Genetic Analysis of Cultured and Wild Populations of *Mytilus coruscus* Based on Mitochondrial DNA

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**Abstract**: DNA sequences from the mitochondrial gene cytochrome oxidase subunit I (mtDNA COI) were used to estimate the genetic variability in two wild populations and two cultured populations of the hard shelled mussel, *Mytilus coruscus*. Thirty haplotypes were identified in the four populations. The cultured populations exhibited a lower number of haplotypes and genetic diversity than those of the wild populations, suggesting that a small number of effective founding breeders contributed to the genetic variation of the cultured populations. No significant differentiation was observed between the cultured population and local wild population, implying that persistent gene flow occurred in these populations. This genetic survey is intended as a baseline for future genetic monitoring of *M. coruscus* aquaculture stocks.

**Key words**: *Mytilus coruscus*; Population differentiation; Genetic diversity; mtDNA COI gene

厚壳贻贝养殖群体与野生群体线粒体 DNA 的遗传分析

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摘要：采用线粒体 DNA COI 基因序列对厚壳贻贝 2 个养殖群体与 2 个野生群体的遗传多样性进行了研究。4 个群体共获得 30 个单倍型。结果显示：在养殖群体中单倍型的数量和遗传多样性要比野生群体的低，可能是由于只有少量的有效父母本对养殖群体的遗传变异有贡献所致。养殖群体与当地野生群体之间也未发生显著的遗传分化，可能是因为它们之间存在基因交流。在今后厚壳贻贝养殖过程中，本研究可以用在对养殖群体进行遗传监测，从而保证养殖群体的遗传多样性水平。

关键词：厚壳贻贝；群体分化；遗传多样性；线粒体 DNA COI 基因

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厚壳贻贝，*Mytilus coruscus*，是一种经济上很重要的贝类，分布广泛于中国、日本和韩国（Wang, 1997）。它是中国特有物种，主要分布在大连至厦门之间。目前，*M. coruscus*的养殖主要集中在少数地区。由于自然群体的减少以及过度捕捞，自然群体的遗传多样性也在逐渐降低。因此，寻找有效的繁殖方法以增加养殖群体的遗传多样性是非常重要的。

The hard shelled mussel, *Mytilus coruscus*, is an economically important mussel which is widely distributed from coast of China, Japan, and Korea (Wang, 1997). It is documented that this species occurred from Dalian to Xiamen in China. The culture of *M. coruscus* has been carried out in only a few regions of China in the past decades. The cultured juveniles mainly originated from the collection of natural populations. In recent years, natural juveniles have decreased while mussel farmers have increased. Due to overexploitation, most mussel stocks have dramatically declined. Therefore, it is very important to obtain juveniles that are produced by artificial breeding to increase the juvenile population.
programs must be implemented to preserve genetic variability, and prevent inbreeding depression. However, for such programs to be successful, information on the genetic relationships among cultured and wild populations is essential.

Mitochondrial DNA has been used extensively for studies in molecular ecology (Avise, 2000). In comparison to allozyme or nuclear DNA, the higher mutation rate, smaller effective population size is expected to provide greater power to identify population structure. Additionally, mtDNA gives a better estimate of genetic differentiation than nuclear markers since it is approximately fourfold more sensitive to genetic drift and founder effects (Birky et al, 1983). Mitochondrial Cytochrome Oxidase I gene (mtCOI) has been used widely in marine species, such as Tegillarca granosa (Zheng et al, 2009), due to adequate levels of variability and easy amplification via universal primers (Folmer et al, 1994).

In this study, we used the mitochondrial Cytochrome Oxidase I gene (mtCOI) to describe the genetic variability of two cultured, and two wild populations and also to quantify the genetic differentiation between them.

1 Materials and Methods

1.1 Samples

Specimens of M. coruscus obtained from both cultured and natural populations are listed in Tab. 1 and Fig. 1. The two wild populations were randomly sampled by divers from the subtidal zone of Shengsi and Lianjiang in 2007, respectively (coded WSS and WLJ). The two cultured populations were of Shengshan (coded CSS) and Huaniao (coded CHN), and also collected in 2007. The CSS population was collected from the cultured area of M. coruscus. In this area, the aquaculture practice had been carried out for three decades. A large number of the natural spat collected were commonly reared. The CHN population hatchery stock was the first-generation of offspring produced in spring 2005 using hundreds of wild caught M. coruscus in Shengsi (exact numbers not documented). Gill tissues were obtained and stored in 100% ethanol at room temperature until DNA extraction.

| Origin | Site | Abbreviation | Longitude | Latitude | Year |
|--------|------|--------------|-----------|----------|------|
| Wild   | Shengsi | WSS            | 122°41’   | 30°51’   | 2007-11 |
| Wild   | Lianjiang | WLJ           | 119°53’   | 26°02’   | 2007-05 |
| Cultured | Huaniao | CHN            | 122°40’   | 30°52’   | 2007-05 |
| Cultured | Shengshan | CSS            | 122°48’   | 30°43’   | 2007-05 |

1.2 Extraction of DNA

Genomic DNA was isolated from gill using the standard proteinase K digestion and phenol/chloroform extraction procedures described by Shen et al (2006). DNA quality was assessed by running samples on 1% agarose gels, and DNA concentration was measured with an UV/visible spectrophotometer (Eppendorf AG 22331 Hamburg) for absorption at 260 nm. DNA was diluted to 50 ng/μL for polymerase chain reaction (PCR) amplifications.

1.3 Amplification of DNA and sequencing

PCR was carried out in 50μL reactions containing 100 ng DNA sample, 5μL 10×PCR buffer, 2.0 μmol/L MgCl₂, 200μmol/L dNTPs, 0.2 μmol/L primer, 1 U Taq polymerase. A pair of universal primers was used in this study (forward primer LCO1490: 5'-GGTCAACAAATCATAAAGATTTG-3'; reversal primer HCO2198: 5'-TAAACTTCAGGGTGACCAAAAAATCA-3'(Folmer et al, 1994). PCR was performed using the Eppendorf PCR system programmed for an initial denaturation step of 3 min at 94°C followed by 35 cycles, each consisting of 94°C denaturation for 50 second, 48°C annealing for 50 second and 72°C extension for 1 min. A final extension of 10 min was performed at 72°C and the PCR products were then held indefinitely at 4°C. A negative control, consisting of all the reaction components except template DNA, was also included for each of amplification.

PCR products were visualized using 1.5% agarose gel stained with ethidium bromide. All amplified products were purified using TIANquick Midi Purification Kit (Tiangen, China). Purified PCR products were directly sequenced in both directions using the PCR primers on an Applied Biosystems ABI 3730 DNA sequencer.

1.4 Data analysis

For all sequence analyses, sequences were aligned with BioEdit Sequence Alignment Editor version 7.0.9
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Fig. 1  Sample locations of two wild and two cultured *Mytilus coruscus* (Hall, 1999) and saved in the Fasta format. The identical haplotypes in the aligned matrix were identified and collapsed using COLLAPSE version 1.2 (Posada, 2006). Nucleotide composition was computed in MEGA version 4.0 (Tamura et al, 2007). Genetic diversity among wild and cultivated populations was estimated using haplotype number \( N \), gene diversity \( h \), and nucleotide diversity \( \pi \) as implemented in DnaSP version 4.0 (Rozas et al, 2003). Gene diversity was calculated according to Nei (1987), using the probability that two randomly chosen haplotypes of the sample are different. Nucleotide diversity was also computed according to Nei (1987), as the probability that two randomly chosen homologous sites are different. Genetic diversity was compared between farmed and wild populations of mussel using FSTAT (Goudet, 1995).

Pairwise estimates of \( F_{st} \) and corrected average pairwise population distances among all populations were obtained using the program Arlequin3.1 (Excoffier et al, 2005). The significance of these estimates was tested by comparing observed \( F_{st} \) with a null distribution obtained by 10000 random permutations of the data set (Excoffier et al, 1992).

2 Results
2.1 Characteristics of mtDNA COI of *M. coruscus*

Once all sequences were aligned, a total segment length of 573 bp of cytochrome oxidase subunit I (COI) was obtained. The average nucleotide composition in our samples is A=33.6%, C=23.9%, G=15.8%, T=26.6%, with an average G+C content of 39.7%. These sequences include 59 variable sites, of which 41 are singleton variable sites and 18 are parsimony informative sites. Sequences have been deposited in GenBank under the following accession number range: FJ495257-FJ495286.

2.2 Genetic variability and population structure within populations

The samples examined show a wide range of values for the number of haplotypes, gene diversities and nucleotide diversities (Tab. 2). A total of 30 haplotypes were obtained for wild and cultured populations of *M. coruscus* (Tab. 3). The number of individuals of different haplotypes ranged from 1 to 18. The haplotype Hap2 had the greatest number of individuals across all samples. The wild WSS population had the greatest number of haplotypes, whereas the cultured CHN population originating from the Shengsi area had the fewest number of haplotypes. Every population had population-specific haplotypes. In the cultured WLJ population, only 3 specific haplotypes were found, exhibiting a decrease of specific haplotypes. In contrast, the samples from the wild WSS population exhibited the greatest number of population-specific haplotypes. The samples from natural populations exhibited the greatest number of haplotypes and population-specific haplotypes compared to cultured samples.

![Image](image_url)

| Population | Number of individuals (n) | Number of haplotypes (N) | Gene diversity (h) | Nucleotide diversity (π) |
|------------|---------------------------|--------------------------|-------------------|-------------------------|
| WSS        | 20                        | 13                       | 0.911             | 0.00898                 |
| CHN        | 13                        | 6                        | 0.718             | 0.00293                 |
| CSS        | 20                        | 12                       | 0.911             | 0.00834                 |
| WLJ        | 13                        | 10                       | 0.923             | 0.00948                 |
| Overall    | 66                        | 30                       | 0.895             | 0.00832                 |

The samples from wild WSS population had an H value of 0.911 and π of 0.00898, compared to the aquaculture samples CHN and CSS with H values of 0.718, 0.911 and π values 0.00293, 0.00834, respectively. The wild WSS population had 3-fold higher nucleotide diversity than the cultured CHN population obtained through artificial propagation. All cultured populations exhibited the less genetic diversity for gene diversity and nucleotide diversity compared to the wild populations.

2.3 Genetic differentiation among populations

Tab. 4 shows different indices of dissimilarity between pairs of populations, including genetic distance and *F*<sub>st</sub> statistics. When populations were compared pairwise, the highest *F*<sub>st</sub> values appeared in CHN WLJ pairs (*F*<sub>st</sub>=0.2991, *P*<0.01). The *F*<sub>st</sub> values for WLJ/WSS were also statistically significant (*F*<sub>st</sub>=0.1414, *P*<0.05). The comparison of populations WSS and CHN, CSS show low *F*<sub>st</sub> values, indicating that these two populations were not highly divergent. But interestingly, genetic differentiation between CHN and CSS was significant (*F*<sub>st</sub>=0.1376, *P*<0.05). In concordance with *F*<sub>st</sub> values, the pairwise Nei’s genetic distance value was low between WSS and CSS, CHN populations (0.099 and 0.298, respectively). The largest genetic distance was between WLJ and CHN (1.735).

3 Discussion

The artificial breeding program for this species starts for a short time and will expand accordingly. There is no previous genetic record of this species and no attempt has been made to assess the genetic status of both wild and cultured populations of this species. This is the first study to demonstrate that a mitochondrial marker can be used to monitor changes in the genetic diversity of the hard-shelled mussel (*M. coruscus*) during domestication.

Genetic variability is an important attribute of species under domestication, since those with higher levels of variation are most likely to present high additive genetic variance for production traits (Alarcon et al, 2004). In this study, genetic analysis of mitochondrial COI gene sequences revealed higher genetic variability for gene diversity and nucleotide diversity both in wild and cultured *M. coruscus* than for the same sequence regions in other marine organism. Results from mitochondrial COI gene sequences in crayfish showed...
Tab. 3 mtDNA haplotypes distribution of *Mytilus coruscus* populations (GenBank accession no and number of individuals)

| Name   | GenBank accession No | WSS | CHN | CSS | WLJ | Total |
|--------|----------------------|-----|-----|-----|-----|-------|
| Hap1   | FJ495257             | 1   |     |     |     | 1     |
| Hap2   | FJ495258             | 6   | 7   | 4   | 1   | 18    |
| Hap3   | FJ495259             | 2   | 1   | 1   | 4   |       |
| Hap4   | FJ495260             | 1   | 2   | 1   | 4   |       |
| Hap5   | FJ495261             | 1   |     |     |     |       |
| Hap6   | FJ495262             | 1   |     |     |     |       |
| Hap7   | FJ495263             | 1   |     |     |     |       |
| Hap8   | FJ495264             | 2   | 5   | 4   |     | 11    |
| Hap9   | FJ495265             | 1   |     |     |     |       |
| Hap10  | FJ495266             | 1   |     |     |     |       |
| Hap11  | FJ495267             | 1   |     |     |     |       |
| Hap12  | FJ495268             | 1   |     |     |     |       |
| Hap13  | FJ495269             | 1   |     |     |     |       |
| Hap14  | FJ495270             |     | 1   |     |     |       |
| Hap15  | FJ495271             | 1   | 2   | 1   | 4   |       |
| Hap16  | FJ495272             |     |     |     |     |       |
| Hap17  | FJ495273             |     |     | 1   | 1   |       |
| Hap18  | FJ495274             |     |     |     | 1   |       |
| Hap19  | FJ495275             |     |     |     | 1   |       |
| Hap20  | FJ495276             |     |     |     | 1   |       |
| Hap21  | FJ495277             |     |     |     | 1   |       |
| Hap22  | FJ495278             |     |     |     | 1   |       |
| Hap23  | FJ495279             |     |     |     | 1   |       |
| Hap24  | FJ495280             |     |     |     | 1   |       |
| Hap25  | FJ495281             |     |     |     | 1   |       |
| Hap26  | FJ495282             |     |     |     | 1   |       |
| Hap27  | FJ495283             |     |     |     | 1   |       |
| Hap28  | FJ495284             |     |     |     | 1   |       |
| Hap29  | FJ495285             |     |     |     | 1   |       |
| Hap30  | FJ495286             |     |     |     | 1   |       |

Tab. 4 Pairwise estimates of Nei’s genetic distance (above diagonal) and $F_{st}$ (below diagonal) between *Mytilus coruscus* populations

|       | WSS | CHN  | WLJ  | CSS   |
|-------|-----|------|------|-------|
| WSS   | 0.099 NS | 0.755* | 0.298 NS |
| CHN   | 0.0230 NS | 1.735** | 0.954 NS |
| WLJ   | 0.1414* | 0.2991** | -0.050 NS |
| CSS   | 0.0466 NS | 0.1376* | -0.0087 NS |

*P<0.05; **P<0.01; NS, not significant.

Nucleotide diversity ranging from 0.01% to 0.43% (Trontelj et al, 2005). In the mud crab *Scylla serrata*, the COI sequence divergence ranges from 0.17% to 0.46% and gene diversity ranges from 0.37 to 0.85 (Fratini & Vannini, 2002). Relatively high levels of DNA diversity characterized the population of the bivalve mollusc *Congeria kusceri* (haplotype diversity=0.66 in the COI gene) (Stepien et al, 2001). However, the mtDNA nucleotide and gene diversity were reduced in the cultured population. A slight decrease of genetic variability in cultured populations had been observed in many fish and mussel species (Lundrigan et al, 2005; Pampoulie et al, 2006; Wang, 2007; Kong & Li, 2007; Shu et al, 2008). The reduced genetic variability we observed in the farmed strains is probably due to a low number of successful breeders during the foundation period, similar to a recent bottleneck in terms of impact on genetic variability (Allendorf, 1986). The greatest reductions in number of haplotypes, nucleotide diversity and gene nucleotide observed in cultured CHN population in this study are probably caused by the use of small numbers of brood-stock collected from wild populations. The reductions in the cultured CSS population are probably contributed to collection of natural spat from small numbers of parents and samples examined. A more precise assessment of the genetic variability in cultured populations can be made, were the magnitude of the genetic variation of wild populations.
made available. This is almost a requirement when the number of generations of the cultured populations is small and there has not been enough time for the variation to be reduced to a detectable level.

The comparison of the $F_{st}$ values (Tab. 4) between CSS, CHN and WSS populations showed that the values were not significantly different. This indicates that no significant genetic differentiation was detected between CHN, CSS and WSS populations. Similar findings were reported for fish (Yang et al, 2008), marine mussel (Jiang et al, 2007; He et al, 2008). The slow genetic differentiation might be due to persistent gene flow caused by cultured juvenile practice in open sea, close to the wild population. But significant genetic differentiation observed between WLJ and WSS, CHN populations, was probably associated with geographic factors. This regional variation could be an important source of diversity for both genotypic and phenotypic traits to be selected in accordance with aquaculture goals (Lundrigan et al, 2005).

Large scale approaches to assess the genetic structure of wild and cultured populations, such as those reported here for *M. coruscus*, are most suitable to provide insights about the evolutionary history of a population and its potential as a source of variation for cultured stock. More detailed information obtained in future studies will be used as a baseline for genetic monitoring of *M. coruscus* aquaculture stains, in particular, the first-generation, recently cultured population. Through population management, inbreeding can be prevented through the maintenance of population size above a critical level, with regular observation of heterozygosity levels and breeding to maximize genetic variability and minimize inbreeding (Barroso et al, 2005). Future farming practice should avoid culturing in areas in which local wild population inhabit, since wild populations represent the primary source of genetic variability for aquaculture stocks. This genetic survey is intended as a baseline for future genetic monitoring of *M. coruscus* aquaculture stocks.

References:

Alarcon JA, Magoulas A, Georgakopoulos T, Zourous E, Alvarez MC. 2004. Genetic comparison of wild and cultivated European populations of the gilthead sea bream (*Sparus aurata*) [J]. *Aquaculture, 230*: 65-80.

Allendorf FW. 1986. Genetic drift and the loss of alleles versus heterozygosity [J]. *Zoo Biol, 5*(2): 181-90.

Avise JC. 2000. Phylogeography: The History and Formation of Species [M]. Cambridge: Harvard University Press.

Barroso RM, Hilsdorf A, Moreira H, Cabello PH, TraubiCzeko YM. 2005. Genetic diversity of wild and cultured populations of *Brycon opalinus* (Cuvier, 1819) (Characiforme, Characidae, Bryconinae) using microsatellites [J]. *Aquaculture, 247*: 51-65.

Birky CW, Manuyama T, Fuerst P. 1983. An approach to population and evolutionary genetic theory for genes in mitochondria and chloroplast and some results [J]. *Genetics, 103*(3): 513-527.

Excoffier L, Smouse PE, Quattro JM. 1992. Analysis of molecular variance inferred from metric distances among DNA haplotypes: Application to human mitochondrial DNA restriction data [J]. *Genetics, 131*(2): 479-491.

Excoffier L, Laval G, Schneider S. 2005. Arlequin version 3.0: An integrated software package for population genetics data analysis [J]. *Evolutionary Bioinformatics, 1*: 47-50.

Folmer O, Black M, Hoeh W. 1994. DNA primers for amplification of mitochondrial cytochrome c oxidase subunit I from diverse metazoan invertebrates [J]. *Molecular Marine Biology and Biotechnology, 5*(5): 294-299.

Fratini S, Vannini M. 2002. Genetic differentiation in the mud crab *Scylla serrata* (Decapoda: Portunidae) within the Indian Ocean [J]. *Journal of Experimental Marine Biology and Ecology, 272*(1): 103-116.

Goudet J. 1995. FSTAT (version 1.2): a computer program to calculate F-statistics [J]. *Heredity, 86*(6): 485-486.

Hall TA. 1999. BioEdit: A user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT [J]. *Nucleic Acids Symp Ser, 41*: 95-98.

He CB, Cong LL, Ge LL, Liu WD, Zhou ZC, Gao XG. 2008. AFLP analysis of cultured and wild hard clam (*Meretrix meretrix*) populations [J]. *Journal of Fishery Sciences of China, 15*(2): 215-221.

Jiang ZY, Niu DH, Chen H, Shen HD, Li JL. 2007. The genetic analysis of ITS-1 and ITS-2 between wild and cultured populations of *Sinoovocula constricta* in Fujian [J]. *Marine Fisheries, 29*(4): 314-318.

Kong LF, Li Q. 2007. Genetic comparison of cultured and wild populations of the clam *Coelomactra antiquata* (Spengler) in China using AFLP markers [J]. *Aquaculture, 271*: 152-161.

Lundrigan TA, Reist JD, Ferguson MM. 2005. Microsatellite genetic variation within and among Arctic herring (*Salvelinus alpinus*) from aquaculture and natural populations in North America [J]. *Aquaculture, 244*(1-4): 63-75.

McGinnity P, Prodohl PA, Ferguson A, Hynes R, Omoleilighigh N, Baker N, Cotter D, Ohea D, Cooke D, Rogan G, Tlaggart J, Cross T. 2003. Fitness reduction and potential extinction of wild populations of Atlantic salmon *Salmo salar* as a result of interactions with escaped farm salmon [J]. *Proceedings of the Royal Society of London (Series B), 270*(1532): 2443-2450.

Nei M. 1987. Molecular Evolutionary Genetics [M]. New York: Columbia Unvi Press.

Pampoulie C, Jorundsdottir TD, Steinarsson A, Petursdottir G, Stefansson MO, Danielsdottir AK. 2006. Genetic comparison of experimental farmed strains and wild Icelandic populations of Atlantic cod (*Gadus morhua* L.) [J]. *Aquaculture, 261*: 556-564.

Posada D. 2006. Collapse: Describing Haplotypes from Sequence Alignments[M]. Computation Evolutionary Biology Lab,
University of Vigo, Vigo, Spain.
Rozas J, Sánchez-DelBarrio JC, Meseguer X, Rozas R. 2003. DnaSP, DNA polymorphism analyses by the coalescent and other methods [J]. Bioinformatics, 19(18): 2496-2497.
Shen YB, Li JL, Mou YJ. 2006. Molecular identification of introgression between the native Mytilus coruscus and the introduced Mytilus edulis using inter-simple sequence repeat marker (ISSR) [J]. Marine Fisheries, 28(4): 195-200.
Shu J, Li Q, Yu RH, Tian CY. 2008. Microsatellites Analysis on Genetic Variation Between Wild and Cultured Populations of Pacific Abalone (Haliotis discus hannai) [J]. Periodical of Ocean University of China, 38(1): 52-58.
Stepien CA, Morton B, Dabrowska KA. 2001. Genetic diversity and evolutionary relationships of the troglodytic ‘living fossil’ Congeria kusceri (Bivalvia: Dreissenidae) [J]. Molecular Ecology, 10(8): 1873-1879.
Tamura K, Dudley J, Nei M, Kumar S. 2007. MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0 [J]. Molecular Biology and Evolution, 24(8): 1596-1599.
Trontelj P, Machino Y, Sket B. 2005. Phylogenetic and phylodogeographic relationships in the crayfish genus Austropotamobius inferred from mitochondrial COI gene sequences [J]. Molecular Phylogenetics and Evolution, 34(1): 212-226.
Wang ZR. 1997. Fauna Sinica [M]. Beijing: Science press.
Wang SF, Du JY, Su YQ. 2007. The genetic structure of Nature and reared groups of Hapalogenys nitosus by ISSR analysis [J]. Acta Oceanologica Sinica, 29(4): 105-110.
Yang C, Zhu XP, Sun XW. 2008. Development of microsatellite markers and their utilization in genetic diversity analysis of cultivated and wild populations of the mud carp (Cirrhina molitorella) [J]. J Genet Genomics, 35(4): 201-206.
Zheng WJ, Zhu SH, Shen XQ, Liu BQ, Pan ZC, Ye YF. 2009. Genetic differentiation of Tegillarca granosa based on mitochondrial COI gene sequences [J]. Zool Res, 30(1): 17-23.

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上海海洋大学水产动物种质资源与创新团队简介

水产动物种质资源与创新团队是上海海洋大学水产养殖国家重点学科的骨干研究力量，也是省部共建水产种质资源发掘与利用教育部重点实验室的基本研究队伍。

上海海洋大学是国内最早开展水产动物种质资源与创新研究的单位，世界水产养殖终身成就奖获得者——李思发教授80年代初回国后创建了这个研究领域，至今已有近30年的历史，在国内外产生了广泛的影响。李思发教授领导的课题组历时20年经过6代系统选育，获得了生长速度比原种快30%、体形好、遗传性状稳定的团头鲂新品种“浦江一号”，它是世界上第一个经选育的草食鱼类新品种，也是上海市育成的第一个水产动物良种，该项目获2002年度上海市科技进步一等奖、2004年度国家级科技进步二等奖。他领导的课题组还于2006年初选育出新吉富罗非鱼新品种，以该新品种为核心的“从吉富到新吉——尼罗罗非鱼种质创新与应用”项目荣获2007年度上海市科技进步一等奖。

该团队年轻学术带头人李家乐教授是李思发教授的学生，他领导的课题组从1998年开始，对我国具有悠久养殖历史、产量占世界产量95%以上的淡水珍珠蚌，开展了系统的种质评价与筛选，获得了三角帆蚌鄱阳湖新品系，并率先将三角帆蚌和从日本引进的池蝶蚌进行杂交，获得了新品种“康乐蚌”。“淡水珍珠蚌新种选育和养殖关键技术”项目获2008年度上海市科技进步一等奖。

目前，该团队拥有教师16名，其中教授6人，副教授5人，是一支以中青年和具有海外留学经历的教师为主的创新型团队。该团队拥有研究生75名，其中博士研究生12人。

最近五年来，该团队获得3000多万科研经费，其中重要的科研项目有：“973”前期研究专项、“863”、科技支撑、农业产业体系、国家自然科学基金重点等。获国家科技进步二等奖1项，上海市科技进步一等奖3项，省部级二等奖2项、三等奖10余项；在公开的学术刊物上发表论文253篇，其中SCI、EI论文26篇；主编或参编专著5部、教材5部，其他编著6部；申请专利12项，其中获得3项。

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