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Song Yang,Hu Linlin,Huang Weiwei,et al.Diversity of gastric flora in Mongolian gerbil model with *Helicobacter pylori* infection

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[J].Journal of Third Military Medical University,2012,34(09):805-808.

## 幽门螺杆菌感染蒙古沙鼠模型胃黏膜菌群多样性研究(PDF)

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Title: Diversity of gastric flora in Mongolian gerbil model with *Helicobacter pylori* infection

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摘要: 目的 对幽门螺杆菌(*Helicobacter pylori*, Hp)感染蒙古沙鼠模型胃黏膜菌群多样性进行研究,探讨Hp感染与胃内菌群的关系。方法 建立Hp感染的蒙古沙鼠模型,空白对照组、阴性对照组、直接感染组和预处理感染组各15例,4周后采集胃黏膜样本,同时检测Hp定植率,并提取细菌基因组DNA,采用聚合酶链反应-变性梯度凝胶电泳技术(PCR-DGGE)对黏膜局部菌群进行指纹图谱分析,并对特异性条带进行测序鉴定分析。结果 预处理感染组感染率(93.3%)与直接感染组感染率(26.7%)有明显差异( $P<0.05$ );各实验组PCR-DGGE指纹图谱分析显示条带数量,空白对照组( $21.6\pm 2.5$ )、阴性对照组( $3.3\pm 1.1$ )、直接感染组( $14.6\pm 2.4$ )和预处理感染组( $7.2\pm 2.2$ ),经统计学分析,各组间均有明显差异( $P<0.05$ ),提示蒙古沙鼠各组间菌群多样性存在显著的差异性。结论 Hp感染与胃黏膜菌群结构的变化密切相关。

Abstract: Objective To clarify the relationship between the diversity of gastric flora and *Helicobacter pylori* (Hp) infection in the stomach in the Hp-infected Mongolian gerbil. Methods A total of 60 Mongolian gerbils were divided into 4 groups, blank control, negative control, direct infection group and pretreatment infection group, with 15 animals in each group. The gerbils in the later group was induced to Mongolian gerbil model with Hp infection by gastric gavage of Hp stain M12, with or without pretreatment of 0.3 ml 50% ethanol and 0.3 ml antibiotics suspension. The gastric mucosa samples were collected in 4 weeks later, and the infection rates of

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*Hp* were counted at the same time. Total bacterial genomic DNA was collected from the Mongolian gerbils from 4 groups. Samples were analyzed by PCR-denaturing gradient gel electrophoresis (DGGE), and specific bands on fingerprints were sequenced. Results There was a significant difference in the infection rates of *Hp* between the pretreatment infection group (93.3%) and the direct infection group (26.7%) ( $P<0.05$ ). The average number of bands was  $21.6\pm 2.5$  in blank control group,  $3.3\pm 1.1$  in negative control group,  $14.6\pm 2.4$  in direct infection group,  $7.2\pm 2.2$  in pretreatment infection group, and there were significant differences among them ( $P<0.05$ ), which suggested there were significant diversities in gastric flora among 4 groups. Conclusion *Hp* infection is closely related to the changes of composition of gastric flora.

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#### 参考文献/REFERENCES

宋阳, 胡琳琳, 黄薇薇, 等. 幽门螺杆菌感染蒙古沙鼠模型胃黏膜菌群多样性研究[J]. 第三军医大学学报, 2012, 34(9): 805-808.

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