

# DETECTION OF GROWTH-RELATED QTLs IN TURBOT (*SCOPHTHALMUS MAXIMUS*)

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**GOBIERNO  
DE ESPAÑA**

**MINISTERIO  
DE CIENCIA  
E INNOVACIÓN**

➤ **Turbot (*Scophthalmus maximus*)**



- Diploid flatfish
- 22 chromosome pairs
- Small genome (< 800 Mb)
- Gonocoric with no sexual dimorphism

**INTRODUCTION**

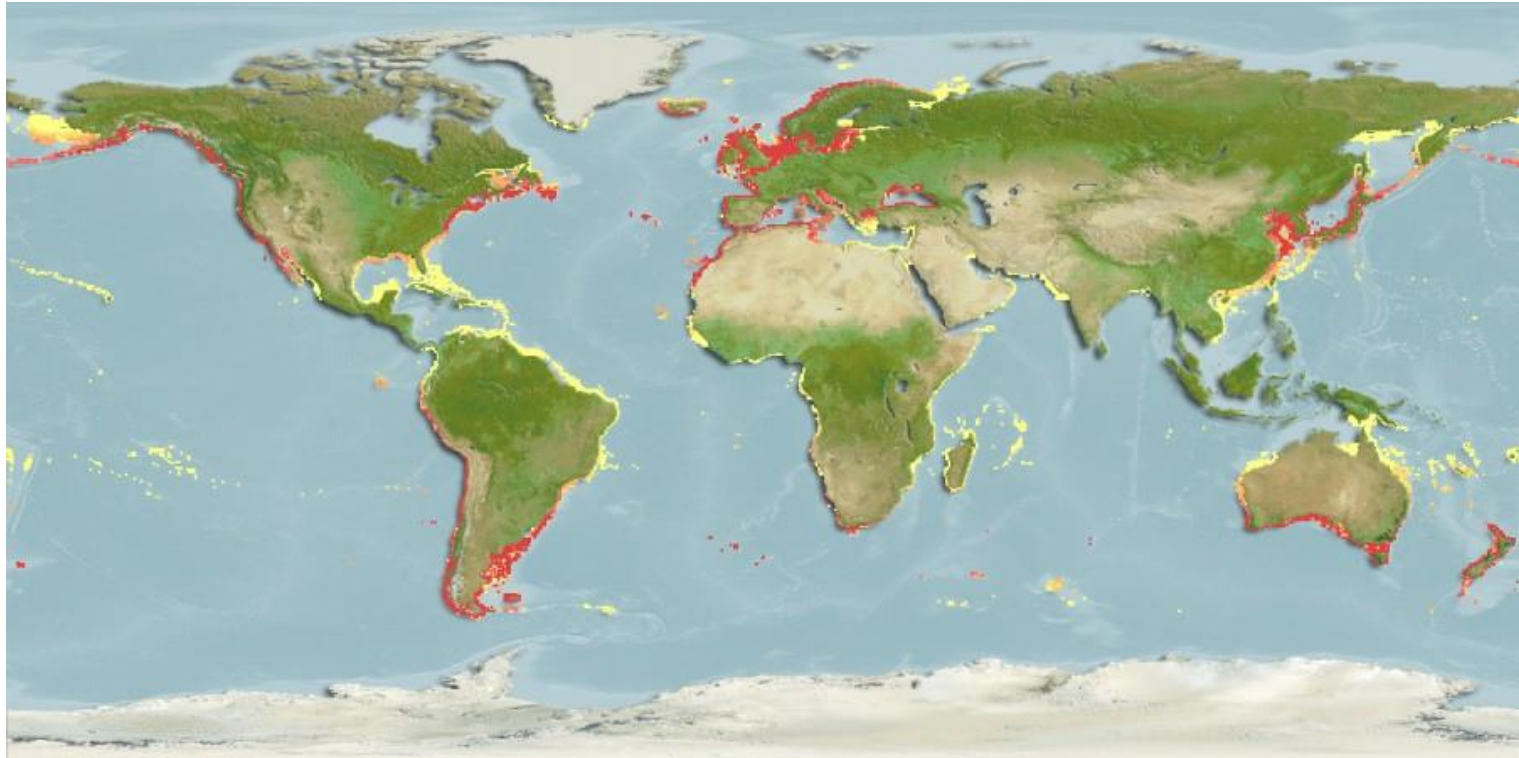


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## ➤ Distribution



- European northern coasts
- Baltic and Mediterranean sea
- Chile, Argentina, South Australia and China

➤ **Interest**

- Food fish

➤ **Culture programs in Europe**

- Since 90's in European Atlantic
- Optimum results in Galician coasts (Spain)
- Increased production

➤ **QTL studies**

- Sex determination (Martínez *et al.* 2009)
- Body length (Ruan *et al.* 2010)



## INTRODUCTION

### OBJECTIVES

- **Detect and locate QTL affecting**
  - Body weight
  - Body length
- **Determine marker-trait associations**



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INTRODUCTION

OBJECTIVES

**METHODS**

- **8 turbot full-sib families**
  - *01, 03, 04, 06* (8 months)
  - *AS-1, AS-2, AS-3, AP* (5 months)
- **Microsatellite markers**
  - Average 100 microsatellites/family
  - 26 linkage groups
  - Genetic map by Martínez *et al.* 2009
- **2 methods**
  - GridQTL: Linear regression
  - QTLMap: Maximum likelihood



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INTRODUCTION

OBJECTIVES

**METHODS**

Uncontrolled factors



Separate analyses

Different QTL between families



**Two methods  
(concordant QTL)**



**QTL repeatability  
(repeated QTL)**



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➤ Linkage groups with detected QTL for weight

<i>Family</i>	<i>01</i>		<i>03</i>					<i>04</i>	<i>06</i>		
<i>GridQTL(LR)</i>	15	17	5	12	16	17	20	14	11		
<i>QTLMap (ML)</i>	1	15	16	1	5	16	17	20	14	15	2

<i>Family</i>	<i>AS-1</i>	<i>AS-2</i>	<i>AS-3</i>	<i>AP</i>	
<i>GridQTL(LR)</i>	13	1	6	18	3
<i>QTLMap (ML)</i>			6		12

- High concordance between methods
- Similar results observed for length





INTRODUCTION

OBJECTIVES

METHODS

RESULTS

- **Associated markers on weight**
  - 4 significant markers 6.8% - 17.9%
- **Associated markers on length**
  - 5 significant markers 7.7% - 16.2%
- **Special case**
  - Sma-USC220 in *Fam01* LG14



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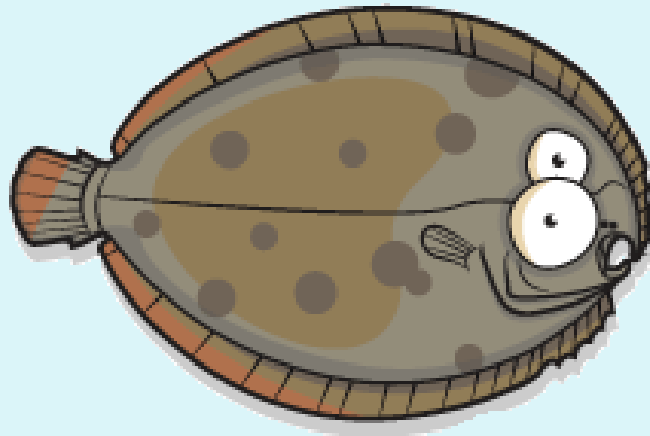
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- **First wide QTL analysis for growth traits**
- **Use of two methods → High consistent results**
- **Incipient studies → Increase marker density**
- **Comparative genomics → focus on regions**



Thanks for your attention!!



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