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Effects of morphological traits on living body weight of wild *Cyclina sinensis* in different geographical populations

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Abstract

Eleven coastal geographical populations of wild *Cyclina sinensis* in China were collected in February 2020, and the effects of four morphological traits (shell length; shell height; shell width; external ligament length) on one weight trait (living body weight) were studied by correlation analysis, path analysis, determination coefficient analysis, and regression analyses. The statistical results showed that the coefficient of body weight variation was generally greater than morphological traits ($P < 0.05$). The correlation analysis results showed that the coefficient of correlation between morphological traits (except for external ligament length) and body weight are significantly positive ($P < 0.05$) in all populations. Based on the results of path analysis and determination coefficient analysis, shell length has the greatest direct effect on body weight in the Yancheng population; shell height has the greatest direct effect on body weight in Dandong, Fuzhou and Tangshan populations; shell width has the greatest direct effect on body weight in Zhanjiang, Wenzhou, Dongtai, Ningbo, Tianjin, Dongying, and Wanning populations. Multiple regression equations were obtained with body weight as the dependent variable, shell length, height, and width and external ligament length as independent variables. The results of systematic clustering showed that there are no apparent geographical differentiation characteristics among eleven geographical populations in morphology. This study provided a scientific basis for selective and genetic breeding and can guide the development and utilization of wild *C. sinensis* seed resources.

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Introduction

Cyclina sinensis is widely distributed in the north and south coastal areas of China, Japan and North Korea. It has wide adaptability and strong resistance ability and is one of the aquatic shellfish with high commercial and nutrient value (Wei et al., 2022). However, the yield was restricted due to the lack of high quality seeds, the market supply is still dominated by fishing wild *C. sinensis* in some areas of China. In order to meet the market demand, it is urgent to develop high-quality and large scale seeds.

Wild populations are necessary original germplasm resources, and developing wild populations that have rich variation can cultivate superior varieties (Seker et al., 2004). There are abundant geographical populations of *C. sinensis* in coastal areas in China, and the wild *C. sinensis* populations in coastal China have extensive genetic diversity, which provides adequate genetic variation resources for *C. sinensis* to conduct extensive selective breeding (Yuan et al., 2008). Production activities select populations with stable traits, but selective breeding selects populations with high phenotypic and genetic variation. A highly varied population is more likely to breed offspring with desired traits.

Shell morphological traits and weight traits of shellfish are the main contents of genetic and selective breeding research. Studies have shown a significant correlation between shell morphological traits and the weight traits of shellfish. Therefore, individual weight can be judged by shell morphological traits. For example, three selective generations diversity studies were conducted in the *Meterix meretrix* based on shell height (SH), and living body weight (BW) was used as the selection indicators. The results showed a clear genetic correlation between SH and BW (Ibraar et al., 1999). A study of reciprocal hybrid abalone showed that the correlation of coefficient (COR) morphological traits and BW were positive (Luo et al., 2013). Another study showed that SH has the greatest direct effect on BW in the yesso scallop *Patinopecten yessoensis* (Chang et al., 2008), and shell thickness and shell length (SL) are the significant factors affecting BW in different specifications *Mercenaria Mercenaria* (Song et al., 2010). Weight traits of shellfish are directly related to yield and individuals with stable body weight can significantly increase the total yield (Zou et al., 2020). Due to the strong correlation between morphological traits and BW and morphological traits of shellfish that are more intuitive than weight traits, it is of great significance to guide selective breeding to give full play to these advantages (Du et al., 2017). A study on the different geographical populations of *Paphia textile* showed that major shell morphological traits affecting software quality differ in three geographical populations. The results provided an essential reference for artificial breeding (Yi et al., 2022). Research about *Volutharpa ampullacea* showed that shell width (SW) is the primary morphological trait when considering BW as the target trait for selective breeding (Han et al., 2021). Therefore, studying the relationship between morphological traits and target traits of shellfish, especially the target traits that can determine the economic value, is critical.

Selective breeding can effectively improve the yield of aquatic products, and the application of statistical theory to selective breeding can optimize breeding strategies (Chen et al., 2021). These theories have been applied and achieved some results in the selective breeding of a variety of marine organisms. Path analysis splits the COR into direct path coefficient and indirect path coefficient and can analyze the degree of effect respective independent variables have on dependent variables. Correlation analysis can determine the degree of correlation between the two variables. Path analysis was used to study the effect of the measurable traits on adductor muscle weight in three *Argopecten irradians* populations. The results showed that the effect of the morphological traits on adductor muscle weight varied significantly (Sun et al., 2017). Correlation analysis and path analysis were used to study the

effect of morphological traits on BW in two kinds of shell color *M. meretrix*, and the results showed that SH and SW are the main factors in determining the black blotching *M. meretrix* BW, and SL is the main factor in determining the BW of red color *M. meretrix* (Fang et al., 2017). Wang studied the effect of the morphological traits of *Ruditapes philippinarum* in different geographical populations on BW by path analysis. The results provided an essential scientific basis for morphological identification, germplasm resource analysis, and genetic breeding research (Wang et al., 2022).

In this study, we aim to: (1) explore the variation degree of morphological traits and BW in different populations; (2) determine the degree of correlation among traits in each population; (3) find out the morphological traits with the most significant direct effect on BW in each population to facilitate the parental selection of breeding and optimize the breeding strategies. We applied statistical methods such as path analysis, correlation analysis, determination coefficient analysis, and regression analysis for these aims. Our study provided a scientific basis for selective breeding, genetic breeding, and developing original germplasm resources of wild *C. sinensis*.

Materials and Methods

Experimental Materials

Eleven geographical populations of wild *C. sinensis* were collected from the coastal areas of China in February 2020, including Guangdong Zhanjiang (ZJ), Zhejiang Wenzhou (WZ), Jiangsu Dongtai (DT), Zhejiang Ningbo (NB), Jiangsu Yancheng (YC), Liaoning Dandong (DD), Tianjin(TJ), Shandong Dongying (DY), Fujian Fuzhou(FZ), Hebei Tangshan(TS), Hainan Wanning (WN) populations (**Figure 1**). Thirty individuals were randomly selected for morphological traits and BW measurement from each geographical population.

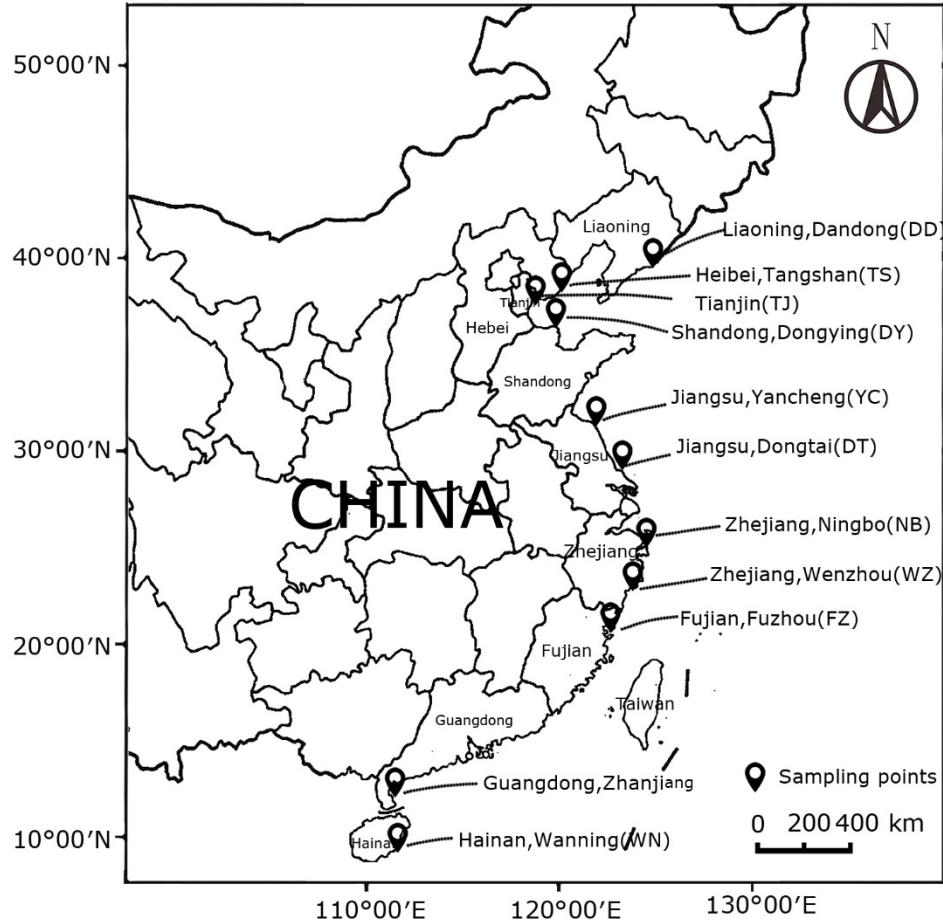


Figure1 Sampling locations of 11 different geographical populations of *C. sinensis*

Experimental Methods

Remove the adhesion of the samples surface and blot the moisture. BW was measured with an electronic balance (accuracy, 0.01g). Four morphological traits (SL; SH; SW; external ligament length, EL) were measured with a digital vernier caliper (accuracy, 0.01mm). The specific method of measurement is as follow (**Figure 2**):

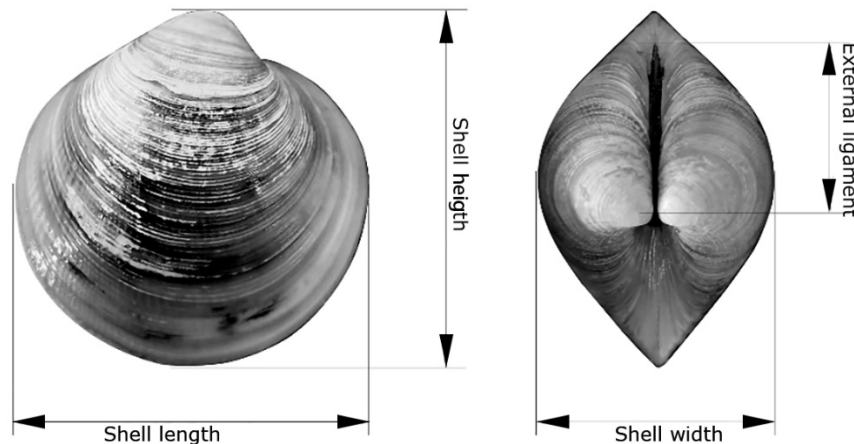


Figure 2 Schematic representation of *C. sinensis* morphological traits

Statistical Analysis

The parameters of morphological traits and BW were recorded, and the coefficient of variation (CV) was calculated by Excel 2016 software. Correlation, path, and coefficient of determination analysis were executed by SPSS 26.0 software and established multiple regression equations by regression analysis. The function "scale" of R software (R version 4.2.1) is used to normalize the data composed of the mean values morphological traits and BW, the function "dist" calculates the Euclidean distance, the function "hclust" performed cluster analysis, and the function "plot" plotted the cluster model graph. Significance was set at $P < 0.05$. The detailed calculation formulas are as follow:

$$CV = \frac{S}{X} \times 100\%$$

where CV is correlation coefficient, S is sample standard deviation, X is sample mean value

$$r_{xy} = \frac{\sum_{i=1}^n (x_i - \bar{x}) \sum_{i=1}^n (y_i - \bar{y})}{\sqrt{\sum_{i=1}^n (x_i - \bar{x})^2 \sum_{i=1}^n (y_i - \bar{y})^2}}$$

where r_{xy} indicates the coefficient of correlation between the two traits

$$P_i = b_{xi} \times \frac{\sigma_{xi}}{\sigma_y}$$

where P_i indicates the direct path coefficient, b_{xi} is the regression coefficient of independent variables, σ_{xi} is the standard deviation of independent variables, σ_y is the standard deviation of dependent variable

$$P_{ij} = r_{ij} P_{iy}$$

where P_{ij} indicates the indirect path coefficient, r_{ij} is the correlation coefficient between the two traits, P_{iy} is the direct path coefficient of independent variable x_i to dependent variable y

$$d_i = P_i^2$$

where d_i is the determination coefficient of single trait on BW.

$$d_{ij} = 2r_{ij} \times P_i \times P_j$$

where d_{ij} is the co-determination coefficient between the two morphological traits.

Results

The Parameters and CVs of Morphological Traits and BW

The ranges of the CVs for between SL, SH, SW and EL in eleven geographical populations are 0.035~0.087, 0.052~0.089, 0.043~0.089, 0.087~0.137 respectively (**Table 1**). The range of CVs for BW in all populations is 0.117~0.211. The results showed that the CVs of BW are generally greater than morphological traits ($P < 0.05$).

Table 1 Statistical parameters and coefficients of variation of morphological traits and BW¹

Pop ²	SL/cm	SH/cm	SW/cm	EL/cm	BW/g
ZJ	3.053±0.266 (0.087)	3.113±0.257 (0.082)	1.881±0.167 (0.089)	1.258±0.160 (0.127)	9.085±1.818 (0.200)
WZ	3.103±0.158 (0.051)	3.141±0.190 (0.061)	1.996±0.097 (0.049)	1.312±0.118 (0.090)	10.485±1.486 (0.142)
DT	3.552±0.221 (0.062)	3.624±0.213 (0.059)	2.090±0.153 (0.073)	1.418±0.167 (0.118)	15.648±3.233 (0.207)
NB	3.401±0.204 (0.060)	3.462±0.182 (0.052)	2.074±0.116 (0.056)	1.431±0.146 (0.102)	12.758±1.879 (0.147)
YC	3.024±0.181 (0.06)	2.919±0.260 (0.089)	1.849±0.079 (0.043)	1.278±0.176 (0.137)	9.012±1.345 (0.149)
DD	3.237±0.246 (0.076)	3.19±0.268 (0.084)	1.955±0.131 (0.067)	1.331±0.168 (0.126)	10.102±2.053 (0.203)
TJ	3.152±0.150 (0.048)	3.094±0.183 (0.059)	1.856±0.097 (0.052)	1.264±0.110 (0.087)	9.293±1.385 (0.149)
FZ	3.234±0.114 (0.035)	3.198±0.189 (0.059)	2.056±0.089 (0.043)	1.456±0.151 (0.103)	11.365±1.326 (0.117)
DY	3.077±0.188 (0.061)	3.035±0.211 (0.070)	1.872±0.111 (0.059)	1.279±0.157 (0.123)	8.844±1.497 (0.169)
TS	3.721±0.227 (0.061)	3.693±0.227 (0.062)	2.353±0.190 (0.081)	1.48±0.166 (0.112)	17.154±3.611 (0.211)
WN	3.784±0.158 (0.042)	3.639±0.197 (0.054)	2.147±0.132 (0.061)	1.422±0.166 (0.117)	15.171±2.154 (0.142)

¹ Data are presented as "mean ± SD", CVs are shown in "()"

² Pop: populations

Correlation analysis among the traits

Morphological traits and BW of *C. sinensis* were tested by Shapiro-Wilk normality test and the results obeys normal distribution. The CORs among the traits are positive and generally

reached significant level ($P < 0.05$) (**Figure 3**). The minimum of COR is 0.150 between SL and SW in FZ population, and the maximum of COR is 0.957 between SW and BW in DT population. Non-significant CORs were mostly related to EL.

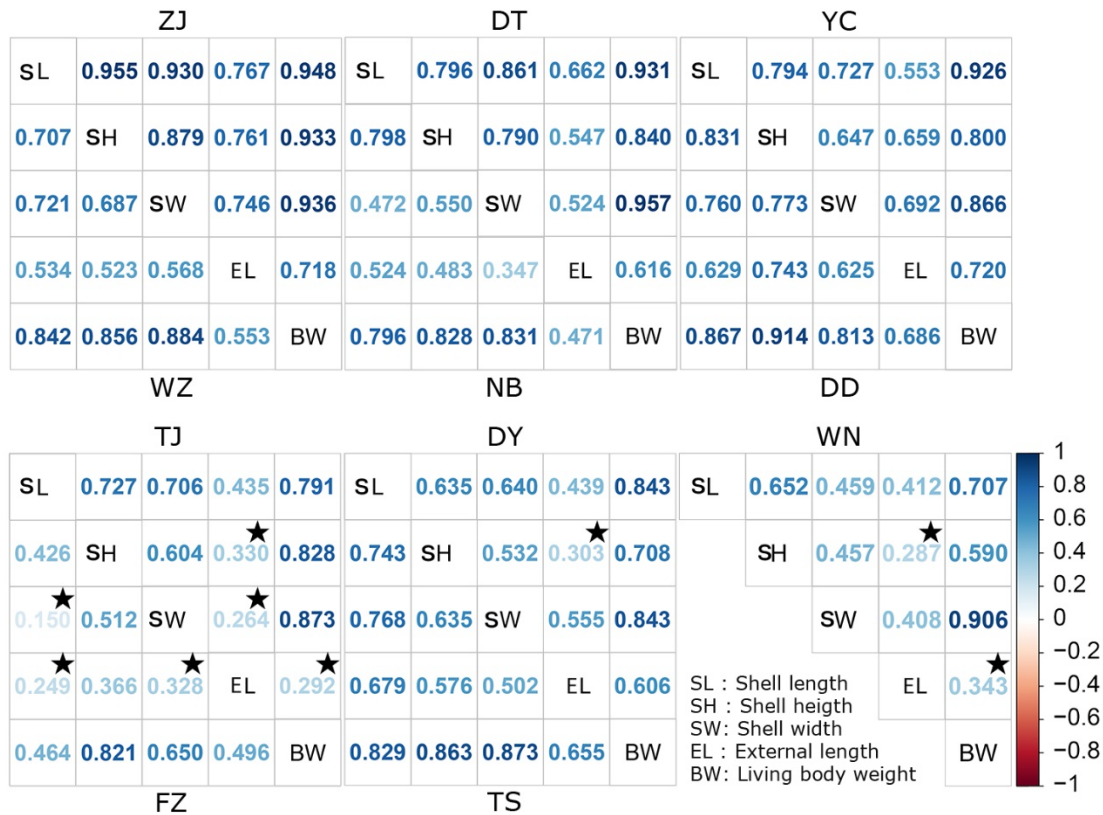


Figure 3 Correlation coefficients among the traits*

* The upper triangle represents the CORs for the population shown in the top text, the lower triangle represents the CORs for the population shown in the bottom text; numbers indicate the CORs between the traits shown by the horizontal and vertical letters; the color depth of the numbers indicates the degree of the correlation; with "★" indicates the insignificant CORs between the two traits.

Path Analysis between Morphological Traits and BW

Path analysis was conducted by taking the SL, SH, SW and EL as independent variables and BW as dependent variable (**Table 2**). The SL has the greatest direct effect on BW in YC population; the SH has the greatest direct effect in DD and FZ populations; the SW has the greatest direct effect in ZJ, WZ, DT, NB, TJ, DY, TS and WN populations. EL has negative effect on BW in ZJ, WZ, NB, DD, TJ and WN populations and only have significant positive effect in YC population. EL has positive effect on BW in DT, FZ, DY and TS populations, but the effect is slight. The largest value of indirect effect was produced by SL through SW in DT population (0.486), while the smallest value was produced by SL and SH through EL in ZJ population (-0.065).

Table 2 Effects of morphological traits on BW

Pop ¹	Trait	PC ²	Indirect PC				Σ
			SL	SH	SW	EL	
ZJ	SL	0.241		0.361	0.411	-0.065	0.948
	SH	0.378*	0.230		0.389	-0.065	0.932
	SW	0.442*	0.224	0.332		-0.063	0.935
	EL	-0.085	0.185	0.288	0.330		0.717
WZ	SL	0.273*		0.264	0.330	-0.026	0.842
	SH	0.374*	0.193		0.315	-0.025	0.857
	SW	0.458*	0.197	0.257		-0.027	0.885
	EL	-0.048	0.146	0.195	0.260		0.553
DT	SL	0.330*		0.085	0.486	0.028	0.930
	SH	0.107	0.263		0.446	0.024	0.840
	SW	0.565*	0.284	0.085		0.023	0.956
	EL	0.043	0.218	0.059	0.297		0.617
NB	SL	0.335*		0.226	0.248	-0.013	0.796
	SH	0.283*	0.267		0.289	-0.012	0.828
	SW	0.526*	0.158	0.156		-0.009	0.831
	EL	-0.025	0.175	0.137	0.183		0.470
YC	SL	0.600*		0.013	0.220	0.093	0.926
	SH	0.016	0.477		0.196	0.111	0.799
	SW	0.303*	0.436	0.010		0.116	0.866
	EL	0.168*	0.331	0.011	0.210		0.720
DD	SL	0.276*		0.458	0.140	-0.008	0.867
	SH	0.551*	0.230		0.142	-0.009	0.914
	SW	0.184	0.210	0.426		-0.008	0.812
	EL	-0.012	0.174	0.409	0.115		0.686
TJ	SL	0.111		0.315	0.384	-0.019	0.792

	SH	0.433*	0.081		0.329	-0.014	0.828
	SW	0.544*	0.078	0.262		-0.011	0.873
	EL	-0.043	0.048	0.143	0.143		0.291
	SL	0.145		0.234	0.044	0.040	0.463
FZ	SH	0.550*	0.062		0.150	0.059	0.821
	SW	0.293*	0.022	0.281		0.053	0.649
	EL	0.162	0.036	0.201	0.096		0.496
	SL	0.394*		0.126	0.256	0.066	0.843
DY	SH	0.199*	0.250		0.213	0.046	0.709
	SW	0.401*	0.252	0.106		0.084	0.843
	EL	0.151	0.173	0.060	0.223		0.607
	SL	0.007		0.342	0.393	0.088	0.829
TS	SH	0.460*	0.005		0.324	0.074	0.864
	SW	0.511*	0.005	0.292		0.065	0.873
	EL	0.129	0.005	0.265	0.256		0.655
	SL	0.401*		0.010	0.355	-0.058	0.708
WN	SH	0.015	0.262		0.354	-0.041	0.590
	SW	0.774*	0.184	0.007		-0.058	0.907
	EL	-0.142*	0.165	0.004	0.316		0.343

¹ Pop: populations;

² PC: path coefficient; with "*" indicates significance reached significant level ($P < 0.05$)

Determination Coefficient Analysis Morphological Traits on BW

The results (**Table 3**) showed that the highest determination coefficients of morphological traits on BW were SH (0.360, YC), SH (0.304, DD), SW (0.599, WN) and EL (0.028, YC) respectively. Including both determination coefficients and co-determination coefficients, the maximum of determination coefficients in the ZJ, WZ, DT, DY and TS populations appeared in the co-determination coefficients, which indicates that the joint effect of two traits has a greater degree of relative determination on BW than that of a single trait in some populations.

Table 3 The determination coefficient of morphological traits on BW

Pop ¹	Trait	DC ²	Co-DC ³						Σ	CI(R ²) ⁴
			SL-SH	SL-SW	SL-EL	SH-SW	SH-EL	SW-EL		
ZJ	SL	0.058								
	SH	0.143								
	SW	0.195	0.174	0.198	-0.031	0.294	-0.049	-0.056	0.933	0.933
	EL	0.007								
WZ	SL	0.075								
	SH	0.140								
	SW	0.210	0.144	0.180	-0.014	0.235	-0.019	-0.025	0.929	0.929
	EL	0.002								
DT	SL	0.109								
	SH	0.011								
	SW	0.319	0.056	0.321	0.019	0.096	0.005	0.025	0.964	0.964
	EL	0.002								
NB	SL	0.112								
	SH	0.080								
	SW	0.277	0.151	0.166	-0.009	0.164	-0.007	-0.009	0.926	0.926
	EL	0.001								
YC	SL	0.360								
	SH	0.000								
	SW	0.092	0.015	0.264	0.111	0.006	0.004	0.070	0.951	0.951
	EL	0.028								
DD	SL	0.076								
	SH	0.304								
	SW	0.034	0.253	0.077	-0.004	0.157	-0.010	-0.003	0.884	0.884
	EL	0.000								
TJ	SL	0.012								
	SH	0.187								
	SW	0.296	0.070	0.085	-0.004	0.285	-0.012	-0.012	0.909	0.909
	EL	0.002								
FZ	SL	0.021	0.068	0.013	0.012	0.165	0.065	0.031	0.789	0.789

	SH	0.303								
	SW	0.086								
	EL	0.026								
	SL	0.155								
DY	SH	0.040	0.100	0.202	0.052	0.085	0.018	0.067	0.903	0.903
	SW	0.161								
	EL	0.023								
	SL	0.000								
TS	SH	0.212	0.005	0.005	0.001	0.298	0.068	0.066	0.934	0.934
	SW	0.261								
	EL	0.017								
	SL	0.161								
WN	SH	0.000	0.008	0.285	-0.047	0.007	-0.001	-0.090	0.942	0.942
	SW	0.599								
	EL	0.020								

¹ Pop: populations

² DC: determination coefficient

³ Co-DC: co-determination coefficient

⁴ CI(R²): correlation indices

Multiple Regression Equations of Morphological Traits Relative to BW

The optimal multiple regression equations (**Table 4**) were established by taking BW as the dependent variable, SL, SH, SW, and EL as the independent variables, and excluded morphological traits with insignificant bias regression coefficients. The results of multiple regression analysis showed a significant linear relationship between the independent variable and the dependent variables in different populations, indicating that the regression equations can commendably explain the quantitative relationship between morphological traits relative to BW.

Table 4 The optimal regression equations of morphological traits relative to BW

Pop ¹	Optimal regression equations	R ²
ZJ	BW=-11.134+3.952SL+4.335SW	0.915
WZ	BW=-19.764+2.496SL+2.853SH+6.788SW	0.918
DT	BW=-32.422+6.054SL+12.71SW	0.956
NB	BW=-25.036+2.999SL+3.892SH+8.48SW	0.918
YC	BW=-15.898+4.542SL+5.122SW+1.333EL	0.947

DD	$BW = -14.545 + 2.881SL + 4.802SH$	0.864
TJ	$BW = -17.296 + 3.59SH + 8.34SW$	0.898
FZ	$BW = -13.076 + 4.648SH + 4.657SW$	0.727
DY	$BW = -17.532 + 3.348SL + 1.348SH + 6.4SW$	0.874
TS	$BW = -37.611 + 8.238SH + 10.345SW$	0.916
WN	$BW = -30.616 + 5.584SL + 12.71SW - 1.853EL$	0.938

¹ Pop: populations

Systematic Clustering among Different Geographical Populations

Systematic clustering was established by standardizing the mean values of morphological traits and BW (**Figure 4**). WZ, DD, YC, TJ, ZJ, and DY populations were gathered into a category, and NB, FZ, TS, DT, and WN populations were gathered into another category. The results of systematic clustering analysis showed no obvious geographical differentiation characteristics among eleven populations. The north and south geographical populations cluster alternately.

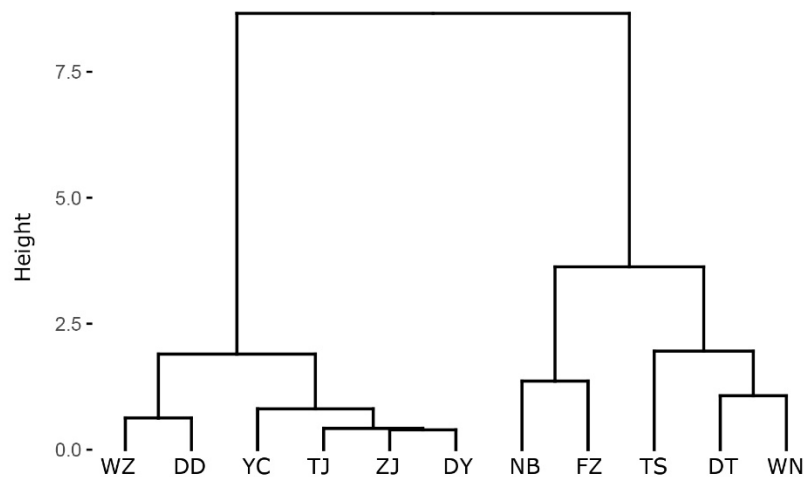


Fig.4 Systematic clustering among different geographical populations of *C. sinensis*

Discussion

Significance of The Morphological Traits and BW Variation for Selective Breeding

Selective breeding is selecting individuals with target traits as parents from populations or families to obtain offspring with stable target traits (Sun et al., 2022). Selective breeding requires determining the extent to which genetic factors and ensuring such traits determine morphological trait variation can stably be inherited (Boudry., 2009). The target traits with a

high CV meaning have the abundant genetic diversity to conduct selective breeding (Gjedrem et al., 2009). In this study, the CV of BW ranged from 0.117 to 0.211. Except for the ZJ population, the CV of BW in northern populations (DD, TJ, TS, DY, YC, DT) was generally larger than in southern populations (NB, WZ, FZ, WN), northern populations have a higher selection potential in BW. Similarly, northern populations were generally larger than southern populations in various morphological traits. The southern populations had a more stable phenotype, and the northern populations had a higher potential of selection.

Phenotypic traits are the comprehensive action process that can be summarized as "Natural Selection-Microevolution-Heritability" (Liu et al., 2021). Due to differences in genetic effects and living environment, even if the same species, there will be significant differences in morphology and BW. Morphological traits and BW as quantitative traits are poly genetically controlled, so weight traits and morphological traits also mutually influence (Li et al., 2022, Zhai et al., 2022, Yu et al., 2022). In this study, the eleven geographical populations span a wide range of latitudes (21°20') and greatly differ in the living environment. There is a rich genetic diversity among different populations (Lou et al., 2012), which may be the reason for the large fluctuations in the variation of morphological traits and BW. ZJ population showed a higher CV in morphological traits (SL, 0.087; SH, 0.082; SW, 0.089; EL, 0.127) and BW (0.200) than other populations the ZJ population is the population with the greatest potential for selective breeding among the eleven populations.

The major morphological traits affecting BW

In shell morphological traits of shellfish, SL, SH, and SW are the most important morphological indicators (Guo et al., 2013). In this study, the CORs between SL, SH, SW and BW all reached significant levels ($P < 0.05$) in all populations. However, Dong (Dong et al., 2011) pointed out that the CORs indicate the total effect of a single trait on BW. Only analyzing the simple CORs between morphological traits and BW cannot indicate the degree of effect of a single trait on BW. Comprehensive analysis of the direct effect of a single trait and the indirect effect of a single trait through other traits can improve the reliability of the research results. The path coefficient is an important parameter that reflects the direct and indirect effects of the independent variables on the dependent variable. In this study, the results of path analysis showed that not all morphological traits can exert significant direct effects on BW, but SL, SH, and SW were still the main traits affecting BW. SL has the greatest direct effect (0.600) on BW in the YC population; SH has the greatest direct effect on BW in DD (0.551) and FZ (0.550) populations; SW has the greatest direct effect on BW in ZJ (0.422), WZ (0.458), DT (0.565), NB (0.526), TJ (0.544), DY (0.401), TS (0.511) and WN (0.744) populations. EL only has a significant positive direct effect on BW in the YC population (0.168), while it has a negative effect on BW of partial populations.

The coefficient of determination indicates the relative degree to which the cause determines the outcome. In the study of path analysis, the sum of the coefficients of determination ≥ 0.850 is an important criterion for determining the main influencing factors (Liu et al., 2004). Among the eleven geographical populations, the total coefficient of determination of the FZ population is less than 0.85 (0.789), and the total coefficient of determination of other populations is greater than 0.85. Furthermore, the determination coefficient of EL is very slight or negative in all populations; SL, SH, and SW are still the main factors affecting BW.

The quantitative relationship between morphological traits and BW and a cluster of population characteristics

To establish the multiple regression equations, it is necessary to exclude the traits with insignificant partial regression coefficients and the traits of the variance expansion factor (VIF) greater than 10 in the results of the collinearity analysis. The optimal multiple regression equations were obtained by the stepwise method. There was a significant linear relationship between the retained traits and BW, indicating that the regression equations can better explain the quantitative relationship between morphological traits and BW and reliably predict BW. In addition, the cluster analysis results showed no geographical difference within the clusters divided into two clusters in morphology. This may be because 11 populations belong to the same species and the breeding and harvesting of wild *C. sinensis* and the disorderly exchange of seeds to cause germplasm mixing (Yao et al., 2007).

Conclusion

The selection of breeding parents directly affects the quality of the seeds. The larger CV of BW in the shellfish populations, the greater the potential of breeding parental selection. The intuitively selectable characteristics of morphological traits and the significant correlation relationship between morphological traits and BW is helpful for the selection of breeding parents. Due to there is a difference the main morphological traits affecting BW in different populations, selective breeding needs to focus on the morphological traits with the largest effect on BW. For selective breeding of ZJ, WZ, DT, NB, TJ, DY, TS and WN populations, SW should be selected as the main morphological trait; SH should be selected as the main morphological trait for DD and FZ populations; SL should be selected as the main morphological trait for YC population. ZJ population showed high CV in SL(No.1), SH(No.3), SW(No.1), EL(No.2), BW(No.4), which may be the population with the most selective potential.

With the continuous development of the aquaculture industry, high-quality seeds with excellent and stable traits are essential for selective breeding, and wild populations with high genetic diversity are highly valuable for selective breeding. Through statistical methods, this study provides a certain scientific basis for morphological discrimination, genetic and selective breeding research and development of primitive germplasm resources of wild *C. sinensis* geographical populations.

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