

研究报告

鲤正、反交F2群体的AFLP遗传图谱构建及其QTL定位

王军,王成辉,刘豪,马玉清,杨新鑫

(上海海洋大学,农业部水产种质资源与利用重点开放实验室,上海 201306)

摘要:

以高代选育的荷包红鲤和兴国红鲤的正、反交F2群体为材料,利用AFLP标记构建了鲤正、反交群体的遗传图谱,并进行了生长相关性状的QTL定位。在正交群体中,14对AFLP引物共产生542个多态性标记,其中325个标记符合3:1的孟德尔分离比例,利用其构建的遗传图谱涵盖50个连锁群,图谱总长度3 676.1 cM,并获得了与全长、体长、体高、尾柄长和尾柄高5个生长性状相关的17个QTL,可解释表型变异的1.66%~70.49%;在反交群体中,14对AFLP引物共产生605个多态性标记,其中333个标记符合3:1孟德尔分离比例,构建的遗传图谱也涵盖50个连锁群,图谱总长度3 943.1 cM,获得了与体重、全长、体长、体高和尾柄长5个生长性状相关的15个QTL,可解释表型变异的1.58%~63.89%。还对正、反交群体构建的遗传图谱及QTL定位差异及结果进行了初步分析和探讨。

关键词: 鲤;正反交F2群体;AFLP标记;遗传图谱;QTL

AFLP Genetic Map Construction and QTLs Identification from F2 Reciprocal Populations in Common Carp, *Cyprinus carpio* L.

WANG Jun, WANG Cheng-hui, LIU Hao, MA Yu-qing, YANG Xin-xin

(Key Laboratory of Aquatic Genetic Resources and Utilization, Ministry of Agriculture, Shanghai Ocean University, Shanghai 201306, China)

Abstract:

Taking F2 reciprocal populations derived from a diallel cross of Purse red common carp and Xingguo red common carp as material, we constructed genetic maps in the common carp (*Cyprinus carpio* L.) using AFLP marker and identified the growth-related quantitative trait loci (QTL). In positive mating population, 542 polymorphic markers were produced from 14 pairs of AFLP primers, in which 325 markers were accord with the ratio of 3:1. A genetic map containing 50 linkage groups were constructed with genome length of 3 676.1 cM, and 17 QTLs related to total length, standard length, pre-dorsal height, caudal peduncle length and caudal peduncle height were achieved, which could explain 1.66% to 70.49% of the total variation. In negative mating population, 605 polymorphic markers were produced with 14 pairs of AFLP primers, in which 333 markers were accord with the ratio of 3:1. Another genetic map containing 50 linkage groups were also constructed with genome length of 3 943.1 cM, and 15 QTLs related to body weight, total length, standard length, pre-dorsal height, caudal peduncle length were also gained, which could explain 1.58% to 63.89% of the total variation. Furthermore, this paper carried out initial analysis and discussion on genetic maps constructed from reciprocal population, the differences between QTL identification and their results.

Keywords: common carp F2 reciprocal populations AFLP marker genetic map QTL

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通讯作者:王成辉,副教授,主要从事水产动物种质资源与遗传育种研究。Tel:021-61900439;E-mail:wangch@shou.edu.cn

作者简介:王军,硕士研究生,主要从事水产动物种质资源与遗传育种研究。

作者Email:

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