/L chymosin	2.3	[109]
		ΔAoatg13: 37 mg/L chymosin	1.4	
		ΔAoatg4: 80 mg/L chymosin	3.1	
		ΔAoatg8: 66 mg/L chymosin	2.5	
		ΔAoatg15: 24 mg/L chymosin	1	
		Control: 26 mg/L chymosin	-	

Due to typographical errors concerning reference [126] and [51], replace:

Table 10. Approaches for improving recombinant protein production through disruption of protease genes.

Process	Modification	Performance	Improvement Factor	Reference
Proteases	Deletion of *pepA* in *A. awamori* strains	Decreased extracellular proteolytic activity compared to the wild type (immunoassay using antibodies specific for PepA, but absolute values for PepA concentration were not determined)	-	[125]
	Deletion of *pepA* in *A. awamori*	430 mg/L of chymosin compared to 180 mg/L in the parental strain	2.4	[128]
	Deletion of *pepA* in *A. niger* (AB1.1)	15–20% proteolytic activity compared to the parent strain AB4.1	-	[126]
	Mutation on *prtT* (UV irradiation) in *A. niger* (AB1.13)	1–2% proteolytic activity compared to the parent strain AB4.1	-	[126]
	Deletion of *prtR*, *pepA*, *cpI*, *tppA* in *A. oryzae*	ΔprtR/pepA/cpI: 24.23 mg/L of *Acremonium cellulolyticus* cellobiohydrolase	1.2	[133]
		ΔprtR/pepA/tppA: 21.30 mg/L	1.1	
		ΔprtR/cpI/tppA: 22.08 mg/L	1.1	
		ΔprtR/pepA/cpI/tppA: 19.93 mg/L compared to 19.54 mg/L in the control strains	1.02	
	Deletion of *alp* and *Npl* in *A. oryzae*	1041 U/g of *Candida antarctica* lipase B compared to 575 U/g in the parental strains	1.8	[132]
	Deletion of various proteases in *A. niger*	Δdpp4: 6% increase in *Tramete* laccase	1.1	[99]
		Δdpp5: 15.4% increase	1.2	
		ΔpepB: 8.6% increase	1.1	
		ΔpepD: 4.8% increase	1.0	
		ΔpepF: 5.3% increase	1.1	
		ΔpepAa: 0.5% increase	1.1	
		ΔpepAb: 13.4% increase	1.1	
		ΔpepAd: 2.7% increase	1.0	
		Δdpp4/dpp5: 26.6% increase	1.3	
	Disruption of *tppA* and *pepE* in *A. oryzae* strains	25.4 mg/L of human lysozyme compared to 15 mg/L in the parental strains	1.7	[118]
	Disruption of *tppA*, *pepE*, *nptB*, *dppIV* and *dppV* in *A. oryzae*	84.4 mg/L of chymosin compared to the 63.1 mg/L in the double protease gene disruptant (ΔtppA/pepE)	1.3	[130]
	Disruption of *tppA*, *pepE*, *nptB*, *dppIV*, and *dppV*, *alpA*, *pepA*, *AopepAa*, *AopepAd* and *cpI* in *A. oryzae*	109.4 mg/L of chymosin and 35.8 mg/L of human lysozyme compared to the quintuple protease gene disruptant (ΔtppA/pepE/nptB/dppIV/dppV; 84.4 mg/L and 26.5 mg/L, respectively)	1.3 and 1.35	[131]
	Deletion of *prtT* in *A. niger*	36.3–36.7 U/mL of mL *G. cingulate* cutinase compared to 21.2–20.4 U/mL in the parental strain	1.7	[127]
		Stability: Cutinase activity retained at 80% over the entire 14-day incubation period, while the parental lost more than 50% of their initial activities after six days of incubation and retained negligible activity after 14 days	-	
	Deletion of *dppV* and *pepA* in *A. nidulans*	*P. sanguineus* laccase activity 500,000 U/mL compared to 40,000 U/mL in the control strain	12.5	[51]
	Deletion of *mnn9* and *pepA* in *A. nidulans*	*P. sanguineus* laccase activity 300,000 U/mL compared to 40,000 U/mL in the control strain	7.5	[51]

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Table 10. Approaches for improving recombinant protein production through disruption of protease genes.

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Proteases	Deletion of *pepA* in *A. awamori* strains	Decreased extracellular proteolytic activity compared to the wild type (immunoassay using antibodies specific for PepA, but absolute values for PepA concentration were not determined)	-	[125]
	Deletion of *pepA* in *A. awamori*	430 mg/L of chymosin compared to 180 mg/L in the parental strain	2.4	[128]
	Deletion of *pepA* in *A. niger* (AB1.18)	15–20% proteolytic activity compared to the parent strain AB4.1	-	[126]
	Mutation on *prtT* (UV irradiation) in *A. niger* (AB1.13)	1–2% proteolytic activity compared to the parent strain AB4.1	-	[126]
	Deletion of *prtR*, *pepA*, *cpI*, *tppA* in *A. oryzae*	ΔprtR/pepA/cpI: 24.23 mg/L of *Acremonium cellulolyticus* cellobiohydrolase	1.2	[133]
		ΔprtR/pepA/tppA: 21.30 mg/L	1.1	
		ΔprtR/cpI/tppA: 22.08 mg/L	1.1	
		ΔprtR/pepA/cpI/tppA: 19.93 mg/L compared to 19.54 mg/L in the control strains	1.02	
	Deletion of *alp* and *Npl* in *A. oryzae*	1041 U/g of *Candida antarctica* lipase B compared to 575 U/g in the parental strains	1.8	[132]
	Deletion of various proteases in *A. niger*	Δdpp4: 6% increase in *Tramete* laccase	1.1	[99]
		Δdpp5: 15.4% increase	1.2	
		ΔpepB: 8.6% increase	1.1	
		ΔpepD: 4.8% increase	1.0	
		ΔpepF: 5.3% increase	1.1	
		ΔpepAa: 0.5% increase	1.1	
		ΔpepAb: 13.4% increase	1.1	
		ΔpepAd: 2.7% increase	1.0	
		Δdpp4/dpp5: 26.6% increase	1.3	
	Disruption of *tppA* and *pepE* in *A. oryzae* strains	25.4 mg/L of human lysozyme compared to 15 mg/L in the parental strains	1.7	[118]
	Disruption of *tppA*, *pepE*, *nptB*, *dppIV* and *dppV* in *A. oryzae*	84.4 mg/L of chymosin compared to the 63.1 mg/L in the double protease gene disruptant (ΔtppA/pepE)	1.3	[130]
	Disruption of *tppA*, *pepE*, *nptB*, *dppIV*, and *dppV*, *alpA*, *pepA*, *AopepAa*, *AopepAd* and *cpI* in *A. oryzae*	109.4 mg/L of chymosin and 35.8 mg/L of human lysozyme compared to the quintuple protease gene disruptant (ΔtppA/pepE/nptB/dppIV/dppV; 84.4 mg/L and 26.5 mg/L, respectively)	1.3 and 1.35	[131]
	Deletion of *prtT* in *A. niger*	36.3–36.7 U/mL of mL *G. cingulate* cutinase compared to 21.2–20.4 U/mL in the parental strain	1.7	[127]
		Stability: Cutinase activity retained at 80% over the entire 14-day incubation period, while the parental lost more than 50% of their initial activities after six days of incubation and retained negligible activity after 14 days	-	
	Deletion of *dppV* and *pepA* in *A. nidulans*	*P. sanguineus* laccase activity 0.5 U/mL compared to 0.04 U/mL in the control strain	12.5	[51]
	Deletion of *mnn9* and *pepA* in *A. nidulans*	*P. sanguineus* laccase activity 0.3 U/mL compared to 0.04 U/mL in the control strain	7.5	[51]

Due to a typographical error concerning reference [144], replace:

Table 12. Approaches for improving recombinant protein production through bioprocessing modifications.

Process	Modification	Performance	Improvement Factor	Reference
Fermentation conditions	Effect of growth medium and temperature on hen egg white lysozyme (HEWL) production in *A. niger*	20–25 °C 8–10 mg/L HEWL while 30–37 °C 3–5 mg/L HEWL	Temperature: 2–2.6	[141]
		soluble starch: 8.0 mg/L HEWL	Carbon source: 1.7–2	
		maltose: 4.5 mg/L HEWL	-	
		glucose: 4.0 mg/L HEWL	-	
		xylose:0.2 mg/L HEWL	-	
		soy milk medium: 30–60 mg/L HEWL	Rich medium: 3.8–7.5	
	Effect of organic nitrogen sources on recombinant glucoamylase production in *A. niger*	Unsupplemented: 44 mg glucoamylase/g biomass	-	[143]
		L-alanine: 32 mg glucoamylase/g biomass	0.7	
		L-methionine: 26 mg glucoamylase/g	0.6	
		casamino acids, yeast extract, peptone, and gelatin: 100 mg glucoamylase/g	2.2	
	Effect of agitation intensity on recombinant amyloglucosidase (AMG) production in *A. oryzae*	Titer at the end of the batch phase 525 rpm: 110 U/L AMG	-	[146]
		675 rpm: 230 U/L AMG	1.6	
		825 rpm: 370 U/L AMG	3.3	
	Effects of bioprocess parameters—agitation intensity, initial glucose concentration, initial yeast extract concentration, and dissolved oxygen tension (DO)—on heterologous protein production in *A. oryzae*	Highest GFP yields were achieved under these conditions: agitation 400 rpm, glucose 25 g/L, yeast extract 0 g/dm^3, DO 15%	-	[142]
	Effect of agitation intensity on recombinant glucose oxidase production in *A. niger*	200 rpm: 300 mkat/L of glucose oxidase	-	[144]
		500 rpm: 800 mkat/L of glucose oxidase	2.6	
		800 rpm: 600 mkat/L of glucose oxidase	1.3	
	Effect of temperature on *Pleurotus eryngii* versatile peroxidase production in *A. nidulans* and *A. niger*	-*A. nidulans* 31 °C: 24 U/L peroxidase activity	-	[145]
		28 °C: 80 U/L peroxidase activity	3.3	
		19 °C: 466 U/L peroxidase activity	19.4	
		-*A. niger* 28 °C: 107 U/L peroxidase activity	-	
		19 °C: 412 U/L peroxidase activity	3.8	
Fungal morphology	Effect of raising the viscosity of the medium by addition of polyvinylpyrrolidone-PVP (transition from aggregated mycelia (pellets) to dispersed mycelia) on hen egg white lysozyme (HEWL) in *A. niger*	Medium with no PVP: 110 mg/L fresh and 8 mg/g dry weight of HEWL	1.7	[147]
		Medium with PVP: 190 mg/L fresh and 14 mg/g dry weight of HEWL		

Table 12. *Cont.*

Process	Modification	Performance	Improvement Factor	Reference
	Effect of addition of microparticles (linked to the formation of freely dispersed mycelium) on titers of native glucoamylase (GlaA) and recombinant fructofuranosidase (FF) produced in *A. niger*	No microparticles: 17 U/mL GlaA and 42 U/mL FF	3.5 GlaA 2–3.8 FF	[148]
		Talc microparticles: 61 U/mL GlaA and 92 U/mL FF FF production can reach up to 160 U/mL (10 g/L talc microparticles of size 6 mm)		
	Effect of addition of titanate microparticles ($TiSiO_4$, 8 mm) on titers of native glucoamylase (GlaA) and recombinant fructofuranosidase (FF) produced in *A. niger*	No microparticles: 19 U/mL GlaA and 40 U/mL FF	9.5 GlaA 3.7 FF	[149]
		Microparticles: 190 U/mL glucoamylase and 150 U/mL fructofuranosidase		
	Effect of growth type on hen egg white lysozyme (HEWL) production and protease activity in *A. niger*	Free suspension: 5.8 mg/g HEWL 95.3 U/g Protease activity	1.5	[140]
		Mycelial pellets: 5.0 mg/g HEWL 58.6 U/g Protease activity	1.2	
		Celite-560-immobilized cultures: 4.1 mg/g HEWL 56.3 U/g Protease activity	-	

with

Table 12. Approaches for improving recombinant protein production through bioprocessing modifications.

Process	Modification	Performance	Improvement Factor	Reference
Fermentation conditions	Effect of growth medium and temperature on hen egg white lysozyme (HEWL) production in *A. niger*	20–25 °C 8–10 mg/L HEWL while 30–37 °C 3–5 mg/L HEWL	Temperature: 2–2.6	[141]
		soluble starch: 8.0 mg/L HEWL	Carbon source: 1.7–2	
		maltose: 4.5 mg/L HEWL	-	
		glucose: 4.0 mg/L HEWL	-	
		xylose:0.2 mg/L HEWL	-	
		soy milk medium: 30–60 mg/L HEWL	Rich medium: 3.8–7.5	
	Effect of organic nitrogen sources on recombinant glucoamylase production in *A. niger*	Unsupplemented: 44 mg glucoamylase/g biomass	-	[143]
		L-alanine: 32 mg glucoamylase/g biomass	0.7	
		L-methionine: 26 mg glucoamylase/g	0.6	
		casamino acids, yeast extract, peptone, and gelatin: 100 mg glucoamylase/g	2.2	

Table 12. *Cont.*

Process	Modification	Performance	Improvement Factor	Reference
	Effect of agitation intensity on recombinant amyloglucosidase (AMG) production in *A. oryzae*	Titer at the end of the batch phase 525 rpm: 110 U/L AMG	-	[146]
		675 rpm: 230 U/L AMG	1.6	
		825 rpm: 370 U/L AMG	3.3	
	Effects of bioprocess parameters—agitation intensity, initial glucose concentration, initial yeast extract concentration, and dissolved oxygen tension (DO)—on heterologous protein production in *A. oryzae*	Highest GFP yields were achieved under these conditions: agitation 400 rpm, glucose 25 g/L, yeast extract 0 g/dm^3, DO 15%	-	[142]
	Effect of agitation intensity on recombinant glucose oxidase production in *A. niger*	200 rpm: 300 µkat/L of glucose oxidase	-	[144]
		500 rpm: 800 µkat/L of glucose oxidase	2.6	
		800 rpm: 600 µkat/L of glucose oxidase	1.3	
	Effect of temperature on *Pleurotus eryngii* versatile peroxidase production in *A. nidulans* and *A. niger*	-*A. nidulans* 31 °C: 24 U/L peroxidase activity	-	[145]
		28 °C: 80 U/L peroxidase activity	3.3	
		19 °C: 466 U/L peroxidase activity	19.4	
		-*A. niger* 28 °C: 107 U/L peroxidase activity	-	
		19 °C: 412 U/L peroxidase activity	3.8	
Fungal morphology	Effect of raising the viscosity of the medium by addition of polyvinylpyrrolidone-PVP (transition from aggregated mycelia (pellets) to dispersed mycelia) on hen egg white lysozyme (HEWL) in *A. niger*	Medium with no PVP: 110 mg/L fresh and 8 mg/g dry weight of HEWL	1.7	[147]
		Medium with PVP: 190 mg/L fresh and 14 mg/g dry weight of HEWL		
	Effect of addition of microparticles (linked to the formation of freely dispersed mycelium) on titers of native glucoamylase (GlaA) and recombinant fructofuranosidase (FF) produced in *A. niger*	No microparticles: 17 U/mL GlaA and 42 U/mL FF	3.5 GlaA 2–3.8 FF	[148]
		Talc microparticles: 61 U/mL GlaA and 92 U/mL FF FF production can reach up to 160 U/mL (10 g/L talc microparticles of size 6 mm)		
	Effect of addition of titanate microparticles ($TiSiO_4$, 8 mm) on titers of native glucoamylase (GlaA) and recombinant fructofuranosidase (FF) produced in *A. niger*	No microparticles: 19 U/mL GlaA and 40 U/mL FF	9.5 GlaA 3.7 FF	[149]
		Microparticles: 190 U/mL glucoamylase and 150 U/mL fructofuranosidase		
	Effect of growth type on hen egg white lysozyme (HEWL) production and protease activity in *A. niger*	Free suspension: 5.8 mg/g HEWL 95.3 U/g Protease activity	1.5	[140]
		Mycelial pellets: 5.0 mg/g HEWL 58.6 U/g Protease activity	1.2	
		Celite-560-immobilized cultures: 4.1 mg/g HEWL 56.3 U/g Protease activity	-	

This update does not change any of the scientific results of the paper. The authors would like to apologize for any inconvenience caused to the readers by these changes. The manuscript will be updated and the original will remain online on the article webpage: https://www.mdpi.com/2073-4344/10/9/1064.

Reference

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