# An overview of culturing and breeding of Chinese Fleshy Shrimp *Fenneropenaeus chinensis* in China


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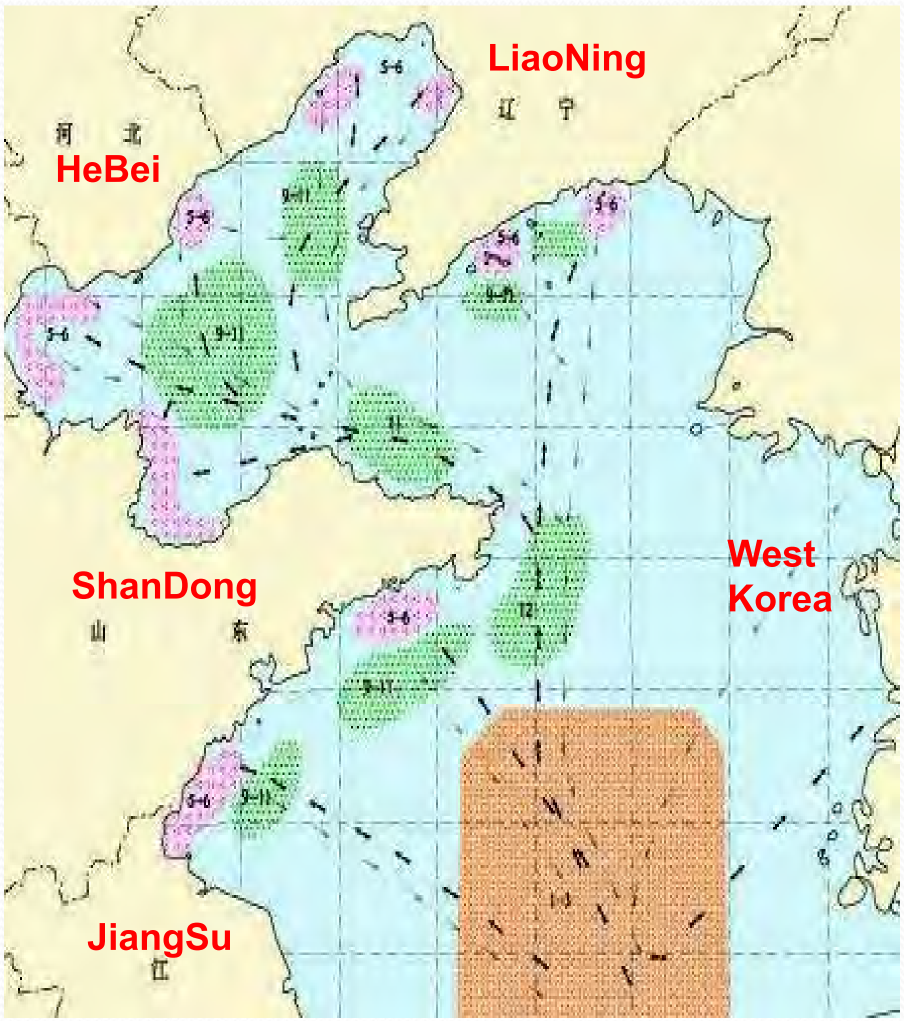
# Introduction





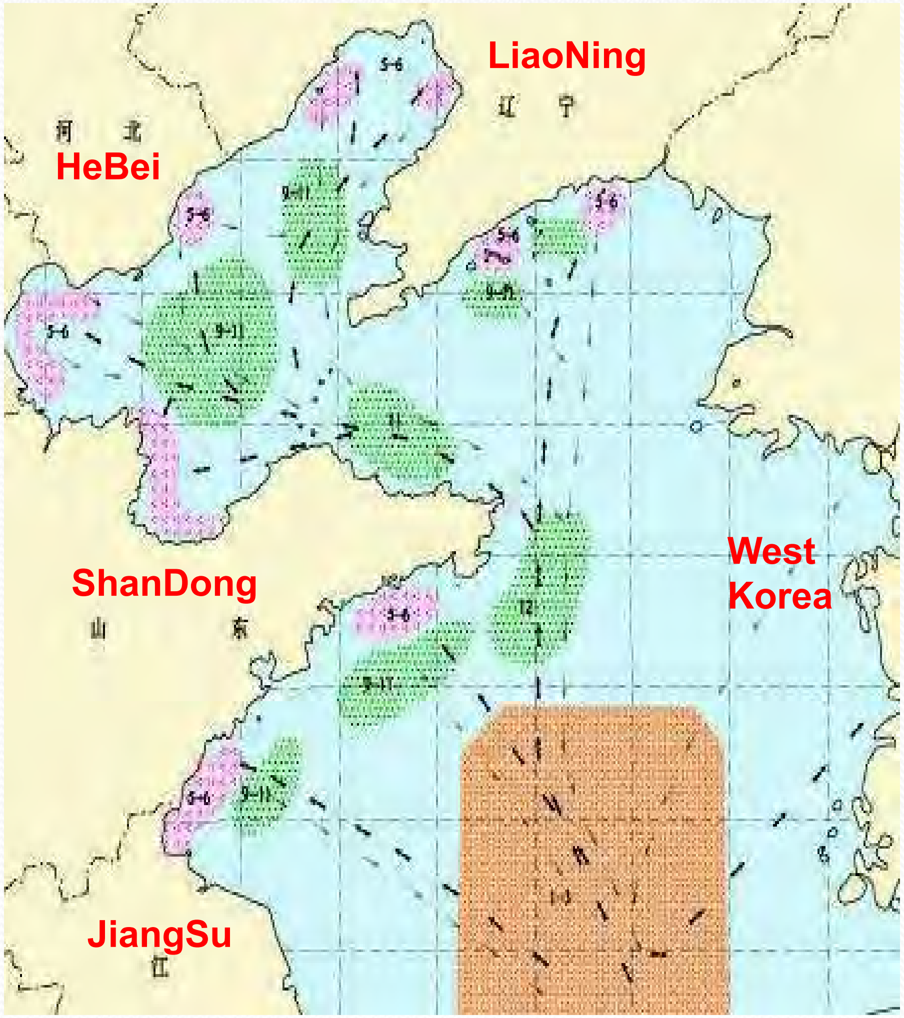
**Chinese Fleshy Shrimp**

***Penaeus* (*Fenneropenaeus*) *chinensis* :**

**Osbeck,1765**

**A cold-water shrimp: mainly distributed along the North-western coast of Pacific Ocean.**

# Introduction




**Chinese Fleshy Shrimp**

***Penaeus* (*Fenneropenaeus*) *chinensis***

**Osbeck,1765**

**A cold-water shrimp, mainly distributed along the North-western coast of Pacific Ocean.**

**One-year life cycle, three migrations:**

**over-wintering migration (Jan-Mar)**

**spawning migration (Apr-Jun)**

**feeding migration (Sep-Nov)**

**Male breeders die after mating (Oct/Nov)**

**Female breeders over-winter, spawn the following spring (Apr-May) and die after the spawning**

# A brief history of initial study of *F.chinensis*

1952.3.30

- Earliest record research of *F.chinensis* in China by Shuping Zhu and Dizhou Tong, mainly focused on life history, gonad maturity, water environment and feed.

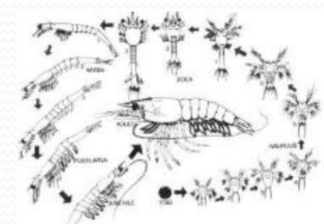
1959

- The first successful rearing of shrimp larvae in TianJin and the first report on its life history was published.

1960

- Chinese scientists succeeded in experimentally breeding *F. chinensis* seedstock.

1965



- Systematically research on development of shrimp larvae was published, which provided the theoretical basis for artificial breeding of shrimp seedstock.

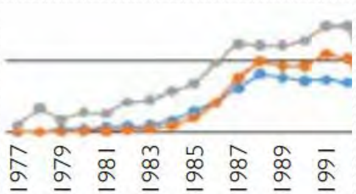
1976

• Seed breeding in concrete tanks and muddy ponds made substantial progress and promoted farming production.

1981

• Techniques for large-scale, industrial seedstock production was validated.

1987-1992




• Farming peak period in China (total yield 200,000 mt, and farm pond area of 40,000 ha).

1993

• Nationwide outbreak of white spot syndrome (WSS) in shrimp culture has seriously affected *F. chinensis*.
**Farming production has been reduced to 50 000t since 1993.**

solutions?
and how do we do?


## Traits in the breeding objective:

- ✓ *Growth,1997*
- ✓ *White Spot Syndrome Virus (WSSV) resistance, 1998*
- ✓ *pond survival, 2004 (multi-traits)*
- ✓ **ammonia nitrogen resistance, 2009**
- ✓ *Low temperature resistance,* 2011

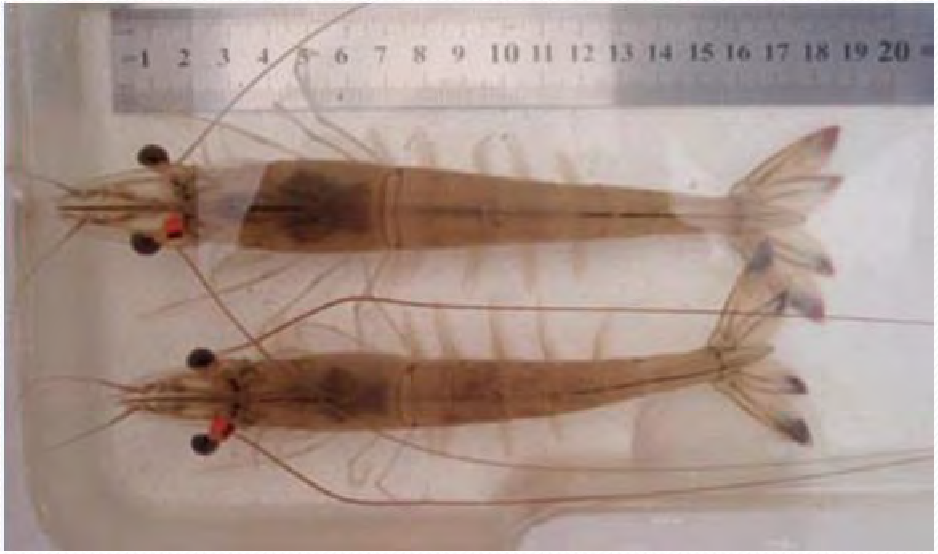
**Great efforts have been made to its recovery due to nationwide outbreak of WSSV. YSFRI conducted new shrimp varieties selection programs which has been confirmed as the most effective way to recover the shrimp farming in China.**

# New Varieties of *F. chinensis*


Huanghai No.1: The first new variety of *F. chinensis*

- Obtained in 2003 after 7 generations of selective breeding incorporating biotechnology with a selective approach.

- The average body length increased by 8.40%, while the body weight increased 26.86% from the values achieved by the unselected control population.




Huanghai No.2

- Obtained in 2008 after 11 generations selection with faster growth, higher pond survival and stronger disease resistance.

- The harvest body weight increased by over 20.0%, resistance to WSS was increased by 15.8%, and the shrimp demonstrated lower morbidity or slowed death after infection with disease.

Huanghai No.3

- Obtained in 2013 after 5 generations selective breeding.

- The resistance of the new varieties of juvenile shrimp to ammonia nitrogen increased by 21.2%, the survival rate increased by 15.2%, and average weight rose by 11.8%.

# An example: Process of breeding a new variety

**Technology line of Huanghai 201**

Collection of germplasm resources

↓

Large-scale family construction

↓

Character test of WSSV resistance, growth rate and survival

↓

Estimate of genetic parameter and genetic progress

↓

Prediction of breeding value; Decision of selection index

↓

Selection plan and its optimization

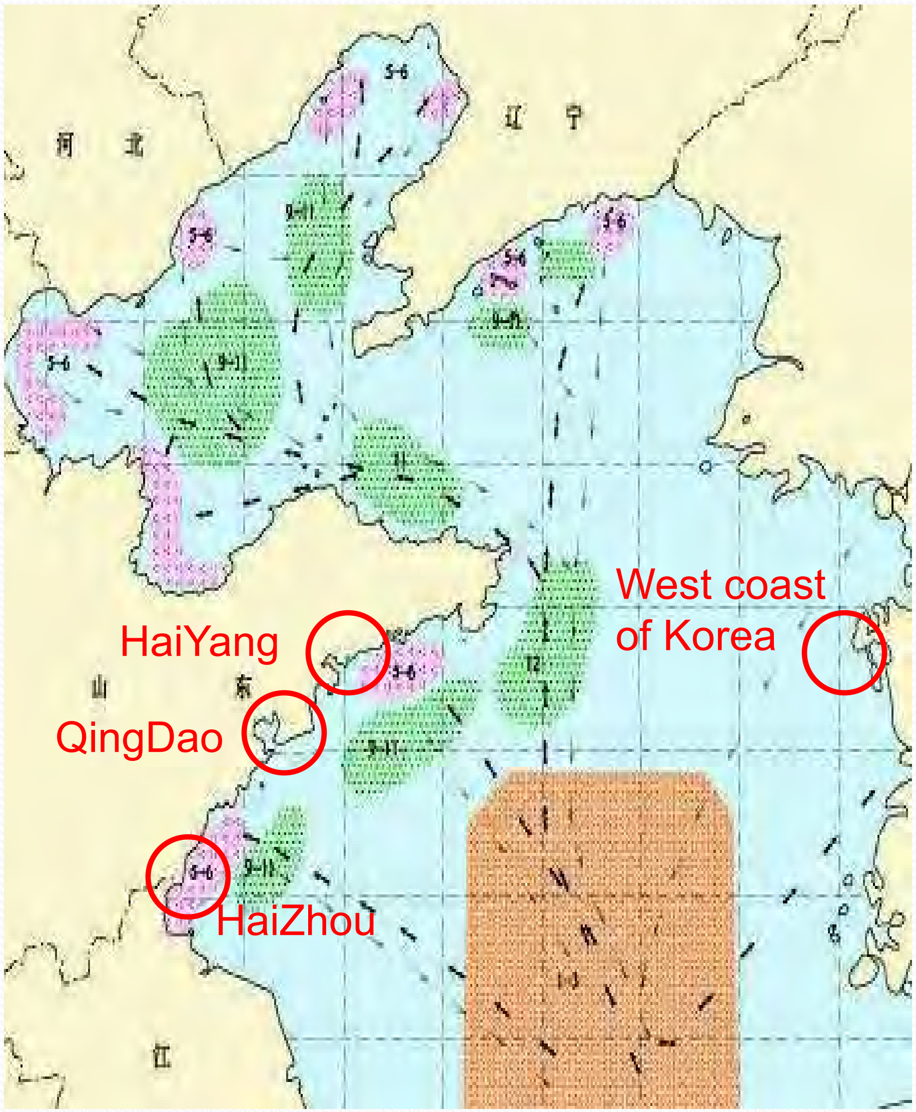
↓

Family and individual selection

↓

Production of seed shrimp and offspring seed

# 1. Source of parents




- Core breeding population of "Huanghai No.2" in QingDao.
- Yellow Sea population near HaiYang.
- Population in HaiZhou Bay.
- Population near West coast of Korea.

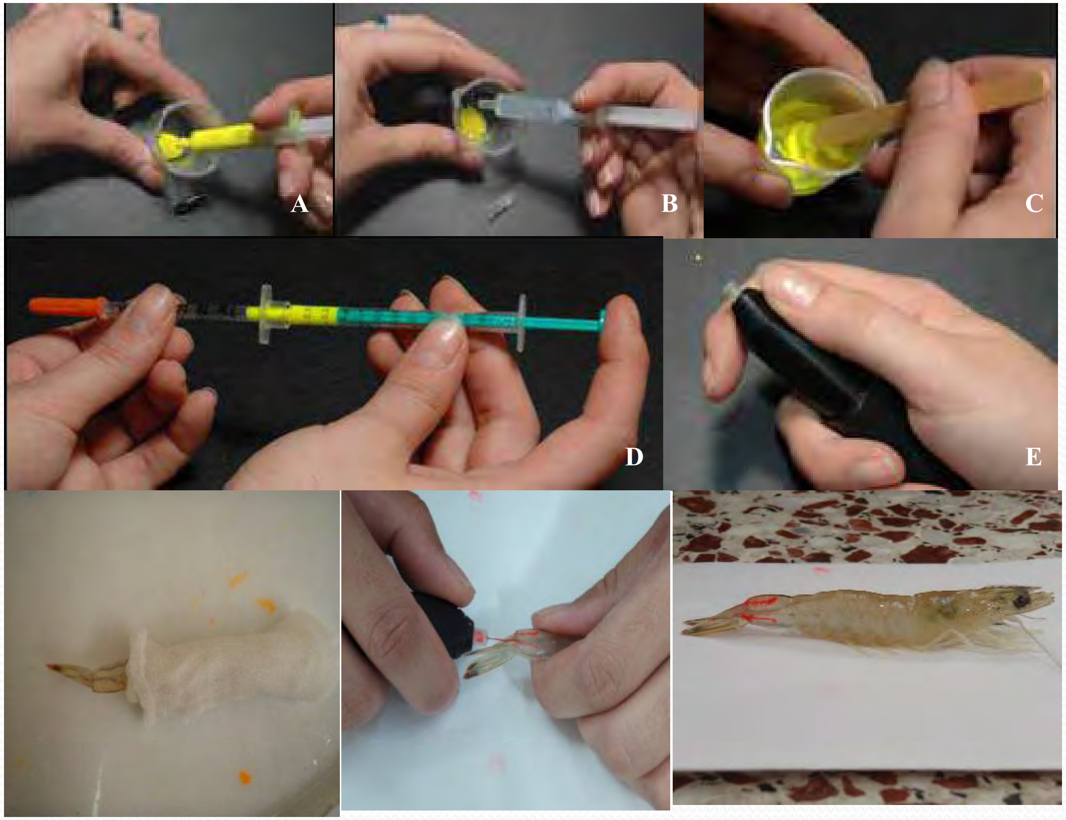
# 2. Family construction


Genetic breeding center of our institute in QingDao

◆ Family constructed in recent years

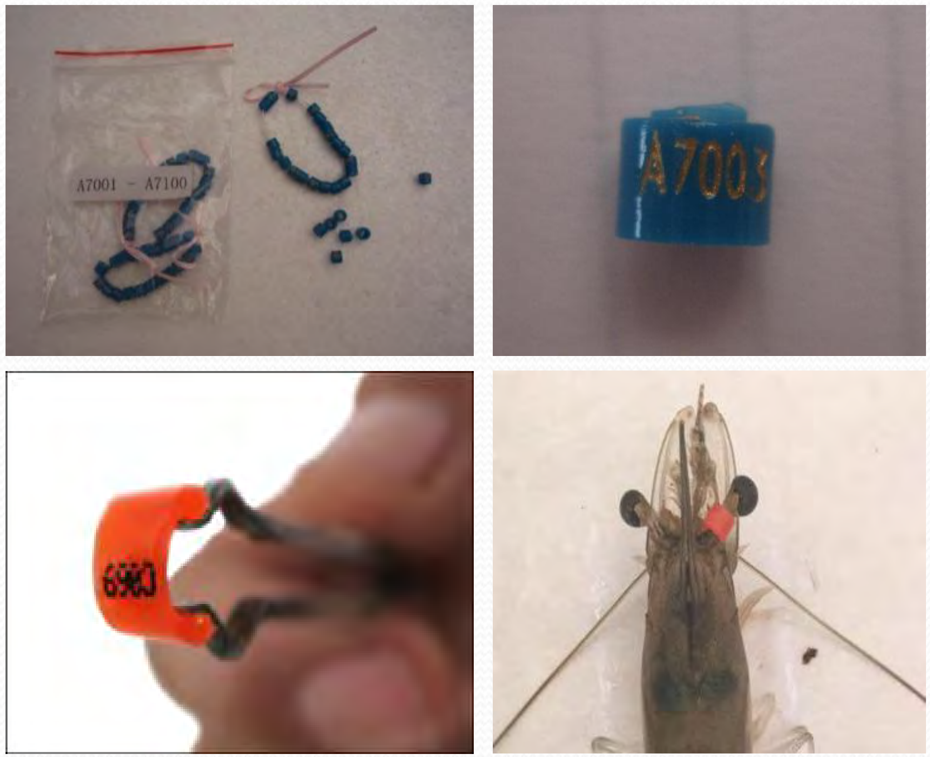
| Year | Family Num | Propagation parent shrimp | Larval rearing (million) | Demonstration area (ha) |
|---|---|---|---|---|
| 2009 | 112 | 1020 | 3.38 | 2111 |
| 2010 | 129 | 2894 | 124.4 | 9482 |
| 2011 | 104 | 7003 | 239 | 1160 |
| 2012 | 65 | 3100 | 177.6 | 3310 |
| 2013 | 93 | 2775 | 210 | 1110 |
| 2014 | 107 | 14200 | 210 | 1200 |
| 2015 | 125 | 6200 | 190 | 7200 |
| 2016 | 132 | 72000 | 113 | 18200 |
| Total | 867 | 109192 | 1267.38 | 43773 |

# Family and individual labeling technique




Family label: VIE fluorescence labeling

# Family and individual labeling technique




Individual label: eyestalk-ring labeling

# 3. Traits test

Traits we concerned

- Growth rate
- Survival rate
- WSSV resistance

Mixed

- each families are equalized in number and mixed into ponds/tanks after labeling to ensure the same environmental conditions.

# Test locations

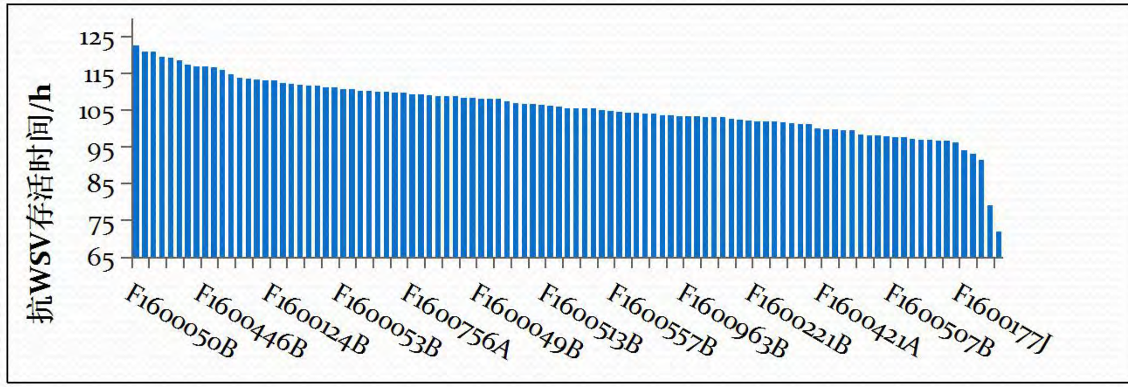

**Shrimp breeding center（growth, survival rate, low temperature）**

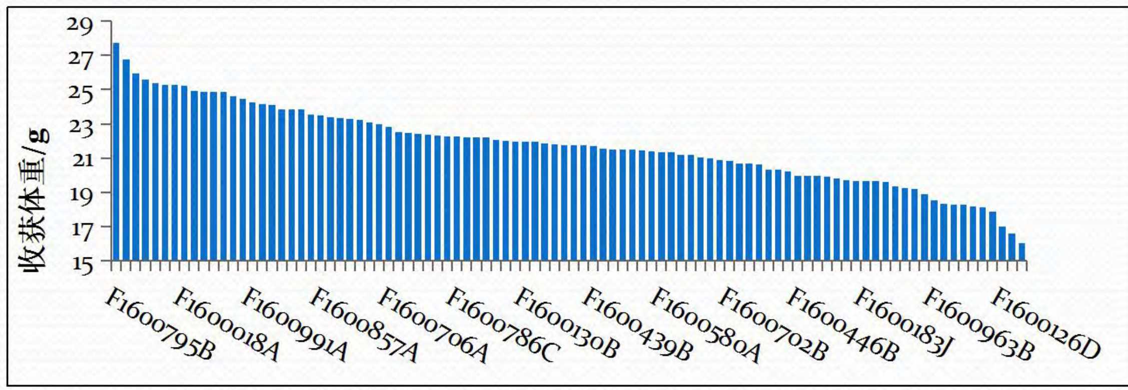
**WSSV resistance**

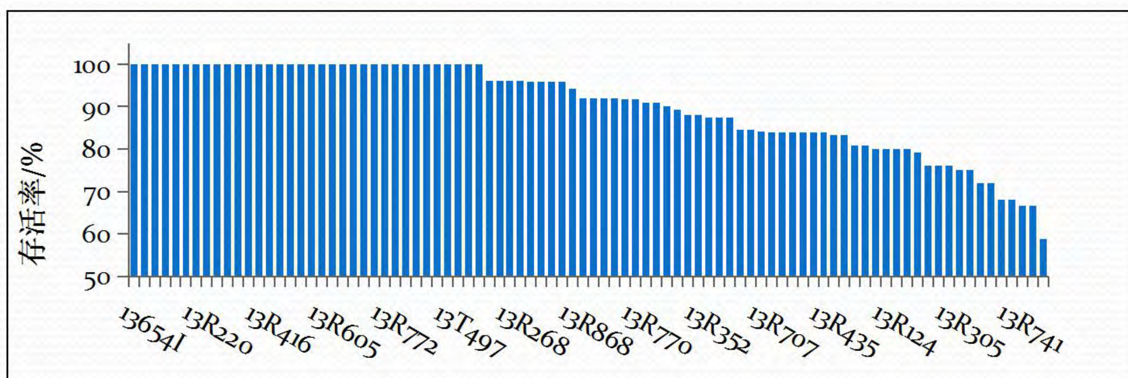
# 中国对虾各家系经济性状排名情况

中国对虾育种核心群各家系抗WSSV存活时间、收获体重及养殖存活率均有一定差异。

各家系收获体重的差异与抗WSSV存活时间和养殖存活率相比更为明显。



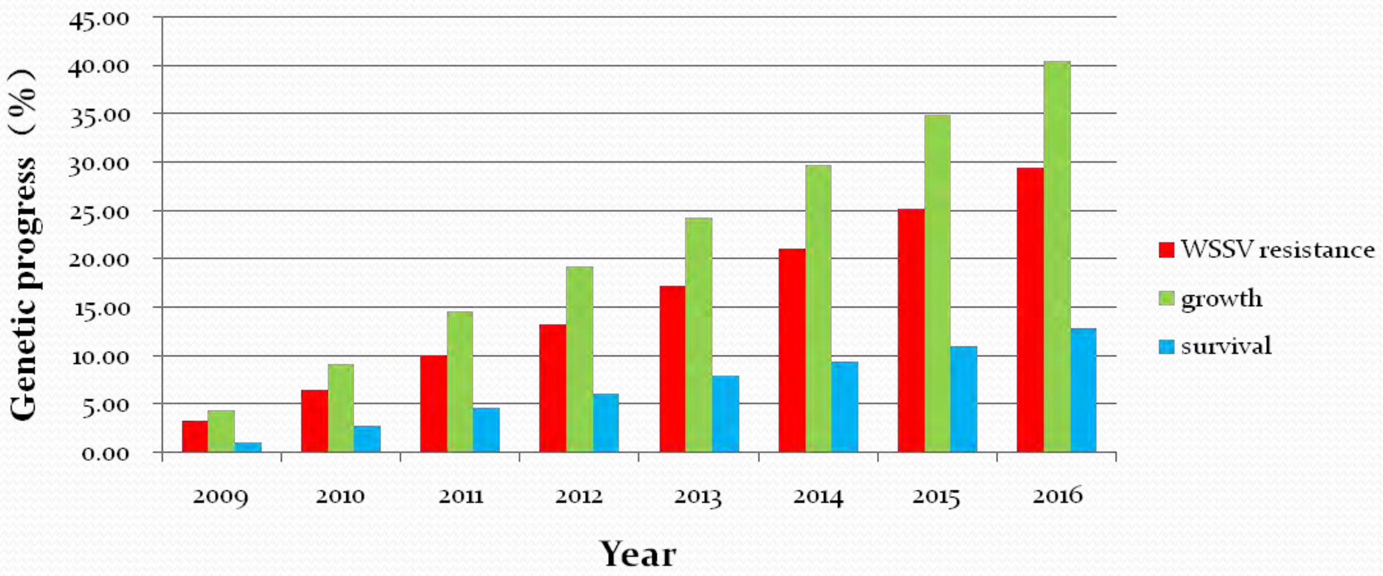



# 4. Estimate of genetic parameter and genetic progress

- Using REML method and data from 2009, we have estimated that, heritability of survival time after virus infection was 0.083±0.023, heritability of harvest weight was 0.132±0.011, and heritability of survival was 0.058±0.026, all shows low heritability.

| Traits | | Variance component | | | Heritability | Common environmental effect |
|---|---|---|---|---|---|---|
| **WSSV resistance** | 147.32 | - | 1633.94 | 1781.3 | 0.083±0.023 | - |
| **Harvest weight** | 1.74 | 1.70 | 9.48 | 12.93 | 0.135±0.025 | 0.132±0.011 |
| **Survival** | 0.066 | 0.106 | 1.000 | 1.140 | 0.058±0.026 | 0.093±0.014 |

# Genetic progress




- After 8 generations selection, accumulative genetic progress of WSSV resistance was 29.52%, the average genetic progress of each generation was over 3%; Accumulative genetic progress of growth was 40.45%, the average genetic progress of each generation was over 5%; Accumulative genetic progress of survival was 12.81%, the average genetic progress of each generation was over 1.5%.

# 5. Prediction of breeding value



- We have developed our own automatically computer system of breeding value estimation using BLUP methods.

- Coefficient of consanguinity was set up to strictly control the inbreeding. Inbreeding coefficient was monitored in each generation.

# Comparison testing results by now


中国对虾优良性状鉴定报告

优良性状鉴定报告

• Survival time of “Huanghai 201” after WSSV infection was 172.09h, increased by 30.10% compared with wild population;

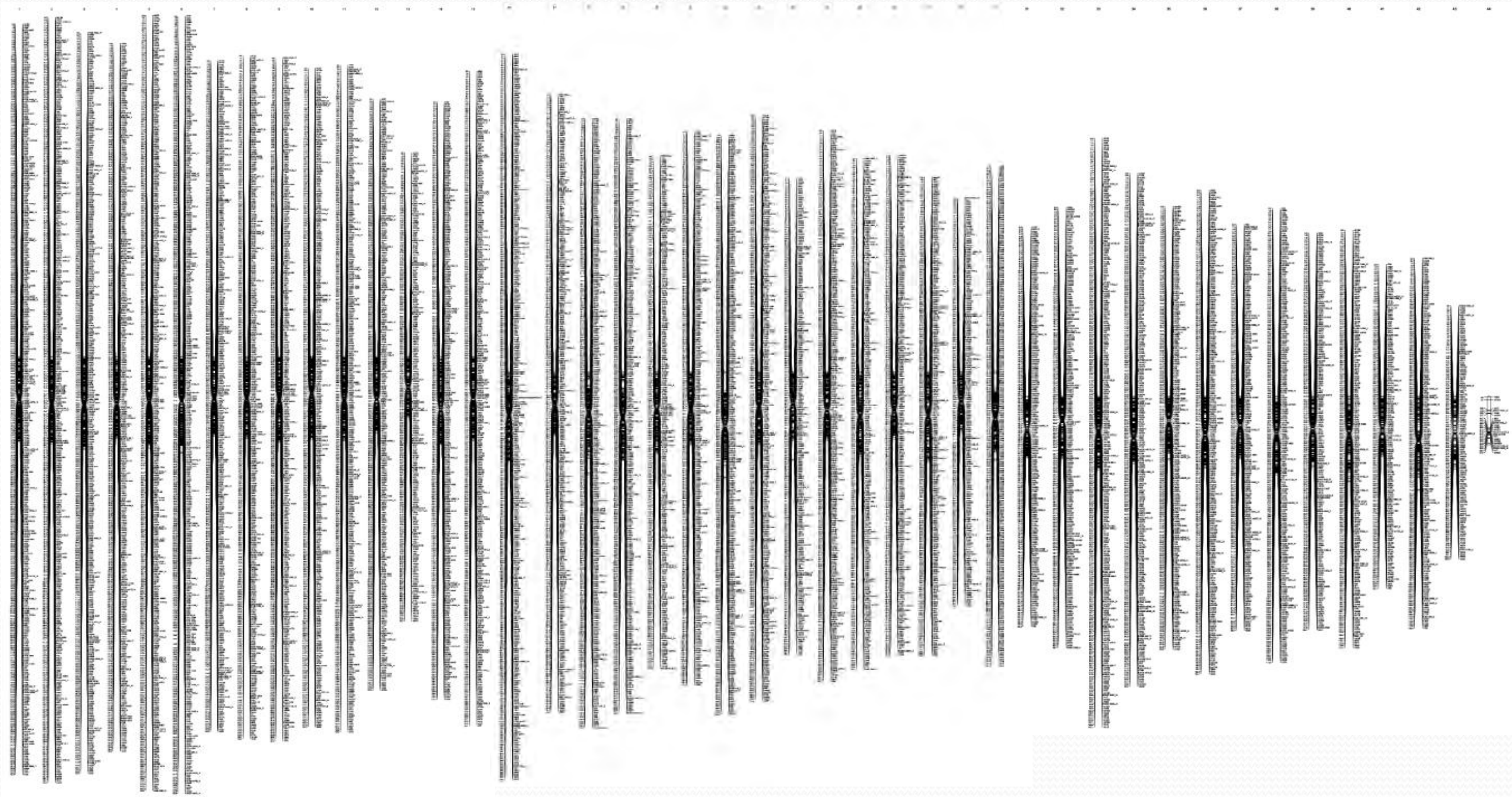
• Harvest weight of “Huanghai 201” was 20.23g, increased by 32.05% compared with wild population;

• Survival of “Huanghai 201” was 86.93%, increased by 13.51% compared with wild population;

# Latest research progress

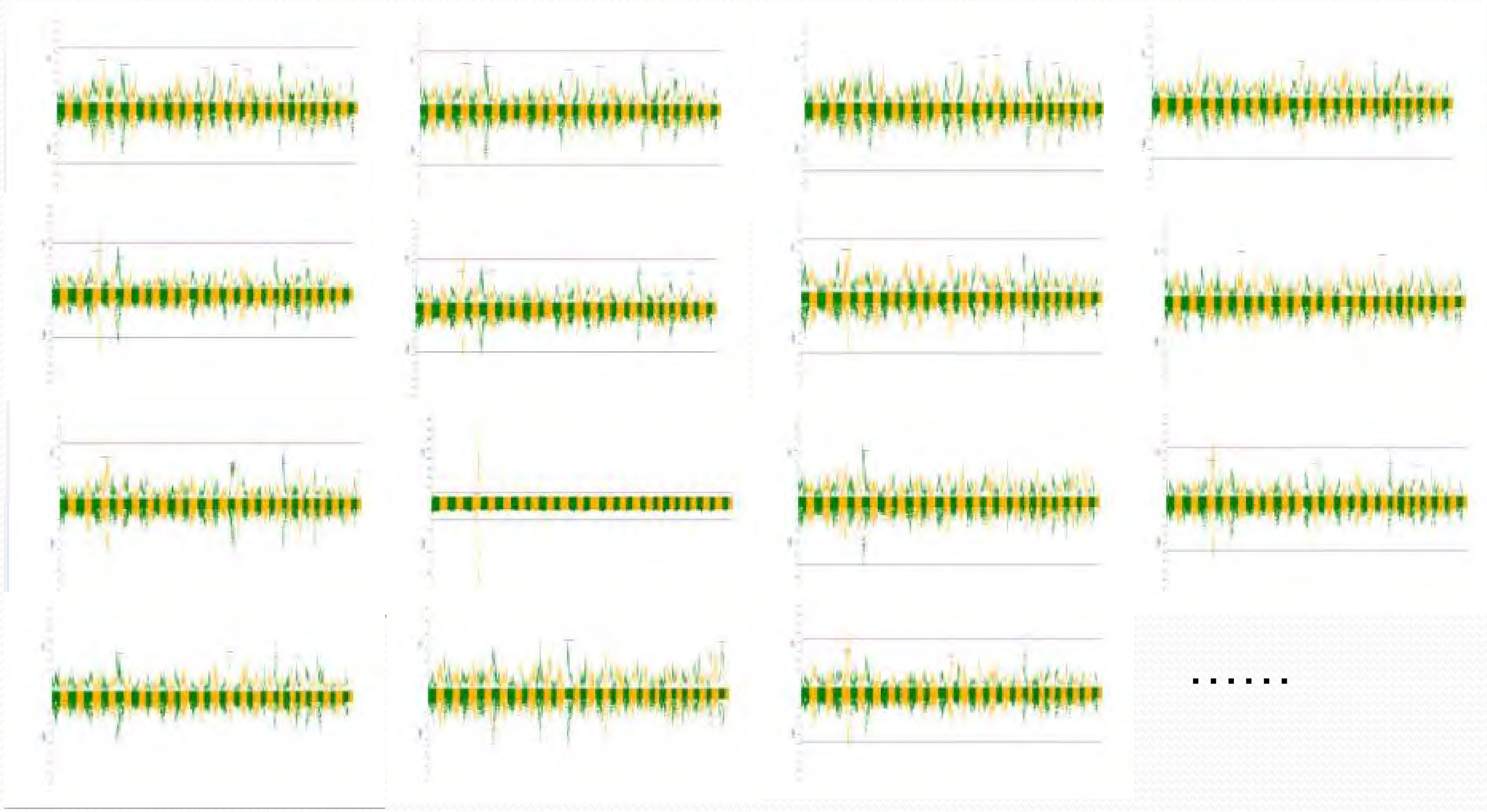
- High-density genetic linkage map using NGS reduced genome sequencing

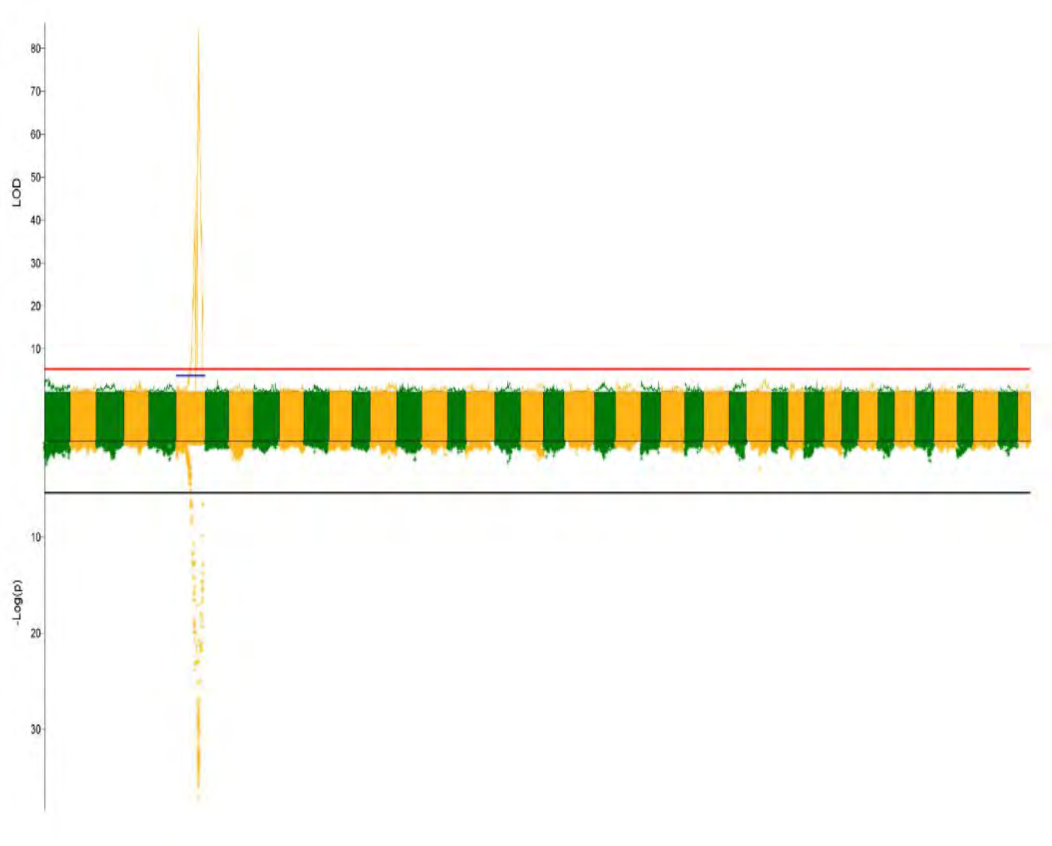
| Parameter | Male-map | Female-map | Integrated-map |
|---|---|---|---|
| Num of SNP | 6509 | 7138 | 12884 |
| Num of linkage group | 44 | 44 | 44 |
| Average marks per linkage group | 147 | 162 | 292 |
| Average marker spacing | 0.58 | 0.72 | 0.41 |
| Average linkage group length | 84.35 | 115.22 | 119.49 |
| Total map length | 3711.41 | 5069.74 | 5257.81 |



High-density linkage map of *F.chinensis*

• Using this map and markers we developed, QTL and GWAS analysis was conducted in 29 main economic trait.






• Variation of sex character was precisely located in linkage groups 6, which explains 75.9% of the variation.

• Totally, 102 QTLs of 28 traits were located in 25 linkage groups, phenotypic variation explained by these loci were between 4.5%~75.9%.

• Results of GWAS were highly consistent with QTL, indicating the reliability.

• Transcriptome sequencing was also used to reveal the genetic basis of WSSV resistance.

• We have obtained the full length cDNA of *FcCBP* and other 12 genes possibly related with WSSV resistance.

• 5 SNPs were confirmed with significant frequency diversity in resistance/sensitve populations.

| SNP locus | Genotype | Population | P |
|---|---|---|---|
| C283-145AG | G/G | R<br>S | 0.008 |
| C364-89AT | A/A | R<br>S | 0.020 |
| C2635-527CA | A/A | R<br>S | 0.025 |
| C12355-592CT | C/T | R<br>S | 0.004 |
| C12355-592CT | C/C | R<br>S | 0.005 |

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Thank you!