

Litopenaeus vannamei 55K Panel

The globally important whiteleg shrimp or Pacific white shrimp, *Litopenaeus vannamei*, is an aquaculture species that would benefit substantially from integration of genomic selection into traditional breeding programs, particularly for disease resistance and low heritability traits.

The research team led by Dr. Kong Jie from Chinese Academy of Fishery Science have sequenced 443 varieties for SNP discovery, which provides a foundation for the Molbreeding GenoBaits 55K shrimp panel design. In this design, total 53,128 SNP sites were targeted, including 3,086 functional sites, such as ammonia tolerance, VpAHPND resistance, WSSV resistance, feed conversion efficiency, harvest weight, etc.. This panel has been validated in different mapping populations and can be used for research work such as analysis of genetic structure and genetic diversity. This 55K panel is also a great tool for genome selection to improve breeding efficiency of disease resistance and select high-quality varieties of *Litopenaeus Vannamei*.

Application

For discovery application

Genetic map construction, genetic diversity analysis, gene/QTL mapping, GWAS analysis, functional gene mapping and cloning.

For breeding services

Variety identification, germplasm resource evaluation and protection, molecular marker-assisted selection, genome-wide selective breeding.

For high-throughput screening

Detection of dominant trait loci, prediction of hybrid combinations, and detection of disease/stress resistance traits.

Trait and resistance related markers and SNP cluster numbers

Markers Contained	SNP Marker Number
Ammonia tolerance related	7
Shrimp white spot syndrome virus (WSSV) resistance	86
Feed conversion efficiency on the transcriptome-DEG	155
Feed conversion efficiency CDS	1,751
Feed conversion efficiency UTR	891
Acute hepatopancreatic necrosis disease associated with <i>Vibrio parahaemolyticus</i> (AHPND) resistance	17
Harvest weight related	77
Morphological traits	102
Framework markers	53,128



Service process



Submit sample
for DNA QC



Library construction
and sequence capture



High-throughput
sequencing



Data quality control and
sequence trimming



Automatic Bioinformatics
analysis on cloud

Report visualization



Figure 1 Distribution of SNP numbers on chromosomes

56,214 SNP markers evenly distributed on prawn chromosome. Due to the prawns genome is of the Scaffold level, there are a large number of scaffolds. In order to better select sites evenly and display the effect, 9 sequences are connected in sequence, 8 of which are about 200M in length.

Definition of ruler: marker region numbers of each sliding window in genome (along a window size of 150000bp)

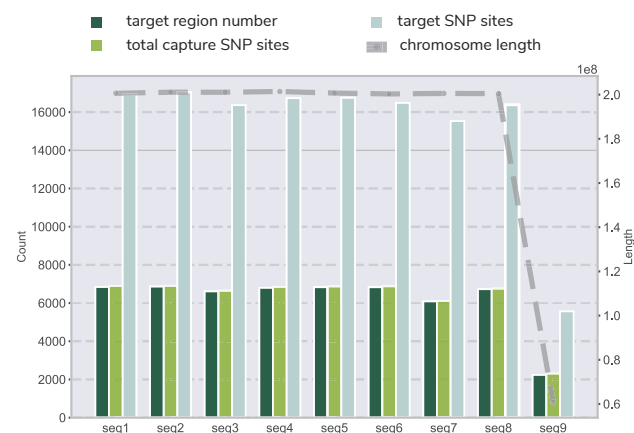


Figure 3 Distribution of SNP regions numbers on chromosome

56,214 SNP markers evenly distributed on each chromosome after splicing, moreover, there are rich mSNP in the regions.

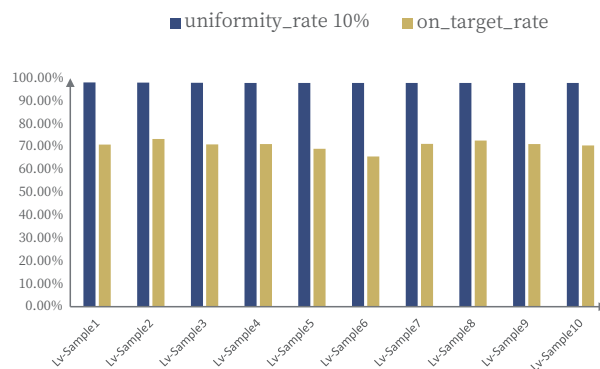


Figure 2 On_target_rate and uniformity_rate 10%

The uniformity_rate 10% were 97.93%-98.17%, on_target_rate were 65.73%-73.39% of 10 test samples by using GenoBaits@Litopenaeus vannamei 55K Panel.

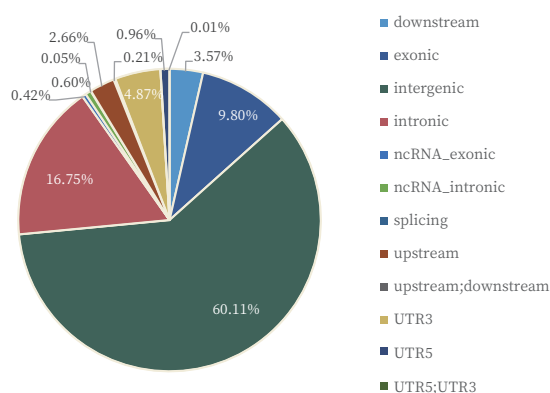


Figure 4 Annotation of the markers

The number of markers in the exonic region of the GenoBaits@Litopenaeus vannamei 55K Panel accounted for 9.80% of all the markers.

Bioinformatics analysis

GBTS Basic analysis

QC and reference sequence comparison: sequencing data QC, reference sequence comparative analysis, sequencing depth and coverage statistics;
Detection and Annotation of the variation loci include SNP, indel, STR/SSR.

Advanced analysis

Phenotypic analysis;
Population genetic study;
Species identification, Species fingerprint construction;
Genome-wide selection;

Genome-wide association study;
Genetic map construction and QTL mapping;
BSA mixed pool sequencing analysis.

According to customer requirements, customized bioinformatics analysis content can be confirmed in the project stage.