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论著

## 应用CO I 短序列片段鉴定常见嗜尸性麻蝇

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**摘要:** 目的:利用线粒体DNA(mtDNA)中278 bp的细胞色素氧化酶辅酶I (cytochrome oxidase I, CO I)序列鉴定我国常见嗜尸性麻蝇,寻求快速、准确的嗜尸性麻蝇种类鉴定方法。方法:从12个省16个地区户外草地家兔尸体上采集麻蝇科3属4种共计19个样本。利用十二烷基硫酸钠-蛋白酶K法提取蝇类胸肌mtDNA; Eppendorf 5331型扩增仪对278 bp的CO I 基因片段进行PCR扩增; 检测扩增产物, PCR胶回收纯化, 测序并上传GenBank; 利用MEGA4.0 软件按邻近法构建无根系统发育树, 通过序列分析建立种内及种间进化分歧表。结果:邻近法构建的发育树中4种麻蝇各自聚群, 与形态学鉴定结果一致, 上述麻蝇按照不同属、种分别聚类, 其种内分歧整体均数均小于或等于3%, 种间进化分歧均数在8%~12%之间。结论: CO I 中278 bp基因序列能有效地鉴定常见嗜尸性麻蝇种类, 进一步完善我国嗜尸性麻蝇基因库, 为今后在实际案例中应用分子标记鉴定嗜尸性麻蝇进而推断死亡时间奠定基础。

**关键词:** 法医昆虫学 嗜尸性麻蝇 分子鉴定 细胞色素氧化酶辅酶 I

## Identification of common *Sarcophagidae* by short cytochrome oxidase I fragment

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**Abstract:** Objective: To identify the common *Sarcophagidae* with a 278 bp fragment of cytochrome oxidase I in mitochondrial DNA and to obtain an unambiguous and rapid identification method for *Sarcophagidae* in forensic investigations.

Methods: Nineteen Sarcosaprophagous flies were collected from 16 locations in 12 Chinese provinces. All specimens were comprised of 4 species. The mtDNA of flies was extracted with SDS-PK extraction method. Polymerase chain reaction was conducted in an Eppendorf 5331 thermal cycler. The PCR products were purified and sequenced and the obtained sequences were uploaded to GenBank. A neighbor-joining tree was constructed with MEGA4.0 package.

Results: The 19 Sarcosaprophagous flies were well clustered. The intraspecific variation within species varied from 0% to 3%, while the interspecific variations between species varied from 8% to 12%.

Conclusion: Congeneric species can be separated by the short fragment (278 bp region in the cytochrome oxidase subunit I gene), which will be instrumental for implementation of the Chinese *Sarcophagidae* database and lay a foundation for post mortem interval estimation in future forensic cases.

**Keywords:** forensic entomology *Sarcophagidae* molecular identification cytochrome oxidase I

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