

A CRE1- regulated cluster is responsible for light dependent production of dihydrotrichotetronin in *Trichoderma reesei*

Alberto Alonso Monroy¹, Eva Stappler¹, Andre Schuster², Michael Sulyok⁴ and Monika Schmoll¹

Supplementary material

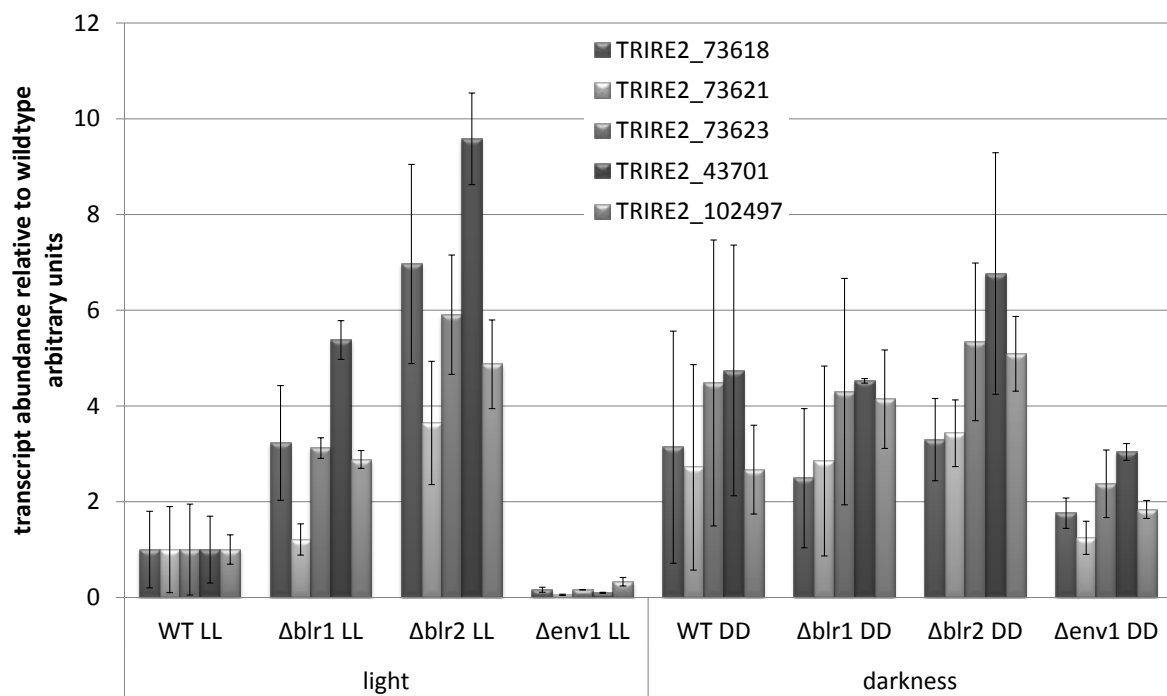


Figure A. Regulation of cluster genes upon growth in light and darkness in wildtype and in deletion mutants of the photoreceptors BLR1, BLR2 and ENV1. Errorbars show standard deviations. Data are taken from (Tisch et al., 2013).

Table A. Oligonucleotides used in this study.

Name	Sequence: 5'-XXXXXX-3'	Purpose	Amplicon size in bp
pdel_43701_5F	GTAACGCCAGGGTTTCCAGTCACGACGGTAGAAGGCATCGTAGGTCC	Amplification of 43701 gene 5' flanking region for deletion	1099
pdel_43701_5R	ATCCACTTAACGTTACTGAAATCTCCAACGTGGTTATACTCCGAAGTCC		
pdel_43701_3F	CTCCTTCAATATCATCTTCTGTCTCCGACGCCCTCTCTCATACATCAGC	Amplification of 43701 gene 3' flanking region for deletion	1132
pdel_43701_3R	GCGGATAACAATTTACACAGGAAACAGCGTGTTCAGCTCTTGAAGTGG		
pdel_53238_5F	GTAACGCCAGGGTTTCCAGTCACGACGATCTACAGAGGCACTAGG	Amplification of 53238 gene 5' flanking region for deletion	1248
pdel_53238_5R	ATCCACTTAACGTTACTGAAATCTCCAACGAGATGTACGAGTGATGAGC		
pdel_53238_3F	CTCCTTCAATATCATCTTCTGTCTCCGACCTATCCATCTGCCATAGACC	Amplification of 53238 gene 3' flanking region for deletion	1107
pdel_53238_3R	GCGGATAACAATTTACACAGGAAACAGCCTCCATGCCTAATACCTACC		
pdel_53776_5F	GTAACGCCAGGGTTTCCAGTCACGACGACACTCACCTTCTCATCTCC	Amplification of 53776 gene 5' flanking region for deletion	1082
pdel_53776_5R	ATCCACTTAACGTTACTGAAATCTCCAACGACTCTCCACTTACATTCC		
pdel_53776_3F	CTCCTTCAATATCATCTTCTGTCTCCGACCTATAGTGCTAGACCCGAGC	Amplification of 53776 gene 3' flanking region for deletion	1031
pdel_53776_3R	GCGGATAACAATTTACACAGGAAACAGCATCTAGCCGTGATACTCTGG		
pdel_73604_5F	GTAACGCCAGGGTTTCCAGTCACGACGAGTACCCGACTAATGACTGG	Amplification of 73604 gene 5' flanking region for deletion	1158
pdel_73604_5R	ATCCACTTAACGTTACTGAAATCTCCAACCTCTATTCTGCTCCCTGCTACC		
pdel_73604_3F	CTCCTTCAATATCATCTTCTGTCTCCGACTCTGTGAGAGAGAGAGAGAGG	Amplification of 73604 gene 3' flanking region for deletion	1177
pdel_73604_3R	GCGGATAACAATTTACACAGGAAACAGCTAGCACCAAGAGTAAGCTCC		
pdel_73618_5F	GTAACGCCAGGGTTTCCAGTCACGACGATCTGGCTTGGATACTCACC	Amplification of 73618 gene 5' flanking region for deletion	1216
pdel_73618_5R	ATCCACTTAACGTTACTGAAATCTCCAACGATCAGCAGATCTGTGAAGC		
pdel_73618_3F	CTCCTTCAATATCATCTTCTGTCTCCGACCACACTCATCTTTCAGC	Amplification of 73618 gene 3' flanking region for deletion	1016
pdel_73618_3R	GCGGATAACAATTTACACAGGAAACAGCGCTGTACTATCCGTAGAACC		
pdel_73621_5F	GTAACGCCAGGGTTTCCAGTCACGACGGTCGAAGAAGTGAGAGATGC	Amplification of 73621 gene 5' flanking region for deletion	1133
pdel_73621_5R	ATCCACTTAACGTTACTGAAATCTCCAACGAGTTGAGATACTCCGATGC		
pdel_73621_3F	CTCCTTCAATATCATCTTCTGTCTCCGACGTAGTCAATTTGCTGGTGTGG	Amplification of 73621 gene 3' flanking region for deletion	1081
pdel_73621_3R	GCGGATAACAATTTACACAGGAAACAGCGTCTTCACTACCAACATCC		
pdel_73623_5F	GTAACGCCAGGGTTTCCAGTCACGACGCTCTTCTATCAGCAGTGG	Amplification of 73623 gene 5' flanking region for deletion	1014
pdel_73623_5R	ATCCACTTAACGTTACTGAAATCTCCAACACACAGCAAAATGACTACC		
pdel_73623_3F	CTCCTTCAATATCATCTTCTGTCTCCGACGCGTAGCATTACTCCATAGC	Amplification of 73623 gene 3' flanking region for deletion	1182
pdel_73623_3R	GCGGATAACAATTTACACAGGAAACAGCTACGGTCGCTCACTATTAGG		
pdel_73631_5F	GTAACGCCAGGGTTTCCAGTCACGACGACCTGAAAGGTAAGGTGACG	Amplification of 73631 gene 5' flanking region for deletion	1123
pdel_73631_5R	ATCCACTTAACGTTACTGAAATCTCCAACAGCTGTATTGAACAGAGG		
pdel_73631_3F	CTCCTTCAATATCATCTTCTGTCTCCGACTCCGTTTACACTGAGACAGC	Amplification of 73631 gene 3' flanking region for deletion	1035
pdel_73631_3R	GCGGATAACAATTTACACAGGAAACAGCCATACGTCCGAAGAGTCACC		
102497_5F	GTAACGCCAGGGTTTCCAGTCACGACGGACGAGTAGATTGTCTATGG	Amplification of 102497 gene 5' flanking region for deletion	1088
102497_5R	ATCCACTTAACGTTACTGAAATCTCCAACAGTACTCATTGGTCAGAGC		
102497_3F	CTCCTTCAATATCATCTTCTGTCTCCGACCTGGTTAAGGTAAGCAGAGC	Amplification of 102497 gene 3' flanking region for deletion	1055
102497_3R	GCGGATAACAATTTACACAGGAAACAGCGCCCTTACCATTGTGTCTGG		
RT_43701_F	GTACGACCATTTGGCTTCGGC	qRT PCR, diagnostic PCR for deletion	264
RT_43701_R	TCCCTGACAACTGCGCCATAGC		
RT_53238_F	AGCGTCATCACCATGTCTCCGC	qRT PCR, diagnostic PCR for deletion	264
RT_53238_R	CGCTTCACTGACGACGAGGGAG		
RT_53776_F	GCGCACTGGAGTATCTGCACGA	qRT PCR, diagnostic PCR for deletion	257
RT_53776_R	CGGTAGCCCTGTGACGATCTCG		
RT_73604_F	AAGACCTCCAGCCGACCGATA	qRT PCR, diagnostic PCR for deletion	253
RT_73604_R	AACGTCTCGTACTCGCACCAGC		
RT_73618_F	ATGACGAGGATAGCAAGGCGGC	qRT PCR, diagnostic PCR for deletion	248
RT_73618_R	AATGGACAACCTGCTCCCGCC		
RT_73621_F	GCAACCTCGTCGATTTGGCTGC	qRT PCR, diagnostic PCR for deletion	218
RT_73621_R	AAGTGTCTCGAGAAGGACGCGC		
RT_73623_F	GACGAGGATGACGTGAAGCGCT	qRT PCR, diagnostic PCR for deletion	266
RT_73623_R	GCCAAGACCAGCGAGTCTTCCA		
RT_73631_F	AACGGCTCCGAAATCACTGCGA	qRT PCR, diagnostic PCR for deletion	232
RT_73631_R	CCCGGCATCAGATATCGCAGG		
int102497_F1	TGCTTGGTGGTACCGGGTCTA	qRT PCR, diagnostic PCR for deletion	250
int102497_R1	TCGTCCAAAGCCATGATGCCGT		

Table B. Copy number determination of strains used in this study.

gene ID	strain	copy number
controls	GNA3QL	1
	Δ gng1	3
43701	Δ 43701 20A	1
	Δ 43701 27A	1
53238	Δ 53238 18A	1
	Δ 53238 40A	1
73604	Δ 73604 1A	1
	Δ 73604 2B	2
73618	Δ 73618 1A	2
	Δ 73618 18AA	3
73621	Δ 73621 10aa	1
	Δ 73621 16aa	3
73623	Δ 73623 29A	2
	Δ 73623 48B	2
102497	Δ 102497 51AA	1
	Δ 102497 52AA	1