

**EXTENSIVE MINISATELLITE POLYMORPHISM
IN INTRONS OF THE GROWTH HORMONE GENE
IN THE SPARIDAE FAMILY**

Bruria Funkenstein
National Institute of Oceanography, Israel Oceanographic & Limnological
Research Institute, Tel-Shikmona, P.O.Box 8030, Haifa 31080, ISRAEL.
Tel: 972-4-8515202; Fax: 972-4-8511911;
E-mail: bruria@ocean.org.il

R. Almuly, A. Dyman, B. Cavari,
Israel Oceanographic & Limnological Research, ISRAEL

M.C. Alvarez
University of Malaga, SPAIN

C. Batargias , A. Magoulas
Institute of Marine Biology of Crete, GREECE

EXTENDED ABSTRACT ONLY – DO NOT CITE

Introduction

GH plays a major role in stimulating somatic growth in vertebrates, including teleosts. Its potential implication in enhancing growth rate of fishes in aquaculture prompted the cloning and characterization of the GH cDNAs and genes from cultured fish species. Comparison of their structure demonstrates a higher variability compared to that found for mammalian GH genes. We are interested in the structure and regulation of expression of growth-related genes in the gilthead seabream, *Sparus aurata* - a member of the Sparidae family (common name, seabreams). Sparidae is an important family of marine fish, most of which are of notable commercial value and display worldwide distribution with many species common to the Mediterranean Sea and East Atlantic Ocean. Domestication of the gilthead seabream, the major aquacultured species to date in the Mediterranean region, started less than 30 years ago. Its successful performance has prompted the domestication of other sparid species and production of interspecific hybrids. Both domestication of new species and

hybrid production require extensive information on the phylogenetic relationships between the species, degree of genetic variation of the aquacultured stocks and the wild population, and geographical differences among cultured and wild stocks.

Results and Discussion

Cloning and structure characterization of the GH gene of the gilthead seabream (saGH) showed that it spans approximately 4.3 kb and consists of six exons and five introns, as found for all cloned teleost GH genes with the exception of carps and catfish. The first and third introns contain long stretches of repetitive tandem repeats. The second intron, which is unusually long compared with that in other teleosts (and other vertebrates) contains several inverted repeats. Intron-targeted polymerase chain reaction (PCR) analysis identified length polymorphism of the first and third introns. Sequence analysis of several variants of the first intron revealed that the variation in length is due to differences in the number of the repeat monomers as well as minor changes in their length (Almuly et al., 2000). Analyses of geographically different cultured stocks of gilthead seabream for GH intron I length revealed a considerably high degree of polymorphism and high level of heterozygosity. The fragment size ranged from about 400 bp to about 1450 bp with more than 12 alleles found.

Intron-targeted PCR was also used for analysis of GH intron I polymorphism in several species of the Sparidae family. High variation in the length of the first intron was found between several sparids studied (8 species) that ranged from about 250 nt to 1450 nt. Preliminary sequence analysis suggests that a consensus repeat unit is found in all sparid GH intron I studied sofar, with species-specific variations. In addition, it appears that sparid species with long GH intron I show length polymorphism, which results from different number of repeat units.

These studies will be useful for establishing the phylogenic relationship between members of Sparidae family based on GH intron sequences, for analysis of genetic variation of populations and for testing the potential application of GH intron polymorphism to serve as genetic marker for desirable traits, such as growth rate.

References

Almuly, R., B. Cavari, H. Ferstman, O. Kolodny, and B. Funkenstein. 2000.
Structure and sequence of the gilthead sea bream (*Sparus aurata*)
growth hormone-encoding gene: identification of minisatellite
polymorphism in intron I. *Genome*, in press.

Acknowledgement

This work was supported in part by the US-Israel Binational Agricultural
Research and Development Fund (BARD, Project No. IS-2769-96CR)

