



中国水产科学研究院黄海水产研究所

YELLOW SEA FISHERIES RESEARCH INSTITUTE CHINESE ACADEMY OF FISHERY SCIENCES

Genetic evaluation for growth traits of *Artemia. sinica*

Luan Sheng, Kong Jie, Zhang Zhiwei

Yellow Sea Fisheries Research Institute
Qingdao, China

2009-06-14

Outline

- ◆ 1. Introduction
- ◆ 2. Breeding program
- ◆ 3. Results
 - ◆ 3.1 Correlation of growth traits between different developmental stages
 - ◆ 3.2 Analysis of heterosis for four strains
 - ◆ 3.3 Evaluating genetic parameters and genetic gain of body length



1. Introduction

- ❖ Brine shrimp distributed worldwide, is one important food for fish and crustaceans .
- ❖ *Artemia.sinica* is only found in China and named as an unique bisexual species.



※ Advantages as an promising model animal for selective breeding:

Short reproduction cycle, small size (adult is over a centimeter), easy mating, resting eggs.



2、Breeding program

❖ 2.1 Breeding object

- Growing faster, body length

❖ 2.2 Founder populations



2.3 Production of families

- ❖ Families of base population (generation G0) were formed using diallel cross including four wild strains.
- ❖ The G1 generation was produced from the mating of G0 individuals, which had breeding values for body length above the population mean in the actual population.
- ❖ The control population was established for the G1 generation using single broodstock pairs from G0. The broodstock of control population had breeding values around the population mean in each generation.



- ❖ In the G0 and G1 generations, full-sib and half-sib families were produced by a nested mating design, in which two dams were mated to the same sire.
- ❖ Half-sibs families were produced by moving the sire to the second dam after mating with the first dam.



The facilities of eggs hatching

400L illumination incubator



culture dish



- ❖ After hatching, nauplius of families were transferred to 500ml plastic beaker and reared separately.



2.4 common testing of trait

❖ Tagging:

- The RFID and VIE were not useful because of the small size of *brine shrimp*
- Each Larva of families was transferred to the 50ml plastic vial which containing 30ml seawater at the 10d .



2.5 Data capture

- ❖ Raw data (2 sets):
 - After tagging
 - After harvesting
- ❖ Data for 'after tagging':
 - Sire ID, dam ID & individual ID
 - Eggs collection date, larva collection date & tagging date
 - Environment and replicate.



❖ Data for after harvesting:

- Harvesting date
- Individual ID
- Final body weight, body length, survival
- Sex (Male, Female)
- Line (Selection, control)



2.7 Evaluation of genetic parameter

- ❖ Heritability (h^2)
- ❖ Common environmental effects (c^2)
- ❖ Genetic, phenotypic and environmental correlations
- ❖ Animal model for growth trait
- ❖ REML: Restricted Maximum Likelihood
- ❖ The complete pedigree

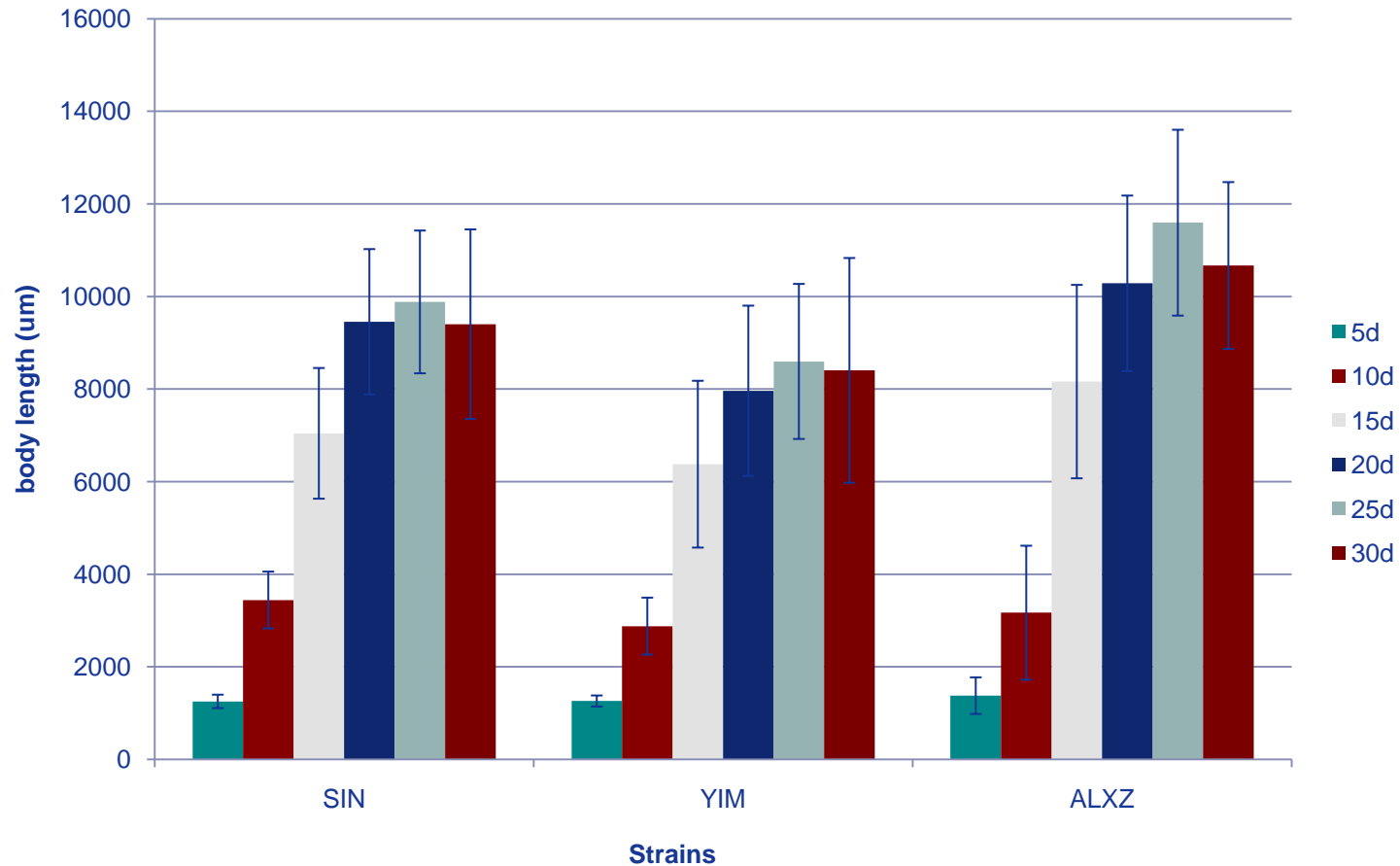


2.8 SELECTION OF NEW BREEDERS

- ❖ Breeding values for harvest body length within generation and across generations were obtained using the estimates of heritability and common full-sib effect across generation by best linear unbiased prediction (BLUP).
- ❖ Selection index was calculated based on EBV and breeding object. Animals with high selection index will be selected as new breeders
- ❖ Rational mating scheme:
 - Control inbreeding, less than 1% inbreeding rate each generation
 - Maximum genetic gain



3.1 Correlation analysis of growth traits between six developmental stages

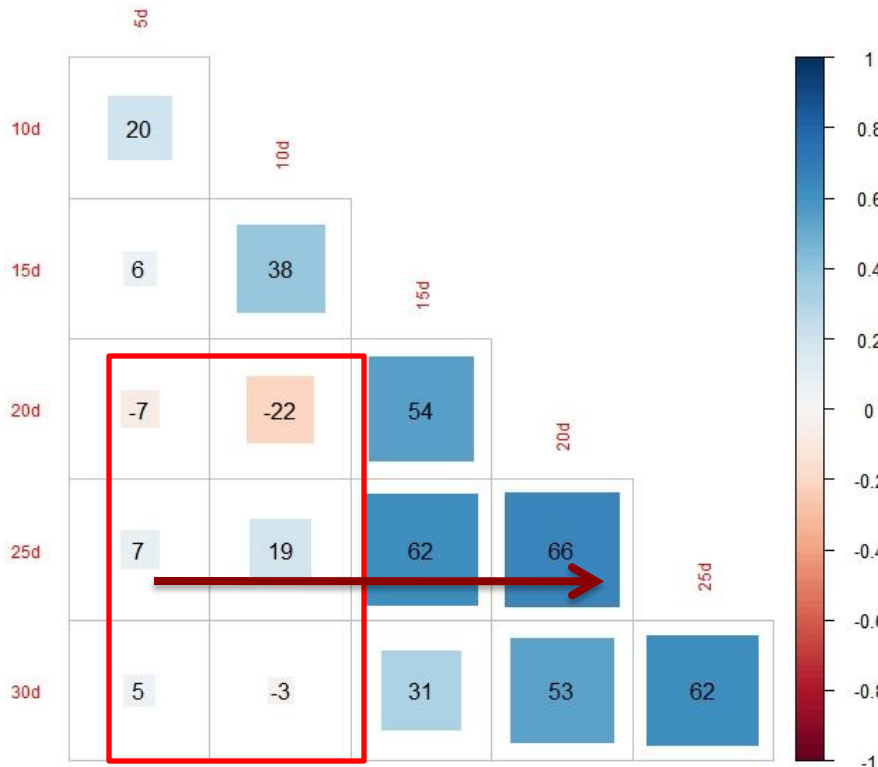


Mean body length of 3 strains at six developmental stages

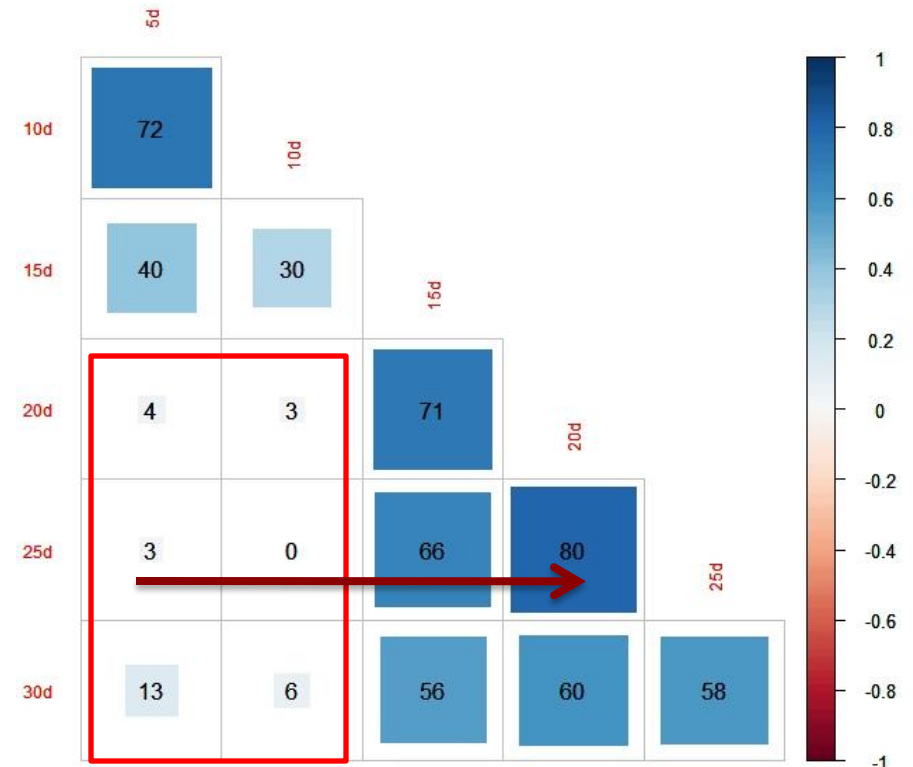


Correlation coefficients of total length at six developmental stages

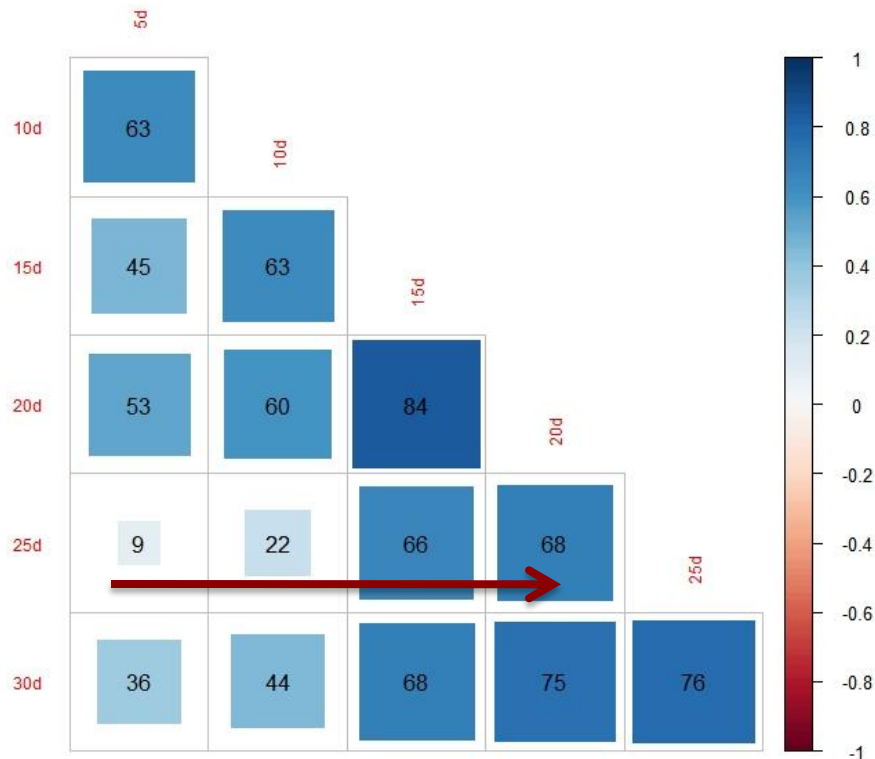
SIN



ALXZ



YIM



❖ Early stage selection especially selecting at stages **before 15d** was **not** reasonable for improving growth trait.



3.2 Analysis of heterosis for four strains

❖ The formula of heterosis ratio:

$$\text{HE}(\%) = \frac{M_{F1} - \frac{1}{2}(M_{P1} + M_{P2})}{\frac{1}{2}(M_{P1} + M_{P2})}$$

$$\text{HEM}(\%) = \frac{M_{F1} - M_{P1}}{M_{P1}}$$

$$\text{HEF}(\%) = \frac{M_{F1} - M_{P2}}{M_{P2}}$$

where, M_{F1} , M_{P1} and M_{P2} represent the average of the first generation post-crossing, maternal and fatherly populations, respectively.



Heterosis of growth traits and survival rate

Group	Trait	HE (%)	HEM (%)	HEF(%)
SIN×BDJL	BL (um)	15.71	19.10	12.51
	BW (mg)	48.72	52.49	45.13
	Suvival(%)	0.43	14.61	-1.52
YIM×SIN	BL (um)	8.92	14.02	4.26
	BW (mg)	20.24	25.98	14.99
	Survival (%)	-5.08	-1.49	6.72
YIM×BDJL	BL (um)	-3.41	4.20	-9.99
	BW (mg)	1.24	8.89	-5.40
	Survival(%)	0.55	6.02	-1.31
ALXZ×YIM	BL (um)	9.85	10.19	9.51
	BW (mg)	-8.85	2.79	-18.12
	Survival(%)	-27.70	-32.05	17.10
ALXZ×BDJL	BL (um)	-0.95	7.22	-7.96
	BW (mg)	-11.96	7.63	-25.52
	Survival(%)	21.61	7.22	72.00



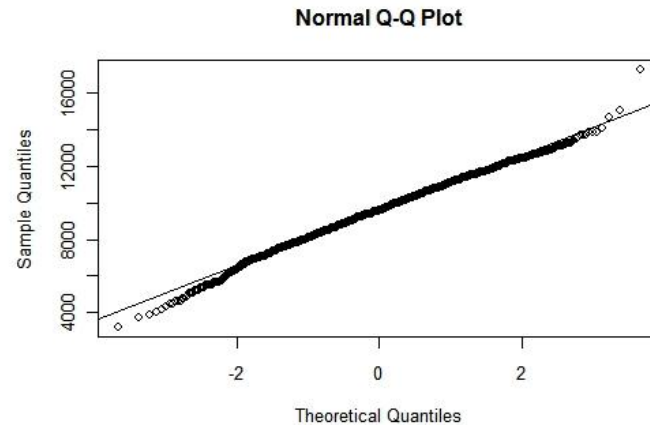
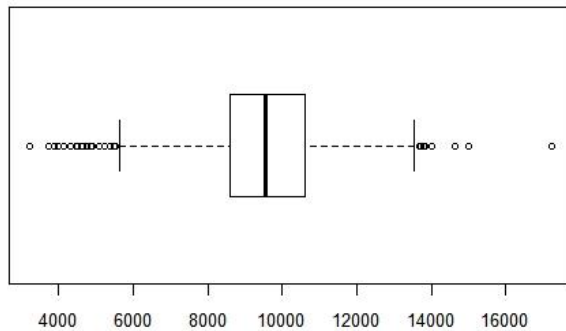
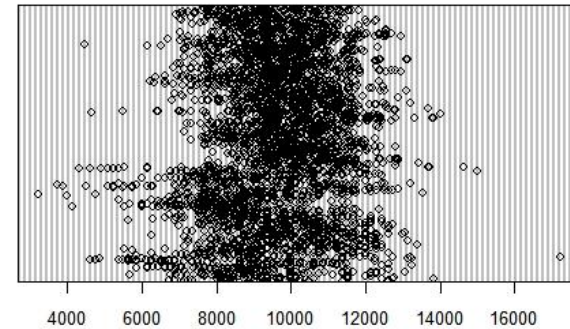
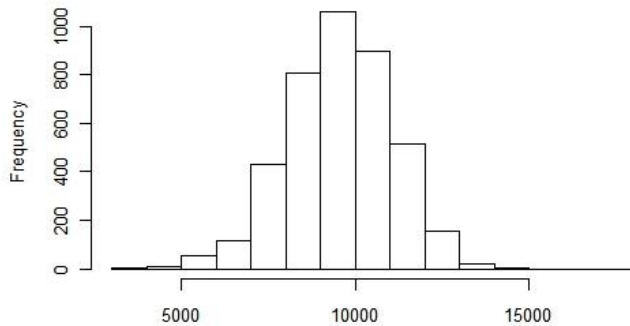
Conclusion

- ❖ Strains of **SIN**、**YIM**、**BDJL** as founder population were more appropriate for improving growth traits.
- ❖ For improving survival, while **ALXZ** and **BDJL** were more appropriate.
- ❖ **None** of these combinations was appropriate for both growth and survival.



3.3 Genetic parameters and genetic gain

Exploratory data analysis of body length



Statistical description of body length for generation G0 and G1

Generation	Population	Tank	N	Harvest body length(um)		Survival(%)
				Mean (um)	CV(%)	
G0	Base	PY0100	805	9417	16.33	73.10
		PY0200	875	9024	20.72	83.44
G1	Selected	PY0100	450	10282	12.54	93.95
		PY0200	467	9716	11.71	94.92
	Control	PY0100	186	9623	13.14	96.38
		PY0200	186	9444	12.75	95.38



Animal model for body length

$$y = Xb + Z_1a + Z_2c + e$$

- ❖ y : vector of observed body length at harvest;
- ❖ b : vector of a fixed effect of the generation (two levels) by tank (two levels) by sex (two levels) subclass (with a total of four levels), and including a covariate of age at harvest for each level of the fixed effect;
- ❖ a : vector of the animal additive genetic effect, $a \sim (0, A\sigma_a^2)$, where A is the additive genetic relationship matrix among all brine shrimps;
- ❖ c : vector of random common full-sib effects, $c \sim (0, I\sigma_c^2)$;
- ❖ e : vector of random residual errors, $e \sim (0, I\sigma_e^2)$.
- ❖ X, Z_1, Z_2 are design or incidence matrices



Genetic parameters of body length

Estimates of the additive, common full-sib, residual and phenotypic variances, heritability and common full-sib effect for harvest body length of *Artemia sinica* within and across generation

Generation	Variance components				Heritability	Common environment coefficient
	σ_a^2	σ_c^2	σ_e^2	σ_p^2	h^2	c^2
G0	720306	4582	786108	1511000	0.48 ± 0.24	0.0030 ± 0.11
G1	695117	26732	294162	1016000	0.68 ± 0.23	0.026 ± 0.086
Across	420238	154847	719645	1295000	0.32 ± 0.08	0.12 ± 0.032



$$Y_{ijk} = \mu + TS_i + bA_k(TS_i) + P_j + e_{ijk}$$

Realized genetic gain

$$Y_{ijk} = \mu + TS_i + bA_k(TS_i) + P_j + e_{ijk}$$

Y_{ijk} is the observed harvest body length of the k th individual of the selected or the control population in G1;

μ is the overall mean;

TS_i is the fixed effect of the i th level of test tank (two levels) by sex (two levels) subclass ($i=1,2,3,4$);

P_j is the fixed effect of the j th population (two levels: control and selected populations);

e_{ijk} is the random residual error of the k th individual.

The covariate age at harvest, nested within the TS effect, on harvest body length was significantly different from zero ($P < 0.05$) and was therefore included in the model.



Realized genetic gain

Generation	Population	Least squares mean (um)	Realized genetic gain	
			Mean (um)	(%)
G1	Control	9517.53		
	Selection	10042.47	524.94	5.52



Predicted genetic gain

Generation	Population	Breeding value (um)	Predicted genetic gain	
			Mean(um)	(%)
G0	Base	-76.45		
G1	Selection	349.97	426.42	4.48



Conclusions

- ❖ Genetic ties across generations increased the accuracy of evaluating the heritability.
- ❖ High heritability for body length, lower genetic gain than expected value.
- ❖ Individual permanent environment effect existed and affected the selective accuracy because each brine shrimp was cultured at one single via. In the current model, this effect couldn't be eliminated effectively.
- ❖ Repeat measure is the possible solution.



Thanks for your attention!

