

Otterlace软件在猪全基因组序列人工注释分析中的应用

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摘要 2009年11月, 美、英等国科学家宣布首次绘制出家猪的基因组草图。近两年, 随着全基因组序列陆续释放, 越来越多的测序片段得到正确拼接组装, 从全基因组水平上对猪功能基因进行注释分析显得尤为迫切。文章以丝切蛋白1(Cofilin 1, CFL1)基因的注释过程为例, 介绍了运用Sanger研究所开发的Otterlace软件对猪全基因组的免疫基因序列进行人工分析与注释。通过详细说明Zmap、Blixem和Dotter 3个注释工具的使用方法, 并给出了注释过程的主要步骤, 以期对Otterlace的应用起一个抛砖引玉的作用。运用Otterlace软件对243个免疫相关基因进行分析, 其中180个基因得到完整或部分注释, 这为后续深入开展这些基因的功能研究奠定了基础。

关键词: 猪 全基因组 人工注释 Otterlace

Abstract: In November 2009, scientists from the US, UK, and other countries announced the complete genome sequence draft of the domestic pig. With the release of improved versions of the pig genome assembly and the increase of correctly assembled sequenced fragments over the past two years, it is particularly urgent to have the pig genes annotated at whole-genome level. This article is aimed at introducing an excellent manual annotation tool, Otterlace software, developed by Sanger institute. We used *CFL1* (Cofilin 1) gene as an example to expound the usage of the three main components of Otterlace, Zmap, Blixem, and Dotter tools, and developed a practical procedure for manual annotations. We have analyzed 243 immune-related genes, among which 180 genes have been completely or partially annotated, offering novel information to the porcine functional genomics.

Keywords: pig, whole genome, manual annotation, Otterlace

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