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GENETIC PARAMETERS AND GENOTYPE x ENVIRONMENT INTERACTIONS FOR GROWTH IN THE RED ABALONE (*Haliotis rufescens*)

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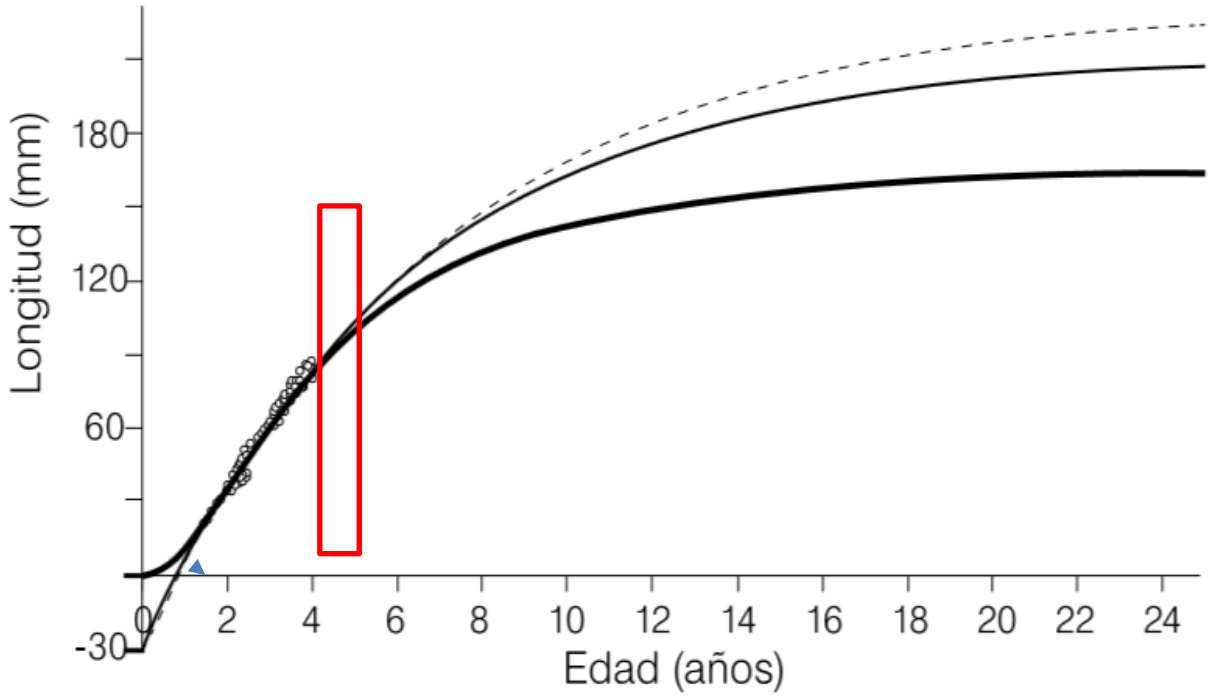
Chilean red abalone production

The red abalone (*Haliotis rufescens*) was introduced in Chile with aquaculture purposes in 1977 from California.

Source: Fisheries Yearbook SERNAPESCA 2013

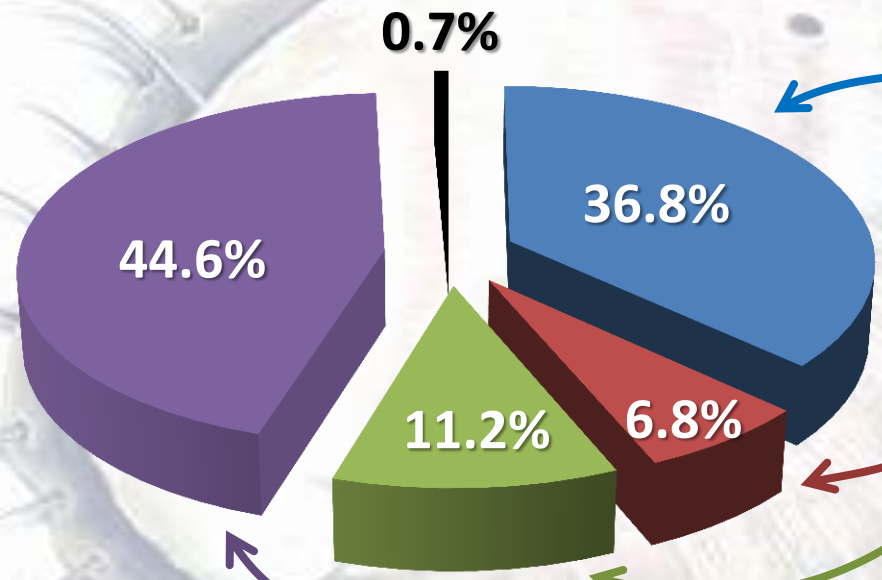
Growth of *H. rufescens* in culture



H. rufescen has a long productive cycle in Chile, usually 40 to 48 month

H. rufescens growth rates can be improved up 10% per generation through selective breeding if the best 5% growers are selected as brooders each generation (Jónasson et al. 1999; Brokordt et al. 2014)

Abalone farming areas in Chile



Atacama
Coquimbo
Valparaíso
Los Ríos
Chiloé

27-32°S

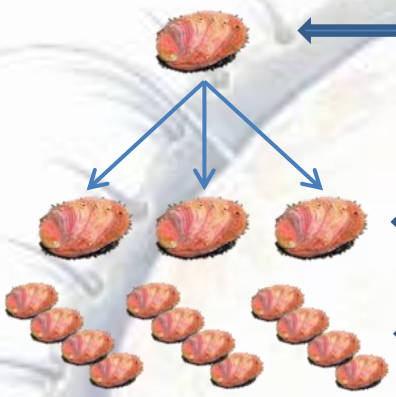
42°- 43°S

Genotype by environment interactions (GEI) may arise as effect of the environmental differences among farms

Objetive

Estimate the heritability and genetic correlations among traits across different environments and to verify the existence of genotype by environment interactions for growth traits in Chilean populations of red abalone.

Family construction and grow-up

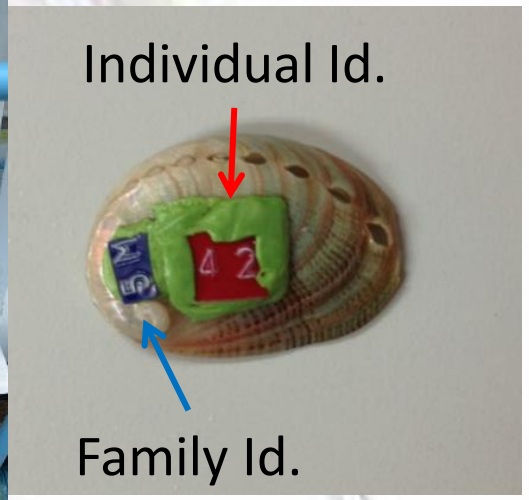


- 2 Cohorts (2007 and 2009)
- 1 sire crossed with 2 - 3 dams
- 59 and 42 full-sib (FS) families
- 24 and 17 half sib (HS) families

Larvae

Settling and nursery

Juvenile grow-up (16 -17 month)



Taging

Experimental farms

Cohort 1

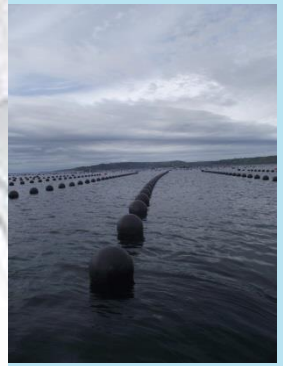
59 FS families were grow up in two farms for 25 month (N° 3,949):

- Cultivos Marinos San Cristóbal (CMSC)
- Abalones Chile (ACh)

Cohort 2

42 FS families were grow up in two farms for 12 month (N° 469):

- Universidad Católica del Norte (UCN)
- Live Seafood (LSF)



Methods

Fed *ad libitum* with fresh macro algae once a week.

Macrocistys pyrifera

Lessonia spp.

Ulva spp.

Gracilaria spp.

Studied traits

Shell width

Shell length

Total weight

Cohort 1: measured at 32 and 42 months of age

Cohort 2 was measured at 48 months of age

Statistical analysis

Estimation of heritability

$$y = Xb + Za + Zf + e$$

ASReml v 3.0

Fixed

Random and covariates

Additive genetic

Estimation of Correlations and genotype environment interaction

Cohort 1

Cohort 2

CMSC ⟺ ACh

UCN ⟺ LSF

Mean weight (g) and trait heritabilities in two cohorts of *H. rufescens* cultured in four farms

Cohort	Farm	Age (Months)	Mean (SD)	h^2 (SE)	CV_a	CV_p
2007	CMSC	32	26.83 (7.57)	0.34 (0.09)*	16.7	28.6
	ACh	32	20.71 (7.79)	0.31 (0.08)*	21.4	38.5
	CMSC	42	85.67 (19.96)	0.40 (0.11)*	15.1	23.8
	ACh	42	53.61 (17.54)	0.24 (0.08)*	16.1	32.9
2009	LSF	48	45.89 (20.61)	0.53 (0.16)*	33.1	45.7
	UCN	48	57.26 (26.49)	0.53 (0.17)*	33.8	46.5
	h^2	Range	0.24 - 0.53	Average =	0,39	

* => $h^2 \neq 0$; $p < 0,05$

Mean shell length (mm) and trait heritabilities in two cohorts of *H. rufescens* cultured in four farms

Cohort	Farm	Age (Months)	Mean (SD)	h^2 (SE)	CV_a	CV_p
2007	CMSC	32	54.99 (5.32)	0.33 (0.09)*	5.7	9.9
	ACh	32	49.34 (6.43)	0.36 (0.09)*	8.0	13.4
	CMSC	42	78.17 (6.17)	0.30 (0.10)*	4.4	8.01
	ACh	42	60.97 (7.73)	0.22 (0.08)*	6.1	12.9
2009	LSF	48	65.41 (9.37)	0.62 (0.17)*	11.5	14.6
	UCN	48	67.11 (11.34)	0.46 (0.16)*	11.0	16.4
	h^2	Range	0.22 – 0.62	Average =	0.38	

* => $h^2 \neq 0$; $p < 0,05$

Mean with (mm) and trait heritabilities in two cohorts of *H. rufescens* cultured in four farms

Cohort	Farm	Age (Months)	Mean (SD)	h^2 (SE)	CV_a	CV_p
2007	CMSC	32	38.12 (4.70)	0.21 (0.07)*	5.8	12.4
	ACh	32	34.07 (4.64)	0.35 (0.09)*	8.3	14.0
	CMSC	43	54.55 (4.57)	0.18 (0.08)*	3.6	8.4
	ACh	43	44.20 (5.85)	0.16 (0.07)*	5.6	13.3
2009	LSF	48	45.57 (6.87)	0.58 (0.17)*	11.7	15.4
	UCN	48	48.17 (8.46)	0.33 (0.15)*	9.7	17.0
	h^2	Range	0.16 – 0.58	Average =	0.30	

* => $h^2 \neq 0$; $p < 0,05$

Genotype by Environment Interactions

Trait	CMSC / ACh		LSF / UCN
	32 month	43 month	48 month
Total Weight	0.966 (0.069)	1.112 (0.049)	0.722 (0.165)
Shell Length	0.959 (0.065)	1.061 (0.071)	0.565 (0.206)
Shell Width	0.945 (0.075)	1.133 (0.104)	0.505 (0.238)
model	simple	Cov: Age	cov Age; Fix Sampling order

* => $r \neq 1$; $P < 0,05$

Genetic correlations between weight, shell length and shell width in *H. rufescens*

Age (Months)	Farm	*r* (range)	EE (range)
32	CMSC	0.86 – 0.95	0.02 – 0.06
	ACh	0.94 – 0.98	0.01 – 0.03
42	CMSC	0.82 – 0.95	0.04 – 0.07
	ACh	0.89 – 0.97	0.02 – 0.04
48	UCN	0.88 – 0.98	0.01 – 0.05
	LSF	0.88 – 0.98	0.01 – 0.05

All genetic correlations hight ($P < 0.05$) and positives

Conclussions

- Chilean populations of cultured red abalone have substantive additive genetic variance to support a selective breeding program.
- Genetic correlations among growth traits are high.
- Genotype by environmental interactions are low between farms in northern Chile, but they can be significant between northern and southern locations.

Thanks!

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