Running head: Functions of fungal Cdc14

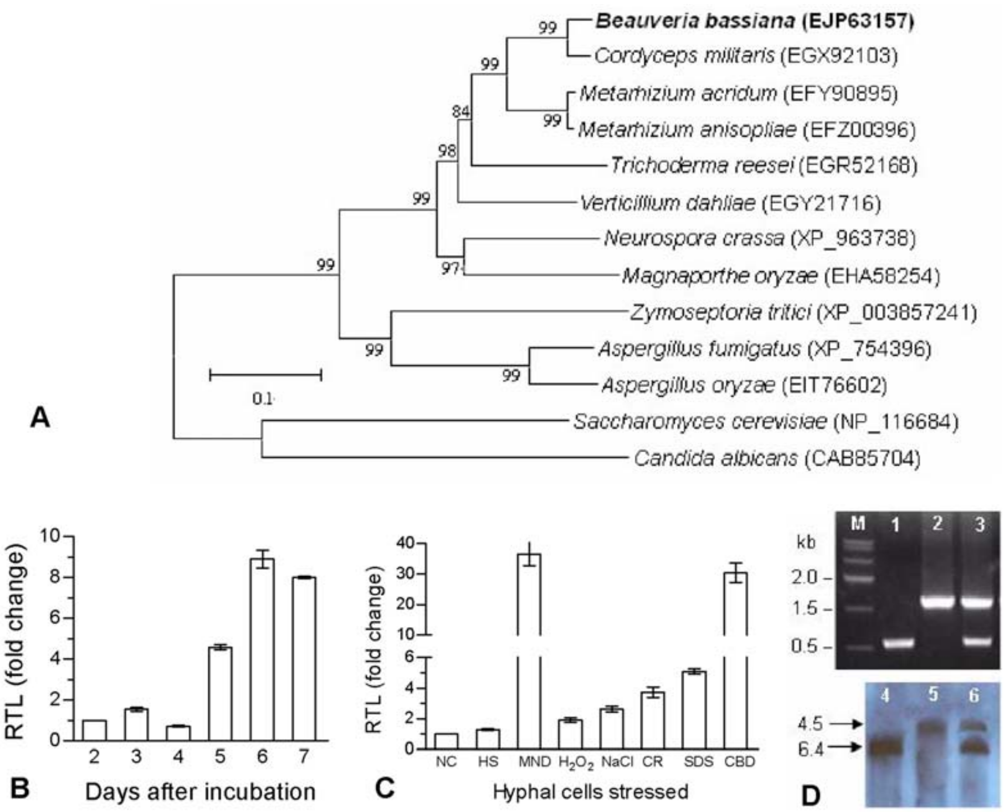
Cytokinesis-required Cdc14 is a signaling hub of asexual development and multi-stress tolerance in *Beauveria bassiana*

Jie Wang, Jing Liu [†], Yue Hu [†], Sheng-Hua Ying and Ming-Guang Feng [*]

Institute of Microbiology, College of Life Sciences, Zhejiang University, Hangzhou, Zhejiang, 310058, People's Republic of China

[†] These authors contribute equally to the study.

* Corresponding author: M.-G. Feng, Institute of Microbiology, College of Life Sciences, Zhejiang University, Hangzhou, Zhejiang, 310058, People's Republic of China. Phone and fax: 86-571-88206178. E-mail: mgfeng@zju.edu.cn



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Primers	Paired sequences (5'-3')	Purpose
5'Cdc14-F/R	AAAAA**GAATTC**GGAGCAGGAAAACGAGGTGT / AAAAA**GGATCC**TTTTGCGATTATTT GCGTGC	Cloning 5'-end for *Cdc14* deletion
3'Cdc14-F/R	AAAAA**AGATCT**CGACATTCTCGGTGCCAAGG / AAAAA **ACTAGT**GCCAATGTTCTCGG CGTCTC	Cloning 3'-end for *Cdc14* deletion
rCdc14-F/R	**GGGGACCACTTTGTACAAGAAAGCTGGGT** GCGTTGGTGGATGGGATAC / **GGGGAC AAGTTTGTACAAAAAAGCAGGCT**ACGCACGCTTTGGAGCAGTC	Cloning full-length *Cdc14* for complement
pCdc14-F/R	AGGCACAACATCACAGCAAC / CGGCTTACTTCTTGGGTCAG	Mutant ID by PCR
sCdc14-F/R	GAAGCCCCTGTATCCAATCG / AGACAGTTGCCAAGGGTGCT	Mutant ID by Southern
qCdc14-F/R	TTACGATTGATGATAGCCTCTTCT / AATGGCGAAGCGGTAGAG	Mutant ID by qRT-PCR
18S-F/R	TGGTTTCTAGGACCGCCGTAA / CCTTGGCAAATGCTT TCGC	Mutant ID by qRT-PCR

Fig. S1. Phylogenetic and transcriptional features of *B. bassiana* Cdc14 and creation of its disruption and complemented mutants. (A) Phylogenetic tree for Cdc14 orthologues in fungal and yeast species (NCBI accession codes in parentheses). Scale bar: branch length proportional to genetic distance assessed with neighbor-joining method. (B) Relative transcript levels (RTL) of *Cdc14* (assessed via qRT-PCR) in wild type during 7-day growth (versus day 2) on SDAY at 25°C. (C) RTL of *cdc14* in wild-type cultures grown for 3 days on 1/4 SDAY supplemented with menadione (MND, 0.2 mM), H_2O_2 (2 mM), NaCl (0.8 M), Congo red (CR, 0.5 mg/ml), SDS (0.2 mg/ml) and carbendazim (CBD, 0.5 μg/ml) at 25°C respectively or exposed for 1 h to heat shock (HS) at 40°C (NC: normal culture not stressed). Error bars: SD. (D) Identification of C*dc14* disruption and complement mutants via PCR (lanes 1–3) and Southern blotting (lanes 4–6). Lanes 1 and 4: wild type. Lanes 2 and 5: *ΔCdc14*. Lanes 3 and 6: *ΔCdc14/Cdc14*. (E) Paired primers used for the manipulation of *B. bassiana Cdc14* and the identification of its mutants (Blue: the sites of restriction enzymes *Eco*RI/*Bam*HI and *Bgl*II/*Spe*I. Red: fragments for gateway exchange).

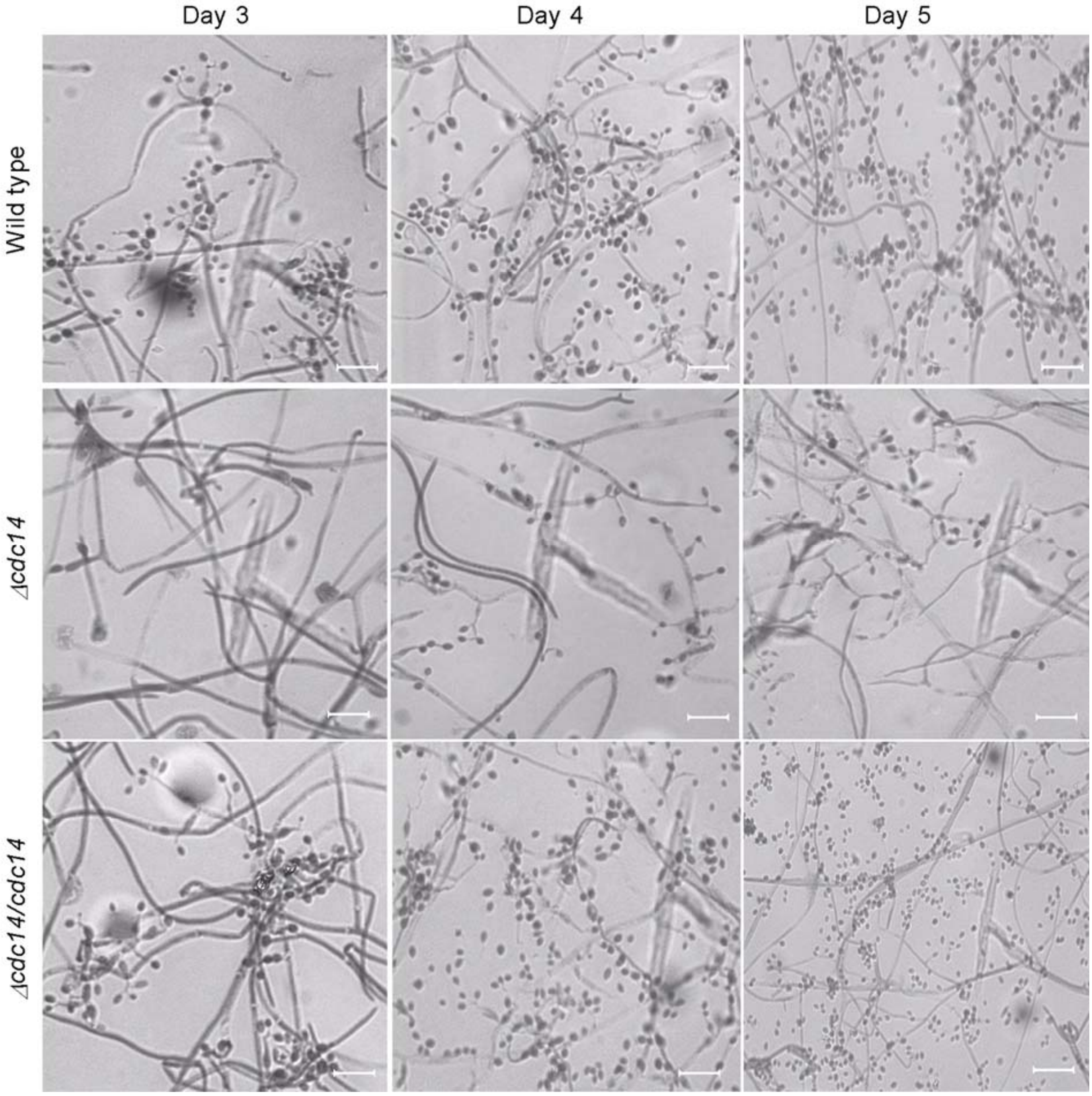

Fig. S2. Morphological comparison of colony samples taken during the conidiation of *B. bassiana* wild-type strain and *cdc14* mutants grown on SDAY plates at 25°C. Scale bars: 10 μm.

Table S1. Paired primers used for assessing the transcript levels of 88 genes in the *Cdc14* disruption and complement mutants versus wild type of *B. bassiana* via qRT-PCR.

Tag code*	**Gene**	**Annotation**	**Sequences (5'-3') of paired primers**
Involved in cytokinesis			
BBA_08543	*wee1*	WEE protein kinase	CTCGTCTACCAGCATCTT / CACCTGTTCAACCTTGTC
BBA_07180	*mid1*	calcium channel subunit	ATGAATTACACAGACAAG / ACATATCGGTGATAGTAG
BBA_01304	*ace2*	transcription factor	CAAGAAGAAGACATTATGC / ATCATCATTCGTGAACAT
BBA_03872	*eng1*	endo-1,3-beta-glucanase	AACACCTACTACAATGAT / TAGTCCTTGTTCTTATCG
BBA_01202	*dse1*	WD domain-containing protein	ATCTCTACTGTTATTGTAAG / ATGATAATATCGGTGTCT
BBA_01489	*sli15*	inner centromere protein	CTCCAGATTGTTCAGTCAG / GTTTCGTTCTCATCAAATATAC
BBA_00440	*ask1*	subunit Ask1	CAAGCAGAAATATGAAATCG / TTTGTAATAGTTTGGATGGT
BBA_05079	*ase1*	microtubule associated protein	AAGAAGGAAATGATTGAC / GGATAAGTTATTGTGATGT
BBA_03315	*cdc15*	CDC15 protein kinase	AATCTACCAACTGCCTCAAC / GTCATATACACGCCAACAAG
BBA_03150	*mob1*	Mob1 family protein	ATGAAGGCTACTGACGAATT / AGGTCATCAACTGCTCAAT
BBA_08042	*plo1*	serine/threonine-protein kinase	CATCATCTCTTCCAAGACAGT / ATCGTTGAGGATATAGCCAAG
BBA_03681	*spg1*	septum-promoting GTP-binding protein 1	ATCAAGGAGTGGTATAGAC / ATCTTGGATTGGAAAGTTG
BBA_02370	*sid2*	serine/threonine-protein kinase	CGACAGGAGTATCTATCTTG / AGAACATTTCCGCAATATAG
BBA_04438	*cbk1*	Serine/threonine-protein kinase	CTTTCCAGGACACTTACTTT / AATGTAGAAGCGAGTTATGT
BBA_06124	*cts1*	CTP synthase	TATCTTGGCATTCGTCTCAG / CGGTCTTCCCTAAATAGTCTC
BBA_08017	*scw11*	cell wall glucanase	AACATTTGGCAGCAGACT / TTGAAGAAGGCGTGGATG
BBA_10084	*hym1*	conidiophore development protein hymA	AAGACCTTGTTCCACGATAT / TTAATAGACTGACGCTTGGT
BBA_04198	*tao3*	cell morphogensis protein	CCTTGTTCAAATATCTCATT / ATCTGTAAATATGGATGTTG
Involved in growth and asexual development			
BBA_04942	*fluG*	developmental protein	CCTCCCTAGTTTGGTCGCTTTCTC / CGCTGTCGGTAATCTGCTCCTC
BBA_02968	*flbA*	developmental regulator	CCAATCCACTCGCCGCTCTC / CGGAGGAAAGAGAATCGGTAGAGG
BBA_06988	*flbB*	bZIP transcription factor	GCACTGACACGCCGACAAGAGC / CCGCCGCCGAAGCCTGTTG
BBA_03181	*flbC*	C_2H_2 conidiation transcription factor	TCCATCTCCAACTTGCTGGGTCTC / GGCGGCGTAGGCGGAAGG
BBA_07259	*flbD*	MYB conidiophore development protein	CGGCAAGCGATGGGCAGAGATTG / ACGAGCAAGGTGACGGTAGAGGTG
BBA_06599	*hyd1*	hydrophobin	TTCTCAGCGATCTTGATCTT / GCACTTGTTGTCGATTGG
BBA_03015	*hyd2*	class I hydrophobin	CATGGTGGAAAGGATCTG / ATCTTGGTCGTCTTCTCG
BBA_10084	*hymA*	conidiophore development protein	TCGCAAGATGGTTCAGTA / GGACAAGAAGGTAAGAAGTT
Involved in response to oxidative stress			
BBA_02311	*sod1*	Cu/Zn superoxide dismutase	GCGGCTTCCACATCCACACCTTTG / GGTCCAGCGTTGCCAGTCTTGAG
BBA_09706	*sod2*	cytosol Mn-superoxide dismutase	CCAGTGTTTGGCATTGACATG / TCAGCCGTCTTCCAGTTGATG
BBA_09382	*sod3*	mitochondrial Mn-superoxide dismutase	TCTCCGGCAAGATTATGGAGC / TTGGCGTCATTCTTGGCCT
BBA_04317	*sod4*	superoxide dismutase	CGAGATGGTCCTTACGGCTTCAG / GCTCCCAGGTGTTGAGGCATAG
BBA_01984	*sod5*	superoxide dismutase	CGGCGACCTCAGCGGCAAGTAC / GCCAGCAACAACAGGGACCGTAGG
BBA_05603	*cat1*	catalase B	CCTCTGACGTTGGCGGCCCTTTC / CCGTGTCCGTGCTGCCTCGTG
BBA_06186	*cat2*	catalase A	CCGTCTGGGCATCAACTGGGAAG / GCTGGGCGTGGTCGTGGTAG
BBA_06567	*cat3*	Catalase	TCAAGTCGGTTCAGGAGATGGAG / TTGTTGCGTCTTCAATCGGAGTG
BBA_09109	*cat4*	catalase C	GAGGAGCCCAGCAACGCACAAGAG / CTGAGGACGACAAGGCCGCCATTC
BBA_09338	*cat5*	catalase P	GCTGGGCTGATCTGCTGGTCCTTG / TCCTTGCTGTAACGGTGGCTGTCG
BBA_09760	*cat6*	catalase D	CGGCTGCGGTGTCTTGTCCATAC / CCTTGTCGGCGTTCTGGCGAAG
BBA_08024	*pod1*	cytochrome c peroxidase	GCCGCCGCTTCTACTCGTCTG / CGTTGCTGCCGCCAGTACCG
BBA_00792	*pod2*	peroxidase	CCGCCAGAATGCCGCCGAGTG / GAATGATGGGTCCGCCGCAGGAG
BBA_08023	*pod3*	NADH oxidase	CACACGCACCGACGACTACG / GTTGCCGCCGCTGCTGAC
Involved in cell wall integrity			
BBA_09307	*chn1*	acidic chitinase endochitinase 1	TGACAACTCGCTTATCAGT / TTATCATACTTGGTCTCAGGAT
BBA_05353	*chn2*	class III chitinase	GCAATTTGACTACCTCTG / CGTATTGGCAATGTTCTT

BBA_02017	*chn3*	chitinase 3	CGGCTCATCACATACTACC / AATGTCGGGCTGCGTAAT
BBA_06297	*chn4*	class III chitinase, chitinase 4	TGAATGGCATAACTCCTG / CGTCTTGATGTCCTCTTC
BBA_09585	*chn5*	chitinase 5	AATCTGGTTACTGTGGTT / TTTGGAGGATCTGAGAAC
BBA_09259	*chn6*	symbiotic chitinase	CAGATGTGAATAATCCAATG / AAGAATATGAGCCAAGTTAG
BBA_02230	*chn7*	chitinase	GTATCAACTACCTCAAGT / TCATATAGACAATGTAATCG
BBA_08982	*chn8*	class V chitinase	TAATGCTAATGCCACTTATG / AGAGATATTGATGCGTTTGT
BBA_00297	*chn9*	class V chitinase	TACATCTCCAATGCTGAAATC / CCACTGGTTCTTGTCGTAT
BBA_03814	*chn10*	chitinase	AATGTATACTCTACCGTCAG / CTTGCTGGAAATGTAACTTT
BBA_06317	*chn11*	chitinase	GACCATTGTGCCGATTCT / GGTGGACAGGGTGTTTATG
BBA_04667	*chs1*	chitin synthase 1	ACCTATATCAACATTCTC / GACAATCTCATTCTTCTC
BBA_03236	*chs2*	chitin synthase 2	TGTGTCTTACTGATTGCT / TAATGATGGCGTAGATGAT
BBA_03590	*chs3*	chitin synthase 2	TCTTCAACACCGTCAACAT / TCCTACCGAGCAAGTCTT
BBA_08043	*chs4*	chitin synthase 4	CAGTCAGATTATCCTTATGTCAT / GATATACCAGTCACCTTCC
BBA_02360	*chs5*	chitin biosynthesis protein	ATGAGAGCGTGATTGAAG / CTGCTTTTCCTTTTCCTC
BBA_06858	*chs6*	chitin synthase 6	TGGAATTGTATCAAGAACT / GAGAATAATGGCACAGAT
BBA_03793	*chs7*	chitin synthase chaperone-like protein	CGTAATGATGGTCTACAAG / CTCCTCAGGAAGTAACTC
BBA_06859	*chs8*	class V chitin synthase	GACTACAAGAACAACAAC / ACGAGTATCATTGGTATAG
BBA_08396	*chs9*	chitin synthase	CAACAAGAAGAAGCCAAG / ATAATGACGAGTCCACTAAT
BBA_07346	*chs10*	class VII chitin synthase	CCTCTTTATTCTCTTTATCG / GGTTGTTGATGTAATGAC
BBA_06846	*chs11*	class VII chitin synthase	GGAGATTATGGAAGCGAT / TAGACAATAGTGCGATGAC
BBA_06144	*mhp1*	cell wall biogenesis protein	GGACCAACCTCCATCACCACAAGC / GCTCACCGATAGGACACCGTTCTC
BBA_06689	*ssd1*	cell wall biogenesis protein phosphatase	GCTCTCCCACCGTCGCAACCAATC / CACCTCCACCACCCCTTCCACCTC
Involved in response to osmotic stress			
BBA_08887	*sho1*	high osmolarity signaling protein	AGCGTCAACAACCTCGTCTAC / AGGCGTGGAGTTCTCAAAG
BBA_02191	*sln1*	sensor histidine kinase/response regulator	TCGGTGCCATCACTCCTTCCAACG / GCGGACGAGCAATGCCAACAGC
BBA_02621	*ssk1*	two-component response regulator	AGAACTTTAGCACCGAGCCCTTTC / AGAAGCAGCAGCAGACGATTGG
BBA_07057	*ypd1*	phosphotransmitter protein	TGACCAGGTCGAGGAGACGTTTGC / TCGGCGTCGGGTTCTGATGAGC
BBA_00971	*msn2*	stress response element binding protein	GCCCGCCACGCCCATCTAC / ACCGAGGTCTCAACCGAGTCAAAC
Involved in signal transduction pathways			
BBA_05916	*pkA*	cAMP-dependent protein kinase subunit	GCATCCGCAGCAGCAGAAC / GCTTGGACTGAACGAGGTGAAC
BBA_07006	*pkC*	protein kinase C	ATTGAAGAGATATGAAGAAC / AAGATTCGGAGTATTGAT
BBA_04261	*snf1*	Protein kinase	GCGAGAGGAACATATAGC / GGATTCACGACTAGCATT
BBA_04387	*ras1*	Ras GTPase protein	GGCGGTGGCGTCGGTAAATC / TGGCGGGAGGTGATGGAGTAG
BBA_04671	*ras2*	Ras GTPAse protein	CCTCGGTGACGGTGGTGTAG / GACTCCTTGACTCGCTGAATCTG
BBA_01318	*bck1*	MAP kinase kinase kinase (Bck1)	GACGCCTGATTACCTCTAACAC / CCTGACGCTGATTCCTTGAC
BBA_00937	*sskB*	MAP kinase kinase kinase (SskB)	GCAGAAGCACTCGGCACCATTTCG / GCGTTGCGGAAGAGGATCGGACTG
BBA_02280	*ste11*	MAP kinase kinase kinase (Ste11)	TATGCTTAACTCGTATGGT / TCGTGGAGATATGACAGA
BBA_01095	*mkk1*	MAP kinase kinase (Mkk1)	CCGCCGCACCTCAGATTCC / CGGTTGACCACCTTGAGAGACAG
BBA_04254	*mkk2*	MAP kinase kinase (Mkk2)	GCCGAGAACCGCCCAGACTTTG / TGCTCACAGTGCCGCCGTTTC
BBA_02330	*pbs2*	MAP kinase kinase (Pbs2)	CGCTCAATGCCGATGTCTTG / GGGCTGAGTTGATATGCTTGAC
BBA_01660	*mkk4*	MAP kinase kinase (Mkk4)	GAGGCGACTGAGGAGAGGACTGAG / CGGCGAGAGGACGGACCAAGAG
BBA_05588	*Mkk5*	MAP kinase kinase (Mkk5)	TTCTCAGACAGCACCAAT / GGCAGACTCTCATAATGTAT
BBA_01244	*mpk1*	MAP kinase (Mpk1)	CTGCTCCTCAACGCCAACTG / GCTGGTGGTGATAATCCTTGCC
BBA_03334	*slt2*	MAP kinase (Slt2)	ACCGACGCACACTTTCAATCCTTC / GCCCACAGACCACACATCAATAGC
BBA_04298	*maf1*	MAP kinase (Maf1)	CGTTCGTGTTGTGCCCGTCATTTC / CCGCCAATCTCATCGTCGTCTTCC
BBA_05209	*hog1*	MAP kinase (Hog1)	GGCTGGCGTCGTTCATCGTGACC / AAGGGCTTGCCGTCGAGCATCTC
BBA_09043	*sty1*	MAP kinase (Sty1)	ATCGCAGGCTCGCAAATACG / GGCTTGGCTGGCTGTTATCC

* Gene accession codes in the annotated genome of *B. bassiana* under the NCBI accession ADAH00000000.