

猪下丘脑和垂体中生长激素受体、胰岛素样生长因子1型受体的发育性变化

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摘要 GH和IGF-1可作用于垂体或/和下丘脑负反馈性地调节垂体GH的分泌,而这种负反馈作用必须通过下丘脑或垂体的GHR和IGF-1R来实现。为研究猪垂体GH分泌负反馈调节的发育性变化和品种特点,分别在0、3、20、30、90、120和180日龄随机选取纯种雄性二花脸猪和大白猪各4头,屠宰并取下丘脑及垂体,用相对定量RT-PCR分析下丘脑和垂体GHR和IGF-1R mRNA水平。结果表明:下丘脑GHR mRNA表达呈明显的时序性变化,在0到120日龄期间呈逐渐上升趋势,180日龄时显著下降($P<0.05$),提示在快速生长期,GH负反馈调控机制逐渐加强。下丘脑GHR mRNA表达还表现明显的品种间差异,在0到180日龄期间大白猪均显著高于二花脸猪($P<0.05$);而垂体GHR mRNA表达相对稳定,品种和年龄间差异不显著,提示GH的负反馈作用位点可能主要在下丘脑。IGF-1R与GHR的表达发育模式不同。下丘脑IGF-1R mRNA的表达相对稳定,无显著的年龄、品种间差异;而在垂体,大白猪和二花脸猪IGF-1R mRNA水平在出生时均较高,随后显著下降($P<0.05$),20日龄后逐渐上升至90日龄的较高水平,随后再次下降。大白猪垂体IGF-1 mRNA表达在30日龄和90日龄时显著高于二花脸猪($P<0.05$),而180日龄时二花脸猪垂体IGF-1R mRNA水平却显著高于大白猪($P<0.05$)。结果提示,IGF-1长环负反馈作用位点可能不在下丘脑,而主要在垂体。

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分类号

The Discovery, Genetic Analysis and Gene Mapping of Earliness Rice (Oryza sativa L.) D64B

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Abstract

D64B, an achromatic early mutation, was discovered from indica rice preserver line D63B. D64B were crossed with inhomogeneous sterile lines, preserver lines and restorer lines, most of their F1 shared the same heading dates as D64B. The results indicated that D64B possessed the characteristic of dominant earliness. To analyze the earliness trait, positive and negative crosses F2 and BC1 from the cross of D64B and Shuhui 527 were cultivated. Their heading dates showed double apices distributing with same apex values. According to apex value—103 d, plants of the F2 and BC1 were separated into early plants and late plants, which were tested with χ^2 value. The results suggested that the segregation ratio of number of early to late plant fitted to 3:1 and 1:1 for positive and negative cross F2 and BC1, respectively, and that the earliness of D64B was controlled by a single dominant major gene. To map the gene, the polymorphisms between D64B and Shuhui 527 was analyzed with reported 356 SSR primers and 59 primers showed polymorphisms. The earliness-lateness near isogenic pools, early plants and late plants from F2 of Shuhui 527 × D64B were further amplified with the 59 primers. The results indicated that there were polymorphisms on both RM279 and RM71. Their results being analyzed with MAPMAKER/EXP3.0 software, the dominant major gene was located on the top arm of rice chromosome 2 and between the two SSR markers, RM279 and RM71, with genetic distance of 12.6 cM and 13.3 cM, respectively. According to reported data, the gene was first discovered and tentatively named as Ef-3(t). In breeding practice, sterile line D64A had been bred with D64B.

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