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Data Article

Primers and copper responsive promoter design and data of real-time RT-PCR assay in filamentous fungus *Trichoderma reesei*

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ABSTRACT

This data article contains data related to the research article entitled "Copper-mediated on-off control of gene expression in filamentous fungus *Trichoderma reesei*" (Wang et al., 2017) [1]. Four kinds of copper responsive promoters were designed. Quantitative PCR (qPCR) was performed to determine relative mRNA levels of red fluorescent protein gene (*rfp*) extracted from cells grown under different concentrations of $CuSO_4$. Three deletion vectors were constructed by using a copper-mediated self-excision cassette instead of a xylose-mediated self-excision cassette (Zhang et al., 2016) [2] to knock out *xyn1*, one of the two major specific endo-β-1,4-xylanases (Rauscher et al., 2006) [3], *xyr1*, the key transcriptional activator of cellulolytic and xylanolytic genes (Lichius et al., 2015) [4], and *ace3*, a factor essential for cellulase production (Häkkinen et al., 2014) [5]. This data article reports the primers, vector construction, and qPCR assay.

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Specifications Table

Subject area	*Biology*
More specific subject area	*Molecular biology, vector construction, Quantitative real time PCR*
Type of data	*Table, figure*
How data was acquired	*Sequencing data were acquired through NCBI. In silico analysis of gene using online Real-time PCR (TaqMan) Primer Design (GenScript, China) and primer design software version 6.0 (Premier Biosoft, USA).*
Data format	*Raw, analyzed*
Experimental factors	*Gene sequences were retrieved from GenBank database; Plasmid were constructed; rfp expression were analyzed by qRT-PCR*
Experimental features	*Four kinds of copper responsive promoters were designed. qRT-PCR was performed to determine relative red mRNA levels of rfp extracted from cells grown under different concentrations of $CuSO_4$. Three deletion cassettes were constructed to knockout xyn1, xyr1, and ace3, respectively.*
Data source location	*Shanghai, China*
Data accessibility	*Data is provided with this article*

Value of the data

- The modified copper responsive promoter Ptcu1c from *T. reesei* was used for the copper-dependent on-off control of DNA transcription and protein expression.
- The relative levels of *rfp* transcripts increased ~500-fold in the absence or presence of copper.
- The copper-mediated self-excision cassette was more widely used than a xylose-mediated self-excision cassette in some *T. reesei* disruptants for the screening of candidate regulators for cellulase and hemicellulase production.

1. Data

Four copper responsive promoters were designed. Quantitative real-time PCR (qRT-PCR) was performed to determine relative mRNA levels of *rfp* extracted from cells grown under different concentrations of $CuSO_4$. By using the copper-mediated self-excision cassette, three deletion plasmids were constructed to knockout *xyn1*, *xyr1*, and *ace3*.

2. Experimental design, materials and methods

2.1. Modified copper responsive promoters

Sequences of native P_{tcu1} (1715 bp) of *Trichoderma reesei* were downloaded from the genome sequence of *T. reesei* QM6a (http://genome.jgi-psf.org/Trire2/Trire2.home.html). Three truncated promoter forms, P_{tcu1a} (1249 bp), P_{tcu1b} (1085 bp), and P_{tcu1c} (535 bp), were randomly selected by us. The primers were designed using Primer Premier 6.0. The overlap sequences, "TTAATTAAGTTAACTCTAGA" and "CACGTGATGACCCGACGTC" were added to the 5′ ends of forward and reverse primers, respectively. Four kinds of copper responsive promoters were cloned by primers (Table 1).

2.2. Expression levels of rfp in T. reesei transformants

About 100 mg of *T. reesei* mycelium was harvested, and grown under different concentrations of $CuSO_4$ for 36 h. Total RNA was extracted using a FastRNA Pro Red Kit (MPbio, Irvine, CA, USA),

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