



Polymorphism analysis of the intron one of insulin-like growth factor 2 receptor gene (*IGF2R*) in FFRC strain common carp (*Cyprinus carpio* L.) and its relationship with growth performance

Z.J. Dong^{1,2,3}, S.Y. Su², W.B. Zhu², C.F. Zhang², M. Ding³, W.X. Chen³, X.H. Yuan^{2,3} and Z. Xie¹

¹College of Animal Science and Technology, Nanjing Agricultural University, Nanjing, China

²Key Laboratory of Freshwater Fisheries and Germplasm Resources Utilization, Ministry of Agriculture, Freshwater Fisheries Research Center, Chinese Academy of Fishery Sciences, Wuxi, China

³Wuxi Fisheries College, Nanjing Agricultural University, Wuxi, China

Corresponding author: Z.J. Dong
E-mail: dongzj@ffrc.cn

Genet. Mol. Res. 14 (1): 407-418 (2015)

Received January 9, 2014

Accepted March 13, 2014

Published January 23, 2015

DOI <http://dx.doi.org/10.4238/2015.January.23.14>

ABSTRACT. The insulin-like growth factor 2 receptor gene (*IGF2R*) encodes a transmembrane protein receptor and acts to sequester and degrade excess circulating insulin-like growth factor 2, which is critical for normal mammalian growth and development. Thus, *IGF2R* may serve as a candidate gene underlying growth trait in the common carp. In this study, we isolated the intron one of common carp *IGF2R* and detected the diversity in 3 continuous generations of FFRC strain common carp. A total of 8 loci were detected within this region, which were named in accordance with their location (i.e., Loc84, Loc106, Loc119,

Loc130, Loc145, Loc163, Loc167, and Loc265). Loc106, Loc119, and Loc145 were moderately polymorphic; while Loc84, Loc130, Loc163, Loc167, and Loc265 exhibited slight level of polymorphism. However, significant differences between polymorphism information content values were not observed among the different generations. For Loc145, all generations deviated from Hardy-Weinberg equilibrium. The total number of significant linkage disequilibria for all generations equaled 40. Among them, 4 pairs were detected in each population, while 8 pairs were found in the 2nd and 3rd generations. For Loc130, the G/T genotype exhibited higher body weight when compared to that of the G/G genotype. The frequency of the homozygous G/G genotype reached 87.96%; thus, we can improve FFRC strain common carp growth performance by increasing the percentage of the G/T genotype within a breeding population. Therefore, the G/T genotype could be used as a molecular marker for superior growth traits.

Key words: FFRC strain common carp; *IGF2R*; Intron one; Single nucleotide polymorphisms