



Analysis of the Gonadal Transcriptome During Sex Determination, Sex Differentiation and Gonadal Maturation in the Sea Bass (*Dicentrarchus labrax*) and Turbot (*Scophthalmus maximus*) by 454 Sequencing and Two Specific Oligo-based Microarrays

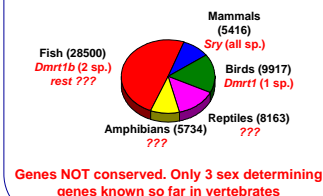
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INTRODUCTION

- Fish comprise close to 30,000 species and exhibit all reproduction types known in vertebrates (gonochorism, hermaphroditism and unisexuality). Thus, fish offer unique opportunities to study the processes of sex determination, sex differentiation and gonad maturation
- In fish, these processes are the result of complex genetic, environmental and social interactions
- Temperature or population density (growth) can easily influence the course of sex differentiation. These effects are one of the most dramatic known examples of phenotypic plasticity
- The gonads are the only organ that can transform from a common undifferentiated rudiment into two completely different developmental pathways, testis or ovary
- In contrast to mammals, in fish the upstream master sex determining gene, if present, is not conserved even in closely related species. However, gonadal aromatase (*cyp19a*) is a key enzyme involved in sex differentiation in all non-mammalian vertebrates
- High temperature-induced masculinization may involve an epigenetic mechanism including methylation of the aromatase gene promoter

Sex determination: A major paradox in evolutionary biology



OBJECTIVE

To better understand the genetic and environmental regulation of sex determination, sex differentiation and gonadal maturation in production fish. Zebrafish is used as a model in some experimental approaches

Sea bass



Dicentrarchus labrax

Turbot



Scophthalmus maximus

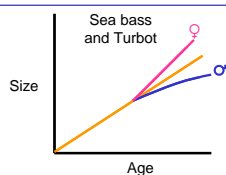
Zebrafish



Danio rerio

STRATEGY

Determine the relationship between age-growth and sex determination, sex differentiation and gonad maturation



Sample gonads during key developmental points and apply a candidate gene approach

Examples of candidate genes

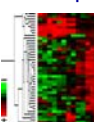
<i>cyp19a</i>	<i>arb</i>
<i>cyp11b</i>	<i>era</i>
<i>foxl2a</i>	<i>erb1</i>
<i>fshr</i>	<i>erb2</i>
<i>amh</i>	<i>shbg</i>
<i>lhr</i>	<i>star</i>

Use 454 sequencing to increase the available numbers of ESTs and to aid in gene discovery in Sea bass and Turbot



Develop species-specific oligo-based microarrays and hybridize with gonad sample collection

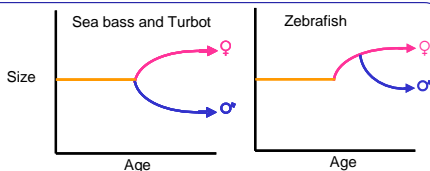
Gonad species-specific microarrays



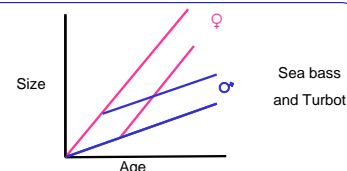
- ✓ Enrichment of Sea bass and Turbot microarrays
- ✓ Analysis of gonad samples in species-specific microarrays (Sea bass, Turbot and Zebrafish)

ONGOING EXPERIMENTS

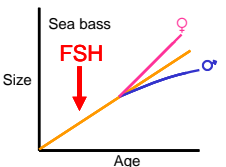
Study the normal course of sex differentiation and gonadal maturation



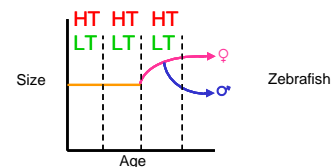
Determine the relationship between growth and sex differentiation



Determine the relationship between sex differentiation and precocious male maturation in fish treated with follicle-stimulating hormone (FSH)



Study the effects of temperature on sex differentiation and *cyp19a* gene promoter methylation in Sea bass and Zebrafish



EXPECTED OUTCOME AND FUTURE PROSPECTS

Contribution to basic knowledge

- Gonadal transcriptomes of model and production fish
- Gene and pathway discovery related to sex determination differentiation and maturation
- Temperature effects on gonadal development
- Assess the influence of environment on the methylome

Applications to fish farming

- Management during early development
- Management during development and maturation
- Brood stock selection

Research supported by project Aquagenomics

