

# Genetic evaluation with uncertain parentage in aquaculture

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➤ **In aquaculture**  $\left\{ \begin{array}{l} \text{physiological} \\ \text{logistic} \end{array} \right\}$  **reasons**

➤ **Mass spawning**

✓ **no control on the contributions of parents**

✓ **impossible to trace paternity of newborn**

➤ **Knowledge of relationships helps to:**

- ✓ **estimate breeding values**
- ✓ **control the loss of diversity and the rise of inbreeding**

**Use of molecular markers to  
reconstruct genealogies**

## We seek

- ✓ every candidate assigned to a father and a mother

## We find

- ✓ some fishes assigned to several possible parents

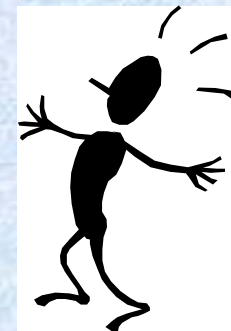
⇒ *usually discarded*

reduced number of markers

population structure

*low cost breeding program*

large proportion  
of the population



**... possible solutions ...**

**enlarge the  
markers' panel**



**higher budget**

*implies*

**deal with uncertain  
paternities/relationships**



**change methodology  
(software)**

**Using more  
candidates**



**Opportunity for higher  
selection pressure**

**Higher accuracy of  
estimates of BV**

**Larger  
response**

## **OBJECTIVE**

- **Study through simulation the advantages of:**
  - ✓ **Genotyping with an increasing number of markers**
  - ✓ **Using individuals with uncertain paternity**

# MATERIAL AND METHODS



## ➤ Population structure

- ✓ First round of sea bream breeding program from ABSA (Culmarex)
- ✓ 1500 selection candidates
  - ⇒ offspring from 50 males and 50 females

## ➤ Mating strategy

- ✓ random (breeders in a single tank)
- ✓ controlled monogamous mating (FS families)

## ➤ Trait (infinitesimal)

- ✓ Measured in candidates themselves
- ✓  $h^2 = 0.5$  or  $0.1$



(cont.)

## ➤ Genotyping

✓ 4 or 8 microsatellites

⇒ real frequencies of sea bream population

✓ 25, 50 or 100 SNP

⇒ equal frequencies

✓ Paternal assignment with tailored FORTRAN program

*probability of every 'trio' ⇒ probability of every possible parent*



only assigned to a single  
mother and a single father



a single parent of one sex  
and several of the other sex



several mothers and  
several fathers





(cont.)

➤ **EBVs calculated through BLUP**

✓ REMLf90 (I. Misztal)

➤ **Relationship matrix (accounting for uncertainties)**

✓ U\_P\_C (J. Fernández)



**BLUP\_U**



**BLUP\_P**



**BLUP\_M**

➤ **Truncation selection of 50 highest EBVs**



**(cont.)**

➤ **Benchmark selection strategies**

- ✓ BLUP with real genealogical relationships
- ✓ truncation based on phenotypes

BLUP\_G

Phenot

➤ **Control parameters**

- ✓ percentage of parentage assignment
- ✓ correlation between selection criteria and TVB
- ✓ mean TVB of selected individuals
- ✓ mean coancestry of selected
- ✓ number of coincident selected

# RESULTS

*100 replicates*

## ➤ Precision of paternity assignment

### Random

	4 mic	8 mic	25 SNP	50 SNP	100 SNP
U	94.42	99.98	48.97	99.70	100.00
P	5.02	0.02	20.52	0.29	0.00
M	0.56	0.00	30.51	0.01	0.00

### FS families

	4 mic	8 mic	25 SNP	50 SNP	100 SNP
U	99.98	100.00	98.72	100.00	100.00
P	0.00	0.00	0.00	0.00	0.00
M	0.02	0.00	1.28	0.00	0.00

- ✓ no genotyping errors
- ✓ unrelated breeders (families)



$h^2 = 0.5$   
Random

➤ **Efficiency of selection**

✓ mean TBV of selected

				Accuracy		
	BLUP_U	BLUP_P	BLUP_M	BLUP_U	BLUP_P	BLUP_M
<b>25 SNP</b>	<b>108.62</b>	<b>109.73</b>	<b>110.31</b>	<b>0.76</b>	<b>0.78</b>	<b>0.75</b>

✓ improvement due to more evaluated

✓ almost no change in the rest of scenarios

✓ BLUP\_G better or equal than anyone

✓ Using phenotype worse (except extreme cases)

✓ **Similar results with the other heritability**

⇒ **but responses lower (obviously)**

		Random					FS families				
		Phenot	BLUP_G	BLUP_U	BLUP_P	BLUP_M	Phenot	BLUP_G	BLUP_U	BLUP_P	BLUP_M
4 mic	TBV	101.92	103.24	103.17	103.22	103.22	101.95	103.58	103.58	103.58	103.58
	$\rho$	0.32	0.53	0.53	0.53	0.53	0.32	0.60	0.60	0.60	0.60
8 mic	TBV	101.90	103.24	103.24	103.24	103.24	101.93	103.54	103.54	103.54	103.54
	$\rho$	0.32	0.53	0.53	0.53	0.53	0.31	0.59	0.59	0.59	0.59
25 SNP	TBV	101.97	103.23	102.34	102.70	102.70	101.96	103.59	103.58	103.58	103.59
	$\rho$	0.31	0.52	0.46	0.48	0.43	0.32	0.59	0.59	0.59	0.59
50 SNP	TBV	101.94	103.17	103.15	103.17	103.17	101.88	103.50	103.50	103.50	103.50
	$\rho$	0.32	0.52	0.52	0.52	0.52	0.31	0.58	0.58	0.58	0.58
100 SNP	TBV	101.89	103.09	103.09	103.09	103.09	101.89	103.43	103.43	103.43	103.43
	$\rho$	0.31	0.52	0.52	0.52	0.52	0.31	0.58	0.58	0.58	0.58

➤ **Percentage of selected individuals coinciding**

BLUP\_U



	$h^2 = 0.5$		$h^2 = 0.1$	
	BLUP_P	BLUP_M	BLUP_P	BLUP_M
4 mic	93.49	93.08	89.34	88.49
8 mic	99.93	99.93	99.82	99.82
<del>25 SNP</del>	<del>99.45</del>	<del>97.50</del>	<del>98.00</del>	<del>96.07</del>
50 SNP	99.30	99.29	98.34	98.30
100 SNP	100.00	100.00	100.00	100.00

- ✓ **very similar with acceptable assignment probabilities**
- ✓ **slightly lower figures for low heritability**



## **TO TAKE HOME**

- Including individuals with multiple paternities is not advantageous**
  
- Paternity assignment improves greatly if mating is controlled**
  
- Uncertain relationships may difficult to implement OC to control the lose of diversity and the rise of inbreeding**

## **FURTHER REMARKS**

- **Some other factors to be accounted for**
  - ✓ genotyping errors may exist
  - ✓ more uncertainty expected if breeders are relatives and/or inbred
  
- **Probably larger benefits when dealing with later generations**
  - ✓ mixed offspring from selected and unselected breeders
  - ✓ more uncertainty expected in selected families (higher inbreeding)
  
- **Repeat study with the second round of selection**





**UNCERTAINTY**

**=**

**PROBLEMS**



**DAD???**

# Thank you!



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