AMERICAN SOCIETY FOR MICROBIOLOGY | genomeAnnouncements

# Draft Genome Sequence of Fungus *Clonostachys rosea* Strain YKD0085

**Shuai Liu,[a,b] Yaowen Chang,[c] Xujia Hu,[d] Xuanyun Gong,[d] Yingtong Di,[b] Jinyan Dong,[a] Xiaojiang Hao[b]**

Key Laboratory of Eco-Environments in Three Gorges Reservoir Region of Ministry of Education, School of Life Science, Southwest University, Chongqing, China[a]; State Key Laboratory of Phytochemistry and Plant Resources in West China, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, Yunnan, China[b]; Shenyang Pharmaceutical University, Shenyang, Liaoning, China[c]; Kunming University of Science and Technology, Kunming, Yunnan, China[d]

**Here, we report the draft genome sequence of *Clonostachys rosea* (strain YKD0085). The functional annotation of *C. rosea* provides important information related to its ability to produce secondary metabolites. The genome sequence presented here builds the basis for further genome mining.**

**Received** 27 April 2016 **Accepted** 17 May 2016 **Published** 23 June 2016

**Citation** Liu S, Chang Y, Hu X, Gong X, Di Y, Dong J, Hao X. 2016. Draft genome sequence of fungus *Clonostachys rosea* strain YKD0085. Genome Announc 4(3):e00538-16. doi: 10.1128/genomeA.00538-16.



Address correspondence to Yingtong Di, diyt@mail.kib.ac.cn, or Jinyan Dong, donjyaa@swu.edu.cn.

The fungus *Clonostachys rosea* belongs to the family *Bionectriaceae* and was previously described as *Gliocladium roseum* (1). *C. rosea* is widely distributed all over the world. The destructive force of this fungus, as a biological control agent, is very strong in nematodes, insects, and many plant-pathogenic fungi, such as *Botrytis cinerea* and *Fusarium graminearum*. Except for the secretion of cell wall-degrading enzymes, *C. rosea* can produce a wide range of bioactive secondary metabolites (2–9).

Genomic DNA of *C. rosea* strain YKD0085 was obtained from a sample cultured in *Aspergillus* minimal medium (AMM) and then sequenced on an Illumina HiSeq 2000 platform. *De novo* assembly of the reads was performed using the SOAP*denovo* assembly protocol version 1.05 (10). DNA sequencing resulted in 1,504,639,412 raw reads, where 78,717,175 unique reads were obtained (estimated genome coverage, 31-fold) and used for genome assembly. The resulting assembly consists of 787 scaffolds and 55.18 Mb ($N_{50}$, 528,196 bp; $N_{90}$, 75,119 bp). The total G+C content was 49.46%.

Protein-coding gene models were predicted using *de novo* prediction tools Genscan (11), Augustus (12), and the homology-based gene prediction tool GeneWise (13), with the default parameters. The homology-based and *de novo* gene sets were merged to form a comprehensive and nonredundant reference gene set by Glean (14). The functional annotation of predicted gene models was mainly based on homology to known annotated genes, and BLAST was the tool mainly used in our analyses. We aligned all protein models by BLASTP to Swiss-Prot and NCBI nr and also mapped them onto functional terms, including GO (15) and KEGG pathways (16) (BLASTP cutoff e value. <1e - 7). The final structural gene prediction resulted in 16,120 gene models. By homology search, we mapped 10,006 predicted proteins to GO terms. The annotation revealed that the genome encodes 28 nonribosomal peptide synthetases, 39 polyketide synthases, and 15 terpenoid synthases. The *C. rosea* genome revealed a rich repertoire of secondary metabolite-encoding genes.

**Nucleotide sequence accession numbers.** The draft genome sequence has been deposited at GenBank under the accession no. LWRQ00000000.The version described in this paper is the first version, LWRQ01000000.

## ACKNOWLEDGMENTS

We acknowledge the contributions by the staff from BGI-Shenzhen, who assisted with the data generation and analysis.

## FUNDING INFORMATION

This work, including the efforts of Yingtong Di, was funded by Xibuzhiguang Project and National Natural Science Foundation of China (NSFC) (81573323). This work, including the efforts of Xiaojiang Hao, was funded by Central Asian Drug Discovery and Development Center of Chinese Academy of Sciences. This work, including the efforts of Jinyan Dong, was funded by National Natural Science Foundation of China (NSFC) (31270091).

## REFERENCES

1. **Schroers HJ, Samuels GJ, Seifert KA, Gams W.** 1999. Classification of the mycoparasite *Gliocladium roseum* in *Clonostachys* as *C. rosea*, its relationship to *Bionectria ochroleuca*, and notes on other gliocladium-like fungi. Mycologia **91:**365–385. http://dx.doi.org/10.2307/3761383.
2. **Song HC, Shen WY, Dong JY.** 2016. Nematicidal metabolites from *Gliocladium roseum* YMF1.00133. Appl Biochem Microbiol **52:**324–330. http://dx.doi.org/10.1134/S0003683816030169.
3. **Chatterton S, Punja ZK.** 2009. Chitinase and beta-1,3-glucanase enzyme production by the mycoparasite *Clonostachys rosea* f. *catenulata* against fungal plant pathogens. Can J Microbiol **55:**356–367. http://dx.doi.org/10.1139/w08-156.
4. **Zhang L, Yang JK, Niu QH, Zhao XN, Ye FP, Liang LM, Zhang KQ.** 2008. Investigation on the infection mechanism of the fungus *Clonostachys rosea* against nematodes using the green fluorescent protein. Appl Microbiol Biotechnol **78:**983–990. http://dx.doi.org/10.1007/s00253-008-1392-7.
5. **Rodríguez MA, Cabrera G, Gozzo FC, Eberlin MN, Godeas A.** 2011. *Clonostachys rosea* BAFC3874 as a *Sclerotinia sclerotiorum* antagonist: mechanisms involved and potential as a biocontrol agent. J Appl Microbiol **110:**1177–1186. http://dx.doi.org/10.1111/j.1365-2672.2011.04970.x.
6. **Tomoda H, Ohyama Y, Abe T, Tabata N, Namikoshi M, Yamaguchi Y,**

**Masuma R, Omura S**. 1999. Roselipins, inhibitors of diacylglycerol acyltransferase, produced by *Gliocladium roseum* KF-1040. J Antibiot **52:** 689–694. http://dx.doi.org/10.7164/antibiotics.52.689.

7. **Dong JY, He HP, Shen YM, Zhang KQ**. 2005. Nematicidal Epipolysulfanyldioxopiperazines from *Gliocladium roseum*. J Nat Prod **68:** 1510–1513. http://dx.doi.org/10.1021/np0502241.
8. **Zhai MM, Qi FM, Li J, Jiang CX, Hou Y, Shi YP, Di DL, Zhang JW, Wu QX**. 2016. Isolation of secondary metabolites from the soil−derived fungus *Clonostachys rosea* YRS-06, a biological control agent, and evaluation of antibacterial activity. J Agric Food Chem **64:**2298–2306. http://dx.doi.org/10.1021/acs.jafc.6b00556.
9. **Dong JY, Zhou W, Li L, Li GH, Liu YJ, Zhang KQ**. 2006. A new epidithiodioxopiperazine metabolite isolated from *Gliocladium rosea* YMF1.00133. Chin Chem Lett **17:**922–924.
10. **Li R, Zhu H, Ruan J, Qian W, Fang X, Shi Z, Li Y, Li ST, Shan G, Kristiansen K, Li SG, Yang HM, Wang J, Wang J**. 2010. *De novo* assembly of human genomes with massively parallel short read sequencing. Genome Res **20:**265–272. http://dx.doi.org/10.1101/gr.097261.109.
11. **Salamov AA, Solovyev VV**. 2000. *Ab initio* gene finding in *Drosophila* genomic DNA. Genome Res **10:**516–522. http://dx.doi.org/10.1101/gr.10.4.516.
12. **Stanke M, Waack S**. 2003. Gene prediction with a hidden Markov model and a new intron submodel. Bioinformatics **19**(Suppl 2):ii215–ii225. http://dx.doi.org/10.1093/bioinformatics/btg1080.
13. **Birney E, Clamp M, Durbin R**. 2004. GeneWise and Genomewise. Genome Res **14:**988–995. http://dx.doi.org/10.1101/gr.1865504.
14. **Elsik CG, Mackey AJ, Reese JT, Milshina NV, Roos DS, Weinstock GM**. 2007. Creating a honey bee consensus gene set. Genome Biol **8:**R13. http://dx.doi.org/10.1186/gb-2007-8-1-r13.
15. **Ashburner M, Ball CA, Blake JA, Botstein D, Butler H, Cherry JM, Davis AP, Dolinski K, Dwight SS, Eppig JT, Harris MA, Hill DP, Issel-Tarver L, Kasarskis A, Lewis S, Matese JC, Richardson JE, Ringwald M, Rubin GM, Sherlock G**. 2000. Gene Ontology: tool for the unification of biology. The Gene Ontology Consortium. Nat Genet **25:** 25–29. http://dx.doi.org/10.1038/75556.
16. **Kanehisa M, Goto S, Kawashima S, Okuno Y, Hattori M**. 2004. The KEGG resource for deciphering the genome. Nucleic Acids Res **32:** D277–D280. http://dx.doi.org/10.1093/nar/gkh063.