猪重要胴体性状的遗传定位 Genetic Location of Body Composition Traits in Pigs

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摘要

为了寻找影响猪重要胴体性状主基因在染色体的位置，我们以大白猪和梅山猪为父母本建立了F2资源家系。随机选留81头F2代个体，经屠宰获得猪胴体性状数据。结合家系个体的48个微卫星标记基因型，用线性模型最小二乘法对各胴体性状进行数量性状基因座（QTL）的区间定位。定位结果表明位于猪染色体（SSC）4号的瘦肉率和瘦肉量QTL达到基因组极显著水平；SSC1、2和4上眼肌面积QTL达到染色体显著水平；位于SSC1和4上的眼肌高度QTL与眼肌面积QTL在同一染色体区域；而眼肌宽度QTL位于SSC6；位于SSC7同一标记区间的皮重、皮率、骨重和骨率QTL表现出很好的一致性，均达到染色体显著水平。SSC6和7的体长QTL达到染色体显著水平。

Abstract: To detect quantitative trait loci (QTL) for body composition traits in pigs, a resource family with three-generation was developed by using Large White grand sires and Meishan grand dams. A total of 81 F2 progenies were phenotyped for body composition. All animals were genotyped for microsatellite markers. The main results are as follows:, the strongest linkages at genome-wise level of lean meat percentage and total meat content were detected on SSC1 and 4. QTLs for loin eye area were located on SSC1, 2 and 4, QTLs for loin eye height on SSC 1 and 4, and QTLs for loin eye width on SSC 6. The best positions estimated for QTLs of skin percentage and of skin weight were in the same marker interval. Two QTLs significant at genome-wise level or highly significant at chromosome-wide level for carcass length were located on SSC6 and 7.

关键词　猪　胴体性状　遗传定位　微卫星标记Key words　swine　body composition　genetic location　microsatellite markers

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