

Elodie Fleury<sup>a,b</sup>, Caroline Fabioux<sup>a,b</sup>, Christophe Lelong<sup>b</sup>, Pascal Favrel<sup>b</sup>, Arnaud Huvet<sup>a\*</sup>

<sup>a</sup> IFREMER, département PFOM, UMR M100 PE2M, Centre de Brest, B.P. 70, 29280 Plouzané, France

<sup>b</sup> Université de Caen, UMR M100 PE2M, 14032 Caen Cedex, France.



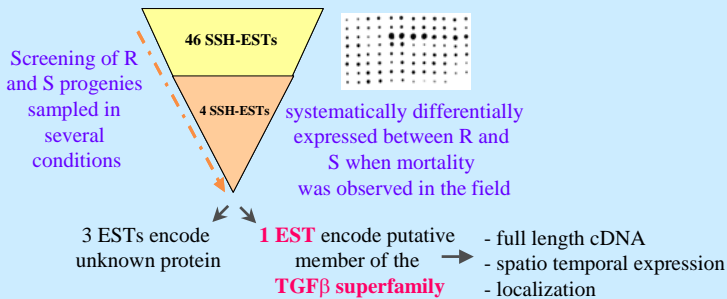
## Introduction

To study the complex and non identified host causes of summer mortality in *C. gigas*, divergent selection criteria based upon summer survival have been applied to produce resistant (R) and susceptible (S) oyster families (Samain et al., 2007). A previous analysis by suppression-subtractive hybridization has characterized 46 differentially-expressed cDNAs between R and S families (Huvet et al., 2004). The present study reports the screening, using nylon array, of the 46 oyster SSH cDNAs from R and S selected families. Among the few differentially expressed genes characterized between R and S samples, one encodes a Transforming-Growth-Factor- $\beta$ -related (TGF $\beta$ ) protein. Members of the TGF $\beta$  superfamily are critical growth factors regulating a variety of important processes. We report the characterization and the spatio-temporal expression of oyster-gonadal-TGF $\beta$ -like (*og-TGF $\beta$ -like*), a TGF $\beta$  superfamily member specifically expressed in the gonad of the cupped oyster, *C. gigas*.

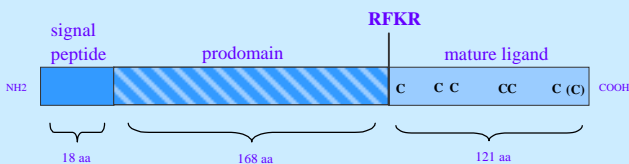
## Results

### 1) cDNA macroarray analysis

cDNA macroarray hybridized by R and S samples collected in 4 experiments to focus on the genetic effect (4 and 16 month-old oysters of 2<sup>d</sup> and 3<sup>d</sup> generations, collected in two sites, and in a nursery)



### 2) Isolation of *og-TGF $\beta$ -like* cDNA



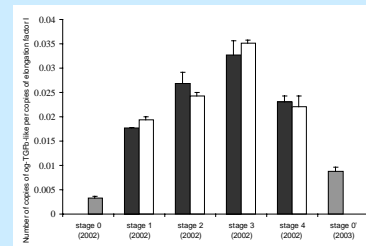
Nucleotide sequence encoding a preproprotein of 307 amino acids

- consensus cleavage site type « RXXR »
- 6 conserved cysteine (lacks the seventh characteristic cysteine)
- percentage of identity with other related ligands very low

➔ **derived member of the TGF $\beta$  superfamily**

### 3) Spatio-temporal expression of *og-TGF $\beta$ -like*

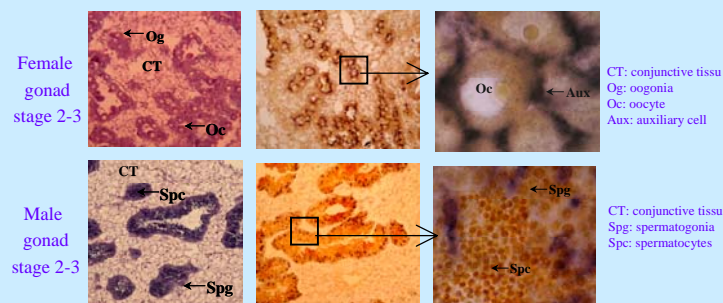
- No significant relative level of transcript detected in any early oyster developmental stage
  - High relative level of transcript detected **exclusively in the gonad**, and not in other tissues, of both male and female
  - Relative quantity of transcript increased continuously during the development of gonadic tubules in both sexes (figure)
- ➔ **maximum level during active gametogenesis (stage 3)**



Level of relative *og-TGF $\beta$ -like* transcript in male (white bar) and female (black bar) during a complete annual reproductive cycle of *C. gigas*

### 4) Localization of *og-TGF $\beta$ -like* by *in situ* hybridization

*og-TGF $\beta$ -like* mRNA detected exclusively in cells **between oocytes**



*og-TGF $\beta$ -like* mRNA detected exclusively in cells **between spermatogonia**

## Conclusion

- ✓ *og-TGF $\beta$ -like* has only 6 conserved cysteine as observed for teleost gonadal soma-derived growth factor (Sawatari et al., 2006)
- ✓ tissue-specific expression, exclusively in the gonad of both sexes and not during developmental stages nor in other tissues
- ✓ strongly expressed when germ cells are fully mature
- ✓ localized in somatic cells surrounding the germ cells, supposed to play a regulatory role in the differentiation and maturation of germ cells

➔ **derived member of the TGF $\beta$  superfamily involved in gonadal development**

- ✓ summer mortality is suggested to interplay with reproduction
- ✓ significant differences in reproduction observed between R and S
- ✓ some TGF $\beta$  members (BMP15, GDF9) play crucial regulatory roles in ovarian follicle or testis development

➔ **Is that different expression of *og-TGF $\beta$ -like* significant to the higher rate of summer mortality of S progeny ?**