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LIST OF ABBREVIATIONS

MAS	Marker Assisted Selection
DNA	Deoxyribonucleic acid
RFLP	Restriction Fragment Length Polymorphism
RAPD	Random Amplified Polymorphic DNA
AFLP	Amplified Fragment Length Polymorphism
EST	Expressed Sequence Tags
SNP	Single Nucleotide Polymorphism
QTL	Quantitative Trait Loci
GH	Growth Hormone
GRF	Growth Hormone Release Factor
IGFs	Insulin-like Growth Factor

SUMMARY AND CONCLUSION

The present work was carried out at Animal Health Research Institute, Cairo (AHRI), Egypt.

The present investigation had been carried out for revealing GH gene polymorphism in Common carp (*Cyprinus carpio L.*) reared under Egyptian conditions, looking for association between growth rate and GH gene variants and detection of SNPs of GH gene and their association with growth trait in common carp. The goal of the present study has been achieved by employing different molecular genetic techniques; Polymerase Chain Reaction-Restriction Fragment Length Polymorphism (PCR-RFLP) and DNA sequencing and SNP analysis.

Blood samples from 37 selected Common carp fish (11 large, 13 medium and 13 small sized fish) were collected into tubes containing an anticoagulant disodium EDTA and then DNA from these samples were extracted using DNA extraction kits (Fermentas). Two primers for Common carp GHI and GHII genes were used to amplify DNA fragments. Only GHI primer amplified a fragment of 2100 bp covering a part of the gene from first exon to the fifth exon.

Growth hormone gene polymorphisms

The genomic DNA from 37 fish was used to amplify GH gene which yield a fragment of 2100 bp for GHI gene.

Restriction analysis of PCR-RFLP-BsaI of GHI gene (2100bp) show two genotypes: HH genotype (1500, 600bp) and GG genotype (undigested fragment, 2100bp).

PCR-RFLP-BanII of GHI gene show two genotypes: HH genotype (1600, 500bp) and GG genotype (undigested fragment 2100bp).

However, PCR-RFLP-HincII of GHI gene, which was expected to cut the 2100bp fragment showed only one band in all tested individuals which means polymorphism at the restriction site of the enzyme.

Results showed the association of BsaI GG genotype with the large size fish and the HH genotype with small size fish. While BanII the HH genotype which appeared in large size fish also appeared in some small size fish BanII cutting pattern unreliable for selection.

DNA sequencing of fragment of GHI gene (2100bp) of six individuals including three largest and three smallest fish in the samples group revealed nucleotide sequence variations among large and small fish. The present experiment showed that individuals no. 7 and 8 (the highest body weight in 37 selected animals), with T (SNP1) nucleotide 49, A (SNP7) nucleotide 658, T (SNP8) nucleotide 806, A (SNP9) nucleotide 861,

T (SNP10) nucleotide 895, G (SNP12) nucleotide 1030, A (SNP13) nucleotide 1082, A (SNP14) nucleotide 1117, C (SNP15) nucleotide 1123, G (SNP16) nucleotide 1187 and T (SNP 20) nucleotide 1417, for the growth hormone gene can be used as a marker-assisted selection (MAS) to select for growth trait. Consequently, these 11 SNP's markers in Common carp GH gene may be useful in genetic improvement of growth trait in Common carp (*Cyprinus Carpio*) in general and in particular those reared under Egyptian conditions.

In conclusion, this work revealed the efficiency of the molecular genetic markers (RFLP and SNPs) in detecting enough GH gene polymorphisms in Common carp and to look for association between growth performance and GH gene polymorphism.

The results of the present work conclude the use of the BsaI restriction enzyme as a marker in selection for growth trait in Common carp as well as SNPs associated with large size fish.