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Transcriptome analysis of *Paecilomyces hepiali* at different growth stages and culture additives to reveal putative genes in cordycepin biosynthesis

Authors: Fang Pang[a], Linping Wang[a], Yu Jin[a], Lanping Guo[c], Lipu Song[b], Guiming Liu[b], Chengqiang Feng[a]*
[a] Beijing Key Laboratory of Protection and Utilization of TCM, Beijing Normal University, Beijing 100875, China
[b] CAS Key Laboratory of Genome Sciences and Information, Beijing Institute of Genomics, Chinese Academy of Sciences, Beijing 100101, China
[c] Resource Center of Chinese Materia Medica, China Academy of Chinese Medical Sciences, Beijing 100700, China
Email address:
Fang Pang: pangfang159bnu@outlook.com
Corresponding author: Chengqiang Feng: fengchengqiang@bnu.edu.cn
Postal Address: No.19 Xinjiekouwai Street, Beijing 100875, China

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Abstract

Paecilomyces hepialid (PH) is an endoparasitic fungus of *Cordyceps sinensis* (CS) and has become a substitute for CS due to their similar pharmacological activities. Because the market demand for CS is difficult to satisfy, and cordycepin, the effective compound of CS, is difficult to industrially produce, we produced 5 samples of PH by culturing for different durations and adding different additives to the culture broth, and detected their cordycepin content with UPLC ESI MS/MS. Then we grouped these cultures into five transcriptome comparisons containing 3 time variable groups and 2 additive variable groups. We used next-generation (NG) sequencing methods to acquire transcriptomic information and investigated the response of gene expression to the additives and the influence of different growth stages. This work will contribute to a better understanding of purine metabolism in PH, and possibly in other *Cordyceps* species. It will provide a useful resource to further advance transcriptomics studies in *Cordyceps* species.

Introduction

Paecilomyces hepialid (PH) is an endoparasitic fungus of *Cordyceps sinensis* (CS) [1]. CS, a kind of caterpillar fungus, is called ‘DongChongXiaCao’ (DCXC) in China [2], and it has been reported that CS has pharmacological properties such as anti-inflammatory activity, antioxidant activity, neuroprotective activity, anti-tumor activity and anti-metastatic activity [3]. The chemical constituents of CS are considered to include cordycepin, ergosterol, polysaccharides, a glycoprotein and

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