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Title: Analysis of the evolutionary pathway of *Streptococcus suis* serotype 2 89K pathogenicity island

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摘要: 目的 分析2型猪链球菌89K致病岛的结构特征,探索其进化历程。 方法 通过BLAST比对,获取89K致病岛的同源序列,构建其同源序列数据库;分析89K致病岛的碱基组成特征,寻找重组热点区域,并对89K进行分区;对各ORF进行功能预测,划分功能模块;对89K致病岛与其同源序列进行系统发育分析及共线性分析,推测其可能的进化历程。 结果 89K致病岛可分为4个保守区,4个主要的非保守区及一段Tn916转座子,呈现多个异源序列相嵌合的结构特征。功能分析发现保守区基因主要参与致病岛的横向转移及其在宿主菌基因组中的稳定,保守区的基因呈现出进化上的一致性,且在某些菌株中保守区以连续状态存在。 结论 保守区在祖先状态时是一个连续整体,不同来源的非保守区经过多次水平转移和重组事件插入到保守区之间,形成了89K致病岛的嵌合结构。

Abstract: Objective To analyze the structure of 89K pathogenicity island (89K PAI) of *Streptococcus suis* serotype 2 (*S. suis* 2), and to explore its evolutionary pathway. Methods BLAST was performed to obtain *S. suis* 2 89K PAI homologous sequences and to establish the homologous sequence database. The base composition pattern of 89K PAI was analyzed to find recombination hotspots, and 89K PAI was divided into several independent regions. The function prediction of each open reading frame (ORF) was performed to distinguish functional modules. Phylogenetic and co-linearity analysis of 89K PAI and its homologous sequences were performed to speculate the possible evolutionary pathway. Results *S. suis* 2 89K PAI was divided into four conserved regions, four main non-conserved regions and a Tn 916 transposon, showing a mosaic structure made up of heterologous sequences. The conserved regions were involved in 89K PAI lateral gene transfer and its maintenance in host bacteria genome. The conserved regions showed a congruent evolutionary pattern and in some bacterial genome the conserved regions were continuous. Conclusion The ancestor status of the conserved regions exists as a continuous entirety, and the non-conserved regions from diverse origins are inserted into the conserved regions by multiple lateral gene transfer and recombination, resulting in the mosaic structure of *S. suis* 2 89K PAI.

参考文献/REFERENCES

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