Session 29: Free communications in Animal Genetics

Detection of QTLs for growth in turbot

Cerna, A., Fernández, J., Toro, M.A., Bouza, C., Hermida, M., Vera, M. and Martinez, P.

ETSIA (UPM),INIA Madrid (Spain), USC Lugo (Spain)

miguel.toro@upm.es

OBJECTIVE

Resistance to disease and growth are the traits that influence more the production

Objective: Detection and location of QTLs that affect traits related to growth

Phenotypic data

- ***Body weight (Pe)***
- ***Body length (Lo)***
- ***Condition factor(FK)*** Fulton (1902)

$$FK= \frac{Pe * 100}{Lo^3}$$

Biological material

Project on QTL detection of resistance to two patogenes *Aeromonas salmonicida* y *Philasterides dicentrarchi*

Two origins

Stolt Sea Farm S.A.

5 families

- Fam03
- Fam04
- FamAS-1
- FamAS-2
- FamAS-3

Pescanova S.A.

1 family

- FamAP

Two ages when measurement were taken:

	FAM03 ***Referenc family DF (Bouza et al. 2007)***			**FAM04**		
	N= 85 → 36 ♂ → 49 ♀			**N**= 91		
	Weight (g)	**Length** (cm)	**FK**	**Weight** (g)	**Length** (cm)	**FK**
Mean	97.05	17.01	1.93	119.28	17.66 ± 1.87	2.08 ± 0.16
Minimum	38	12.9	1.56	26.8	11.4	1.66
Maximum	194	22	2.62	215.2	21	2.48

⇒ ***8 months of culture***

Separated tanks

	FAMAS-1			**FAMAS-2**			**FAMAS-3**			**FAMAP**		
	N= 100			**N**= 100			**N**= 100			**N**= 113		
	Weigth (g)	**Length** (cm)	**FK**	**Weght** (g)	**Length** (cm)	**FK**	**Weigth** (g)	**Length** (cm)	**FK**	**Weight** (g)	**Length** (cm)	**FK**
Mean	**46.31**	**12.81**	**2.18**	**26.69**	**10.69**	**2.15**	**31.62**	**11.33**	**2.14**	**32.13**	**11.43**	**2.14**
Minimum	20.3	10.5	1.52	10.5	8.5	1.71	16.3	9	1.77	20.2	10	1.85
Maximum	69.2	15	2.73	42	12.5	2.82	50.8	13	2.933	44.8	13	2.712

➡ *5 months of culture*

Separated tanks

The families were analysed independently

Genetic map

The **consensus genetic map** of reference used was developed by **Bouza et al. (2007), Martínez et al. (2008) and Martínez et al. (unpublished)**

	No. micros	*Length cM*	*Inteval between markers*	
Fam03	*186*	*1074.87*	*6.87*	26 LG
Fam04	*87*	*1002.88*	*15.45*	24 LG
FamAS-1	*92*	*1093.87*	*16.5*	
FamAS-2	*90*	*1062.21*	*15.48*	26 LG
FamAS-3	*89*	*1041.62*	*16.5*	
FamAP	*90*	*1076.87*	*15.8*	
	122.33	*1058.72*	*14.43*	

QTL Analysis

Two programmes were utilised:

- ❑ ***GridQTL*** (*Seaton et al 2006*)
- ❑ ***QTLmap*** (Gilbert et al., 2008)

-no fixed effect were adjusted (except sex in Fam03)

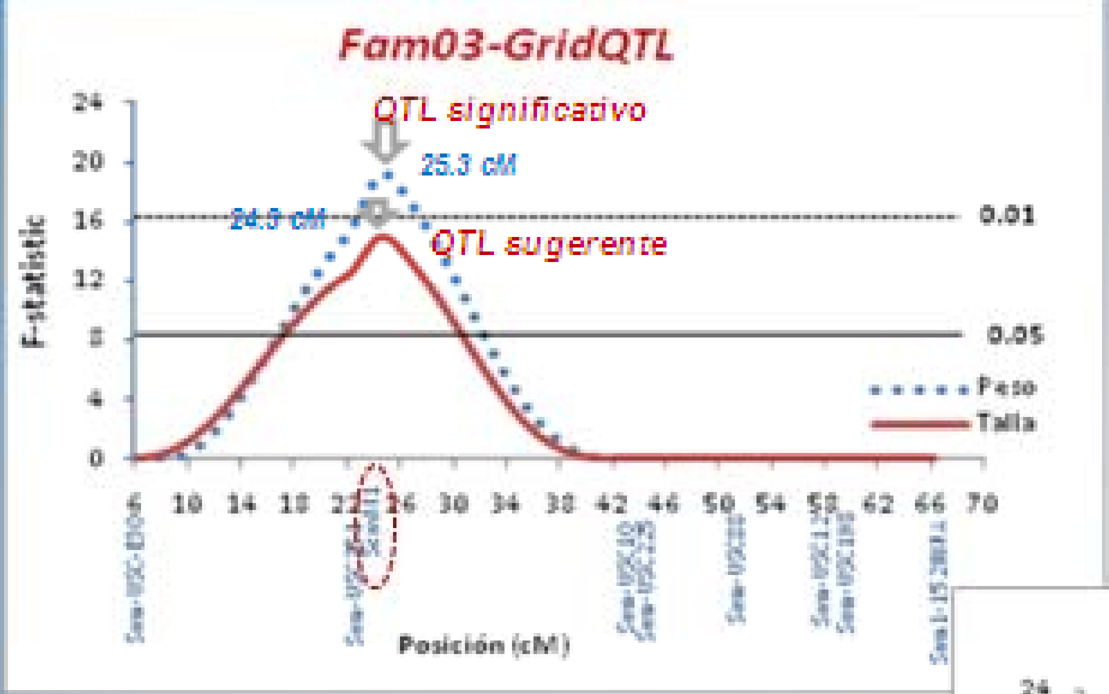
- a **single QTL was assumed**

- Theshold of significance:

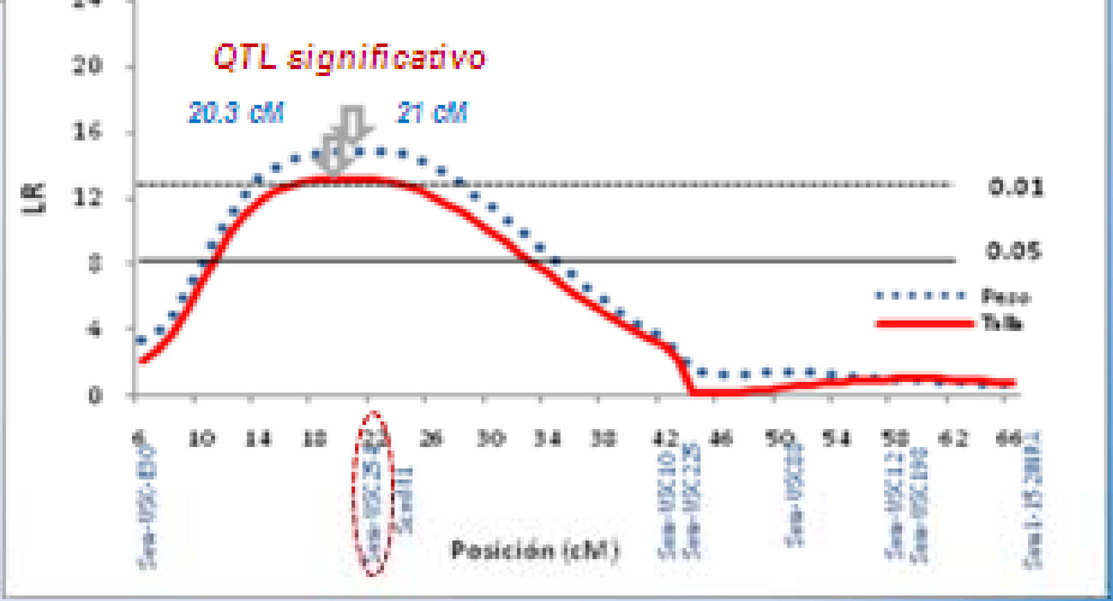
< 5% chromosome-wide → suggestive QTL
< 1% chromosome-wide → significant QTL

Linkage group 5 (LG 5)

Fam03-GridQTL



Fam03-QTLmap



ScmM1

Sma-USC254

CONCLUSIONS

- ✓ We have detected **6 QTLs significant** with both programes

Body weight: *two* QTLs on LG 5 and 14
Body lengt: *two* QTLs on LG 12 and 14
Condition factor: *two* QTLs on LG 3 and 16

- ✓ Additionally, GridQTL detected 2 QTLs for body weight on GLs 12 y 16 (suggestive with QTLmap) whereas QTLmap detected 3 QTLs (suggestive with GridQTL)

CONCLUSIONS

✓ The use of two programmes has allowed to obtain more consistent results and to avoid false positives

✓Future work:

- fine mapping on these GLs increasing the number of observations and the density of markers
- comparative genomics in homologous regions of model fishes