

论著

## 自然感染诺氏疟原虫患者血片样本PCR鉴定

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摘要

目的 对云南省1例诊断为“间日疟”患者血片中形态不典型的疟原虫种进行分子生物学鉴定。方法 分别抽提待鉴定血片和已知感染虫种的4种疟原虫(间日疟原虫、恶性疟原虫、诺氏疟原虫、食蟹猴疟原虫)血片疟原虫基因组DNA, 再根据疟原虫小核糖体亚基(SSU rRNA)序列合成疟原虫属特异性引物, 以及恶性疟原虫、间日疟原虫、诺氏疟原虫种特异性引物, 然后对包括待鉴定血片在内的疟原虫DNA分别进行PCR鉴定。结果 用诺氏疟原虫特异性引物从待鉴定血片DNA中扩增出约150 bp条带, 测序结果表明该序列与诺氏疟原虫SSU rRNA序列完全一致。结论 云南省该例疟疾患者感染了猴疟原虫——诺氏疟原虫。

关键词 [诺氏疟原虫](#) [人体自然感染](#) [SSU rRNA](#)

分类号

## Molecular Identification of Naturally Acquired *Plasmodium knowlesi* Infection in a Human Case

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Abstract

Objective To confirm the diagnosis of a human case with atypical vivax-malaria from Yunnan Province by molecular technique. Methods DNA was extracted from blood films of unidentified sample, and of four known *Plasmodium* species (*P. vivax*, *P. falciparum*, *P. knowlesi*, and *P. cynomolgi*). A DNA-based diagnosis with the polymerase chain reaction (PCR) method targeting the small subunit ribosomal RNA (SSU rRNA) genes of genus- and species-specific (two human malaria species and *P. knowlesi*) was introduced. Results The PCR amplification with primer pair specific for *P. knowlesi* produced a single fragment of 150 bp. Sequence analysis showed that the amplified fragment was identical to the sequence of *P. knowlesi*. Conclusion The patient was naturally infected with *P. knowlesi*.

Key words [Plasmodium knowlesi](#) [Natural infection](#) [Human](#) [SSU rRNA](#)

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