



HELLENIC CENTRE FOR MARINE RESEARCH, INSTITUTE of MARINE BIOLOGY & GENETICS
HCMR/IMBG



BRIDGE-MAP
Bridging Genomes: An integrated genomic approach toward genetic improvement of aquacultured fish species - Q5RS-2000-01797
2001-2005

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BRIDGEMAP Consortium



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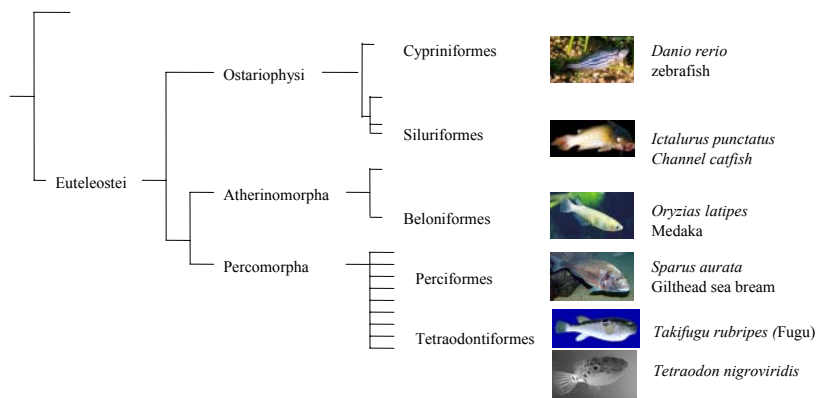
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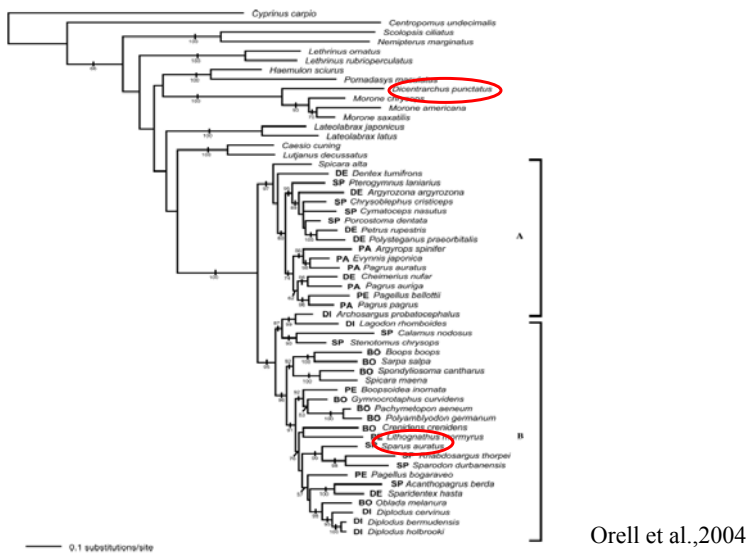
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An Aquaculture motivated Genetics & Comparative Genomics project on the gilthead sea bream



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Objectives

- Develop tools for genetic analysis and MAS in *Sparus aurata*
- Develop tools for comparative genome mapping of Aquaculture species to non model species
- Combine approaches to create short-cuts in linking variation at DNA to phenotypic variation for non-model species
- Initiate breeding project with industrial partners

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In the beginning :

- Batargias C, Dermitzakis E, Magoulas A, Zouros E (1998).
- Characterization of
- six polymorphic microsatellite markers
- in gilthead seabream, *Sparus aurata*.
Molecular Ecology, **8**, 897–899.

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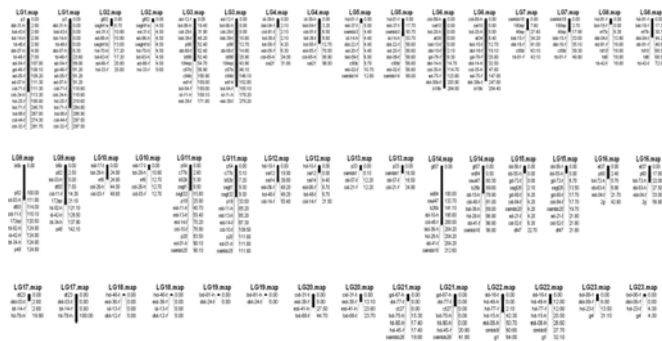
Produced resources

- ✓ Microsatellites: >200 microsatellite markers
- ✓ Linkage panels
- ✓ **Linkage map & partial QTL mapping**
- ✓ >7 cDNA libraries: head kidney, kidney, liver, embryonic/larval, brain, pituitary, intervertebral cartilage
- ✓ ESTs : > 2000 unique EST sequences
- ✓ BAC genomic library: 6x coverage, 120Kb average insert size
- ✓ **Radiation hybrid panel**: 93 hybrid cells + 3 controls
average insert size 6Mb
- ✓ **Radiation hybrid map** ~1000 markers
- ✓ Merging RH map and linkage map

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Genetic linkage map

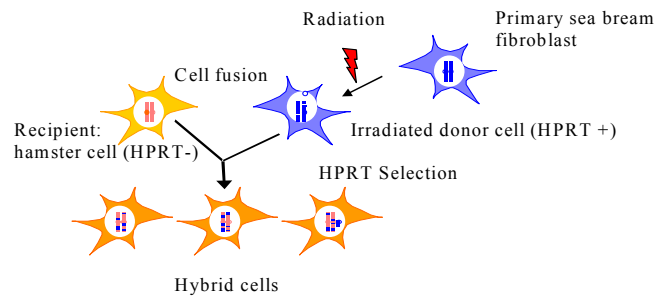


Early draft version of the linkage map **207 microsatellite markers** , **26 linkage groups** -24 chromosomes haploid karyotype, LOD score 3, (Franch et al., in preparation), **chromosome specific differences in male vs. female recombination**

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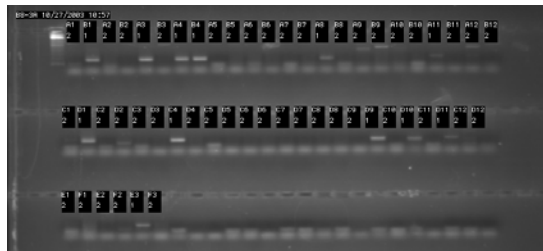


Radiation hybrid panel



Senger *et al.* in press

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1= positive
2= negative
0= undecided

- retention rate over all 100 cell lines 23.5%
- retention rate for clones of >16% (80): 26.8%

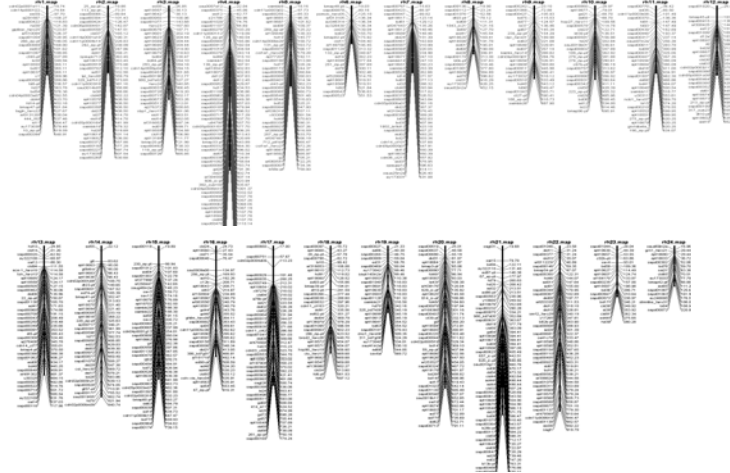
organism	average retention rate
LN54 panel of Zebrafish (93 hybrid cell lines) (Hukriede et al., Proc.Natl.Acad.Sci, vol. 96, 1999)	22%
T51 panel of Zebrafish (94 hybrid cell lines) (Geisler et al., Nature Genetics, vol. 23, 1999)	18.4%
Mouse (93 hybrid cell lines) (Etten et al., Nature Genetics, vol. 22, 1999)	30%

Senger *et al.*, 2006

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RH MAP- 24 Linkage groups

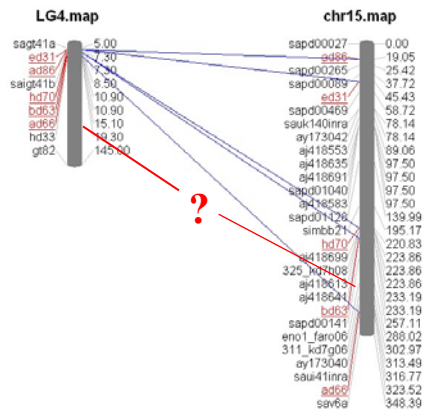


First Draft version of the RH map: about 1000 markers at data analysis stage

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Genetic linkage vs. RH: From almost congealed regions to recombination hot spots



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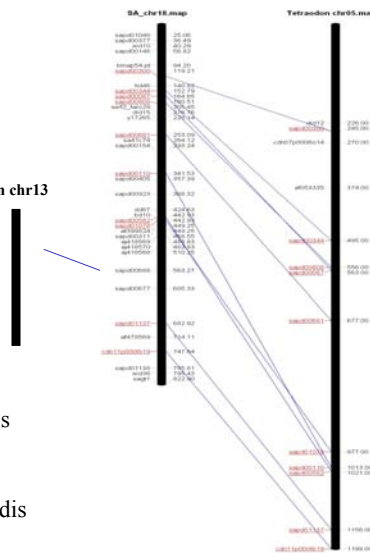
Happy snapshots of comparative genomics

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Comparison of gene order between *Sparus aurata* and *Tetraodon nigroviridis*

Tetraodon chr13



12 genes mapped on *Sparus aurata* RH18, found in *Tetraodon nigroviridis* chromosome 5

1 belonging to *Sparus aurata* RH group18 found in *Tetraodon nigroviridis* chromosome 13

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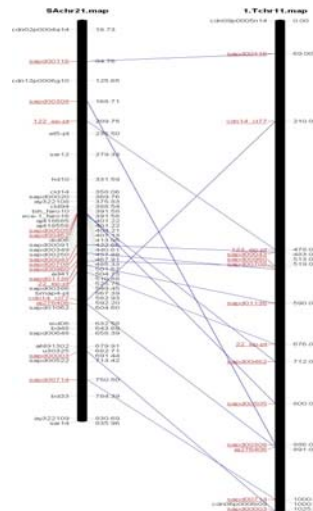


But there evolution took also alternative ways

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Comparison of gene order between Sparus aurata and Tetraodon nigroviridis



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FROM QTL TO CANDIDATE GENES

- Find QTL by genome scan
- Established Synteny => candidate genes in Tetraodon
- Isolate Genes in seabream by PCR
- Confirm synteny by RH mapping
- SNPping and/or functional analysis
- Or Go Vice-versa

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Partial QTL mapping for growth – Towards Combining QTL and candidate genes approaches

How to choose only 2 linkage groups when there are limited resources:

- Sparus aurata prolactin receptor
- Sparus aurata prolactin (PRL)
- Sparus aurata growth hormone receptor
- Sparus aurata growth hormone gene

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Other ways to define interesting candidate genes and /or to tag biological hierarchies:

I. Population genomics -

- a) selective sweeps
- b) outliers F_{st} values & comparative information

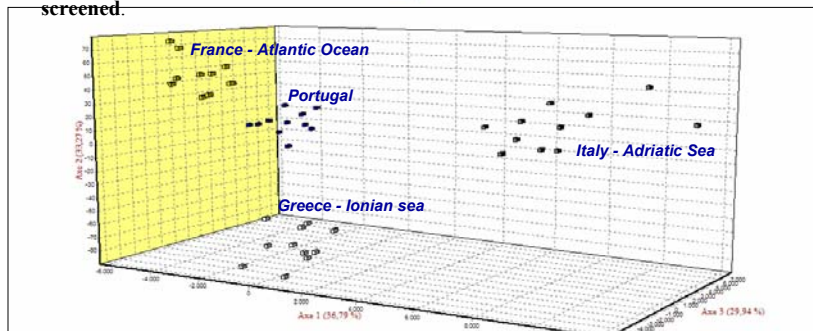
II. Microarray experiments

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Populations may be structured: Traceability, Population genomics, Adaptation

Natural Resources of *Sparus aurata*: – Factorial Correspondence Analysis for samples from the Mediterranean and the Atlantic, genotyped for 33 microsatellite markers. Each point represents a different fish from four different geographic origins. The average θ value is 0.022 /// few annotated genes comprising microsatellites have been also screened.



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Where are we now?

- Thanks to new developments & with relatively small project
- *Sparus aurata* has been transformed from a species with no genetic resources to a species that can easily rich a status of aquaculture model species
- Possibility for applying combined strategies to selective breeding
- Great potential for easily furthering DNA related genetic approaches as well as functional and comparative genomics

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