

赣中南花猪随机扩增多态DNA与群体遗传关系的研究 Population Genetic Relationships of Ganzhongnan Spotted Pig Breed Inferred from Random Amplified Polymorphic DNA Analysis

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收稿日期 修回日期 网络版发布日期 接受日期

摘要 用RAPD技术检测了泰和冠朝猪、永丰藤田花猪、瑞金三花猪、兴国茶园猪、上犹花猪、万安花猪、乐安花猪等7个赣中南花猪地方类群基因组混合DNA的多态性, 经80个随机引物扩增筛选, 16个引物产生了共44个多态标记。遗传距离指数计算结果显示: 泰和冠朝猪和瑞金三花猪亲缘关系最近, 而兴国茶园猪与乐安花猪遗传距离最远。各类群的UPMGA和NJ聚类分析结果与采用生化、免疫和细胞遗传标记分析的结论不尽相同, 在此基础上, 结合现行分类方法, 认为各受试猪群可暂时归并为赣中南花猪类型, 但对泰和冠朝猪和万安花猪的品种归属性应作进一步分析。

Abstract: Random amplified polymorphic DNAs (RAPDs) were used to investigate bulked genomic DNA polymorphism of seven pig populations including Taihe Guanchao, Yongfeng Tengtian Spotted, Ruijin Spotted, Xingguo Chayuan, Shangyou Spotted, Wanan Spotted, and Lean Spotted pig. Eighty random primers were screened, of them, 16 primers generated polymorphic markers with total number of 44. The genetic distance index matrix indicated that the genetic relationship between Taihe Guanchao and Ruijin Spotted pig population was the closest, while that between Xingguo Chayuan and Lean Spotted pig population was the farthest. Our molecular phylogenetic trees constructed by UPMGA and NJ methods were in general consistent with that based on biochemical, immunogenetic and cellular genetic markers except for differences in some populations. It was inferred from this study that all pig populations examined could be temporary classified into one breed, however, the population genetic character of Taihe Guanchao and Wanan Spotted pig populations should be further evaluated.

关键词 [猪](#) [RAPD](#) [群体遗传](#) [系统分类](#) **Key words** [pig](#) [RAPD](#) [population genetics](#) [systematic classification](#)

分类号

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