

MITOS Y VERDADES DE PROGRAMAS DE SELECCIÓN GENÉTICA DE CAMARÓN, A FIN DE DILUCIDAR LOS PROGRAMAS MÁS ADECUADOS PARA SELECCIÓN DE CAMARÓN EN ECUADOR

EU project 2014 - 2019

Grupo de Investigación en Acuicultura
(GIA; www.giaqua.org)



Juan Manuel AFONSO¹, Walter **INTRIAGO²**, Hyun Suk **SHIN¹**, Islam **SAID¹**, Cathaysa **PÉREZ-GARCÍA¹**, Sergio **LEÓN-BERNABEU³**, Álvaro **LORENZO-FELIPE¹**, María Jesús **ZAMORANO¹**

¹ULPGC, ²BIOGEMAR

ECO AQUA
www.ecoaqua.eu

Research and Technology to enhance excellence in Aquaculture development under an Ecosystem approach



UNIVERSIDAD DE LAS PALMAS DE GRAN CANARIA



CAMPUS ATLÁNTICO TRICONTINENTAL CANARIAS 2010/2015

1



Parque Científico Tecnológico Universidad de Las Palmas de Gran Canaria

1

Grupo de Investigación en Acuicultura



MEJORA GENÉTICA EN CAMARÓN

ÍNDICE

- ❑ 1. Estrategias
- ❑ 2. Estructura de la mejora genética en Camarón
 - 2.1. Condicionantes biológicos y de producción
- ❑ 3. Herramientas a desarrollar o disponer
- ❑ 4. Definición de la población base
- ❑ 5. La matriz de parentesco
- ❑ 6. Los caracteres de la selección (objetivos y criterios)
- ❑ 7. Métodos de selección
 - 7.1. Unicarácter
 - 7.2. Multicarácter
- ❑ 8. La estimación de parámetros genéticos
- ❑ 9. Respuesta a la selección
- ❑ 10. Modelo de implementación de la Selección Genética
- ❑ 11. Interacción Genotipo-Ambiente
- ❑ 12. Cruzamiento
- ❑ 13. Selección genómica
 - 13.1. Detección de QTL
 - 13.2. Costes



MEJORA GENÉTICA EN CAMARÓN: 1. Estrategias

Selección
Reproductores



SELECCIÓN

CRUZAMIENTO

BIOTECNOLOGÍA:

- Marcadores moleculares
(*SNP, Microsatélites*)
- QTL

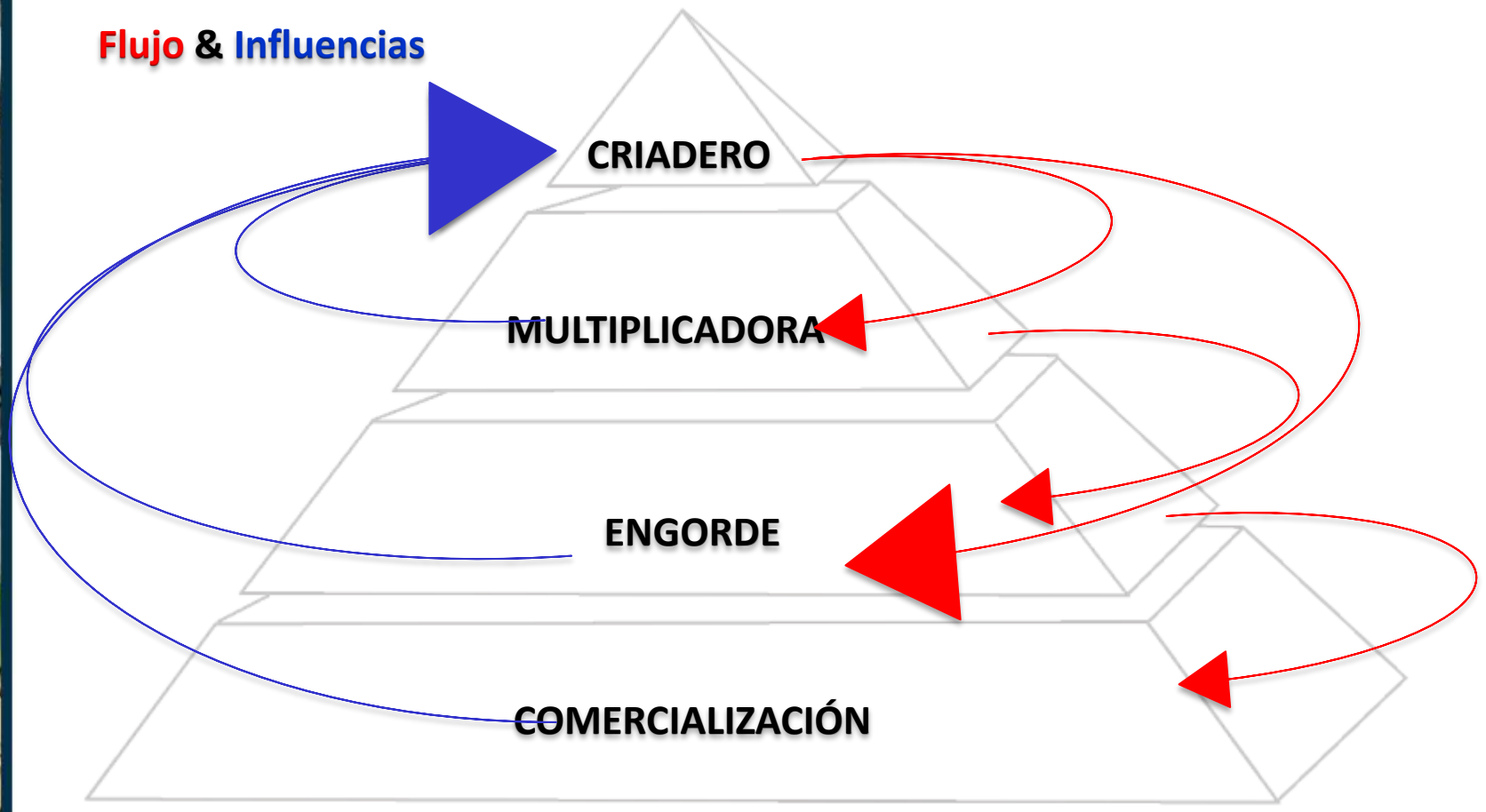


MEJORA GENETICA en Camarón: 2. Estructura



MEJORA GENETICA en Camarón: 2. Estructura

Flujo & Influencias



2.1. Condicionantes biológicos y de producción

- % de desove diario: *con o sin ablación*
- Edad a la madurez sexual: *intervalo entre generaciones, generaciones de selección por año*
- Vida útil del reproductor seleccionado y en producción: *difusión de la mejora*
- Estructura de la producción de la empresa: *millones nauplios, PL12, proporción de sexo por tanque, reproductores totales en producción, etc..*
- Caracteres de interés para la selección: *crecimiento, supervivencia, resistencia, etc..*
- Grado de conocimiento de las relaciones de parentesco de la población: *definición de la población de partida*
- Ambientes para la evaluación genética: *densidad, temperatura, salinidad.*
- Capacidad técnica en herramientas genéticas: *laboratorios de análisis en empresa*

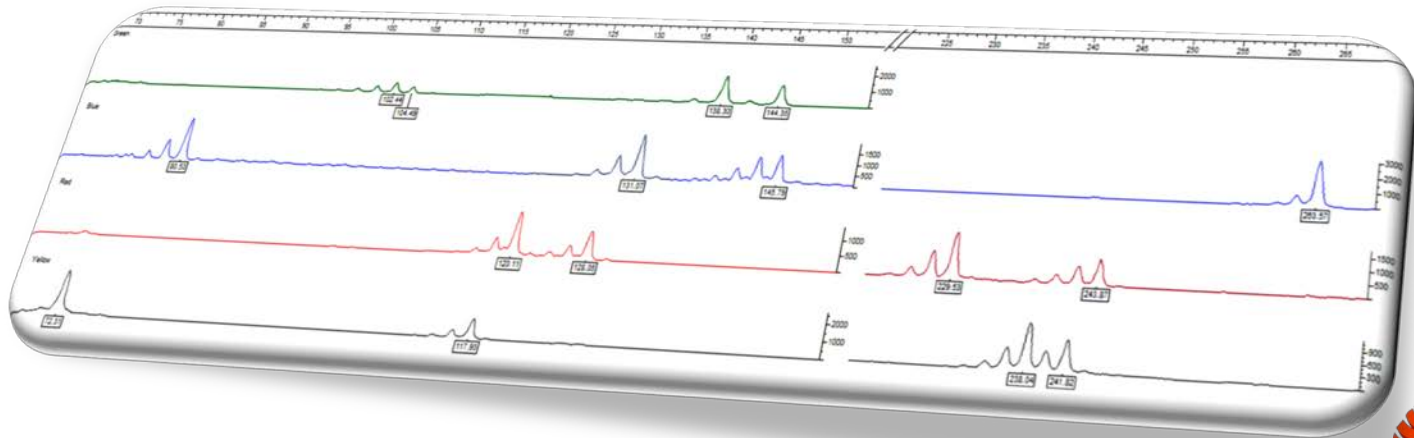


MEJORA GENÉTICA EN CAMARÓN: 3. Herramientas

- ✓ Banco de muestras (ADN y tejidos)

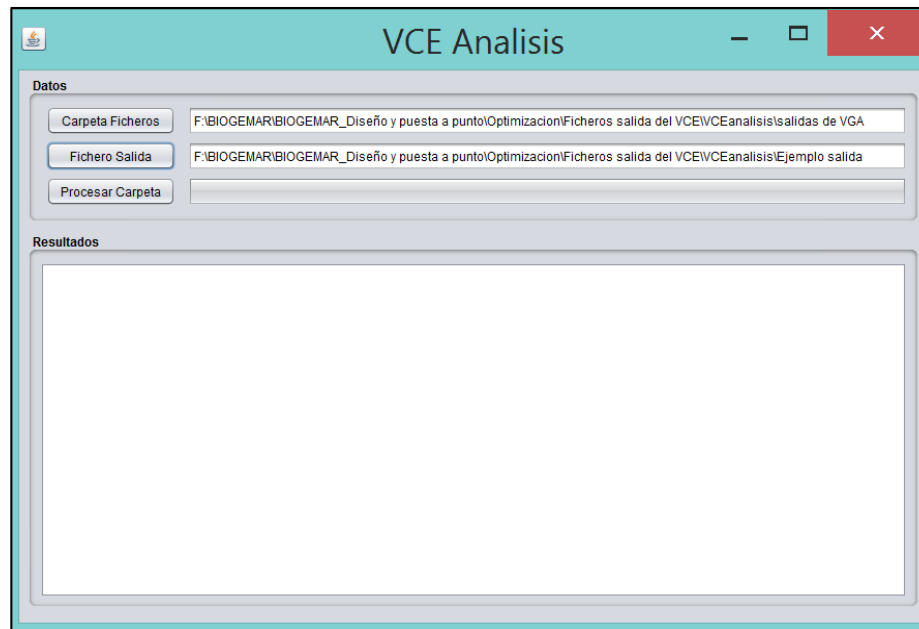


- ✓ Marcadores moleculares específicos (microsatélites o SNP): **SuperMúltiplex Lvann_1 (0,67 / 10)**



MEJORA GENÉTICA EN CAMARÓN: 3. Herramientas

- ✓ Programa que facilite en tiempo record la elaboración matrices de parámetros genéticos (VCE_ánalisis)



MEJORA GENÉTICA EN CAMARÓN: 3. Herramientas

- ✓ Programa que facilite la estructuración de lotes por TALENTO GENÉTICO y MINIMO PARENTESCO en tiempo record (**VCE_optimización** / [FISHBOOSTEL](#))

No of male candidates= 3500

No of female cand = 3500

SOLUTION :

Population Average Relationship (solution) = 0.274338147115317

Genetic merit of parents = 18.6528093059157

No of selected males = 20

Name	%_progeny	EBV	avg_relat
213002	0.000	13.031	0.262
213004	0.000	13.855	0.262
213006	0.000	15.199	0.262
213008	0.000	15.206	0.262



MEJORA GENÉTICA EN CAMARÓN: 3. Herramientas

- ✓ Diagnóstico automático de *Infectious hypodermal and hematopoietic necrosis virus (IHHNV)* – *PCR_{ADN} (GenBank: JN616415.1 – Genome complete) *White spot syndrome virus (WSSV)* – *PCR_{ADN}

IHHNV

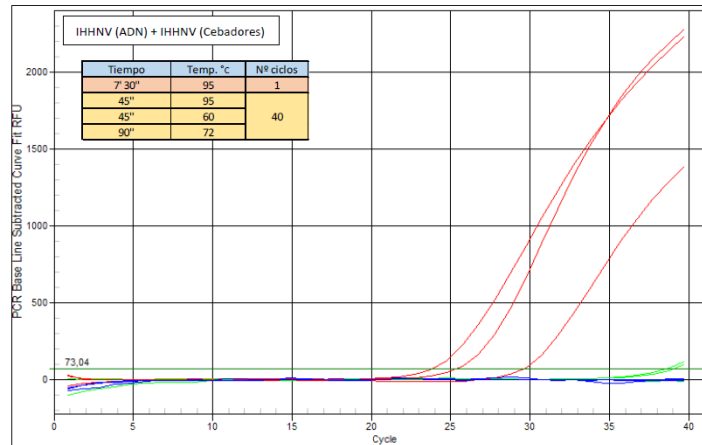


Figura 36. Gráfica que representa la fluorescencia emitida por la sonda de IHHNV (ADN: Blanco, IHHNV, *L. vannamei*).

WSSV

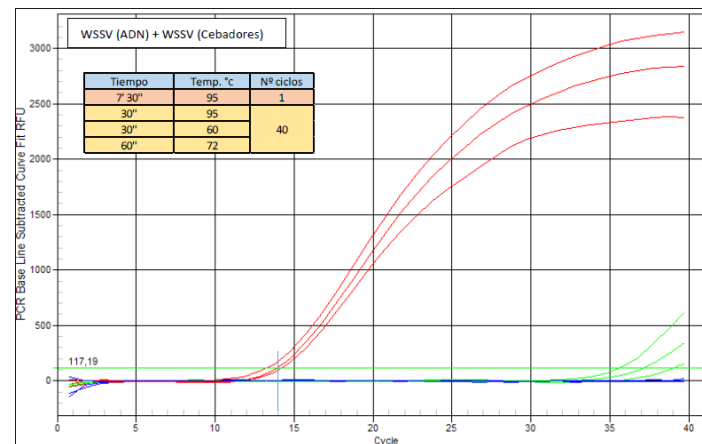


Figura 31. Gráfica que representa la fluorescencia emitida por la sonda de WSSV (ADN: Blanco, WSSV, *L. vannamei*).



MEJORA GENÉTICA EN CAMARÓN: 3. Herramientas

- ✓ Programa de apareamientos: minimizando la consanguinidad y permitiendo apareamientos anidados para machos y hembras (**APAREA_CAMARÓN**)
- ✓ Robótica para la elaboración de MásterMix, Normalización de [ADN], Banco de ADN, extracción ADN (**TECAN, BIOSPRINT96**)

TECAN

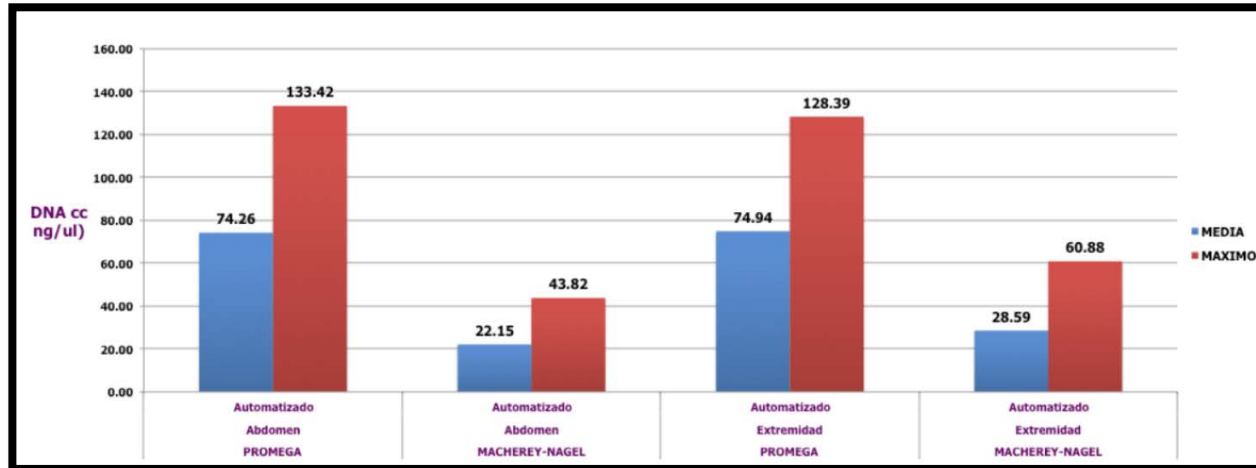


BIOSPRINT96



MEJORA GENÉTICA EN CAMARÓN: 3. Herramientas

- ✓ **Protocolos** de rendimiento de extracción de ADN, a partir de diferentes tejidos



MEJORA GENÉTICA EN CAMARÓN: 3. Herramientas

- ✓ Base de datos (**BBDD**)

Macmicod-BBDD-v5 - Excel

ARCHIVO INICIO INSERTAR DISEÑO DE PÁGINA FÓRMULAS DATOS REVISAR VISTA ACROBAT

Calibri 11 A A Ajustar texto General

Pegar Fuente Alineación Número Estilos Celdas

Portapapeles Fuente Alineación Número Estilos Celdas

S14

	A	B	C	D	E	F	G	H	I	J	K	L
	generation	age	station	label	prebreed_sacrif	sex	survival	weight	length	observations	def	tank origin
1												
2	5	105	C1	9999900	Pepr	Hembra	Vivo	19,40	11,5		Sin Definiendo	1
3	5	105	NSS	9999901	Pepr	Hembra	Muerto	18,80	11,0		Definido12	1
4	5	105	NSS	9999902	Pepr	Hembra		19,50	11,0		Definido13	2
5	5	105	NSS	9999903	Pepr	Macho		11,40	9,0			2
6	5	105	NSS	9999904	Pepr	Macho		23,00	12,6			2
7	5	105	NSP	9999905	Pepr	Hembra	Muerto	10,90	9,0			2
8	5	105	NSP	9999906	Pepr	Hembra	Muerto	9,50	8,0			2
9	5	105	NSP	9999907	Pepr	Macho	Vivo	12,10	9,7			3
10	5	105	NSP	9999908	Pepr	Macho	Vivo	9,30	8,0			3
11	5	105	NSP	9999909	Pepr	Macho		18,50	12,0			1
12	5	105	C1	9999910	Sacrif			23,70	12,0		Definido16	
13	5	105	C1	9999911	Sacrif			21,10	12,0			
14	5	105	C1	9999912	Sacrif			19,00	10,0			
15	5	105	C1	9999913	Sacrif			14,70	10,8			
16	5	105	C1	9999914	Sacrif			18,60	11,2			
17	5	105	C2	9999915	Sacrif			17,20	11,8			
18	5	105	C2	9999916	Sacrif			17,40	11,2			
19	5	105	C2	9999917	Sacrif			15,40	10,0			
20	5	105	C2	9999918	Sacrif			14,00	10,9			
21	5	105	C2	9999919	Sacrif			13,50	9,8			
22	5	105	C3	9999920	Sacrif			18,50	11,7			
23	5	105	C3	9999921	Sacrif			18,70	10,9			
24	5	105	C3	9999922	Sacrif			16,70	11,8			
25	5	105	C3	9999923	Sacrif			20,10	10,1			
26	5	105	C3	9999924	Sacrif			19,80	10,5			
27	5	105	C4	9999925	Sacrif			15,10	9,6			
28	5	105	C4	9999926	Sacrif			13,40	11,0			
29	5	105	C4	9999927	Sacrif			20,50	11,5			
30	5	105	C4	9999928	Sacrif			15,80	11,0			
31	5	105	C4	9999929	Sacrif			11,40	9,1			
32	5	105	C4	9999930	Sacrif			13,40	11,0			
33	5	105	C4	9999931	Sacrif			20,50	11,5			

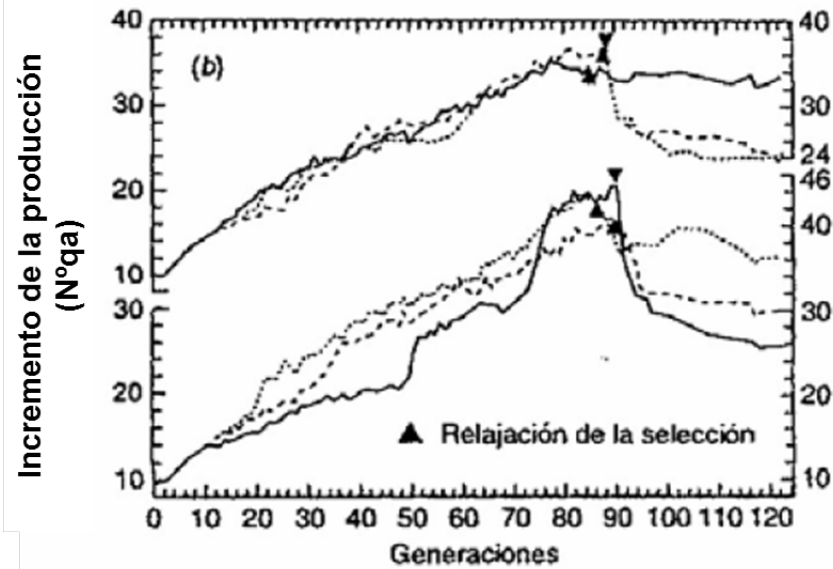
Enviar a la Base de Datos

LIMPIAR EXCEL

NUEVOS INDIVIDUOS Hoja1 WFLI_BLOCK DNA_PLATE PCR_PLATE FAMILY FAMILY_GEN ...

4. Definición de la Población Base

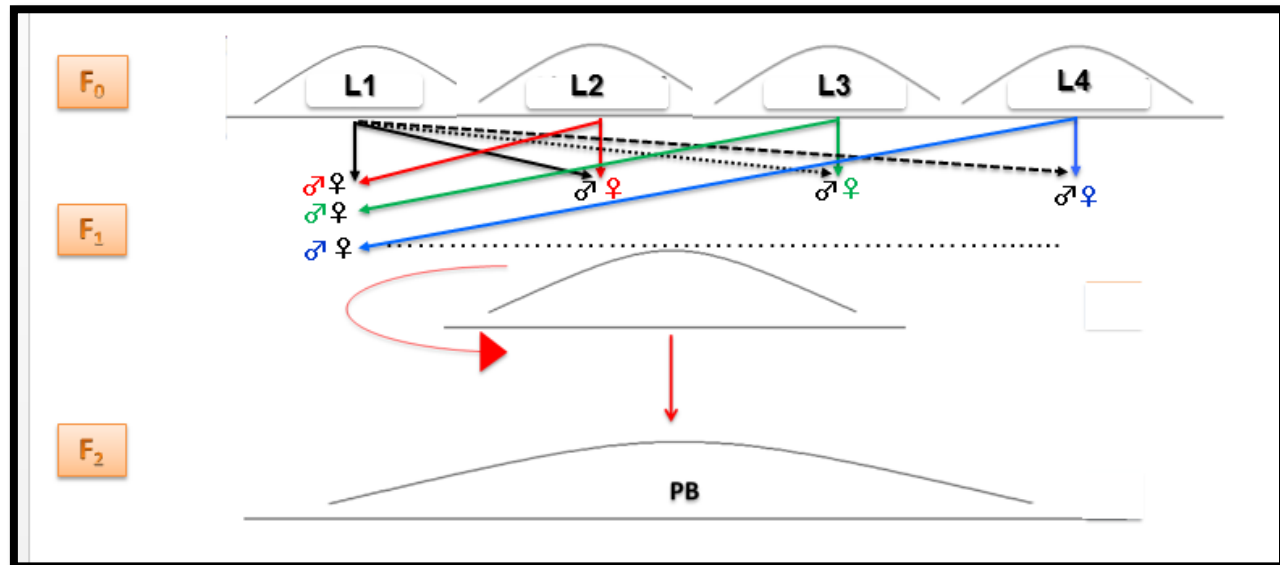
- ✓ Esencial su definición para mantener la longevidad del programa de selección como herramienta de mejora de la producción.



4. Definición de la Población Base

- ✓ Dependiendo del conocimiento de la población (*control de rendimiento y relaciones de parentesco*), se puede utilizar diferentes herramientas.

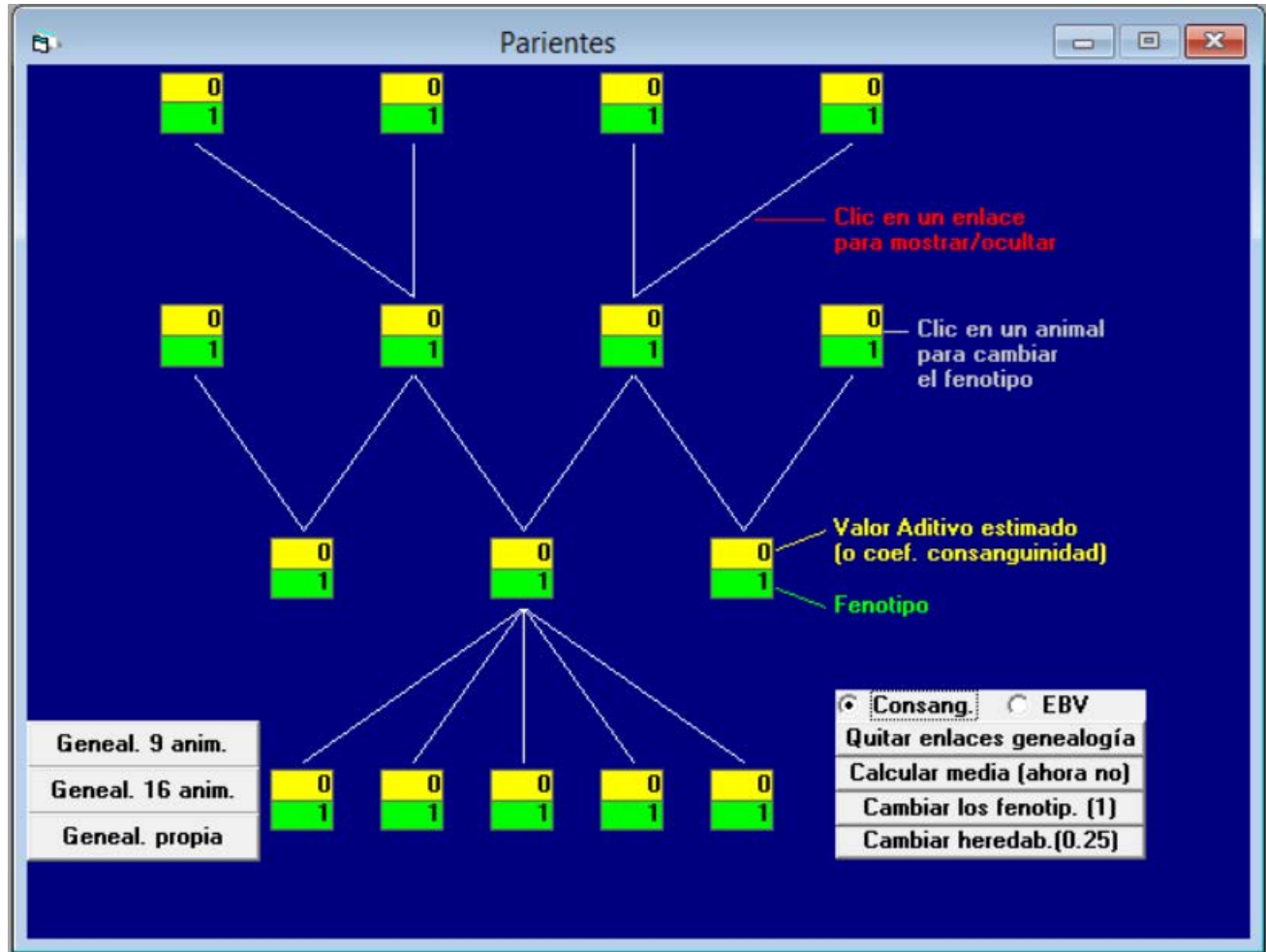
- **CRUCES DIALÉLICOS**



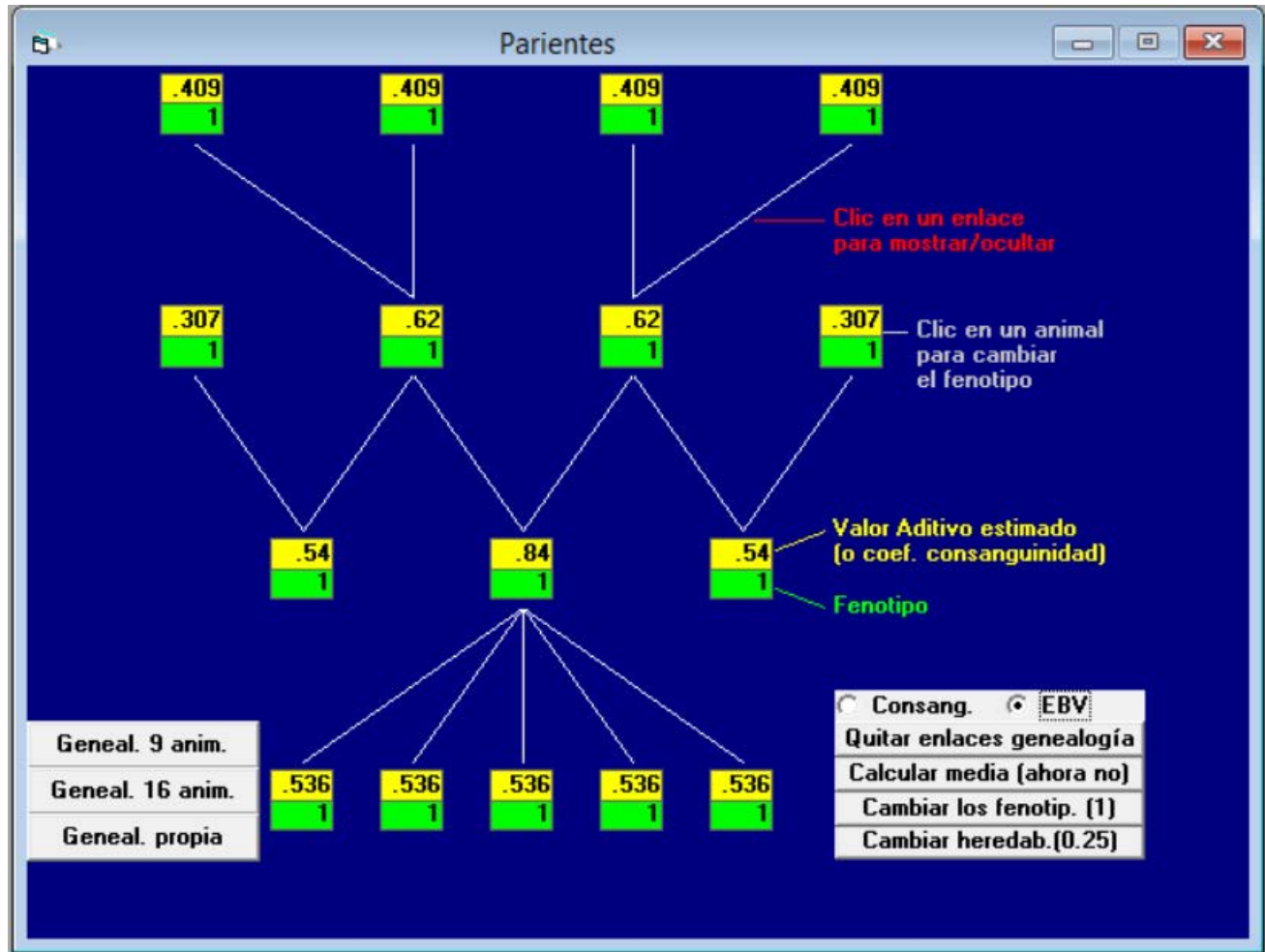
- **MOL_COAN** (basado en marcadores moleculares, *microsatélites*): parentesco molecular
- **BASEPOP** (basado en marcadores moleculares, *microsatélites*): mínimo parentesco y selección



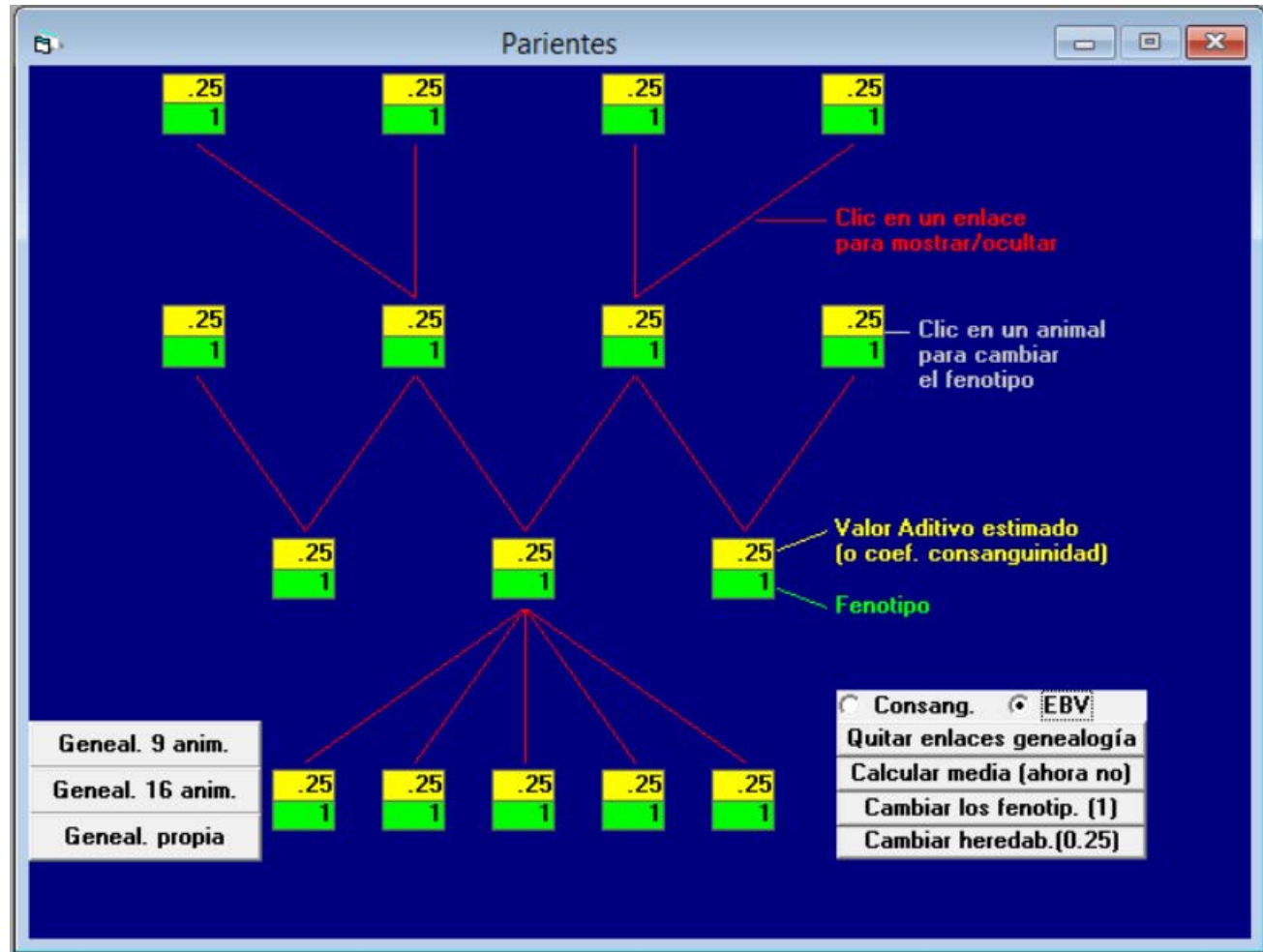
5. Matriz de parentesco



5. Matriz de parentesco

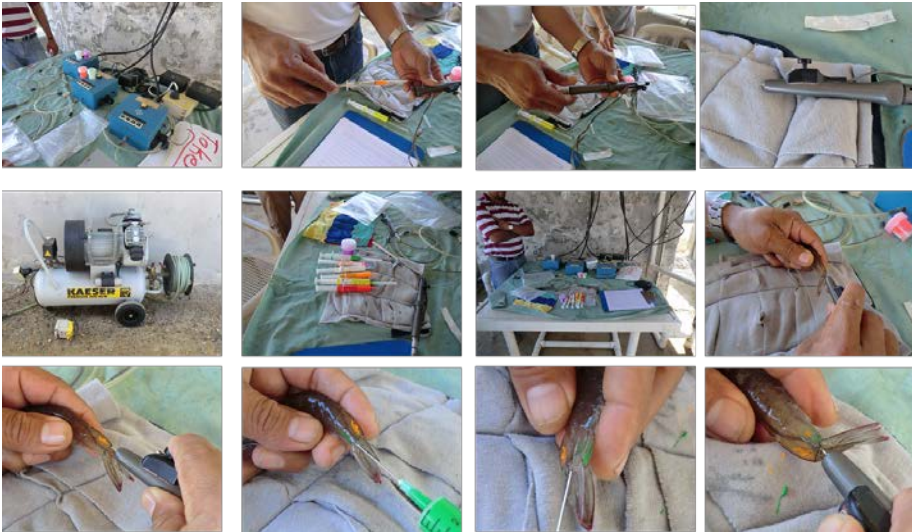


5. Matriz de parentesco



5. Matriz de parentesco

- ✓ Es esencial disponer de sistemas de trazabilidad familiar e individual
 - **VIE** (*marcaje familiar*)



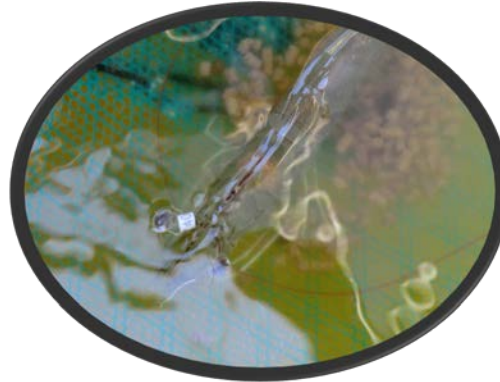
Fecha: _____ Muestreo familias lote 31 genética para realizar ms

Fam	Tq	Cod	1	2	3	4	5	6	7	8	9
		AAV									
		ABN									
		AFB									
		ALP									
		ANA									
		APF									
		ARB									
		AVL									
		BAV									
		BBN									
		BFB									
		AAA									
		BNA									
		BPF									
		BRB									
		BVL									
		FAV									
		FBN									
		FFB									
		FLP									
		ANL									
		FPF									
		FRB									
		FVL									
		LVV									
		LBN									
		LBB									
		LLP									
		LNA									
		LPF									



5. Matriz de parentesco

- **Etiquetas** (*marcaje individual*)



- **NONATEC** (sistema electrónico de *marcaje individual*)



* **NONATEC Lab Bench Bluetooth reader**

* **NONATEC Hand Held Bluetooth reader**



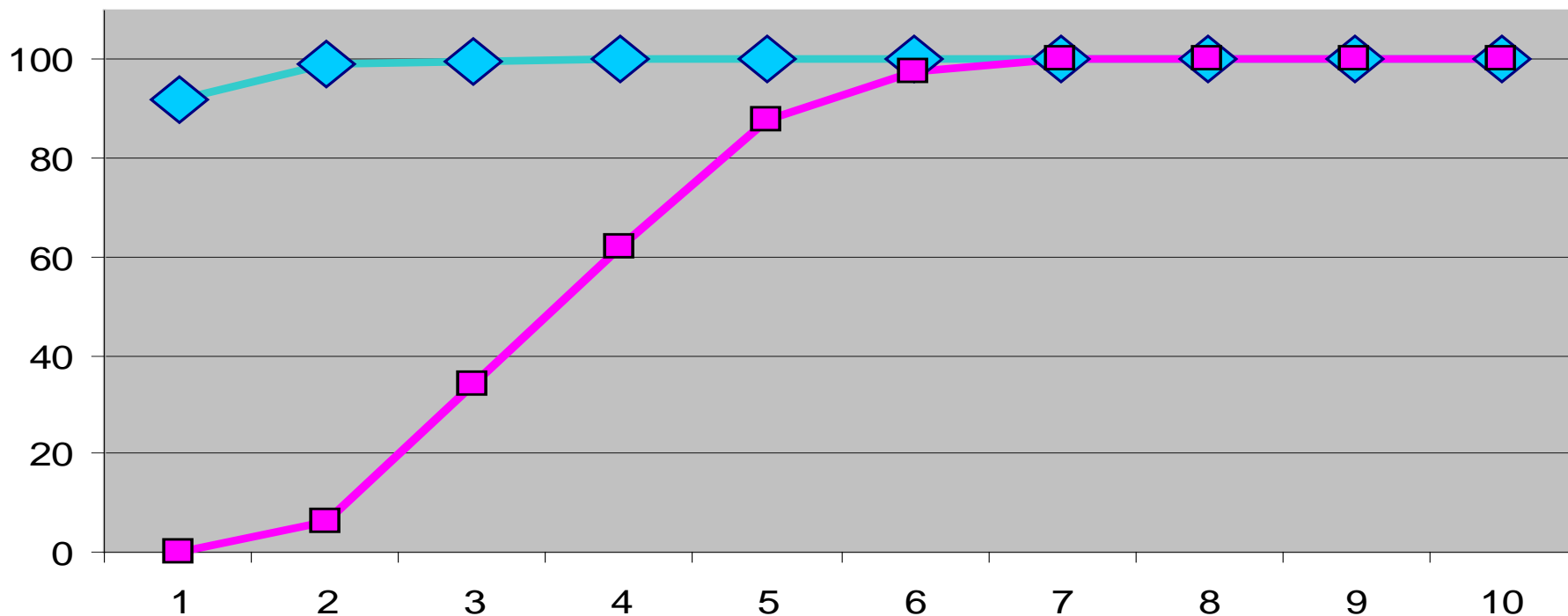


5. Matriz de parentesco

- **Microstatélites** (*reconocimiento individual*)

RimA

	1	2	3	4	5	6	7	8	9	10
P.E.C. (%)	94,8	99,1	99,8	99,9	100	100	100	100	100	100
P.R.A. (%)	0	6,1	34,1	62,2	87,8	97,6	100	100	100	100

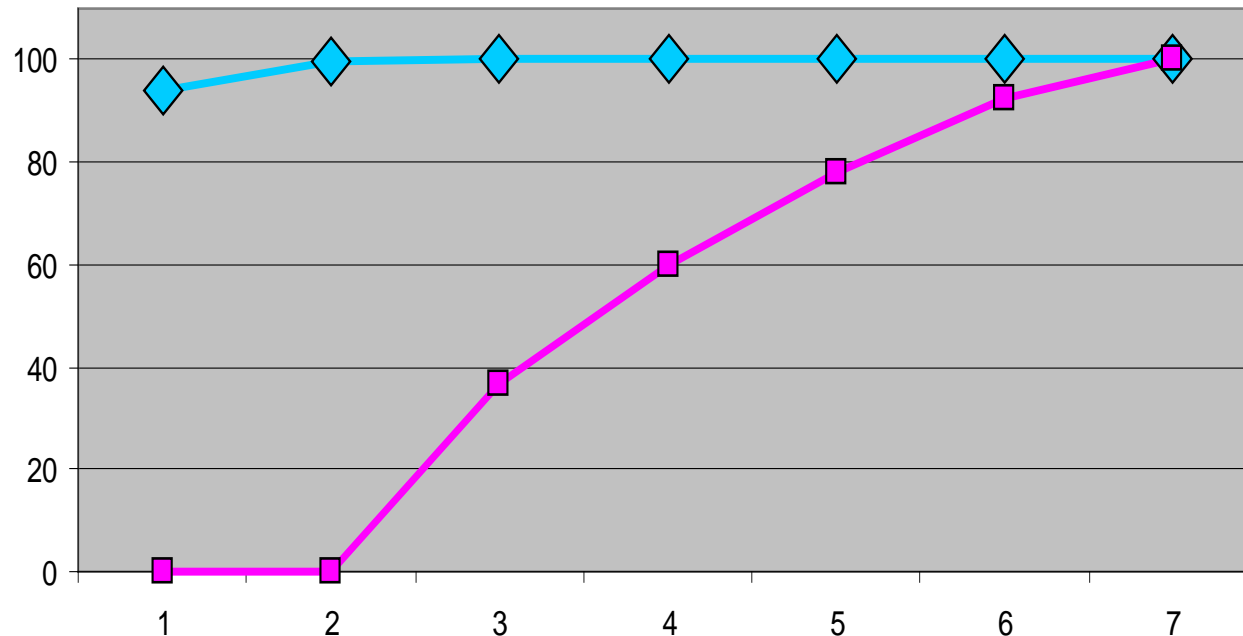


5. Matriz de parentesco

- **Microstatélites** (*reconocimiento individual*)

RimB

	1	2	3	4	5	6	7
P.E.C.* (%)	94,1	99,6	99,9	100	100	100	100
P.R.A.* (%)	0	0	36,6	59,7	78,1	92,7	100



5. Matriz de parentesco

- **SNP** (*reconocimiento individual*)

Equipamiento mínimo ILLUMINA

MiniSeq

MiSeq



TruSeq Genotype N_e

#Samples	#SNPs		
	100	500	1000
384	\$30	\$40	\$50
1056	\$25	\$28	\$35
3072	\$23	\$25	\$27
5088	\$22	\$23	\$25
10080	\$20	\$21	\$22
15072	\$20	\$20	\$21
20064	\$20	\$20	\$20
25056	\$20	\$20	\$20
30048	\$20	\$20	\$20
>30048	\$20	\$20	\$20



6. Los caracteres de la selección (*objetivos y criterios*)

OBJETIVOS

Crecimiento
Conversión del alimento

Resistencia a patógenos

Morfología

Robustez

Éxito reproductivo

CRITERIOS

Peso total al sacrificio
Peso corporal al sacrificio
Longitud total al sacrificio
% (peso corporal / peso total)
SGR

% supervivencia frente a retos
% supervivencia frente a episodios naturales

Longitud de segmentos abdominales
Alto de segmentos abdominales
Ancho de segmentos abdominales

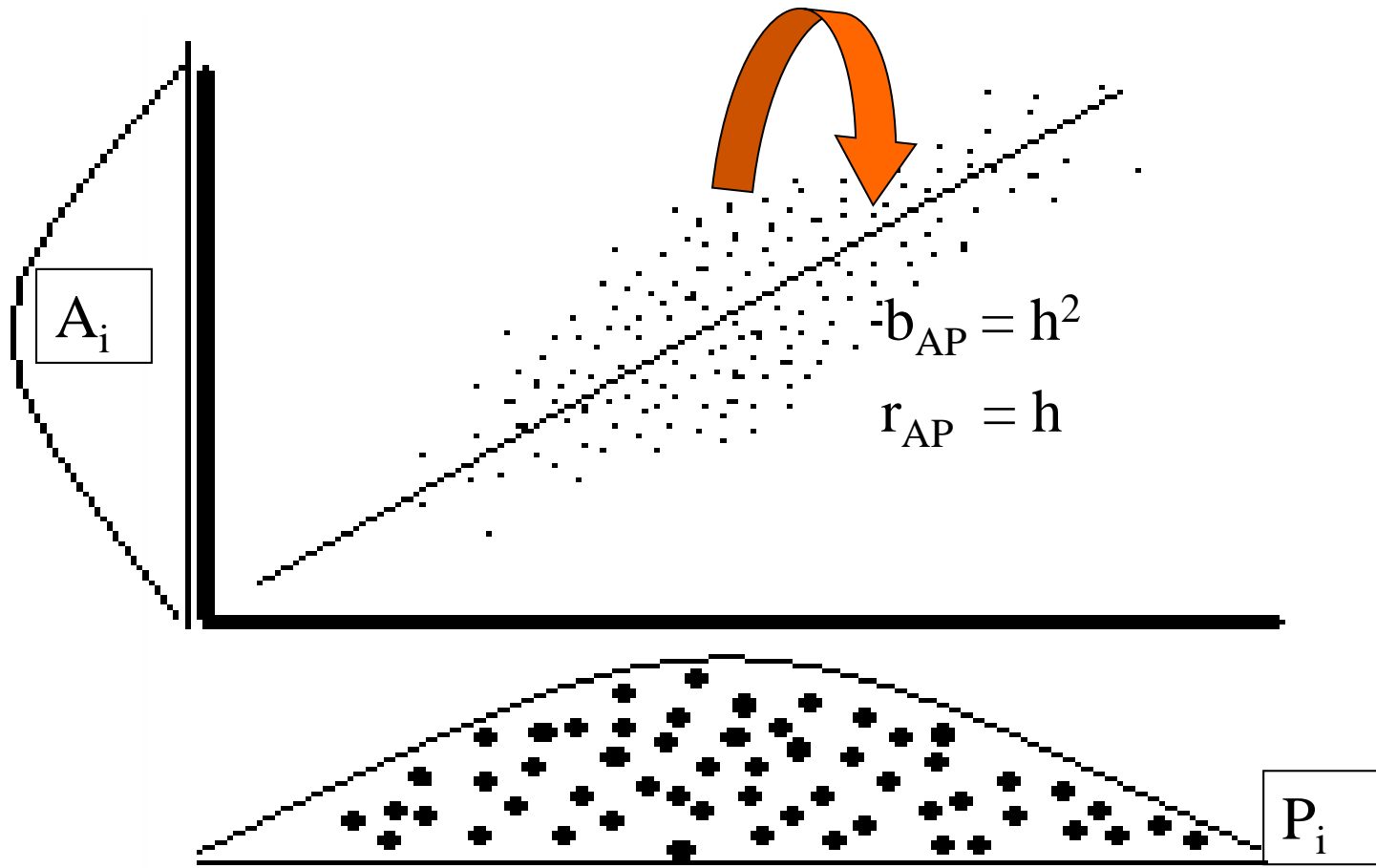
% supervivencia a diferentes edades en laboratorio
% supervivencia en camaronera
% supervivencia en RAS

Nº de puestas / hembra
Periodo entre puestas
Nº de huevos
Diámetro del huevo



7. Métodos de selección: 7.1. Selección unicarácter

Selección FENOTÍPICA (MASAL)

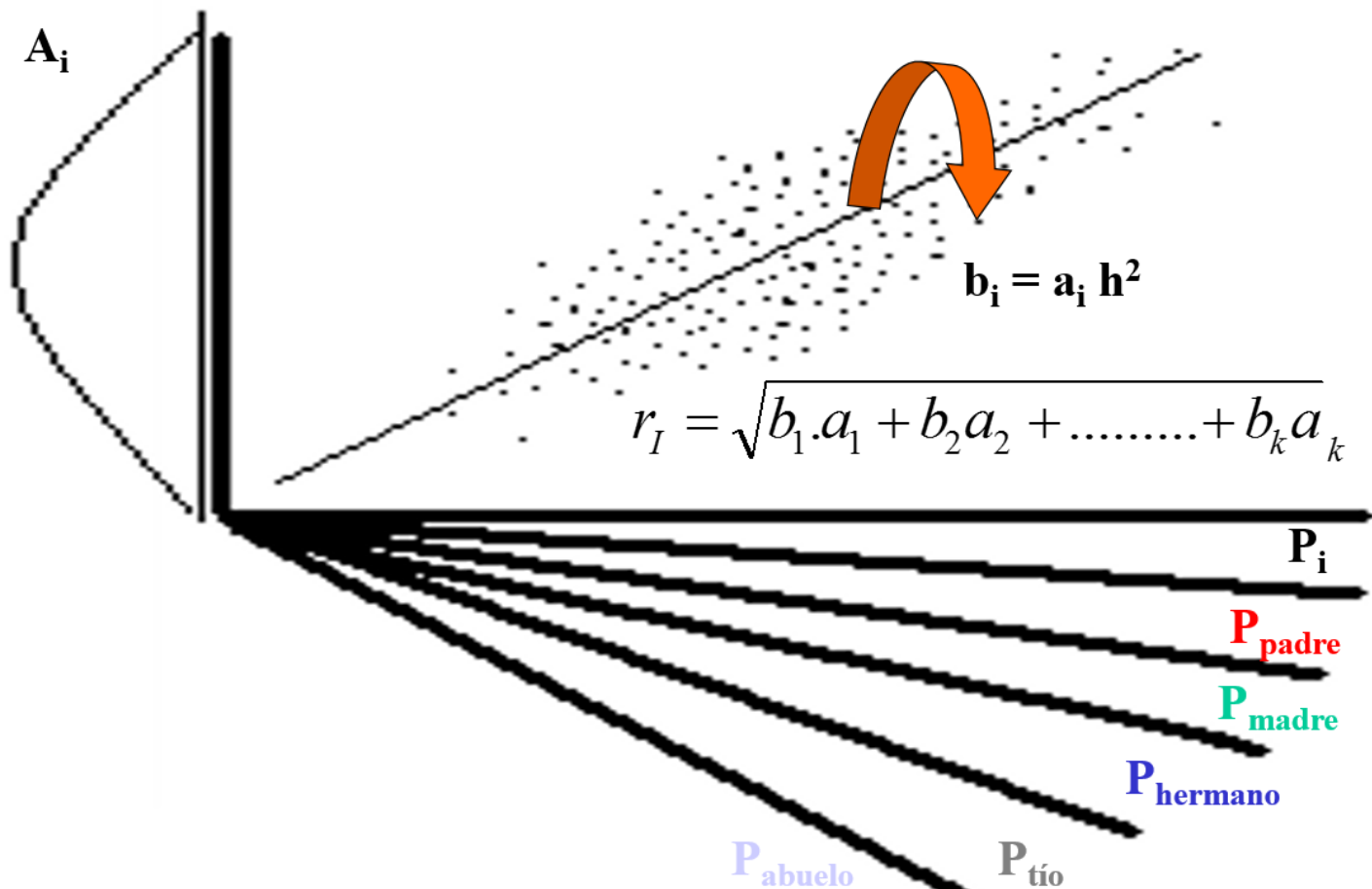


$$A_i = b_{AP} * P_i$$



7. Métodos de selección: 7.1. Selección unicarácter

Selección mediante ÍNDICES



$$A_i = b_i P_i + b_p P_p + b_m P_m + b_h P_h + b_t P_t + b_a P_a$$



7. Métodos de selección: 7.1. Selección unicarácter

Selección mediante ÍNDICES

Respuesta

$$\frac{R}{L} = \frac{i\sigma_A}{L} r_{I,A}$$

Coefficientes

$$r_{I,A} = \sqrt{b_1 a_{1\alpha} + b_2 a_{2\alpha} + \dots + b_k a_{k\alpha}}$$

Valor genético aditivo

$$I = b_1 P_1 + b_2 P_2 + b_3 P_3 + \dots + b_k P_k$$

$$b_1; b_2; b_3; \dots b_k$$

Determinación de coeficientes de regresión

$$\frac{\partial r_{IA}}{\partial b_i} \longrightarrow \left\{ \begin{array}{l} d_1 b_1 + a_{12} b_2 + a_{13} b_3 + \dots + a_{1k} b_k = a_{1\alpha} \\ a_{21} b_1 + d_2 b_2 + a_{23} b_3 + \dots + a_{2k} b_k = a_{2\alpha} \\ a_{k1} b_1 + a_{k2} b_2 + a_{k3} b_3 + \dots + d_k b_k = a_{k\alpha} \end{array} \right.$$



7. Métodos de selección: 7.1. Selección unicarácter

Selección FENOTÍPICA (MASAL)

donde

$$d_i = \frac{1 + (m_i - 1)r + (n_i - 1)a_{ii}}{m_i \cdot h^2 + (n_i - 1)a_{ii}}$$

a_{ij} = coeficiente de relación aditivo entre i e j

a_{ii} = coeficiente de relación aditivo entre dos parientes cualesquiera del individuo i

$a_{i\alpha}$ = coeficiente de relación aditivo entre i y α (individuo y candidato)

m = nº de medidas sobre el individuo o pariente i

n_i = número de individuos o parientes i

Ejemplo: Selección FENOTÍPICA (una medida)

$$d_1 b_1 = a_{1\alpha}$$

$$d_1 = \frac{1 + (m_1 - 1)r + (n_1 - 1)a_{ii}}{m_1 h^2 + (n_1 - 1)a_{ii}} = \frac{1 + (1 - 1)r + (1 - 1)a_{ii}}{1 h^2 + (1 - 1)a_{ii}} = \frac{1}{h^2} \quad a_{1\alpha} = a_{11} = 1$$

$$\frac{1}{h^2} b_1 = 1$$

$$b_1 = h^2$$

$$b_{A,P} = h^2$$

$$r_{I,A} = r_{P,A} = \sqrt{b_1 a_{1\alpha}} = \sqrt{h^2 \cdot 1} = h$$



7. Métodos de selección: 7.1. Selección unicarácter

Método	Respuesta	Valor genético aditivo
- Individual	$\frac{R}{L} = \frac{i\sigma_A}{L} h$	$\hat{A} = h^2 (P_i - \bar{P})$
- Individual con "n" mediciones	$\frac{R}{L} = \frac{i\sigma_A}{L} h \sqrt{\frac{n}{1+(n-1)r}}$	$\hat{A} = \frac{nh^2}{1+(n-1)r} (\bar{P}_{n_i} - \bar{\bar{P}})$
- Genealógica	$\frac{R}{L} = \frac{i\sigma_A}{L} ah$	$\hat{A} = ah^2 (P_i - \bar{P})$
- Fraternal	$\frac{R}{L} = \frac{i\sigma_A}{L} ah \sqrt{\frac{n}{1+(n-1)t}}$	$\hat{A} = \frac{anh^2}{1+(n-1)t} (\bar{P}_{n_i} - \bar{\bar{P}})$
- Progenie o descendencia	$\frac{R}{L} = \frac{i\sigma_A}{L} \frac{1}{2} h \sqrt{\frac{n}{1+(n-1)t}}$	$\hat{A} = \frac{1}{2} \frac{nh^2}{[1+(n-1)t]} (\bar{P}_{n_i} - \bar{\bar{P}})$
- Familiar	$\frac{R}{L} = \frac{i\sigma_A}{L} h \frac{[1+(n-1)a]}{\sqrt{n[1+(n-1)t]}}$	$\hat{A}_f = h^2 \left(\frac{1+(n-1)a}{1+(n-1)t} \right) (\bar{P}_f - \bar{\bar{P}}_f)$
- Intrafamiliar	$\frac{R}{L} = \frac{i\sigma_A}{L} h(1-a) \sqrt{\frac{(n-1)}{n(1-t)}}$	$\hat{A} = h^2 \frac{(1-a)}{(1-t)} (P_i - \bar{P}_f)$
- Familiar + Intrafamiliar	$\frac{R}{L} = \frac{i\sigma_A}{L} h \sqrt{1 + \frac{(a-t)^2(n-1)}{(1-t)[1+(n-1)t]}}$	$\hat{A} = h^2 \frac{(1-a)}{(1-t)} (P_i - \bar{P}_f) + h^2 \frac{[1+(n-1)a]}{[1+(n-1)t]} (\bar{P}_f - \bar{\bar{P}}_f)$



7. Métodos de selección: 7.1. Selección unicarácter

Selección por DESCENDENCIA

Método	Respuesta	Valor genético aditivo
- Progenie o descendencia	$\frac{R}{L} = \frac{i \cdot \sigma_A}{L} \frac{1}{2} h \sqrt{\frac{n}{1+(n-1)t}}$	$\hat{A} = \frac{1}{2} \frac{nh^2}{[1+(n-1)t]} (\bar{P}_{n_i} - \bar{\bar{P}})$

Siendo $1/2$ el coeficiente de **relación aditivo**

Límite ($n \rightarrow \infty$)

$$\lim_{n \rightarrow \infty} r_{\bar{P}_{n(MH/HC),A}} = \frac{1}{2} h \sqrt{\frac{1}{t}} = \sqrt{\frac{(0,5)^2 h^2}{ah^2}} = \sqrt{\frac{(0,5)^2}{a}}$$

$$\left. \begin{array}{l} a_{HC} = \frac{1}{2} \Rightarrow r_{\bar{P}_{n(HC),A}} = \sqrt{0,5} = 0,7 \\ a_{MH} = \frac{1}{4} \Rightarrow r_{\bar{P}_{n(MH),A}} = \sqrt{1} = 1 \end{array} \right\}$$

Comparación entre métodos (ausencia de Ec)

Hermanos carnales

$$h^2 > 0,5 \Rightarrow r_{P,A} > r_{\bar{P}_{n,A}}$$

Medios hermanos

$$\neq h^2 \Rightarrow r_{P,A} < r_{\bar{P}_{n,A}}$$

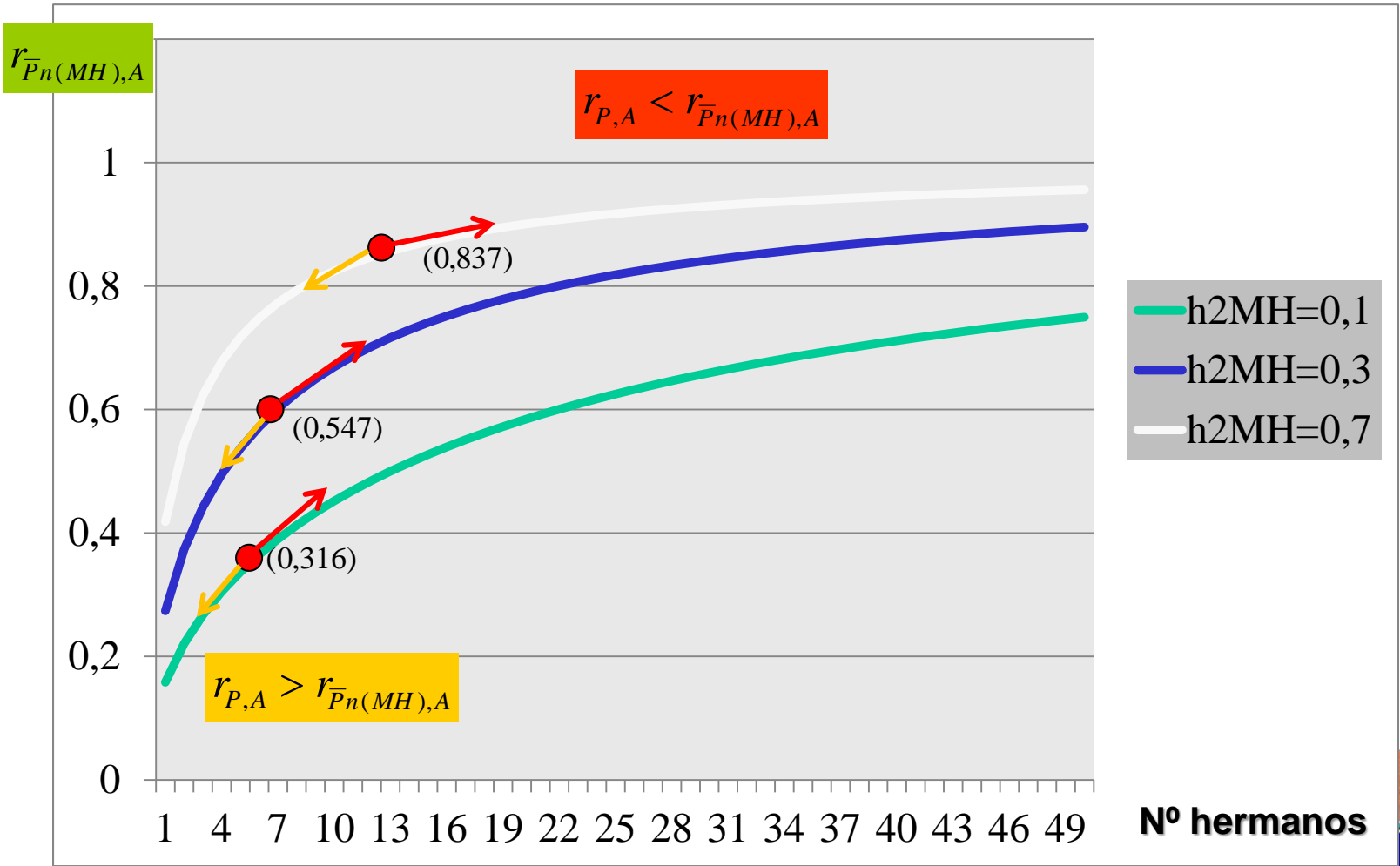


7. Métodos de selección: 7.1. Selección unicarácter

Selección por DESCENDENCIA

$$r_{\bar{P}n(MH),A} = \frac{1}{2}h\sqrt{\frac{n}{1+(n-1)ah^2}}$$

Sin ***E_c***



7. Métodos de selección: 7.1. Selección unicarácter

Selección por FAMILIAR

Coefficientes

$$r_{\bar{P}_f, A_f} = h \frac{[1 + (n-1)a]}{\sqrt{n[1 + (n-1)t]}}$$

$$b_{A_f, \bar{P}_f} = h^2 \left(\frac{1 + (n-1)a}{1 + (n-1)t} \right)$$

Límite ($n \rightarrow \infty$)

$$\lim_{n \rightarrow \infty} r_{\bar{P}_f, A_f} = \sqrt{a} \left\{ \begin{array}{l} a_{MH} = \frac{1}{4} \Rightarrow r_{\bar{P}_f, A_f} = \sqrt{0,25} = 0,5 \\ a_{HC} = \frac{1}{2} \Rightarrow r_{\bar{P}_f, A_f} = \sqrt{0,5} = 0,7 \end{array} \right.$$

Comparación entre métodos (ausencia de Ec)

$$h^2 > 0,25 \Rightarrow r_{P,A} > r_{\bar{P}_f, A_f}$$

$$h^2 > 0,5 \Rightarrow r_{P,A} > r_{\bar{P}_f, A_f}$$



7. Métodos de selección: 7.1. Selección Multicarácter

- Cada **objetivo** tendrá su correspondiente A. Si consideramos todos los objetivos simultáneamente tendremos **el valor genético aditivo conjunto o global o agregado o mérito neto (H)**.

$$H = v_1A_1 + v_2A_2 + v_3A_3 + \dots + v_nA_n$$

V_j = Valor económico neto del objetivo "j", que es el beneficio que produce una unidad de mejora en dicho objetivo.

- De cada animal se estima el valor genético aditivo conjunto mediante los **criterios de selección** → **Criterio de selección conjunto = K**

$$K = b_1F_1 + b_2F_2 + b_3F_3 + \dots + b_nF_n$$

b_i = importancia relativa de cada criterio "i"



7. Métodos de selección: 7.1. Selección Multicarácter

¿Cuándo será K un mejor estimador de H?

- Mejor a medida que r_{HI} sea mayor.
- r_{HI} se puede maximizar derivando respecto a cada b_i y hacer la derivada igual a cero.

Se obtienen las siguientes ecuaciones:

$$b_1 \cdot \text{COV}(F_1 F_1) + \dots + b_n \cdot \text{COV}(F_1 F_n) = v_1 \cdot \text{COV}(A_1 A'_1) + \dots + v_m \cdot \text{COV}(A_1 A'_m)$$

$$b_1 \cdot \text{COV}(F_2 F_1) + \dots + b_n \cdot \text{COV}(F_2 F_n) = v_1 \cdot \text{COV}(A_2 A'_1) + \dots + v_m \cdot \text{COV}(A_2 A'_m)$$

⋮

$$b_1 \cdot \text{COV}(F_n F_1) + \dots + b_n \cdot \text{COV}(F_n F_n) = v_1 \cdot \text{COV}(A_n A'_1) + \dots + v_m \cdot \text{COV}(A_n A'_m)$$

n= número de criterios de selección

m= número de objetivos de selección

v_k = valor económico neto para el objetivo k

$\text{Cov}(F_i F_j)$ = covarianza entre los criterios de selección i y j.

$\text{Cov}(A_i A'_k)$ = covarianza entre los valores genéticos aditivos del criterio i y el objetivo k.

i= 1 → n

j=1 → m



7. Métodos de selección: 7.1. Selección Multicarácter

Camarón

$$\text{Índice de selección (K)} = 0,7 * \text{TSV} + 0,3 * \text{Crecimiento}$$

Salmón del Atlántico

$$I_{\text{market}} = 1,0 \text{ Length-Larvae}_{\text{Family}} + 0,03\% \text{ Smolt}_{\text{Family}} + 0,74 \text{ Length-Harvest}_{\text{Family}} + 0,38 \text{ Length-Harvest}_{\text{Individual}}$$



7. Métodos de selección: 7.1. Selección Multicarácter

Selección por INDIRECTA

Selección indirecta - Mejorar un carácter X mediante selección sobre otro carácter Y correlacionado con el primero.

Respuesta correlacionada es: $CR_X = r_A \cdot i_Y \cdot h_Y \sigma_{AX}$

Respuesta directa: $R_X = i_X \cdot h_X \sigma_{AX}$

$$\frac{CR_X}{R_X} = \frac{r_A \cdot i_Y \cdot h_Y \sigma_{AX}}{i_X \cdot h_X \sigma_{AX}} \qquad \frac{CR_X}{R_X} = \frac{r_A \cdot i_Y \cdot h_Y}{i_X \cdot h_X}$$

Si aplicamos la misma intensidad de selección, la relación entre selección indirecta y directa resulta:

$$\frac{CR_X}{R_X} = \frac{r_A h_Y}{h_X}$$



8. Estimación de parámetros genéticos

- ❑ 8.1. Estimaciones para caracteres de:
 - *Peso cosecha*
 - *Morfología*
 - *Supervivencia a TSV, WSSV, AHPND*
 - *Robustez o supervivencia*

- ❑ 8.2. Mejoras de las estimaciones de heredabilidad
 - ❑ *Caso de IMAFISH_ML en dorada y corvina*



8.1. HEREDABILIDAD: Resistencia a enfermedades

Adriantahina et al. (2012)

BW = peso corporal / **TL** = longitud total / **BL** = longitud corporal

FASD = profundidad 1er segmento abdominal **TASD** = profundidad 3er segmento abdominal

FASW = ancho 1er segmento abdominal

Table 3 Mean and Standard deviation for the accumulation growth of offspring

Trait	BW (g)	TL (cm)	BL (cm)	FASD (cm)	TASD (cm)	FASW (cm)	PCL (cm)
Mean	14.95	12.11	10.36	1.48	1.48	1.32	2.93
Standard deviation	2.73	0.79	0.70	0.11	0.12	0.10	0.21
CV (%)	18.26	6.52	6.76	7.43	8.11	7.58	7.17

Table 4 Heritabilities (h^2) and their standard error (σ_h^2)

Trait	BW (g)	TL (cm)	BL (cm)	FASD (cm)	TASD (cm)	FASW (cm)	PCL (cm)
h^2 (%)	51.50**	39.40**	40.90**	41.20**	42.00**	42.90**	41.50**
σ_h^2	0.03	0.03	0.02	0.02	0.02	0.02	0.02
<i>t</i> -test	17.16	13.13	20.45	20.60	21.00	21.45	20.75

$t_{0.05} = 1.96$, $t_{0.01} = 2.57$. ** denotes very significance ($P < 0.01$).

Table 5 Response to selection, selection differentials, and realized heritability for growth in *L. vannamei*

Parameters	Estimates
Selection response (g)	1.26
Selection response (%)	10.70
Mean selection differential (g)	4.25
Realized heritability (%)	29.65

Table 6 Genetic correlations of body size and the body weight from half-sib correlation method

Traits	BW (g)	TL (cm)	BL (cm)	FASD (cm)	TASD (cm)	FASW (cm)	PCL (cm)
Genetic correlations	1.00**	0.85**	0.84**	0.66**	0.67**	0.77**	-0.08**

** denotes very significance ($P < 0.01$).



8.1. HEREDABILIDAD: Resistencia a enfermedades

Argue et al. (2002)

Heritability (h^2) estimates (\pm s.e.) for Growth line *L. vannamei* reared in the round pond (RP) and recirculating raceway (RR)

Trait	$h^2_{\text{half-sib}}$	$h^2_{\text{full-sib}}$	h^2_x	Realized h^2
RP harvest weight	1.19 \pm 0.59	0.70 \pm 0.15		1.17 \pm 0.18
RP weight—male	1.27 \pm 0.63	0.78 \pm 0.17		0.98 \pm 0.16
RP weight—female	1.33 \pm 0.66	0.82 \pm 0.18		1.38 \pm 0.20
RP weight gain	1.14 \pm 0.57	0.68 \pm 0.15		
RP gain—male	1.22 \pm 0.61	0.75 \pm 0.17		
RP gain—female	1.27 \pm 0.63	0.79 \pm 0.17		
RP pond survival	-0.10 \pm 0.07	0.08 \pm 0.03	-0.19 \pm 0.13	
RR harvest weight	0.84 \pm 0.43	0.71 \pm 0.15		1.00 \pm 0.12
RR weight—male	1.18 \pm 0.59	0.83 \pm 0.18		0.83 \pm 0.11
RR weight—female	0.94 \pm 0.49	0.80 \pm 0.17		1.14 \pm 0.13
RR weight gain	0.82 \pm 0.43	0.68 \pm 0.15		
RR gain—male	1.11 \pm 0.56	0.80 \pm 0.18		
RR gain—female	0.95 \pm 0.44	0.77 \pm 0.17		
RR pond survival	0.10 \pm 0.07	0.15 \pm 0.04	0.21 \pm 0.15	
Percent tail	0.15 \pm 0.12	0.11 \pm 0.04		
Sex ratio—combined	-0.002 \pm 0.012	-0.003 \pm 0.01	-0.003 \pm 0.02	
Sex ratio—RR	-0.007 \pm 0.024	-0.001 \pm 0.01	-0.01 \pm 0.038	
Sex ratio—RP	-0.03 \pm 0.04	0.002 \pm 0.012	-0.05 \pm 0.06	

Heritability on the underlying scale (h^2_x) was calculated from the half-sib h^2 estimate.

Table 6

Heritability (h^2) estimates (\pm s.e.) for TSV line *L. vannamei* selected primarily for resistance to Taura Syndrome Virus (TSV)

Trait	$h^2_{\text{half-sib}}$	$h^2_{\text{full-sib}}$	h^2_x	Realized h^2
TSV—GCRL	0.19 \pm 0.08	0.14 \pm 0.05	0.30 \pm 0.13	0.28 \pm 0.14
Weight—OI	0.58 \pm 0.15	0.58 \pm 0.11		
Survival—OI	0.06 \pm 0.03	0.13 \pm 0.03	0.10 \pm 0.05	
Sex ratio—OI	-0.012 \pm 0.014	0.003 \pm 0.01	-0.02 \pm 0.02	

Shrimp were evaluated at the Gulf Coast Research Laboratory (GCRL) and the Oceanic Institute (OI). Heritability on the underlying scale (h^2_x) was calculated from the half-sib h^2 estimate.

8.1. HEREDABILIDAD: *Resistencia a enfermedades*

Gitterle *et al.* (2005)

Table 4

Heritability ($h^2 \pm SE$) and the effect common to full-sibs other than additive genetic ($c^2 \pm SE$) for WSSV resistance and harvest body weight in *P.vannamei* for each batch and line

Line	Batch	WSSV		Body weight	
		$h^2 \pm SE$	$c^2 \pm SE$	$h^2 \pm SE$	$c^2 \pm SE$
1	4	0.17 ± 0.06	0.00 ± 0.02	0.21 ± 0.11	0.08 ± 0.04
	6	0.03 ± 0.03	0.02 ± 0.01	0.15 ± 0.08	0.08 ± 0.03
	All	0.07 ± 0.02	0.01 ± 0.01	0.21 ± 0.04	0.08 ± 0.02
2	3	0.04 ± 0.04	0.01 ± 0.02	0.11 ± 0.15	0.17 ± 0.07
	5	0.07 ± 0.03	0.00 ± 0.01	0.06 ± 0.09	0.11 ± 0.04
	7	0.03 ± 0.02	0.01 ± 0.01	0.45 ± 0.10	0.00 ± 0.03
	All	0.03 ± 0.01	0.02 ± 0.01	0.20 ± 0.04	0.09 ± 0.02

Table 5

Genetic correlations between harvest body weight and WSSV resistance for each batch and line

Line	Batch	Correlation
1	4	-0.51 ± 0.30
	6	-0.31 ± 0.51
	All	-0.55 ± 0.18
2	3	-0.94 ± 0.64
	5	-0.16 ± 0.61
	7	-0.47 ± 0.32
	All	-0.64 ± 0.19



8.1. HEREDABILIDAD: Resistencia a enfermedades

Gitterle *et al.* (2006)

Table 5

Heritabilities estimates (\pm SE) for harvest weight and for WSSV resistance using individual oral inoculation (IO) and waterborne infection (WB)

Batch	WSSV		Harvest
	IO	WB	Weight
	$h^2 \pm se$	$h^2 \pm se$	$h^2 \pm se$
8	0.01 \pm 0.01		0.05 \pm 0.1
9	0.01 \pm 0.00		0.23 \pm 0.07
10	0.01 \pm 0.01		0.31 \pm 0.11
11	0.02 \pm 0.01	0.00 \pm 0.00	0.39 \pm 0.15
13	0.02 \pm 0.01	0.01 \pm 0.01	0.34 \pm 0.11

Table 6

Product moment correlations between the full-sib family breeding values for resistance to WSSV and harvest weight in each batch

Batch	IO	WB
8	0.06	–
9	0.27*	–
10	0.33**	–
11	0.17	0.07
13	–0.35**	–0.33**

* $P < 0.05$ ** $P < 0.01$.

Individual oral (IO) and waterborne (WB) infection protocol.



8.1. HEREDABILIDAD: *Resistencia a enfermedades*

Ødegård *et al.* (2011)

Diseño:

- Resistencia a TSV
- Determinar si entre el % de supervivientes (CURADOS o NO SUSCEPTIBLES) hay dos caracteres:
 - Dañados (ENDURANCE)
 - Con riesgo o no (SUSCEPTIBLES)
- 15.261 individuos de 513 HC de 3 generaciones analizados mediante retos a TSV en 21 tanques separados

Table 1 Descriptive statistics of the data set

Item	
Shrimp with data	15,261
Full-sib families	513
Sires	266
Dams	484
Generations with data	3
Batches with data	7
Challenge-test tanks per batch	3
Average mortality (across tests)	28%
Median time until death ¹ (across tests)	157 h (56 h)

¹Excluding individuals with censored lifespans. Between-test standard deviation is presented in parenthesis.



8.1. HEREDABILIDAD: Resistencia a enfermedades

Ødegård et al. (2011)

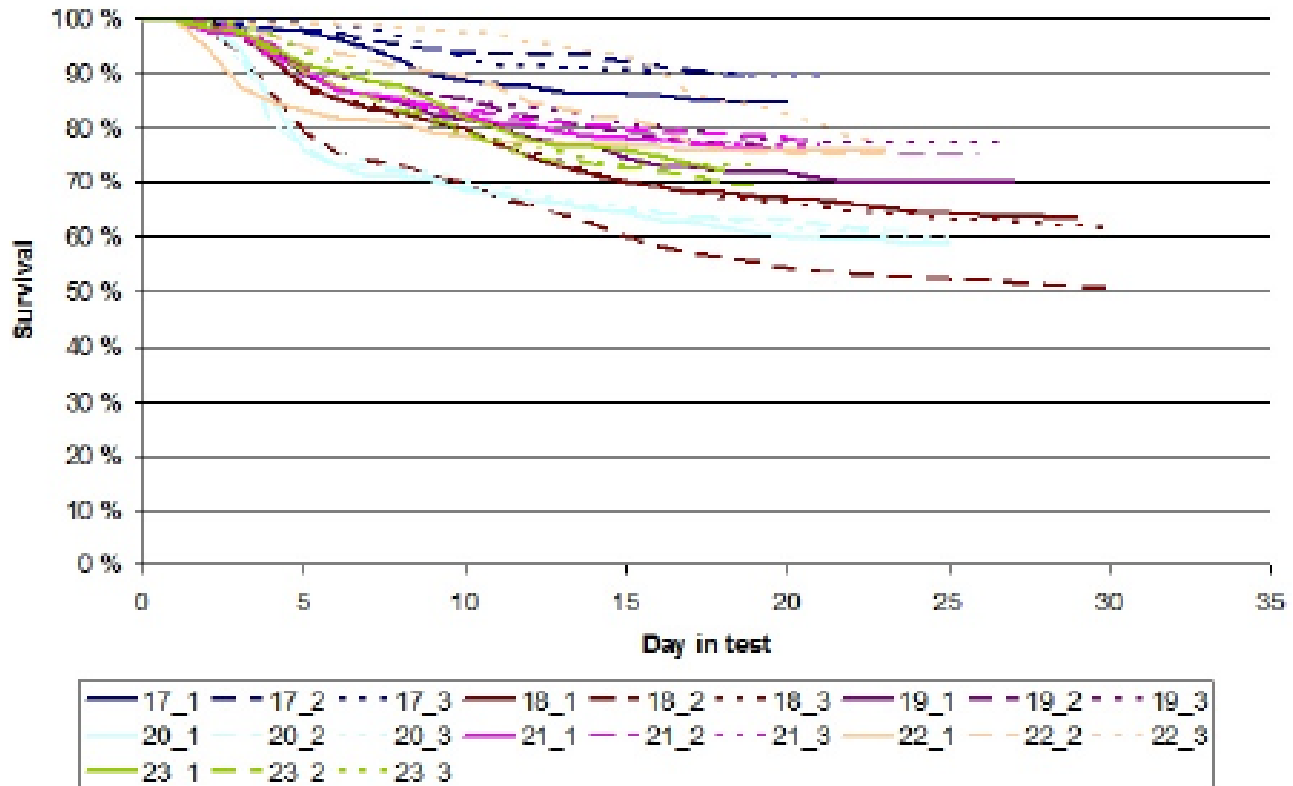


Figure 1 Kaplan-Meier survival curves for the different TSV challenge tests. The different challenge tests are numbered as "batch_tank" (batches 17 to 23).



8.1. HEREDABILIDAD: Resistencia a enfermedades

Ødegård et al. (2011)

Given the endurance scores and the susceptibility statuses, all parameters of the **CURE model** were sampled **as in a standard bivariate threshold model** using Gibbs sampling.

a simple cross-sectional threshold model for **observed survival until the end of test (SIMPLE)**

using a “naïve” (**assuming that all individuals are susceptible**) survival score threshold model (**NAÏVE**)

Table 2 Posterior means of parameters for the CURE, SIMPLE and NAÏVE threshold models (± posterior standard deviations)

Parameters ¹	Trait	CURE	SIMPLE	NAÏVE
Fraction susceptible (%)		38 ± 1	-	100
σ_t^2	Endurance/survival scores	0.14 ± 0.01	-	0.13 ± 0.01
σ_g^2	Endurance/survival scores	0.09 ± 0.04	-	0.21 ± 0.05
	Susceptibility/mortality	0.82 ± 0.23	0.72 ± 0.16	-
r_g	Endurance - susceptibility	0.22 ± 0.25	-	-
σ_f^2	Endurance/survival scores	0.07 ± 0.02	-	0.03 ± 0.01
	Susceptibility/mortality	0.13 ± 0.04	0.08 ± 0.03	-
r_f	Endurance - susceptibility	-0.06 ± 0.05	-	-
σ_b^2	Susceptibility	0.16 ± 0.10	-	-
h^2	Endurance/survival scores ²	0.07 ± 0.03	-	0.16 ± 0.03
	Susceptibility/mortality ³	0.41 ± 0.07	0.39 ± 0.06	-
c^2	Endurance/survival scores ⁴	0.05 ± 0.01	-	0.02 ± 0.01
	Susceptibility/mortality ⁵	0.07 ± 0.02	0.05 ± 0.02	-

¹ σ_t^2 = variance of tank-test-day effects, σ_g^2 = genetic variance, r_g = genetic correlation, σ_f^2 = variance of common environmental family effects, r_f = correlation of common environmental family effects, σ_b^2 = variance of batch-tank effects,

$$^2 h^2 = \sigma_g^2 / (\sigma_g^2 + \sigma_f^2 + \sigma_t^2 + 1), ^3 h^2 = \sigma_g^2 / (\sigma_g^2 + \sigma_f^2 + 1)$$

$$^4 c^2 = \sigma_f^2 / (\sigma_g^2 + \sigma_f^2 + \sigma_t^2 + 1), ^5 c^2 = \sigma_f^2 / (\sigma_g^2 + \sigma_f^2 + 1)$$



8.1. HEREDABILIDAD: *Resistencia a enfermedades*

Ødegård *et al.* (2011)

Table 3 Pearson (above diagonal) and Spearman (below diagonal) correlation coefficients between posterior means of breeding values for the different models

Model		CURE		SIMPLE	NAÏVE
	Trait	Endurance	Susceptibility	End-survival	Survival
CURE	Endurance		0.51	0.57	0.63
	Susceptibility	0.50		0.99	0.98
SIMPLE	End-survival	0.57	0.99		0.99
NAÏVE	Survival	0.61	0.98	0.99	



8.1. HEREDABILIDAD: *Resistencia a enfermedades*

Moss *et al.* (2013)

Diseño:

- Resistencia a TSV: distintas cepas / sistema de cultivo (RAS)
- 180 HC familias (177 machos : 175 hembras)
- Desove individual de hembras y cría separada hasta el marcaje con VI entre 1-2 g
- Reto: a TSV: : 2-3 g alimentados hasta saciedad con el 3% de su peso con tejido infectado.
Mortalidad a los 21 días

Table 1

Taura syndrome virus (TSV) isolates used in *per os* challenges of *P. vannamei*.

Table was modified from Srisuvan *et al.* (2006).

TSV isolate	Collection location	Collection year	GenBank accession #
USTX95	Texas, USA	1995	-
BZ01	Belize	2001	AY590471
TH04	Thailand	2004	AY997025
VE05	Venezuela	2005	DQ212790



8.1. HEREDABILIDAD: Resistencia a enfermedades

Moss *et al.* (2013)

Table 2

TSV challenge data used for the estimation of genetic correlations and heritabilities: number of shrimp families, total shrimp, and mean family (\pm SD) survival by generation. Numbers in parentheses are the number of replicate challenge tanks. Superscripts refer to analyses for which each generation of data was used.

Generation	TSV challenge				
	Isolate	# of families	Total shrimp	Survival (%)	Survival range (%)
7 ^a	USTX95	80 (2)	1701	47.6 \pm 17.5	0–88
7 ^a	BZ01	80 (2)	1716	39.8 \pm 19.9	0–88
9 ^{a,c,d}	USTX95	50 (2)	955	75.0 \pm 18.2	35–100
9 ^{a,c,d}	BZ01	50 (2)	971	43.8 \pm 25.9	0–85
11 ^{ab,c,d}	USTX95	50 (2)	1236	77.7 \pm 14.5	43–100
11 ^{ab,c,d}	BZ01	50 (2)	1236	79.4 \pm 14.5	35–100
11 ^{ab,c,d}	TH01	50 (2)	1236	88.8 \pm 9.9	63–100
11 ^{ab,c,d}	VE05	50 (2)	1236	90.1 \pm 10.7	53–100

^a Bivariate analysis of USTX95 and BZ01 survival data.

^b Four-trait analysis of TSV survival data.

^c Bivariate analyses of TSV survival and RAS growth data.

^d Bivariate analyses of TSV survival and RAS growout survival data.

Table 3

Growout data/performance in a recirculating aquaculture system (RAS) used for the estimation of genetic correlations and heritabilities: number of shrimp families, total shrimp, stocking density, mean family stocking weight (\pm SD), harvest weight (\pm SD), growth (\pm SD), and survival (\pm SD) by generation. Superscripts refer to analyses for which each generation of data was used and correspond to superscripts in Table 2.

Generation	RAS growout						
	# of families	Total shrimp	Density (per m ²)	Stocking wt (g)	Harvest wt (g)	Growth (g/day)	Survival (%)
9 ^{cd}	50	13,276	237	1.9 \pm 1.5	19.1 \pm 1.5	0.213 \pm 0.018	70.0 \pm 14.2
11 ^{cd}	50	8809	401	1.4 \pm 0.2	20.2 \pm 1.0	0.214 \pm 0.011!	80.2 \pm 8.0

^c Bivariate analyses of TSV survival and RAS growth data.

^d Bivariate analyses of TSV survival and RAS growout survival data.



8.1. HEREDABILIDAD: Resistencia a enfermedades

Moss *et al.* (2013)

Table 4

Estimates of heritability ($h^2 \pm SE$; on the diagonal) for four TSV survival traits (i.e. survival to four TSV isolates) and genetic correlations ($r_G \pm SE$; below diagonal) among these traits for a selected population of *P. vannamei*. Estimates were calculated from variance components obtained from multivariate (4) animal model using a single generation of survival data (Generation 11, G11).

Trait	USTX95	BZ01	TH04	VZ05
USTX95	0.26 ± 0.05			
BZ01	0.90 ± 0.31**	0.16 ± 0.04		
TH04	0.56 ± 0.25*	0.35 ± 0.23	0.33 ± 0.07	
VE05	0.87 ± 0.29**	0.99 ± 0.26**	0.50 ± 0.24*	0.27 ± 0.06

* $p \leq 0.05$.

** $p \leq 0.005$.

Table 5

Estimates of heritability ($h^2 \pm SE$) for survival to two TSV isolates and genetic correlations ($r_G \pm SE$) between these two traits for three generations in a selected population of *P. vannamei*. Estimates were calculated from variance components obtained from bivariate animal models using either a single generation of survival data or survival data from three generations (combined analysis).

Generation	h^2		r_G
	USTX95	BZ01	
7	0.22 ± 0.04	0.24 ± 0.05	0.85 ± 0.25**
9	0.19 ± 0.05	0.41 ± 0.07	0.87 ± 0.30**
11	0.26 ± 0.06	0.26 ± 0.06	0.59 ± 0.25*
Combined	0.22 ± 0.03	0.32 ± 0.03	0.75 ± 0.15**

* $p \leq 0.05$.

** $p \leq 0.005$.



8.1. HEREDABILIDAD: Resistencia a enfermedades

Moss *et al.* (2013)

Genetic correlations ($r_G \pm SE$) among growout performance traits (growth and survival) in a recirculating aquaculture system (RAS) and TSV survival traits (i.e. survival to four TSV isolates) for two generations in a selected population of *P. vannamei*. Estimates were calculated from variance components obtained from bivariate animal models using either a single generation of survival data or survival data from both generations (combined analysis).

RAS trait	Generation	r_G			
		USTX95	BZ01	TH04	VZ05
Growth	9	-0.26 ± 0.18	$-0.29 \pm 0.17^*$	-	-
	11	-0.07 ± 0.18	-0.24 ± 0.19	-0.27 ± 0.20	-0.09 ± 0.18
	Combined	-0.12 ± 0.13	$-0.27 \pm 0.13^*$	-	-
Survival	9	0.12 ± 0.19	0.24 ± 0.17	-	-
	11	0.30 ± 0.20	-0.11 ± 0.19	-0.12 ± 0.20	-0.13 ± 0.19
	Combined	0.19 ± 0.13	0.16 ± 0.12	-	-

* $p \leq 0.05$.



8.1. HEREDABILIDAD: *Resistencia a enfermedades*

Caballero-Zamora *et al.* (2015)

Diseño:

- *Peso y Resistencia a WSSV, en poblaciones de cultivo con brotes naturales*

Table 1

Number of shrimp recovered, mean body weight, and family survival percentage for all data and by pond.

Population	Number of shrimp seeded	Number of shrimp recovered	Mean body weight \pm SD ^a	Mean family survival rate % \pm SD
All data	17,850	10,004	21.5 \pm 3.9	56.0 \pm 66.3
P10	5950	4891	23.0 \pm 3.2	82.2 \pm 29.5
P30	5950	4424	21.0 \pm 3.1	74.4 \pm 34.3
K15	5950	688 ^b	14.2 \pm 3.9	11.6 \pm 24.7

^a SD: Standard deviation.

^b From 162 families (8 families had zero survival rate).



Caballero-Zamora *et al.* (2015)

Table 2

Genetic parameter estimates for body weight (BW) and survival in the presence and absence of White Spot Syndrome Virus (WSSV) outbreak in the Pacific White Shrimp (*P. vannamei*) using bivariate within-pond linear models^a.

WSSV	Pond	Trait	Additive genetic variance	Residual variance	Phenotypic variance	Heritability	Genetic correlation
Presence	K15	BW	1.47 (1.86)	10.80 (1.14)	14.44 (0.88)	0.10 (0.13)	-0.98 (0.57)
		Survival	0.006 (0.003)	0.10 (0.003)	0.11 (0.002)	0.06 (0.03)	
Absence	P10	BW	3.16 (0.99)	5.68 (0.50)	10.01 (0.39)	0.32 (0.09)	0.67 (2.59)
		Survival	0.0003 (0.002)	0.14 (0.003)	0.15 (0.003)	0.00 (0.01)	
	P30	BW	1.39 (0.55)	6.77 (0.31)	9.54 (0.31)	0.15 (0.06)	-0.90(0.87)
		Survival	0.003 (0.004)	0.18 (0.41)	0.19 (0.004)	0.01 (0.02)	

^a Standard errors are in parentheses.

Table 3

Heritabilities (h^2) and genetic correlations (r_G) for body weight (BW) using a linear model^a between ponds in *P. vannamei*.

Pond	h^2	r_G
P10	0.33 (0.10)	0.65 (0.38)
K15	0.11 (0.11)	
P30	0.29 (0.09)	0.38 (0.42)
K15	0.09 (0.11)	
P10	0.33 (0.09)	0.99 (0.03)
P30	0.23 (0.08)	

^a Standard errors are in parentheses.

Table 4

Heritabilities (h^2) and genetic correlations (r_G) for survival using a linear model^a between ponds in *P. vannamei*.

Pond	h^2	r_G
P10	0.03 (0.02)	0.49 (0.54)
K15	0.03 (0.02)	
P30	0.00 (0.02)	0.83 (2.22)
K15	0.03 (0.02)	
P10	0.01 (0.02)	0.93 (0.83)
P30	0.01 (0.02)	

^a Standard errors are in parentheses.



8.1. HEREDABILIDAD: *Resistencia a enfermedades*

Castillo-Juárez *et al.* (2015)

Diseño:

- Resistencia a WSSV y AHPND
- Reto AHPND: 2 g con 144 HC familias (28 HC Ecuador; 10 MH Mexico; 16 HC Ecuadorix Mexico). 105 colony-forming units/mL
- Reto WSSV: 4 g con infección oral a 107 copias virales DNA/g

$$h^2_{\text{AHPND}} < 0,10$$

$$h^2_{\text{WSSV}} = 0,20$$



8.1. HEREDABILIDAD: *Estrés*

PLOS ONE | <https://doi.org/10.1371/journal.pone.0173835> March 22, 2017

Estimation of genetic parameters and genotype-by-environment interactions related to acute ammonia stress in Pacific white shrimp (*Litopenaeus vannamei*) juveniles at two different salinity levels

Xia Lu^{1,2}, Sheng Luan^{1,2}, Baoxiang Cao^{1,2}, Xianhong Meng^{1,2}, Juan Sui^{1,2}, Ping Dai^{1,2}, Kun Luo^{1,2}, Xiaoli Shi^{1,2}, Dengchun Hao^{1,2,3}, Guomin Han⁴, Jie Kong^{1,2*}

Table 1. Numbers of samples/families (N) and the means, minima, maxima, standard deviations, and coefficients variation of the ST, SR₅₀, and BL values.

Traits		N		Mean	Minimum	Maximum	Standard deviation	Coefficient variation (%)
ST (h)	30‰	individuals	3624	36.64	2.00	78.00	16.94	46.23
		families	91	36.64	16.32	64.56	10.03	27.38
	5‰	individuals	3597	24.80	2	69.00	13.51	54.48
		families	91	24.80	9.50	50.58	7.26	29.27
SR ₅₀ (%)	30‰	families	91	50.78	0	94.87	26.80	52.78
	5‰	families	91	50.27	2.78	95.00	19.29	38.37
BL (cm)	30‰	individuals	3624	3.77	1.00	8.80	0.93	23.85
		families	91	3.77	2.84	4.94	0.42	11.14
	5‰	individuals	3597	3.70	1.00	9.30	0.90	24.32
		families	91	3.70	2.63	4.79	0.40	10.81



8.1. HEREDABILIDAD: *Estrés*

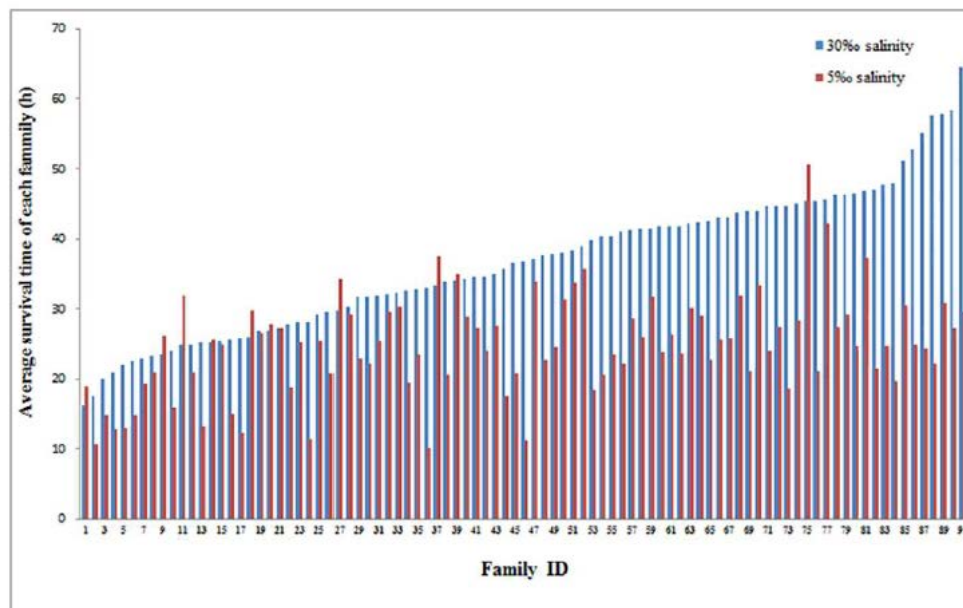


Fig 3. The average survival time for each family of *L. vannamei* juveniles during acute ammonia stress in normal and low salinity conditions.



8.1. HEREDABILIDAD: *Estrés*

Table 2. Variance components and heritabilities of for ST, SS₅₀ and BL.

Traits	Variance components			Heritability	Phenotypic correlation	Genetic correlation
	Additive genetic variance	Random residual error variance	Phenotypic variance	$h^2 \pm SE$		
ST _H	220.852	60.708	281.560	0.784 $\pm 0.070^a$	0.286 \pm 0.076*	0.394 \pm 0.097*
ST _L	111.258	82.145	193.403	0.575 $\pm 0.068^b$		
SS _{50H}	1.085	1.000	1.724	0.402 $\pm 0.061^c$	0.273 \pm 0.100*	0.377 \pm 0.098*
SS _{50L}	0.439	1.000	1.293	0.216 $\pm 0.050^d$		
BL _H	0.315	0.596	0.911	0.346 \pm 0.052	0.248 \pm 0.047*	0.535 \pm 0.096*
BL _L	0.325	0.518	0.843	0.386 \pm 0.054		

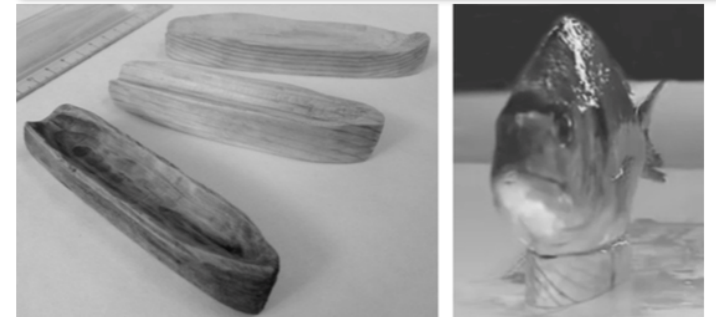
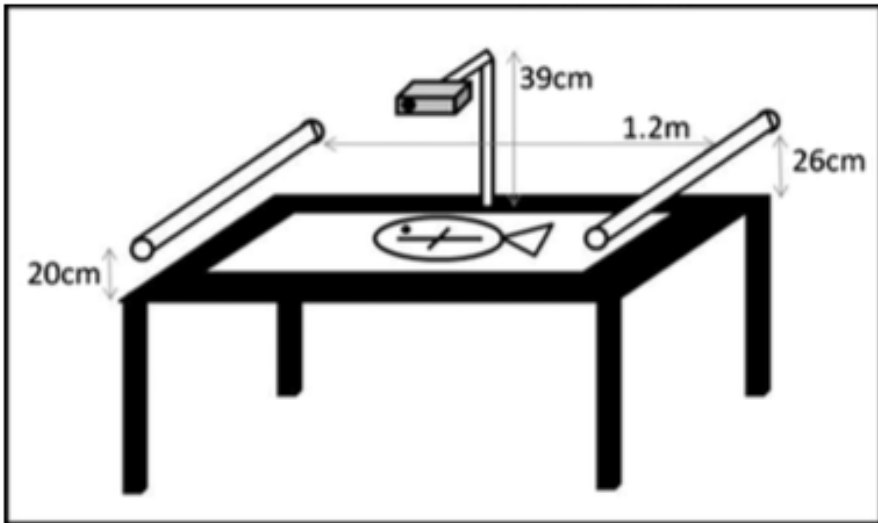




8.2. Mejoras de las estimas de heredabilidad

Navarro *et al.* (2016)

- **IMAFISH_ML (non-invasive technological traits ; NTT)**
 - The measurement of growth and morphological traits in marine fish with an image analysis package IMAFISH_ML. The software can provide up to 27 fish morphometric traits as an easy and fast method to assess fish growth and shape (Navarro *et al.*, 2016)



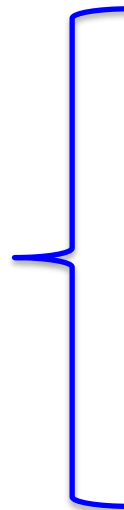


8.2. Mejoras de las estimas de heredabilidad

- Estimate **genetic parameters of morphological traits** in gilthead sea bream and meagre using the **automatic method IMAFISH_ML** (non-invasive technological traits; NTT) and **to demonstrate the applicability to genetic breeding programs**



- **Measurement**
 - Phenotypic traits
 - Genotypic traits



1. Weight
2. Fork length in manual way (FLM)
3. Total lateral area (TLA)
4. Total dorsal area (TDA)
5. Fork length (FoL)
6. Fish maximum height (FMH)
7. Maximum width (MW)
8. Head height (HeH)
9. Fillet area (FilA)

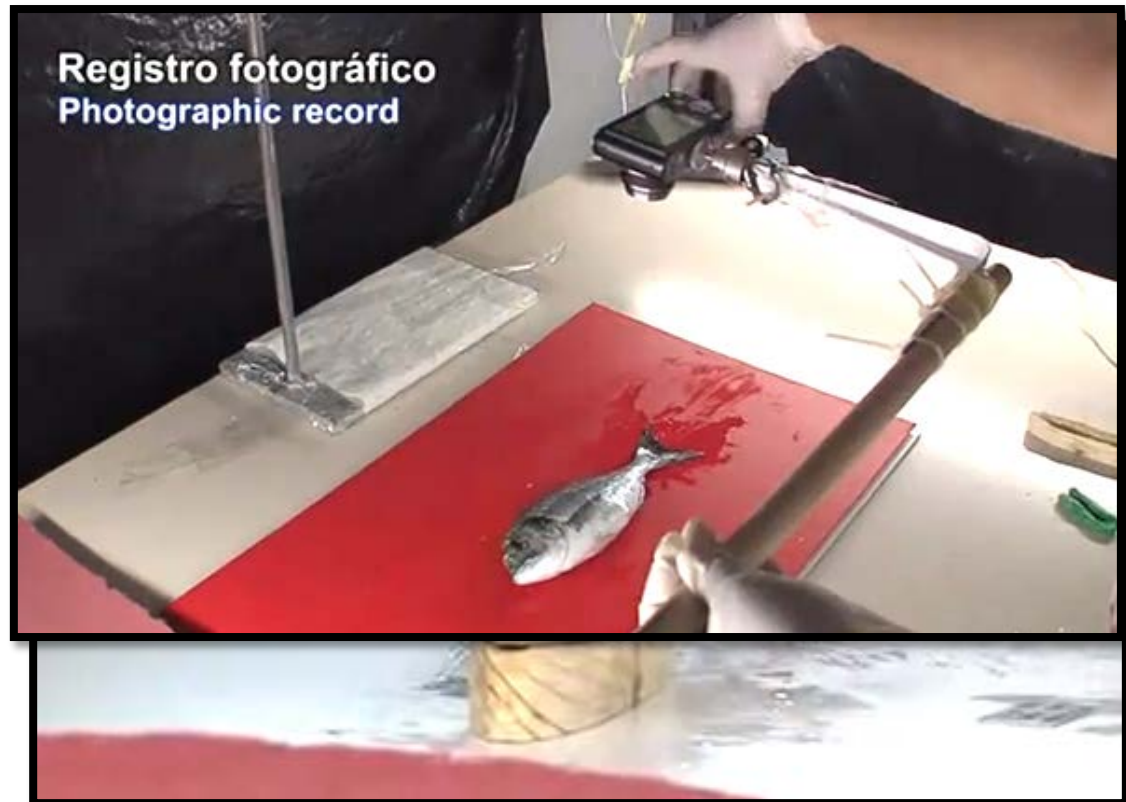


8.2. Mejoras de las estimas de heredabilidad

◆ Specimen measurement

- Olympus digital camera (FE230/X790, Olympus lens 6.3 to 18.9 mm, f3.1 to 5.9, equivalent to 38 to 114 mm on a 35 mm camera) by Navarro et al. (2016) for IMAFISH-ML software

- *Dorsal view*
- *Lateral view*



8.2. Mejoras de las estimas de heredabilidad

◆ Specimen measurement

MORPHOMETRIC TRAITS

IMAFISH_ML

↑
MATLAB v7.5



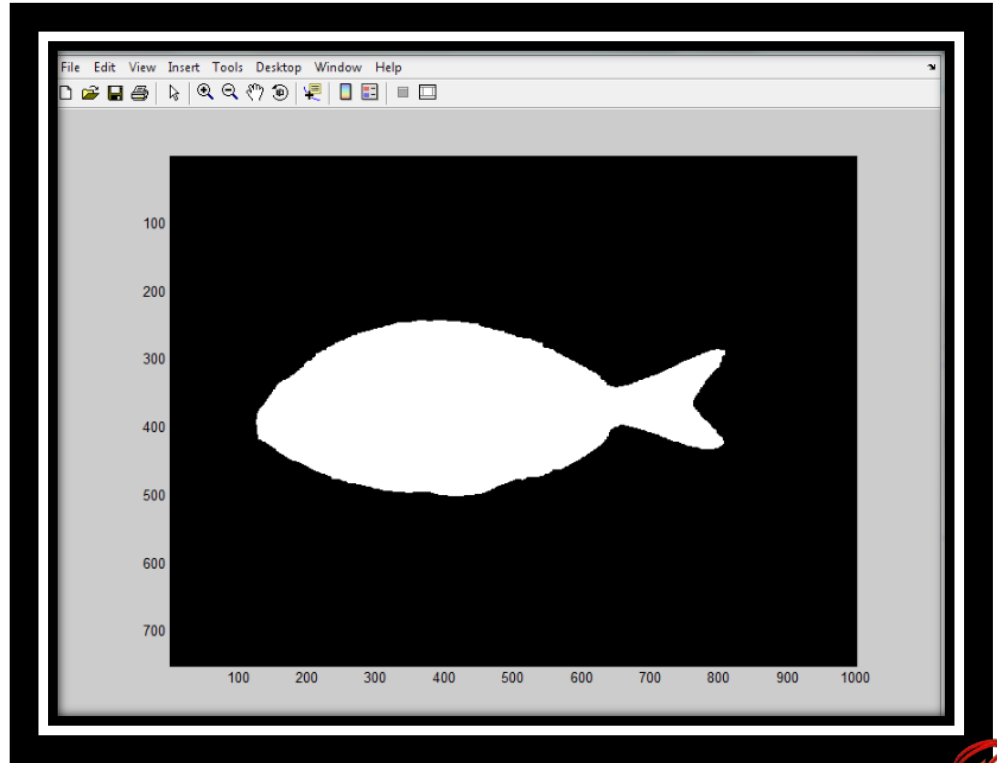
8.2. Mejoras de las estimas de heredabilidad

◆ Specimen measurement

MORPHOMETRIC TRAITS

IMAFISH_ML

MATLAB v7.5



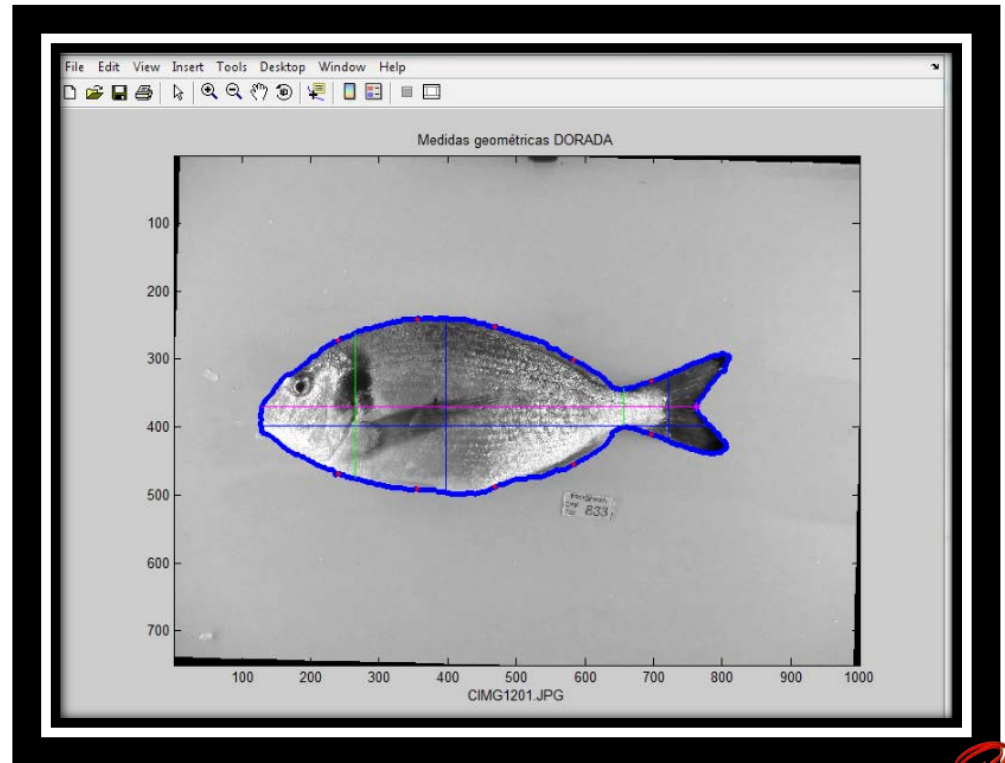
8.2. Mejoras de las estimas de heredabilidad

◆ Specimen measurement

MORPHOMETRIC TRAITS

IMAFISH_ML

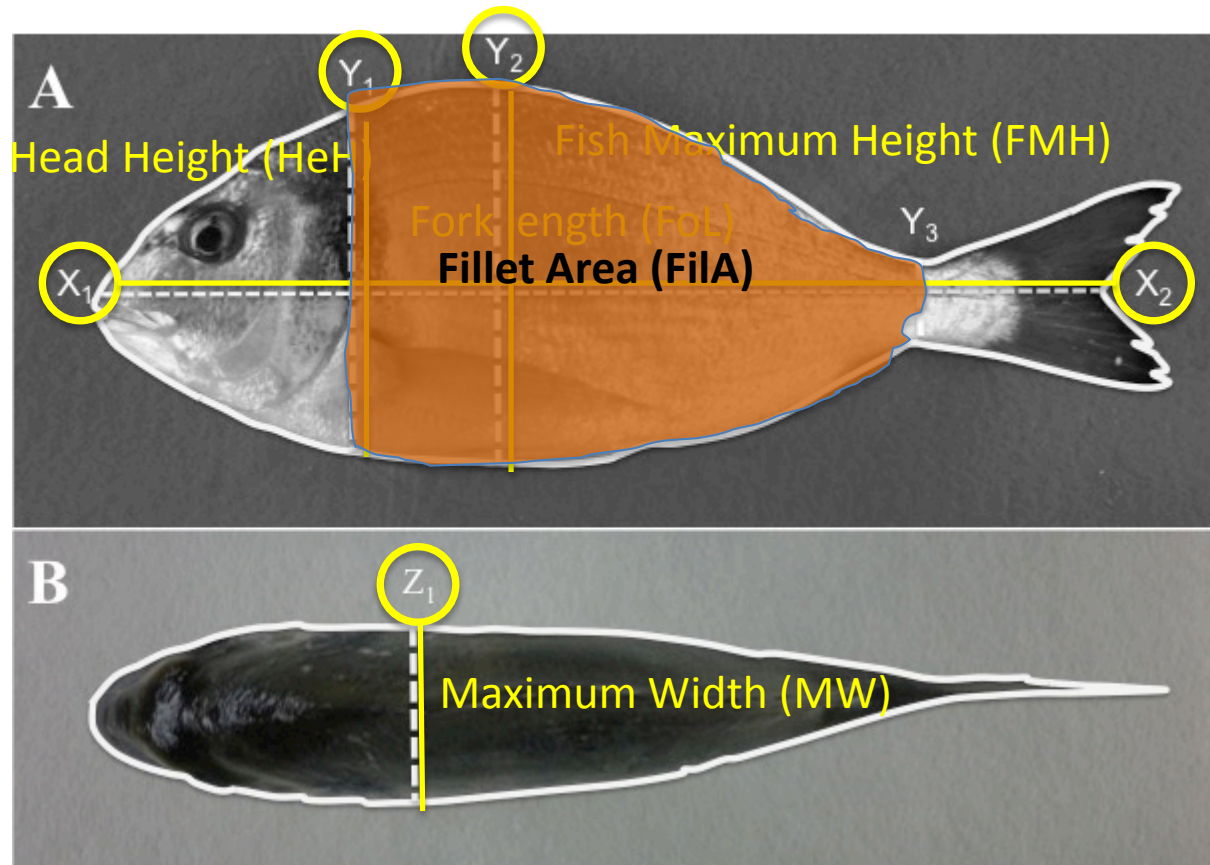
↑
MATLAB v7.5



8.2. Mejoras de las estimas de heredabilidad

◆ Specimen measurement

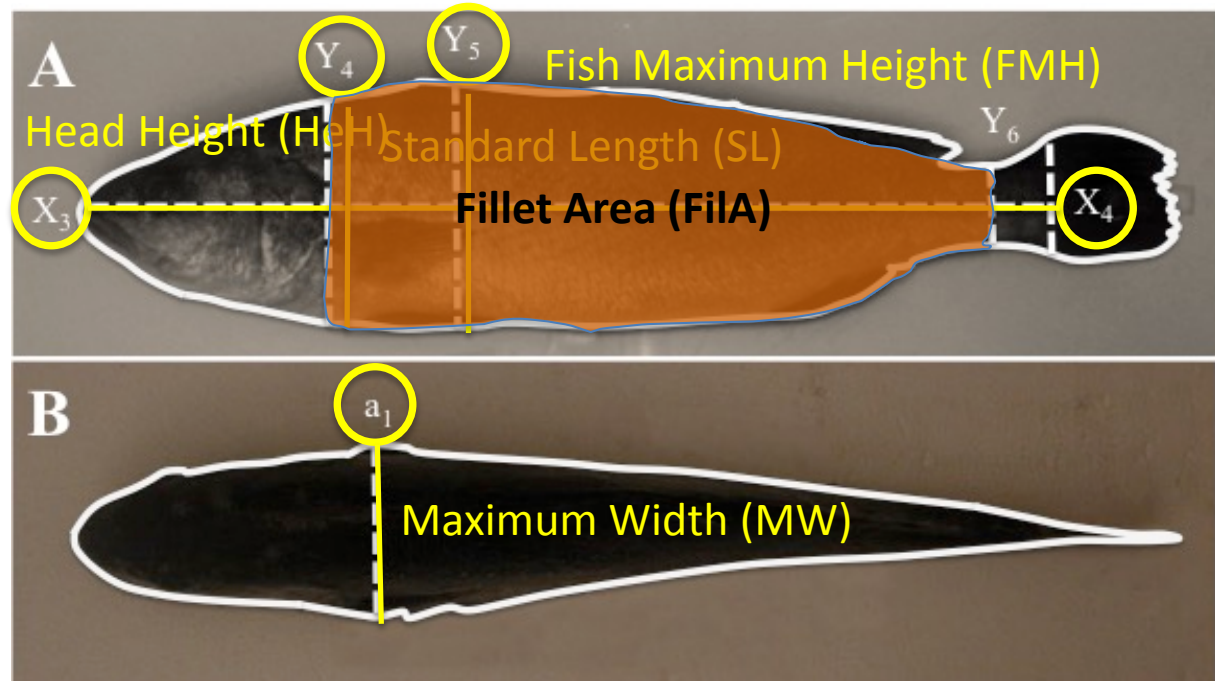
➤ Gilthead sea bream



8.2. Mejoras de las estimas de heredabilidad

◆ Specimen measurement

➤ Meagre



8.2. Mejoras de las estimas de heredabilidad

Genetic parameters (Heritabilities and correlations) in gilthead sea bream

Heritabilities

Genetic correlations

	Weight	FLM	TLA	TDA	FoL	FMH	MW	HeH	Fila
Weight	0.43±0.10	0.98±0.01	0.99±0.00	0.99±0.00	0.99±0.01	0.98±0.01	0.98±0.02	0.98±0.01	0.99±0.00
FLM	0.93	0.40±0.09	0.99±0.01	0.99±0.02	0.99±0.01	0.95±0.02	0.95±0.03	0.96±0.02	0.98±0.01
TLA	0.97	0.96	0.46±0.10	0.99±0.01	0.99±0.00	0.98±0.01	0.95±0.03	0.99±0.01	0.99±0.00
TDA	0.71	0.68	0.73	0.35±0.08	0.99±0.02	0.97±0.02	0.98±0.01	0.96±0.02	0.99±0.01
FoL	0.95	0.98	0.98	0.71	0.43±0.10	0.96±0.02	0.93±0.04	0.97±0.01	0.98±0.01
FMH	0.96	0.91	0.97	0.72	0.93	0.45±0.10	0.94±0.03	0.99±0.00	0.99±0.01
MW	0.63	0.57	0.63	0.94	0.59	0.64	0.36±0.08	0.93±0.04	0.97±0.02
HeH	0.94	0.90	0.96	0.69	0.92	0.96	0.61	0.51±0.10	0.98±0.01
Fila	0.90	0.87	0.99	0.74	0.89	0.96	0.64	0.92	0.45±0.10

Phenotypic correlations

Weight, Fork Length (FLM), Standard Length (SLM), Total Lateral Area (TLA), Total Dorsal Area (TDA), Fork Length (FoL), Standard Length (SL), Fish Maximum Height (FMH), Maximum Width (MW), Head Height (HeH) and Fillet Area (Fila).

8.2. Mejoras de las estimas de heredabilidad

Genetic parameters (Heritabilities and correlations) in meagre

Heritabilities

Genetic correlations

	Weight	SLM	TLA	TDA	SL	FMH	MW	HeH	FilA
Weight	0.22±0.12	<i>0.97±0.03</i>	<i>0.99±0.02</i>	<i>1.00±0.01</i>	<i>0.86±0.13</i>	<i>0.97±0.05</i>	<i>0.95±0.06</i>	<i>0.98±0.02</i>	<i>0.99±0.03</i>
SLM	0.92	0.19±0.11	<i>0.98±0.03</i>	<i>0.96±0.04</i>	<i>0.93±0.06</i>	<i>0.98±0.03</i>	<i>0.98±0.03</i>	<i>0.64±0.06</i>	<i>0.96±0.04</i>
TLA	0.94	0.95	0.22±0.13	<i>0.96±0.02</i>	<i>0.79±0.15</i>	<i>0.96±0.06</i>	<i>0.98±0.04</i>	<i>1.00±0.00</i>	<i>0.99±0.02</i>
TDA	0.93	0.91	0.94	0.25±0.13	<i>0.93±0.06</i>	<i>0.96±0.03</i>	<i>0.98±0.04</i>	<i>1.00±0.00</i>	<i>0.97±0.03</i>
SL	0.87	0.94	0.93	0.9	0.25±0.12	<i>0.99±0.01</i>	<i>0.73±0.22</i>	<i>0.99±0.02</i>	<i>0.94±0.06</i>
FMH	0.9	0.89	0.86	0.89	0.9	0.19±0.1	<i>0.95±0.05</i>	<i>0.97±0.11</i>	<i>0.94±0.06</i>
MW	0.82	0.85	0.96	0.88	0.75	0.83	0.26±0.14	<i>0.99±0.01</i>	<i>0.99±0.01</i>
HeH	0.85	0.85	0.91	0.85	0.87	0.79	0.9	0.25±0.14	<i>1.00±0.00</i>
FilA	0.94	0.92	0.94	0.91	0.9	0.84	0.94	0.82	0.19±0.12

Phenotypic correlations

Weight, Fork Length (FLM), Standard Length (SLM), Total Lateral Area (TLA), Total Dorsal Area (TDA), Fork Length (FoL), Standard Length (SL), Fish Maximum Height (FMH), Maximum Width (MW), Head Height (HeH) and Fillet Area (FilA).

9. Respuesta a la selección

Adriantahina *et al.* (2012)

BW = peso corporal / **TL** = longitud total / **BL** = longitud corporal

FASD = profundidad 1er segmento abdominal **TASD** = profundidad 3er segmento abdominal

FASW = ancho 1er segmento abdominal

Table 5 Response to selection, selection differentials, and realized heritability for growth in *L. vannamei*

Parameters	Estimates
Selection response (g)	1.26
Selection response (%)	10.70
Mean selection differential (g)	4.25
Realized heritability (%)	29.65



9. Respuesta a la selección

Argue et al. (2002)

Diseño:

- *Peso y Resistencia a TSV*
- *Intensidad de selección del 19%*
- *Índice de selección sintético: 70% vs 30% (TSV vs P)*
- *70♀: 30♂ (2♀: 1♂), HC vs MHP*
- *36 HCs – 7 HCc (P) / 65 HCs – 15 HCc (TSV)*
- *Engorde en: Estero (22 semanas) y RAS (16 semanas) a 100 animals / m², 95 animals / familia (completados con no marcados)*
- *Reto TSV: 3-5 g con 3.789 animals en 4 tanques (2 alimentados con el 3% de su peso con cefalotorax infectado una vez un día / 2 alimentados con el 3% de su peso con cefalotorax infectado una vez tres días). Mortalidad a los 21 días*

Table 2

Mean harvest weight (\pm s.d.), weight gain, growth rate, and survival of *L. vannamei* in the recirculating raceway (RR) and the round pond (RP)

	RP (growth line)	RR	RP (TSV line)
Harvest weight (g)	25.0 \pm 5.1	23.5 \pm 4.4	22.8 \pm 2.9
Harvest weight range	7.7–48.6	8.3–40.7	8.5–33.4
Weight gain (g)	23.7 \pm 5.1	22.2 \pm 4.4	21.3 \pm 2.8
Growth rate (g/week)	1.08 \pm 0.23	1.39 \pm 0.27	1.39 \pm 0.19
Survival (%)	76.6 \pm 9.6	82.1 \pm 11.5	81.1 \pm 11.9



9. Respuesta a la selección

Argue *et al.* (2002)

Table 3

Realized response to selection for Growth line *L. vannamei* reared in the OI round pond

Selection	Harvest weight (g ± s.d.)	Weight gain (g ± s.d.)	%Survival (± s.d.)	%Female (± s.d.)
Select	25.8 ± 2.5a	24.5 ± 2.5a	76.4 ± 9.1a	50.1 ± 6.1a
Control	20.9 ± 2.4b	19.6 ± 2.4b	77.9 ± 6.4a	55.6 ± 4.2b
%Gain	+23.4	+25.0	-1.9	

Means in the same column with different letters are significantly different ($P < 0.05$).

Table 4

Realized response to selection for Growth line *L. vannamei* reared in the recirculating raceway

Selection	Harvest weight (g ± s.d.)	Weight gain (g ± s.d.)	%Survival (± s.d.)	%Female (± s.d.)
Select	24.2 ± 2.1a	22.9 ± 2.1a	81.7 ± 11.6a	51.5 ± 5.9a
Control	20.0 ± 2.7b	18.9 ± 2.7b	84.5 ± 11.5a	50.0 ± 4.8a
%Gain	+21.0	+21.2	-3.3	

Means in the same column with different letters are significantly different ($P < 0.05$).



9. Respuesta a la selección

Argue *et al.* (2002)

Table 7

Realized response to selection in the TSV line of *L. vannamei*

Selection	GCRL TSV survival (% ± s.d.)	OI survival (% ± s.d.)	OI weight (g ± s.d.)
Select	46.4 ± 9.8a	81.6 ± 10.8a	22.6 ± 1.5b
Control	39.2 ± 8.0b	78.8 ± 9.9a	23.7 ± 1.6a
%Gain	+18.4	+3.6	-4.6

Shrimp were evaluated at the Gulf Coast Research Laboratory (GCRL) and the Oceanic Institute (OI). Means in the same column with different letters are significantly different ($P < 0.05$).



EJEMPLO de Respuesta a la selección: *peso cosecha*

Considerando:

- i (proporción seleccionados) (5,0%)

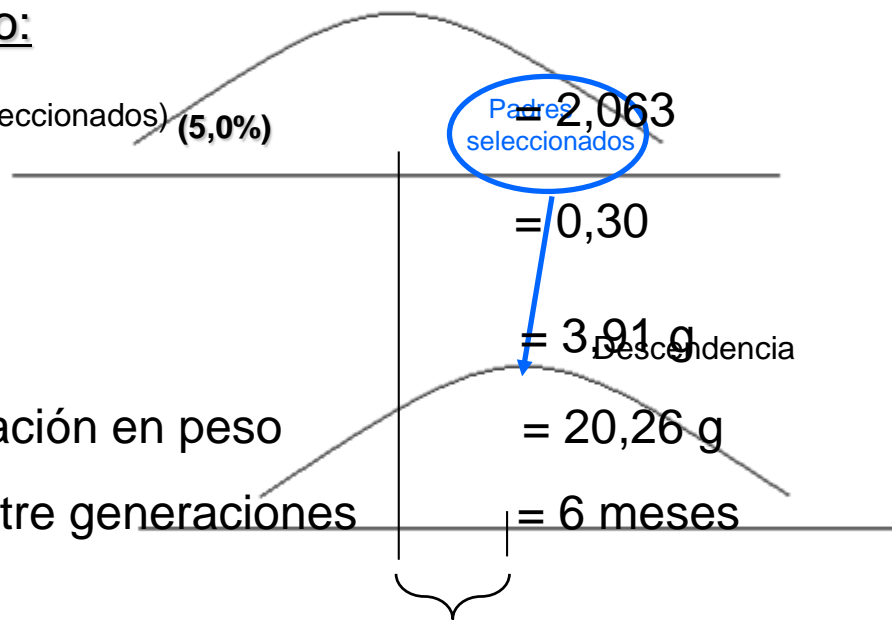
- h^2 (Peso)

- σ_P

- Media población en peso

- Intervalo entre generaciones

Población bajo estudio



$$\text{Respuesta} = R = i h^2 \sigma_P$$

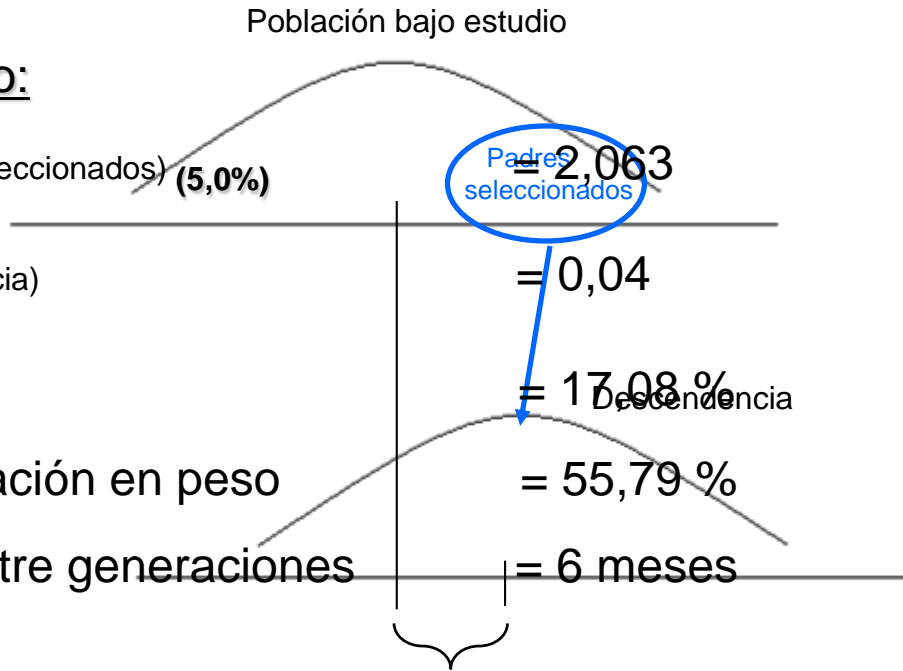
$$R_{g(5\%)} = 2,42 \text{ g} \longrightarrow R_g / \text{media} = 0,1194 \longrightarrow 11,94 \% / \text{generación} \\ 23,88 \% / \text{año}$$



EJEMPLO de Respuesta a la selección: supervivencia a cosecha

Considerando:

- i (proporción seleccionados) **(5,0%)**
- h^2 (Supervivencia) **= 0,04**
- σ_P **= 17,08 %**
- Media población en peso **= 55,79 %**
- Intervalo entre generaciones **= 6 meses**



$R_g(5\%) = 1,41\% \longrightarrow R_g / \text{media} = 0,025 \xrightarrow{R = i h^2 \sigma_P} 2,5\% / \text{generación}$
 $5,0\% / \text{año}$

$$\frac{CR_X}{R_X} = \frac{r_A h_Y}{h_X} \quad r_A = 0,485$$

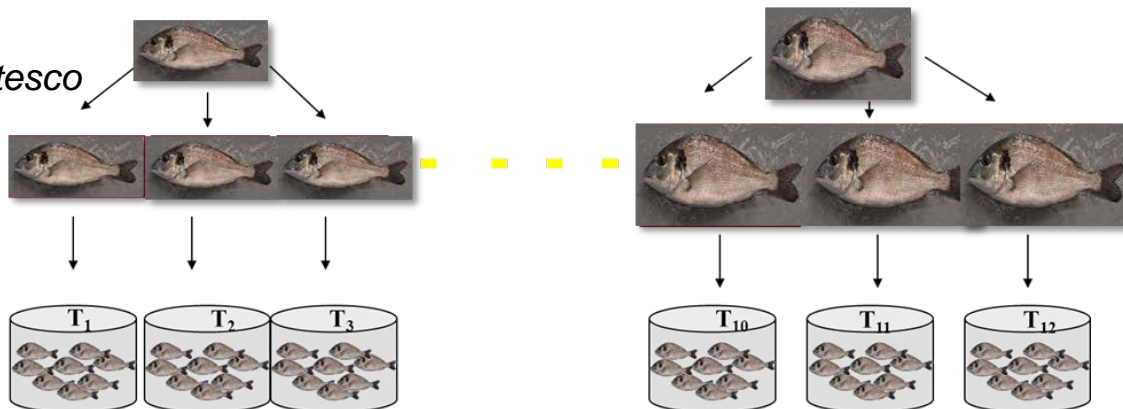
$$\frac{CR_X}{R_X} = 1,32$$



10. Modelo de implementación de la Selección Genética

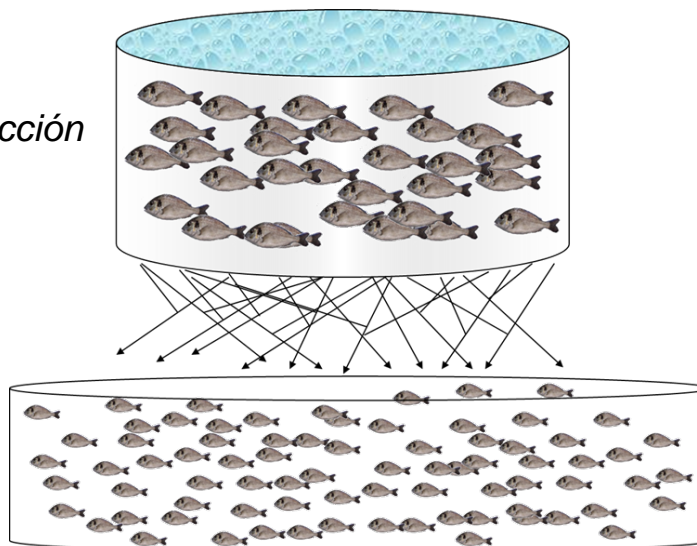
CRUCES DIRIGIDOS

- *No adaptados a los sistemas de producción industrial*
- *Incremento de costes*
- *Mejor control del parentesco*
- *Genealogía conocida*
- *Existe varianza del Ec*



CRUCES BAJO PUESTAS MASALES

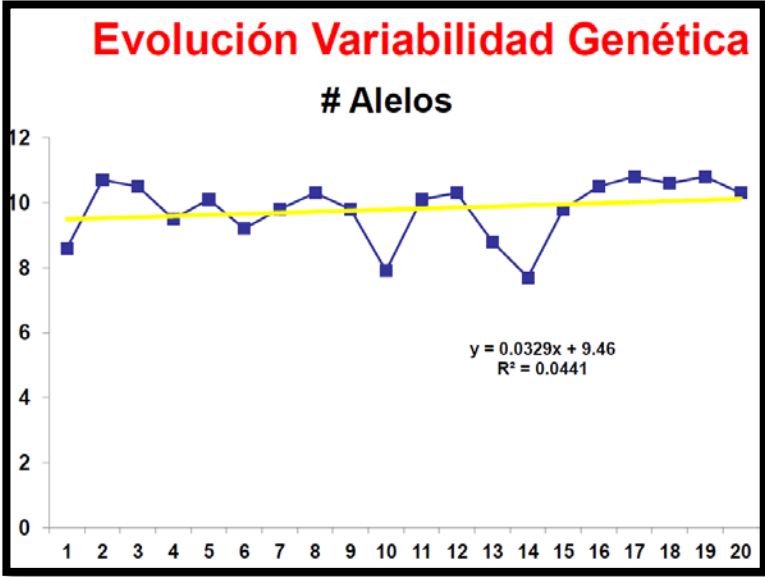
- *Adaptados a los sistemas de producción industrial*
- *Minimización de costes*
- *Peor control del parentesco*
- *Genealogía inferida*
- *No existe varianza del Ec*



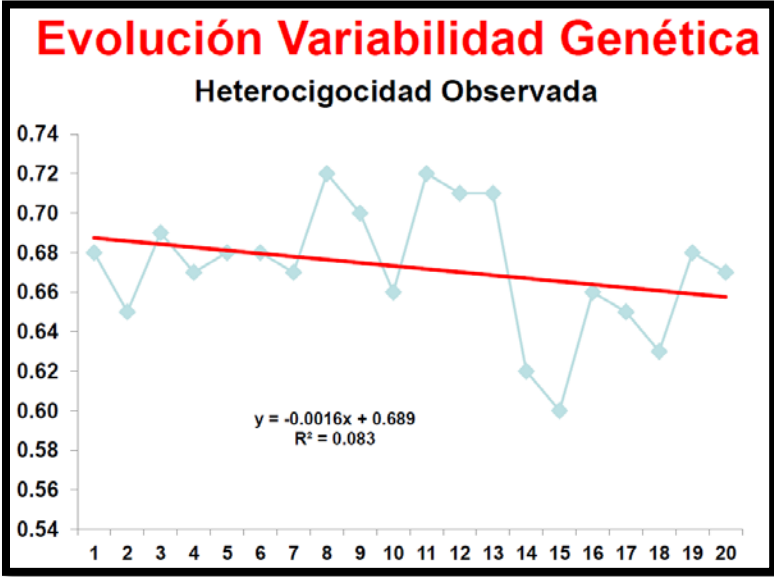
10. Modelo de implementación de la Selección Genética

EVOLUCIÓN DE UN PROGRAMA DE MEJORAMIENTO GENÉTICO EN ECUADOR

Rocha *et al.* (2010)



Retención de la diversidad alélica



Retención del 94% de la heterocigocidad



10. Modelo de implementación de la Selección Genética

Rocha *et al.* (2010)

Balance después de 2 Años y medio

- **Promedio de ganancia anual de 8,7% para crecimiento** en el conjunto de las tres fincas (con incrementos de densidades)
- **Sobrevivencia se mantuvo, productividades mucho más altas, menos días de cultivo mismo con pesos finales más altos, sin problemas de tallas**



11. Interacción Genotipo-Ambiente

Pérez-Rostro Ibarra. (2003)

A captive population of Pacific white shrimp (*Penaeus vannamei*) replicated in two environments was evaluated for genetic variability and covariability of size traits.

Table 1 (a) Mean squares and significance of effects from the mixed-model multivariate analysis of variance (MANOVA) for all size traits in *Litopenaeus vannamei*; (b) least-square means of size traits within the environment and within sex; (c) heritability estimates (\pm standard error (SE)) for size traits after correction for sex and environmental effects

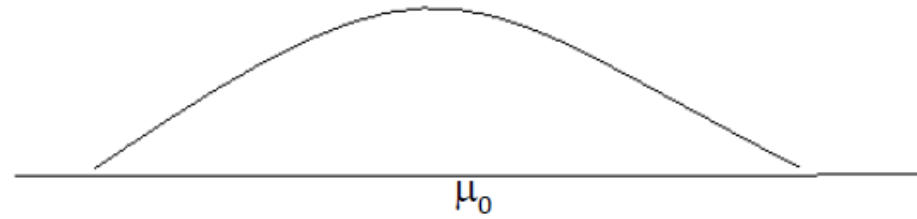
(a) MANOVA mixed-model results

Mean squares for each trait

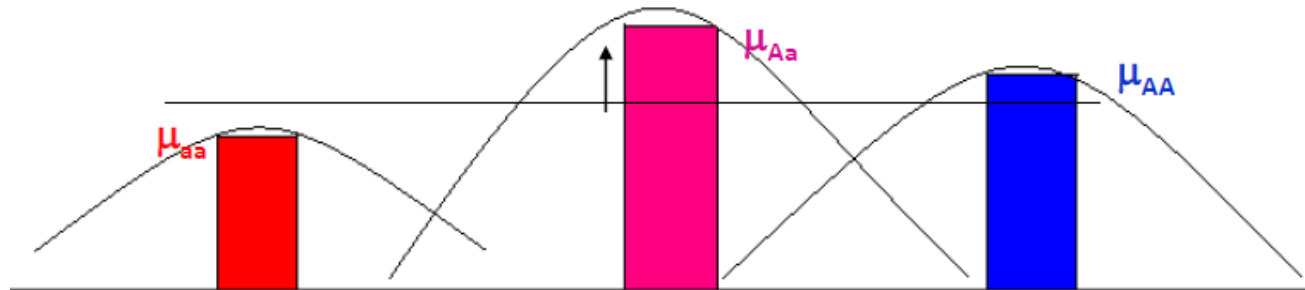
Source of variation	d.f.	TL	CL	AL	TWt	CWt	AWt	WiIAS
Environment	1	164.03*	11.34*	9.09*	3087.11*	517.79*	1076.28*	4.360*
Family	36	1.71*	0.13*	0.97*	19.94*	2.74*	8.40*	0.020*
Sex	1	3.37*	1.59*	0.33	86.82*	31.85*	13.50	0.210*
Env \times fam	36	0.62	0.06	0.35	7.76	1.04	3.31	0.008
Env \times sex	1	0.01	0.01	0.00	0.05	0.17	0.41	0.003
Fam \times sex	36	0.45	0.05	0.24	5.51	0.72	2.43	0.006
Env \times fam \times sex	36	0.53	0.05	0.28	6.60	1.07	2.62	0.009
Error	538	0.47	0.05	0.25	6.17	0.95	2.56	0.008



12. Cruzamiento



$$\text{HETEROSIS POSITIVA} = \mu_{Aa} - (\mu_{AA} + \mu_{aa})/2$$



Modelo: Gen (α) alelos (A, a) \rightarrow Aa



12. Cruzamiento



Contents lists available at ScienceDirect

Aquaculture

journal homepage: www.elsevier.com/locate/aqua-online



Cross breeding of different domesticated lines as a simple way for genetic improvement in small aquaculture industries: Heterosis and inbreeding effects on growth and survival rates of the Pacific blue shrimp *Penaeus (Litopenaeus) stylirostris*

Emmanuel Goyard ^{a,*}, Cyrille Goarant ^a, Dominique Ansquer ^a, Pierre Brun ^a, Sophie de Decker ^a, Robert Dufour ^a, Christian Galinié ^b, Jean-Marie Peignon ^a, Dominique Pham ^a, Elodie Vourey ^b, Yves Harache ^a, Jacques Patrois ^a

Table 3

Individual weights at stocking and harvest and average growth rates observed in experimental earthen ponds and in experimental cages where populations were reared, tagged and mixed together ("communal rearing" conditions) or separately ("separate rearing" conditions)

		initial weight at the time of tagging and mixing (g)			Time of harvest ^a	Final weight (g)			Average growth rate (g/day)			Final survival rate ^b		
		CC	HH	F ₁		CC	HH	F ₁	CC	HH	F ₁	CC	HH	F ₁
Year class 2005	Pond 1	3.3 (0.8 SD)	3.4 (1.3 SD)	2.9 (0.4 SD)	134	25.5 (3.3 SD)	26.6 (2.5 SD)	32.3 (3.0 SD)	0.17	0.17	0.22	52%	60%	61%
	Pond 2	3.3 (0.8 SD)	3.4 (1.3 SD)	2.9 (0.4 SD)	134	24.0 (2.8 SD)	24.5 (2.3 SD)	30.4 (3.1 SD)	0.15	0.16	0.21	50%	60%	60%
Year class 2006	Pond 1	4.0 (1.2 SD)	11.1 (2.9 SD)	3.8 (1.2 SD)	126	25.5 (3.7 SD)	31.2 (5.0 SD)	33.3 (3.2 SD)	0.17	0.16	0.23	37%	27%	55%
	Pond 2	4.0 (1.2 SD)	11.1 (2.9 SD)	3.8 (1.2 SD)	126	26.0 (4.3 SD)	32.8 (4.3 SD)	35.2 (3.7 SD)	0.17	0.17	0.25	32%	38%	52%
Year class 2006	"Separate rearing" cages	3.1 (1.1 SD)	-	3.1 (1.0 SD)	77	16.2 (3.0 SD)	-	23.3 (3.3 SD)	0.17	-	0.26	38%	-	51%
	"Communal rearing" cages	3.1 (1.1 SD)	9.7 (1.6 SD)	3.1 (1.0 SD)	77	17.7 (3.6 SD)	24.0 (3.7 SD)	24.4 (2.7 SD)	0.19	0.19	0.28	44%	40%	52%

^a Days post stocking.

^b From stocking to harvest.



12. Cruzamiento

Gitterle *et al.* (2005)

Table 4

Heritability ($h^2 \pm SE$) and the effect common to full-sibs other than additive genetic ($c^2 \pm SE$) for WSSV resistance and harvest body weight in *P.vannamei* for each batch and line

Line	Batch	WSSV		Body weight	
		$h^2 \pm SE$	$c^2 \pm SE$	$h^2 \pm SE$	$c^2 \pm SE$
1	4	0.17 ± 0.06	0.00 ± 0.02	0.21 ± 0.11	0.08 ± 0.04
	6	0.03 ± 0.03	0.02 ± 0.01	0.15 ± 0.08	0.08 ± 0.03
	All	0.07 ± 0.02	0.01 ± 0.01	0.21 ± 0.04	0.08 ± 0.02
2	3	0.04 ± 0.04	0.01 ± 0.02	0.11 ± 0.15	0.17 ± 0.07
	5	0.07 ± 0.03	0.00 ± 0.01	0.06 ± 0.09	0.11 ± 0.04
	7	0.03 ± 0.02	0.01 ± 0.01	0.45 ± 0.10	0.00 ± 0.03
	All	0.03 ± 0.01	0.02 ± 0.01	0.20 ± 0.04	0.09 ± 0.02

45%

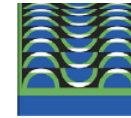




ELSEVIER

Aquaculture

journal homepage: www.elsevier.com/locate/aqua-online



Cross breeding of different domesticated lines as a simple way for genetic improvement in small aquaculture industries: Heterosis and inbreeding effects on growth and survival rates of the Pacific blue shrimp *Penaeus (Litopenaeus) stylirostris*

Emmanuel Goyard ^{a,*}, Cyrille Goarant ^a, Dominique Ansquer ^a, Pierre Brun ^a, Sophie de Decker ^a, Robert Dufour ^a, Christian Galinié ^b, Jean-Marie Peignon ^a, Dominique Pham ^a, Elodie Vourey ^b, Yves Harache ^a, Jacques Patrois ^a

^a Ifremer, Département Aquaculture en Calédonie, Station de Saint Vincent, BP 2059, 98846 Nouméa, New Caledonia

^b Groupement des Femmes Aquacoles, Chambre d'Agriculture, BP 111, 98 845 Nouméa, New Caledonia

ARTICLE INFO

Article history:

Received 26 September 2007

Received in revised form 6 March 2008

Accepted 12 March 2008

Keywords:

Genetic improvement

Cross breeding

Shrimp

Penaeus (Litopenaeus) stylirostris

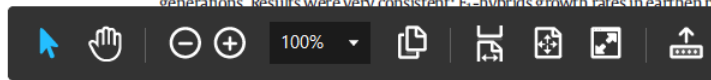
Growth

Survival

Vibriosis

ABSTRACT

Two populations of the Latin American shrimp *Penaeus (Litopenaeus) stylirostris* domesticated in Hawaii and in New Caledonia were previously shown to be genetically differentiated and proven highly inbred. In New Caledonia, where different Vibriosis affect shrimp production and antibiotic use is banned in growing ponds, the Hawaiian population was introduced to increase the allelic variability available for local shrimp farmers and start a genetic improvement program. Growth and survival rates of the two pure populations and the two-way F₁-hybrids obtained by breeding Hawaiian animals with New Caledonian animals were assessed in several simple experiments (earthen ponds, floating cages and experimental infection challenges) during two years on two successive generations. Results were very consistent: F₁-hybrids growth rates in earthen ponds were 37% (±7% SD) higher than in the different populations when in the different populations when showed better survival rates in all conclusion that biomass production is much higher with F₁-hybrid populations than with pure populations using the same quantity of juveniles stocked: biomass production in ponds was increased 1.4 and 2.3 times on year 1 and year 2 respectively, and 1.9 times in



12. Cruzamiento

Acta Oceanol. Sin., 2017, Vol. 36, No. 2, P. 62-68

DOI: 10.1007/s13131-016-0942-6

<http://www.hyxb.org.cn>

E-mail: hyxbe@263.net

Heterosis and heritability estimates for the survival of the Pacific white shrimp (*Litopenaeus vannamei*) under the commercial scale ponds

LU Xia^{1,2}, LUAN Sheng^{1,2}, CAO Baoxiang^{1,2}, SUI Juan^{1,2}, DAI Ping^{1,2}, MENG Xianhong^{1,2}, LUO Kun^{1,2}, KONG Jie^{1,2*}

Table 1. Numbers of families produced from incomplete diallel crosses of eight strains of *Litopenaeus vannamei*

Maternal	Paternal							SIN	Total
	UA1	UA2	UA3	UA4	UA5	UA6	UA7		
UA1	6	-	2	5	2	3	1	5	24
UA2	1	8	1	1	1	1	1	2	16
UA3	1	1	8	1	-	1	1	1	14
UA4	5	1	2	13	4	5	4	1	35
UA5	5	1	-	6	10	4	4	1	31
UA6	5	1	1	7	4	10	5	1	34
UA7	2	1	1	6	6	4	11	-	31
SIN	7	1	1	1	-	1	1	10	22
Total	32	14	16	40	27	29	28	21	207

Note: UA1 represents HAWAII, UA2 GUAMIS, UA3 KONABA, UA4 OCENAI, UA5 SISMAM, UA6 HIGHHA, UA7 OCENA2, and SIN



12. Cruzamiento

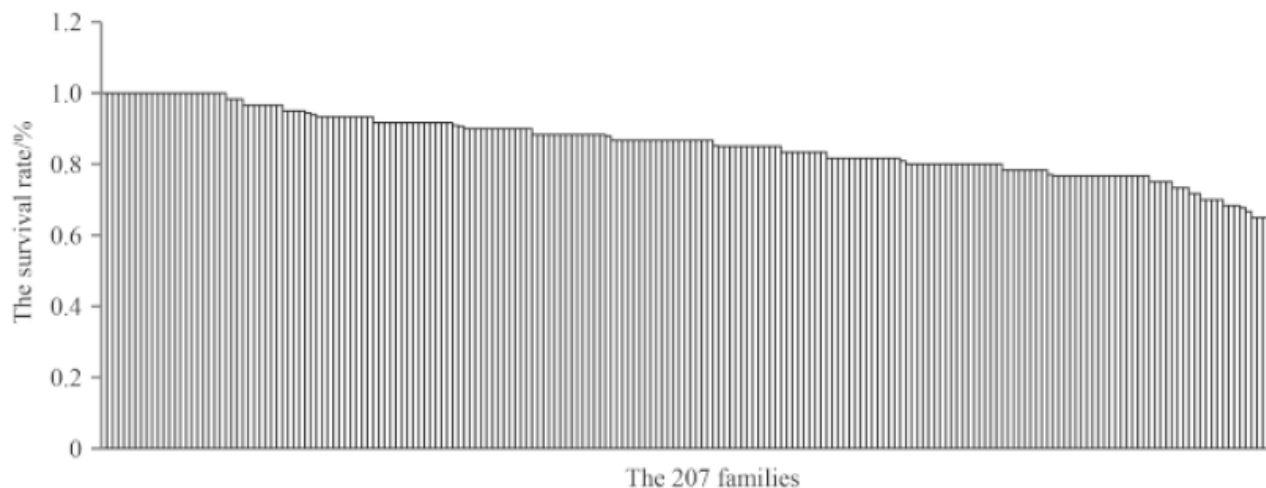


Fig. 1. The distribution of survival rate of all the 207 families.

Table 5. Variance components and heritability estimates for survival in *Litopenaeus vannamei*

Variance components				Heritability $h^2 \pm SE$	Common environ- ment $c^2 \pm SE$
$2\sigma_{sd}^2$	σ_c^2	σ_e^2	σ_p^2		
0.054	0.122	1.00	1.176	0.092 \pm 0.043	0.106 \pm 0.054

Note: $2\sigma_{sd}^2$ is sire-dam variance; σ_c^2 is common environmental effects variance; σ_e^2 is residual variance; c^2 is common environment coefficient.



12. Cruzamiento

Table 4. Analysis of heterosis for survival of eight strains in *Litopenaeus vannamei*

Combination types	Population combinations	Survival rate/%			Heterosis/%
		Orthogonal (♂ × ♀)	Reciprocal (♀ × ♂)	Mean	
Hybridized combinations	UA3×SIN ¹⁾	100.00	100.00	100	20.53
	UA2×UA5 ²⁾	100.00	93.33	96.67	10.79
	UA3×UA4 ²⁾	83.33	100.00	91.67	9.33
	UA7×SIN ²⁾	91.67	-	91.67	8.02
	SIN×UA5 ¹⁾	90.00	-	90.00	7.33
	UA4×SIN ¹⁾	85.00	91.67	88.34	6.80
	UA6×UA3 ¹⁾	100.00	86.67	93.34	6.64
	UA1×UA3 ¹⁾	88.33	91.67	90.00	6.29
	UA6×SIN ¹⁾	93.33	85.00	89.17	3.22
	UA1×UA4 ¹⁾	80.67	92.33	86.50	2.46
	UA4×UA5 ¹⁾	88.33	83.75	86.04	1.54
	UA6×UA4 ¹⁾	90.00	86.90	88.45	1.36
	UA6×UA5 ¹⁾	90.83	86.67	88.75	0.38
	UA6×UA7 ³⁾	91.25	86.00	88.63	-0.88
	UA1×UA5 ⁴⁾	82.00	86.67	84.34	-1.44
	UA2×UA3 ³⁾	81.67	88.33	85.00	-1.57
	UA1×SIN ³⁾	81.90	82.00	81.95	-1.90
	UA2×UA6 ³⁾	93.33	81.67	87.50	-2.54
	UA7×UA4 ⁴⁾	88.75	77.78	83.27	-2.89
	UA1×UA6 ³⁾	83.33	86.67	85.00	-3.51
	UA3×UA7 ⁴⁾	66.67	98.33	82.50	-4.06
	UA2×UA4 ³⁾	85.00	80.00	82.50	-4.19
	UA7×UA5 ³⁾	87.92	78.33	83.13	-4.33
	UA1×UA7 ⁴⁾	82.50	80.00	81.25	-6.15
	UA2×UA7 ³⁾	75.00	90.00	82.50	-6.52
	UA2×SIN ³⁾	80.00	77.50	78.75	-7.60
	UA1×UA2 ³⁾	77.05	-	77.05	-11.37



13. SELECCIÓN GENÓMICA: Mapa genético en Camarón

Yu *et al.* (2016). *Nature Scientific Report*

LG ID	Sex-averaged map		
	Number of markers	Distance (cM)	Average distance (cM)
LG1	279	166.14	0.6
LG2	84	70.64	0.85
LG3	171	88.06	0.52
LG4	101	112.58	1.13
LG5	99	69.02	0.7
LG6	105	113.83	1.09
LG7	104	81.72	0.79
LG8	79	131.56	1.69
LG9	194	90.15	0.47
LG10	143	87.18	0.61
LG11	110	65.07	0.6
LG12	92	83.64	0.92
LG13	186	94.28	0.51
LG14	21	21.36	1.07
LG15	201	76.22	0.38
LG16	169	101.8	0.61
LG17	189	100.68	0.54
LG18	117	98.52	0.85
LG19	183	92.41	0.51
LG20	226	117.02	0.52
LG21	26	33.32	1.33
LG22	113	83.55	0.75

LG ID	Sex-averaged map		
	Number of markers	Distance (cM)	Average distance (cM)
LG23	52	78.37	1.54
LG24	99	95.06	0.97
LG25	178	95.63	0.54
LG26	126	106.17	0.85
LG27	131	102.13	0.79
LG28	181	110.12	0.61
LG29	222	124.16	0.56
LG30	100	103.29	1.04
LG31	175	113.19	0.65
LG32	172	101.38	0.59
LG33	91	48.14	0.53
LG34	222	120.05	0.54
LG35	107	108.42	1.02
LG36	153	108.05	0.71
LG37	154	99.89	0.65
LG38	96	119.54	1.26
LG39	75	131.67	1.78
LG40	156	130.85	0.84
LG41	110	82.65	0.76
LG42	189	111.24	0.59
LG43	178	102.01	0.58
LG44	187	100.67	0.54
Total	6,146	4,271.43	0.7

Mapa de 44 grupos de ligamiento estadísticos construidos como promedio de ambos sexos



13. SELECCIÓN GENÓMICA: SNPs

Jones *et al.* (2017). *Nature Scientific Report*

SNP - putativos	Genotipados	Distancia media entre SNP (cM)	Mapa <i>L.vannamei</i>	cM sexo-promedio
262512 (1.344-234.452)	13.364 (825 - 6.146)	17,22 (0,7 - 50)	44 LG	4.445,37



8.967 SNPs

- Infinium® ShrimpLD-24 v1.0 BeadChip Kit (48 samples)** i
 20013012
[Sign in](#) to see pricing and favorite products.
- Infinium® ShrimpLD-24 v1.0 BeadChip Kit (288 samples)** i
 20013013
[Sign in](#) to see pricing and favorite products.
- Infinium® ShrimpLD-24 v1.0 BeadChip Kit (1152 samples)** i
 20013014
[Sign in](#) to see pricing and favorite products.

Product Highlights

The Infinium ShrimpLD-24 v1.0 BeadChip enables genomic selection and evaluation for family identification within Pacific white shrimp (*Litopenaeus vannamei*), to advance aquaculture breeding programs. This microarray contains over 6400 genome-wide single nucleotide polymorphisms (SNPs), validated using family brood stock from multiple existing breeding programs. The array offers:

- **Excellent call rates and accuracy**
 > 99% mean call rate and > 99.9% reproducibility
- **High-value content with comprehensive coverage**
 Evenly distributed polymorphic SNPs with 1 cM mean spacing
- **High-throughput and flexible format**
 Up to 24 samples can be genotyped in parallel

(Du *et al.*, 2009, 2010; Yu *et al.*, 2016; Jones *et al.*, 2017)



13. SELECCIÓN GENÓMICA: *vs* selección fenotípica

Pérez-Enciso y Toro (2007)

TABLA 2.

Ventaja relativa esperada de la respuesta a la selección fenotípica asistida con marcadores respecto a la selección fenotípica en presencia de desequilibrio de ligamiento poblacional, en función de la heredabilidad del carácter (h^2) y de la fracción de varianza genética explicada por los marcadores (q_m).

	q_m		
h^2	0,10	0,30	0,50
0,10	1,35	1,87	2,29
0,25	1,11	1,31	1,51
0,50	1,03	1,08	1,15



13. SELECCIÓN GENÓMICA: *vs selección combinada*

Pérez-Enciso y Toro (2007)

TABLA 3.

Ventaja relativa esperada de la respuesta a la selección combinada asistida con marcadores respecto a la selección combinada en una población panmíctica como función de la heredabilidad del carácter (h^2), la fracción de varianza genética explicada por los marcadores (q_m), el número de familias (m) y su tamaño (n) (OLLIVIER 1998).

h^2	q_m	$M = 8$			$m = \text{grande}$	
		$n = 1$	$n = 8$	$n = \text{grande}$	$n = 1$	$n = \text{grande}$
0,10	0,50	1,8	1,10	1,21	1,28	1,21
0,50	0,50	1,09	1,05	1,09	1,19	1,13

Existe un número de marcadores y un tamaño de población máximo por encima del cual los aumentos en precisión son despreciables. Para la mayor parte de situaciones, *grosso modo*, no merece la pena genotipar con densidades inferiores a los 5 cM entre marcadores o aumentar el tamaño de población por encima de un millar de individuos.



13.1. QTLs en Camarón: crecimiento

Yu *et al.* (2016). *Nature Scientific Report*

LG	Position (cM)	Markers	LOD	Additive Effect	Dominant Effect	R ² (%)
1	51.3	Marker12047	6.1	-18.4	16.5	13.1
10	39.3	Marker7605	5.7	-10.4	12.1	19.0
12	50.3	Marker2797	5.3	-13.9	15.4	14.7
13	67.3	Marker18522	5.5	-14.7	2.9	15.0
18	66.0	Marker33221	5.5	-9.2	7.7	22.6
33	25.9	Marker24250	6.5	-16.3	20.3	17.9
37	35.6	Marker8838	5.1	-17.7	16.5	11.3
38	53.4	Marker11898	5.9	-15.7	20.2	17.9
38	64.6	Marker42558	5.4	-16.5	19.2	13.8
42	44.9	Marker89109	5.8	-11.7	12.9	16.3
44	17.6	Marker5684	5.1	9.5	11.7	19.7

Table 7. Detected QTLs for Body Length.

LG	Position (cM)	Locus	LOD	Additive Effect	Dominant Effect	R ² (%)
9	46	Marker34000	7.1	-3.6	2.3	20.8
10	39.3	Marker7605	4.1	-4.0	5.1	14.3
22	28.8	Marker33688	4.2	1.1	1.0	7.8
27	13.5	Marker21173	3.8	-4.0	3.1	15.5
35	61.1	Marker58445	4.0	-2.2	0.2	13.8
38	38.7	Marker4670	3.7	-1.4	0.5	6.4
41	38.5	Marker10074	4.1	-5.2	4.7	11.1

Table 8. Detected QTLs for Body Weight.



13.2. SELECCIÓN GENÓMICA: costes

Minimal Laboratory Setup



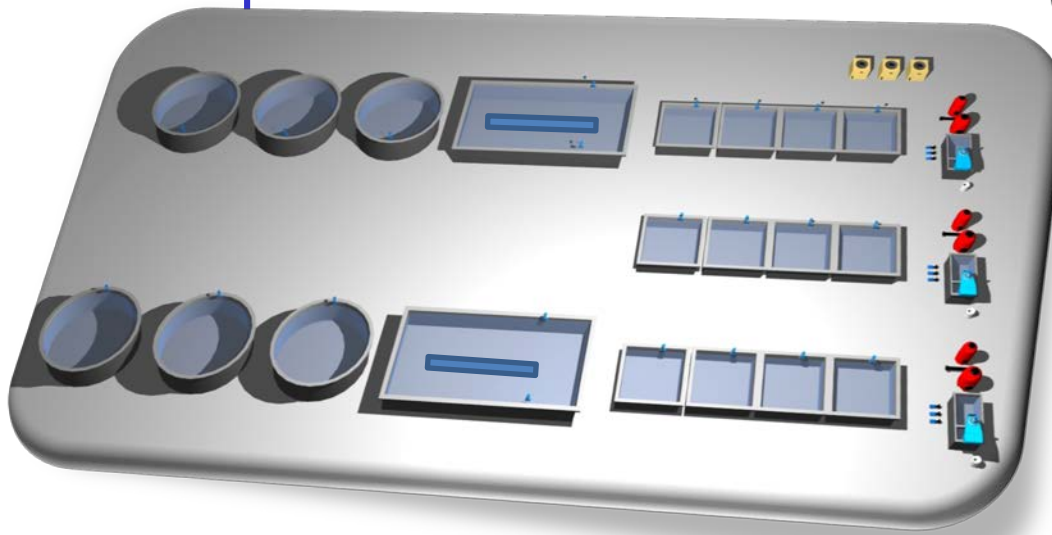
- TruSeq Genotype N_e startup costs are modest

#Samples	#SNPs		
	100	500	1000
384	\$30	\$40	\$50
1056	\$25	\$28	\$35
3072	\$23	\$25	\$27
5088	\$22	\$23	\$25
10080	\$20	\$21	\$22
15072	\$20	\$20	\$21
20064	\$20	\$20	\$20
25056	\$20	\$20	\$20
30048	\$20	\$20	\$20
>30048	\$20	\$20	\$20



PARQUE CIENTÍFICO TECNOLÓGICO DE LA ULPGC (PCTM)

Estación de reproductores



➤ CONTROL Y MONITORIZACIÓN

- 6 Tanques x 40 m³
- 2 Tanques x 80 m³
- 12 Tanques x 10 m³ (RAS)

[AQUAEXCEL2020 - http://www.aquaexcel2020.eu/](http://www.aquaexcel2020.eu/)

[GIA - http://www.giaqua.org/](http://www.giaqua.org/)

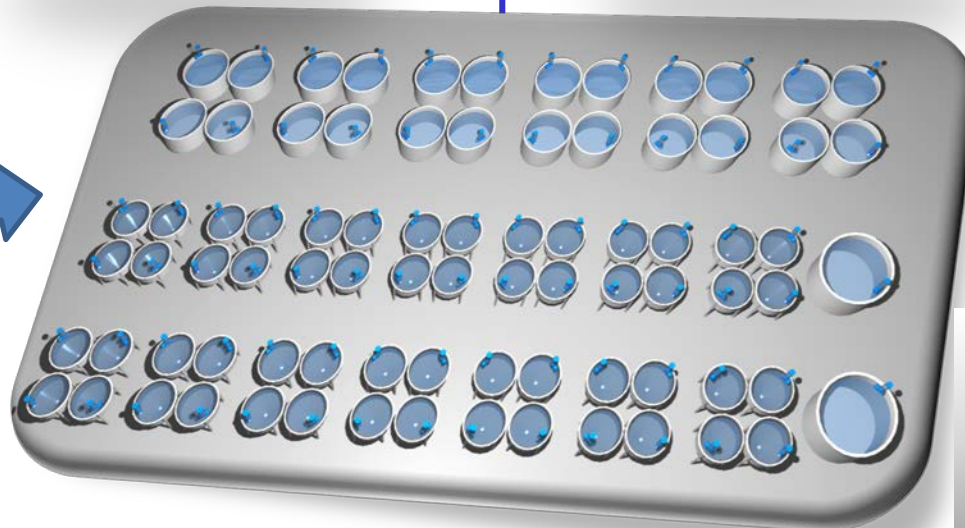
Warm Water Species Selection Unit (WWSSU)



PARQUE CIENTÍFICO TECNOLÓGICO DE LA ULPGC (PCTM)



Warm Water Species Selection Unit (WWSSU)

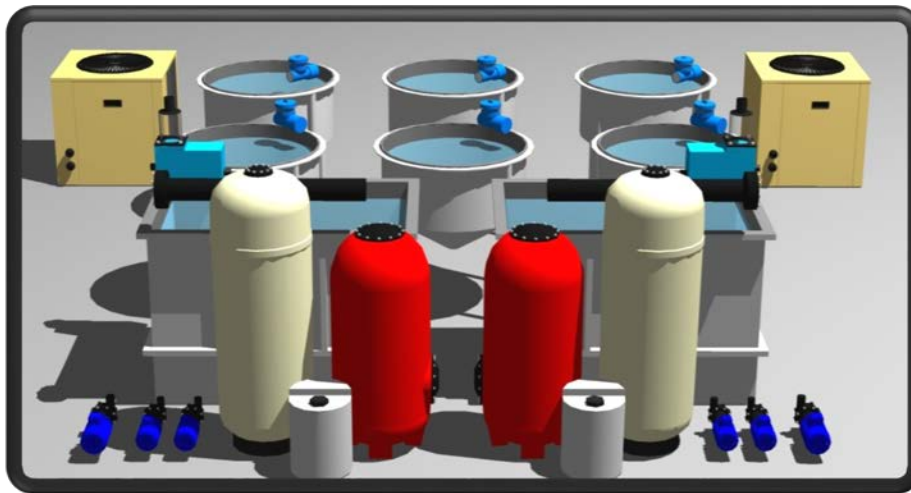


- **CONTROL Y MONITORIZACIÓN**
- 2 Tanques x 2 m³
 - 24 Tanques x 1 m³
(fotoperiodo)
 - 54 Tanques x 0.5 m³





PARQUE CIENTÍFICO TECNOLÓGICO DE LA ULPGC (PCTM)



Estación de Bio-ensayos (MBS)

- **CONTROL Y MONITORIZACIÓ N**
- ☑ **16 RAS**
- ☑ **48 Tanques x 0.5 m³ (total)**

PARQUE CIENTÍFICO TECNOLÓGICO DE LA ULPGC (PCTM)



FITU

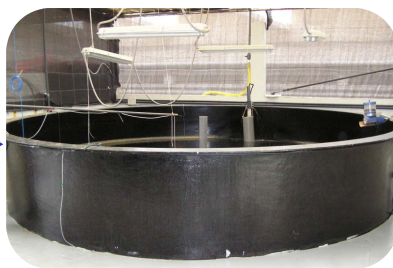
Feed Ingredients-additives
Testing Unit

Feed Ingredients and Additives Testing Unit (FITU)



➤ Manual CONTROL & MONITORIZACION

- 45 Tanques x 1 m³
- 90 Tanques x 0.5 m³
- 2 Tanques x 2 m³
- 48 Tanques x 0.2 m³
- 24 Tanques x 0.1 m³



➤ Manual CONTROL & MONITORIZACION

- 2 Tanques x 40 m³
- 6 Tanques x 2 m³
- 8 Tanques x 10 m³

CONCLUSIONES



Muchas gracias por su atención!

