

# 基于 DNA 宏条形码的庞泉沟不同生境 鳞翅目昆虫物种多样性差异比较

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**摘要:**【目的】为详细了解庞泉沟国家级自然保护区鳞翅目昆虫的物种组成, 并探究不同生境鳞翅目昆虫多样性差异。【方法】在庞泉沟国家级自然保护区的森林和草地两种生境内分别设置采样点, 森林生境内选定 5 块样地, 在草地生境内选定 4 块样地, 各样地内蝶类和蛾类分别使用网捕法和灯诱法采集, 应用经典形态学和宏条形码技术, 鉴定所采集的鳞翅目物种。分析庞泉沟国家级自然保护区两种生境鳞翅目昆虫物种组成与多样性差异。【结果】结果表明, 9 块样地内共采集鳞翅目昆虫样本 2944 头, 隶属于 18 科 80 属 454 种。从两种生境内鳞翅目昆虫的科、属、种组成来看, 两种生境内鳞翅目昆虫组成无明显差异, 但科级水平的昆虫丰度有明显差异, 舟蛾科在黑渠岭样地数量最多, 丰度值高达 40.78; 夜蛾科在主干沟样地数量最多, 丰度值为 33.74; 木蠹蛾科在大草坪样地数量最多, 丰度值为 27.58。从属级水平来看, 草地生境属的数量多于森林生境。从种级水平来看, 森林生境内 5 块样地物种共计 88 种, 草地生境内 4 块样地物种共计 116 种。 $\alpha$ 多样性分析表明, 主干沟样地内的鳞翅目昆虫多样性最高, 黑渠岭样地内鳞翅目昆虫多样性最低;  $\beta$ 多样性分析表明, 不同生境之间鳞翅目昆虫群落组成不存在相似性, 但差异也不显著。【结论】经典形态学耦合了宏条形码技术可以大大提高鉴定效率; 昆虫多样性和相对丰度指标应结合使用, 综合评判昆虫发生情况, 可以为害虫监测提供重要依据。

**关键词:** 庞泉沟国家级自然保护区; 鳞翅目; 宏条形码; 昆虫多样性

## A Comparison of Lepidoptera Species Diversity in Different Habitats of Pangquangou Based on DNA Metabarcoding

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**Abstract:** 【Objective】To thoroughly study the species composition of Lepidoptera insects in the Pangquangou National Nature Reserve and to explore the differences in Lepidoptera diversity across various habitats. 【Method】Sampling plots were established in both forest and grassland habitats within the Pangquangou National Nature Reserve, with five plots selected in the forest habitat and four in the grassland habitat. Butterflies and moths were collected using sweep netting and light trapping methods within each plot. Classical morphology and metabarcoding technology were applied to identify the collected Lepidoptera species. The composition and diversity of Lepidoptera species in the two habitats of the reserve were analyzed. 【Result】A total of 2944 bulk samples were collected from the nine sampling sites, belonging to 18 families, encompassing 80 genera, and 454 species. There were no significant differences in the composition of Lepidoptera insects between the two habitats, but there were notable differences in the abundance

at the family level. The family Notodontidae was most abundant in the Heiquling plot with an abundance value of 40.78; Noctuidae was most abundant in the ZhuGangou plot with an abundance value of 33.74; Cossidae was most abundant in the DaCaoPing plot with an abundance value of 27.58. At the genus level, the number of genera in grassland plot was higher than in the forest habitat. At the species level, the forest habitat had a total of 88 species across the five plots, while the grassland habitat had 116 species across the four plots. Alpha-Diversity analysis showed that the highest diversity of Lepidoptera insects was found in the ZhuGangou plot, while the lowest was found in the Heiquling plot. Beta-Diversity analysis showed no similarity in the community composition of Lepidoptera between different habitats, although the differences were not significant. 【 Conclusion 】 The coupling of classical morphology with metabarcoding technology can greatly improve identification efficiency. Insect diversity and relative abundance indicators should be used in combination to comprehensively assess insect occurrence, providing important basis for pest monitoring.

**Keywords:** Pangquangou National Nature Reserve; Lepidoptera; Metabarcoding; Insect Diversity