

研究报告

鸡 *Myostatin* 基因单核苷酸多态性及其对屠体性状的遗传效应分析

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摘要

以180只3个品系的温岭草鸡为材料, 采用PCR-RFLP方法对鸡 *MSTN* 基因外显子1的2个多态位点进行研究, 并分析对屠体性状的遗传效应。 *Bsh*1236 I 识别G(2100)A突变, 产生 *MN* 和 *NN* 2种基因型, *Msp* I 识别G(2109)A突变, 产生 *AA*、*AB* 和 *BB* 3种基因型, 联合2个位点分析出现了5种基因型。基因型频率在品系间的 χ^2 检验表明差异均不显著 ($P > 0.05$)。方差分析显示不同基因型的屠宰率有显著或极显著的差异 ($P < 0.01$ 或 $P < 0.05$)。多重比较显示: 杂合型 *MN* 的腹脂重和屠宰率显著 ($P < 0.05$) 高于突变型 *NN*; 杂合型 *AB* 的胸肌重和胸肌率显著 ($P < 0.01$ 或 $P < 0.05$) 高于基因型 *AA*, 基因型 *AA* 的腹脂重和腹脂率都极显著 ($P < 0.01$) 高于突变型 *BB*, 在腿肌重性状上, *BB* 型显著 ($P < 0.05$) 低于 *AA* 型和 *AB* 型; 2个位点联合分析时, *NA/MA* 基因型的腹脂重、腹脂率和胸肌率均极显著 ($P < 0.01$) 高于或低于其他基因型。

关键词 [温岭草鸡](#) [Myostatin基因](#) [RFLP](#) [屠体性状](#) [单倍型](#)

分类号

SNPs of *Myostatin* gene and its genetic effects on carcass traits in chicken

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Abstract

<P>Two polymorphic sites in the first exon 1 of MSTN gene in 180 Wenling grass-chicken including 3 lines were studied by PCR-RFLP method, and its genetic effects on carcass traits were researched. The results showed that 2 genotypes (MN and NN) in G(2100)A locus were identified by Bsh1236 I and 3 genotypes (AA, AB and BB) in G(2109)A locus were identified by Msp I, and 5 genotypes were emerged while com-analyzing 2 loci. The χ^2 test indicated genotype frequencies had no significant deviation (P > 0.05) among lines. The analysis of variance showed that the different genotypes had significant deviation (P < 0.01 or P < 0.05) in carcass percent. The multiple comparisons were made. The abdominal fat weight and carcass percent of heterozygosis MN were significantly higher (P < 0.05) than that of mutant NN, and the breast muscle weight and breast muscle percent of heterozygosis AB were significantly higher (P < 0.01 or P < 0.05) than that of AA individuals. In addition, the abdominal fat weight and abdominal fat percent of AA individuals were significantly higher (P < 0.01) than that of mutant BB individuals, but BB individuals were significantly lower (P < 0.05) than AA and AB individuals in leg muscle weight trait. The abdominal fat weight, abdominal fat percent and breast muscle percent of genotype NA/MA individuals were significantly higher or lower (P < 0.01) than those in other genotype individuals while com-analyzing 2 loci. </P>

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