Acta Oceanol. Sin., 2020, Vol. 39, No. 12, P. 76–81
https://doi.org/10.1007/s13131-020-1688-8
http://www.hyxb.org.cn
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Research in migration route of hatchery released Chinese shrimp (*Fenneropenaeus chinensis*) in the Bohai Bay using method of SSR marker

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Received 16 October 2019; accepted 16 December 2019

Abstract

This study provides new insights for the hatchery released Chinese shrimp (*Fenneropenaeus chinensis*), including proportion, dynamic migration route, after they were released into nature for stock enhancement using a new strategy quite different than ever. Chinese shrimp were sampled at 22 survey stations during two investigation voyages acrossing 74 survey stations in the Bohai Sea from July 16 to August 9 in 2015. Among 289 sampled individuals during the second voyage, totally 155 shrimps were identified as hatchery shrimp released into the Laizhou Bay at mid-May in 2015 based on finger-print of eight SSR (simple sequence repeats) markers, and the proportion of hatchery released shrimp in recapture samples were from 41.30%–85.71% in each station with an average value 53.63%, which verified a previous view point that up to 90% of autumn season Chinese shrimp landing in the Bohai Sea were composed of hatchery released. Meanwhile, the dynamic migration route of hatchery released shrimp revealed that part of released shrimp migrated heading northwest along the west coast of the Bohai Sea up to the Bohai Bay but just remained at the Laizhou Bay until over-wintering migration at mid-October when they initiate over-wintering migration. Present unnatural spring season shrimp fishing model cut the throat of spawner shrimp chance to swim back to their respective spawning plants at each spring, it still no chance to clarify whether the hatchery released shrimp could replenish to the reproduce population and complete a whole life cycle as same as their natural relatives.

Key words: *Fenneropenaeus chinensis*, migration route, hatchery release, stock enhancement, SSR marker

Citation: Wang Weiji, Lyu Ding, Wang Mosang, Liu Kefeng, Kong Jie, Shan Xiujuan, Jin Xianshi. 2020. Research in migration route of hatchery released Chinese shrimp (*Fenneropenaeus chinensis*) in the Bohai Bay using method of SSR marker. Acta Oceanologica Sinica, 39(12): 76–81, doi: 10.1007/s13131-020-1688-8

1 Introduction

As one of the most important native marine shrimp species in China, with smaller population was also found along the coast of the Korean Peninsula, the Chinese shrimp (*Fenneropenaeus chinensis*) has played an indispensable role in China fisheries (Deng et al., 1990; Deng, 1998; Liu et al., 2004). However, since the 1980s, once plentiful spring and autumn season landings of Chinese shrimp in the Yellow Sea and Bohai Sea declined. This decline has been mainly attributed to an increase in fishing, pollution and natural habitat destruction. Additionally, the traditional spring shrimp-fishing season disappeared approximately since 1986 (Deng et al., 1990; Deng, 1998). Meanwhile, suffering from the disease (white spot syndrome virus, WSSV) outbreak in shrimp farming, the total annual production of Chinese shrimp dramatically decreased from approximately 200 000 t in the late 1980s to 20 000–40 000 t in the 2000s (Ye et al., 2005). After several decades of continuous practice, hatchery release enhancement was proven to be a useful strategy for natural population recovery of Chinese shrimp, and the fishery was also gradually benefiting from the strategy (Wang et al., 2006). Meanwhile, different methods were developed to assess the recapture rate, a very important index in assessing whether an enhancement program is successful. These methods include marker-recapture methods with physical markers such as eye tags, visible implant elastomers (http://www.nmt.us), code wire tags (http://www.nmt.us) and radio frequency identification (http://www.biomark.com), as the most commonly used (Klima, 1965; Marullo et al., 1976; Luo et al., 2008; Liu et al., 2013; Xu et al., 2017). Considering the huge number of hatchery and the small size of released shrimp, obtaining precise recapture rates for assessing the effect of the enhancement impractical by injecting physical markers is impractical. Therefore, it was necessary to develop a new type of "marker" for "released shrimp tagging", and further to produce precise recapture rate assessment. Wang et al. (2014) provided a new distinguishable from previous physical tagging methods, which was based on individual identification and pedigree tracing using simple se-

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Foundation item: The National Key R&D Program of China under contract No. 2017YFE0104400; the National Basic Research Program (973 Program) of China under contract No. 2015CB453303.

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quence repeat (SSR) markers and was successfully applied in recapture rates estimation in the Jiaozhou Bay and Bohai Bay in China in 2012. Regarding to the limited number of family individuals (named as molecular marker-tagging individuals compared to traditional physical-tagging individuals), including both hatchery released and detected from recaptured shrimp samples, however, previous research only provided limited data that not strong enough to support an overall assessment of shrimp released enhancement activity. Chinese shrimp was with significant migratory habitat. In its whole life cycle, there were three kinds of significant migration (over-wintering, spawning and feeding migration, respectively) that correlated closely with sea water temperature, bait, physiologic phase and hydrography. In addition to assess the enhancement effect, released shrimp identification and migration route tracing are also meaningful to clarify these following two puzzles: (1) Considering the biological behavior, whether the released hatchery shrimp stock is still consistent with their wild counterparts as well? In two fish species Mulloway (*Argyrosomus japonicus*) and Largemouth Bass (*Micropterus salmoides*), in which, higher levels of movement activity of hatchery-reared were discovered to be one of the key biological differences from natural stock, but lower survival probability of hatchery-reared was also found in semi-natural environments (Garlock et al., 2014; Taylor et al., 2017). (2) Could the released hatchery-reared shrimp have chance to develop spawner and further back to spawning plant after over-wintering as same as their wild counterparts at the next spring? Since besides to enhance the shrimp production, another important goal of hatchery release is to maintain self-sustainable wild stock (Araki and Schmid, 2010). It was widely believed that up to 80% or more of Chinese shrimp autumn landing were from hatchery-released (Wang et al., 2006; Li et al., 2019); and it is different from coastal invertebrate species, whose sessile or sedentary behaviors can be helpful for them to form self-replenishing population (Bell et al., 2005), Chinese shrimp need migrate to coastal area, especially estuary, to finish spawning just in part of life time. Hence whether the hatchery-released Chinese shrimp could finish a whole migration cycle is a signal of population self-replenishment and spawning plant improvement. Due to released individuals were too small to injected with physical marks, there were few studies focused on the pattern of feeding, overwintering, and spawning migrations of released Chinese shrimp. These questions were just speculated by the migration patterns of wild Chinese shrimp. Using microsatellite markers, we have an opportunity to do a realistic tracking description of them, which is of great significance for scientific evaluation of the ecological values of enhancement and releasing of Chinese shrimp. In this study, single-parent parentage identification in Chinese shrimp based on 8 SSR loci was used to trace the hatchery released shrimp in the Laizhou Bay in Shandong Peninsula in 2015, subsequently, the dynamic migration route and corresponding quantity changing of hatchery-released shrimp in the Bohai Sea were investigated and outlined. This research would be useful in enhancement effect and natural shrimp resource assessment, autumn fishing season landing amount anticipation, and even the dispute resolution of shrimp-fishing in the Bohai Sea.

2 Materials and methods

2.1 *Materials*

2.1.1 *Shrimp spawner sampling*

By the end of June 2015, all of 1 016 shrimp spawner were collected from Haifeng Aquatic Ltd., Changyi, Shandong Province, China after they finished larvae produce for shrimp hatchery release mission of the Laizhou Bay (lies in southern coast of the Bohai Sea), Haifeng was the only assigned Chinese shrimp seed producer for hatchery release in the Laizhou Bay in 2015. All samples were transferred with carbon dioxide ice to laboratory in the Yellow Sea Fisheries Research Institute, Qingdao, China and maintained in a –75°C super-cold refrigerator for the following DNA isolation.

2.1.2 *Hatchery released shrimp recapture*

All hatchery released shrimps, about 0.2–0.3 billion according to a private communication, were released around the estuary of Weihe River that lies in the southern coast of the Laizhou Bay in mid-May, 2015. Two months after the shrimp larvae were released, they were recaptured for the first time across three sea areas in the Bohai Sea by using traditional trawling net, including the Liaodong Bay sea area, the Bohai Bay sea area and Laizhou Bay sea area from July 16 to 18, respectively. In the Liaodong Bay sea area, there were 20 survey stations covered from 40°00′N to 40°45′ N, 120°10′E to 121°45′E; in the Bohai Bay sea area, totally 25 survey stations distributed, from 38°15′N to 39°00′N, 117°45′E to 119°00′E; and in the Laizhou Bay sea area, totally 21 sampling survey stations covered from 37°11′N to 38°00′N, 119°05′E to 120°30′E. From August 6 to 9, released shrimps were recapture for the second time at the other 8 survey stations that covered from 37°25′N to 38°44′N, 118°16′E to 119°45′E. All the recaptured shrimp samples were preserved in refrigerator aboard, then were transferred with ice to laboratory and maintained in a –75°C super-cold refrigerator for DNA isolation.

2.2 *Methods*

Protocol described by Wang (2008) was used to isolate genomic DNA from the swimming apparatus that dissected from each Chinese shrimp sample. Genomic DNA was dissolved in 0.1 mol/L TE (Tris-EDTA) (pH 8.0), and according to the $OD_{260/280}$ value that measured using GeneQuant (Amersham Biosciences) and 0.7% agarose electrophoresis, the genomic DNA was adjusted to 50 ng/μL and stored at –20°C for subsequent SSR genotyping. One set of a quadruple-fold fluorescent-labeled SSR-PCR system for *F. chinensis* and other four single fold fluorescent-labeled SSR-PCR systems were used for total 8 SSR loci genotyping (Table 1), and the PCR reaction components and procedures were adopted following to the description of Li et al. (2012) and Wang et al. (2016) with slight adjustment. An ABI 3130 autosequencer (Applied Biosystmes) was used to separate the PCR amplification products, and the alleles of each SSR loci were sized with a GeneScanTM-500 LIZ Size DNA Standard (Applied Biosystems). A computer software for assignment of parents to their offspring based on genetic markers, Cervus 3.0 software, (http://www.fieldgenetics.com) was used to identify the released shrimp and trace to their parents. An authentic single-parent parentage relationship was declared only if all the alleles between recaptured sample and spawner were consistent and with an LOD score larger than 3.0.

3 Results

3.1 *Shrimp recapture results*

During the two hatchery released shrimp recapture voyages, totally 74 survey stations were investigated by using trawling net across the whole Bohai Sea from July 16 to August 9, and the first and second voyages covered 66 and 8 survey stations, respectively. Chinese shrimp samples were captured at total 14 survey

Table 1. Details of 8 SSR loci that composed of four single fold and one set of quadruple-fold fluorescent-labeled SSR-PCR system

PCR system	Locus name	GenBank access number	Annealing temperature/°C	Primer sequences (5′–3′) and labeled fluorescent dye
Quadruple-fold PCR system	EN0033	AY132813	64	F: 6-FAM-CCTTGACACGGCATTGATTGG R: TACGTTGTGCAAACGCCAAGC
	RS0622	AY132778	66	F: ROX-TCAGTCCGTAGTTCATACTTGG R: CACATGCCTTTGTGTGAAAACG
	FCKR002	JQ650349	60	F: HEX-CTCAACCCTCACCTCAGGAACA R: AATTGTGGAGGCGACTAAGTTC
	FCKR013	JQ650353	61	F: TAMRA-GCACATATAAGCACAAACGCTC R: CTCTCTCGCAATCTCTCCAACT
Single-fold PCR system	FC019	–	45	F: ROX-GTTGATGCCAGCAGTTAT R: TTCCAAGGGTCAGAGGTG
	RS0683	AY132823	64	F: HEX-ACACTCACTTATGTCACACTGC R: TACACACCAACACTCAATCTCC
	FCKR009	JQ650352	52	F: TAMRA-GCACGAAAACACATTAGTAGGA R: ATATCTGGAATGGCAAAGAGTC
	FC027	–	45	F: ROX-GCGTGTAATGCTTGCTGT R:TTTAGGACCTGCGGAGAA

Note: F represents forward primer, and R reverse primer.

stations during the first voyage, the sampled shrimp number were from 1 to 9 per site with a total number of 37. By the second voyage, Chinese shrimp samples were found at all of 8 survey stations, the samples number were from 2 to 76 at each sea site with a total number of 289 (Table 2).

Table 2. Details of sampling batches of Chinese shrimp in 2015

Voyage	Sampling date	Position	Samples number
First	July 16	37°11′41.76″N,119°28′33.06″E	1
	July 16	37°25′07.20″N, 119°29′40.68″E	3
	July 17	38°45′00.00″N, 118°15′00.00″E	1
	July 17	38°15′00.00″N, 118°00′00.00″E	4
	July 18	38°30′00.00″N, 118°00′00.00″E	1
	July 18	38°30′00.00″N, 118°15′00.00″E	6
	July 18	38°30′00.00″N, 118°30′00.00″E	3
	July 18	38°45′00.00″N, 118°15′00.00″E	1
	July 19	38°45′00.00″N, 118°00′00.00″E	9
	July 19	38°50′01.20″N, 118°15′00.00″E	1
	July 27	38°20′00.00″N, 119°04′58.80″E	1
	July 27	38°45′00.00″N, 119°15′00.00″E	2
	July 27	38°00′00.00″N, 119°15′00.00″E	2
	July 28	37°45′00.00″N, 119°30′00.00″E	2
	Total		37
Second	August 6 (1)	37°25′25.62″N, 119°20′13.26″E	46
	August 7 (2)	37°36′56.58″N, 119°29′58.80″E	7
	August 7 (3)	37°43′41.94″N, 119°29′36.42″E	42
	August 7 (4)	37°44′18.06″N, 119°42′00.06″E	2
	August 7 (5)	38°00′46.80″N, 119°45′11.34″E	12
	August 8 (6)	38°13′43.20″N, 119°10′58.92″E	54
	August 9 (7)	38°44′30.60″N, 118°22′13.50″E	50
	August 9 (8)	38°44′38.16″N, 118°16′04.80″E	76
	Total		289

Note: The number in the parethesis are the survey station numbers.

3.2 *SSR genotyping results*

Genomic DNA for SSR genotyping were isolated successfully from 1 016 shrimp spawner and 289 recaptured shrimp samples in the second voyage (the qualified genomic DNA could not be isolated successfully from all of 37 recaptured shrimp samples in the first voyage due to the poor preserved condition aboard). The total detected number of the alleles on 8 SSR loci after scanned 1 016 shrimp spawner and 289 recaptured shrimp samples were 254 and 238, respectively. The allele numbers at each SSR loci were from 8 to 63 with an average 31.75 and from 6 to 60 with an average 29.75 in spawner and recaptured stocks, respectively. The polymorphic information content (PIC) values of each SSR loci were from 0.780 to 0.952 across both spawner and recaptured stocks, which produced a cumulative probability of exclusion more than 0.999 with only one parent known (Table 3). In a view of genetic polymorphism, moreover, there was no obvious difference was detected between the spawner and recaptured stocks.

3.3 *Hatchery released shrimp identification and single-parent parentage confirmation*

Shrimps that were artificial released into the Laizhou Bay and were identified from all captured shrimps at 8 survey stations in the second voyage (Fig. 1), the number were from 1 to 37 per site with total number 155, and the proportion of released shrimp were from 41.30%–85.71% at each investigation site with an average value 53.63% (Table 4). All of these hatchery released shrimp could be traced to 135 female from 1 016 spawners that used in hatchery released shrimp larvae produced at the Laizhou Bay in 2015, most of spawners (116) have only 1 filial shrimp were detected, eighteen have 2 filial shrimp and there was also one have 3 filial shrimp were detected. According to the distribution of hatchery released shrimps after they were released into the Laizhou Bay, it was suggested that at least part of the hatchery released shrimps migrated heading northwest along the west coast of the Bohai Sea and even up to the Bohai Bay, which was against that the larvae would just remained at the Laizhou Bay until overwintering migration around late October as thought before (Fig. 1), and the estimated swimming distance of part of hatchery released shrimp could be up to 100 km or more during two and a half months after they were released.

4 Discussion

4.1 *More precise recapture ratio assessment could be expected*

As one of the focus topics, recapture rate assessments have

Table 3. Summary of genetic variability, probabilities of exclusion of 8 SSR loci in spawner and recaptured stocks

Locus name	Observed number of Alleles		Observed heterozygosity		Expected heterozygosity		Polymorphic information content		Probability of exclusion (E-2P)
	SP	RP	SP	RP	SP	RP	SP	RP	
EN0033	72	49	0.783	0.756	0.964	0.950	0.962	0.946	0.924
FCKR002	23	19	0.947	0.993	0.920	0.909	0.914	0.900	0.834
RS0622	42	33	0.921	0.949	0.955	0.954	0.952	0.950	0.907
FCKR013	30	25	0.912	0.889	0.940	0.929	0.936	0.923	0.876
RS1101	26	19	0.824	0.806	0.812	0.808	0.787	0.780	0.632
RS0683	46	33	0.796	0.825	0.917	0.914	0.912	0.907	0.836
FC027	53	22	0.953	0.888	0.954	0.902	0.951	0.891	0.900
FCKR009	32	28	0.740	0.802	0.939	0.933	0.935	0.927	0.876
EN0033	72	49	0.783	0.756	0.964	0.950	0.962	0.946	0.924
Cumulative exclusion probability (E-2P)									0.999

Note: SP is spawner population; RP, recaptured population. Probability of exclusion (E-2P): probability of exclusion based on the genotype with one^{-} parent known.

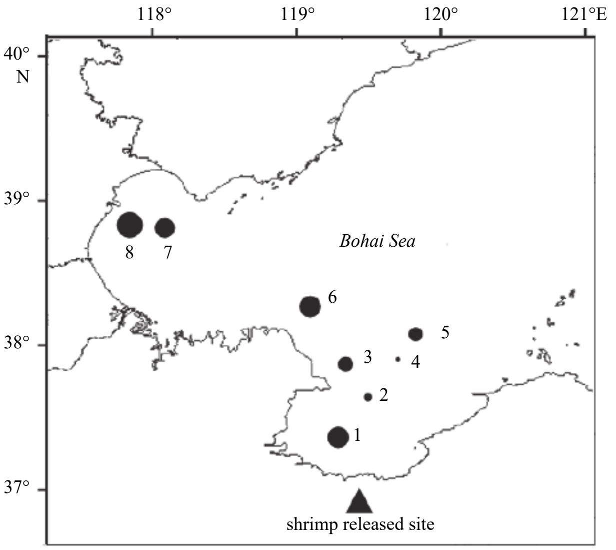

Fig. 1. Position of shrimp released site in Laizhou Bay and survey stations where released shrimp were detected. Black round dots (their sizes were in proportion to the sampled shrimp number at each survey station) indicated the 8 survey stations at the second voyage, and numbers 1–8 by the right were sequenced according to the sample date from 6 August to 9 August. Solid triangle showed the estuary of Weihe river where all hatchery enhancement shrimp were released at the mid-May in 2015.

Table 4. Summary of sampling and released shrimp identified numbers in the second investigation voyage

Sampling date	Number of released shrimp identified	Proportion/%
August 6 (1)	19	41.30
August 7 (2)	6	85.71
August 7 (3)	23	54.76
August 7 (4)	1	50.00
August 7 (5)	6	50.00
August 8 (6)	35	64.81
August 9 (7)	28	56.00
August 9 (8)	37	48.68
Average		53.63

Note: the numbers in the parenthesis are survey station numbers.

been highlighted since the first hatchery released enhancement of Chinese shrimp at Bohai Sea 30 years ago (Deng, 1983). Many methods, most of them were physical-tagging techniques, have been reported before (Klima, 1965; Marullo et al., 1976; Luo et al., 2008), however, these methods either were only suitable in large sized shrimp. For example, the visible implant elastomer was only suitable for 3 cm or above size shrimp, or the numbers of tagging shrimp were very limited. Besides, physical-tagging was harmful to the tagged individual and the tagging process was labor intensive. Previously, the largest numbers of physical-tagging shrimps were 46 679 and 95 272 in the Bohai Bay and Liaodong Bay in 1986, respectively (Deng et al., 1990). Wang et al. (2014) developed "molecular marker-tagging" technique for recaptured rate estimation of Chinese shrimp, and the numbers of molecular marker-tagging were 204 000 and 300 000 in the Bohai Bay and Jiaozhou Bay, respectively. However, just in the Laizhou Bay, the number of released shrimps was more than 0.2 billion each year, and it could increase to 1.5–2.0 billion in the whole Bohai Sea. Hence, the numbers of either physical-tagging or "molecular-marker tagging" were too small to produce an unbiased recapture rate estimate for enhancement effect assessment (Bravington and Ward, 2004). With the accuracy of SSR on single-parent parentage confirmation in Chinese shrimp was verified in a previous study (Zhang et al., 2014), we introduced single-parent parentage identification using SSR marker in present study. Considering that all of the spawners used in the Laizhou Bay were sampled, theoretically, it is equal to that all of the released filial shrimp were "molecular-marker tagged", and could be identified and traced to their maternities. In fact, totally 155 released shrimp were identified directly from 289 recaptured samples, and considering the number of identified hatchery released shrimp and its proportion in the whole recaptured samples, combing with an accuracy resource estimate, it was very hopeful to produce an authentic recapture rate estimate. Moreover, the chance to further understanding the survival rate, genetic variability and some other interested topics between hatchery released and wild populations was good as well, which was incomparable the previous physical-tagging release could be. A previous generally accepted view point considering that more than 90% part of Chinese shrimp landing in autumn fishing season each year in the Bohai Sea were hatchery released since the hatchery enhancement initiated 30 a ago, present results suggested that 41.30%–85.71% of recaptured shrimp at eight survey stations were composed of hatchery shrimp that released from the Laizhou Bay, which supported this view point again. Since the Laizhou Bay was not the only hatchery release site in the Bohai Bay, Hebei Province and Tianjin City along west coast of the Bohai Sea are both mainly responsible for at least one third of Chinese shrimp hatchery release in the Bohai Sea, and several survey stations in present study were more close to Hebei Procince or Tianjin City than to the Laizhou Bay (Gu et al., 2014). So, the most of left part in recaptured shrimp samples were from other Chinese shrimp hatchery released stations was also good. Considering there were more than 35 a since the first large-scale Chinese shrimp hatchery release initiated in Bohai Sea in 1984 (Wang et al., 2006), and to keep sustainable development of Chinese shrimp stock enhancement in the future, we are also supposed to pay more attention to the genetic differentiation between hatchery-released stock and wild population in the Bohai Sea areas , since negative effect (genome-wide introgressive hybridization) in wild Atlantic salmon influenced by hatchery released stock has been observed (Ozerov et al., 2016). At present, we still could not discriminate the wild shrimp from recaptured samples, partly because not all of the spawners for hatchery release along coast of the Bohai Sea areas could be sampled, so we still need a more detailed-designed program in future.

4.2 *Migration route of released shrimp*

Chinese shrimp has long-distance migratory behaviors, the female migratory distance could reach more than 1 000 km during a whole life span. Its life cycle could be divided into three obvious phases: feeding, over-wintering and spawning migration, but only the female individuals can complete the late two phases (in natural, male individuals died gradually after finishing copulation during the over-wintering migration in the late autumn). According to the geographic distribution of spawning plants, the natural Chinese shrimp population was suggested to be composed of the Bohai Bay population, the Laizhou Bay population, the Liaodong Bay population, the west coast of the Korean Peninsula and the other small, or unreported formally population (Zhuang et al., 2001; Liu et al., 2004), and it was generally accepted that although all the populations shared the same over-wintering ground, the shrimps within each population would follow a relatively settled route of feeding, over-wintering and spawning migration. In another word, with respect to population or gene-flow exchange, different geographic populations might share little, or at least there was still lack of strong evidence to support such an exchange.

Today, with continuous implement of hatchery enhancement of Chinese shrimp for 30 a ago, the old problem has been mentioned again: How about the migration routine of hatchery enhancement shrimp after they were released? If the released shrimps have chance escaping from high-intensity shrimp-fishing, could they migrate back to the original released stations to carry out reproduction and accomplish a whole migration cycle with their wild relatives at the next spring? This has puzzled academic fields since the hatchery enhancement was initiated. The reason why these puzzles emerged was mainly because human intervened the natural migration pattern. According to the official regulations of Chinese shrimp enhancement, spawners collection, larvae production and hatchery larvae release must be carried out *in-situ*, namely the hatchery released shrimp larvae must be produced by the spawners that captured just in the domestic spawning plants and the hatchery larvae must be released at the same site. However, due to the dramatically decreasing natural resource, especial the disappearing of shrimp spring fishing season, most of spawners were captured just around the over-wintering site located at the west coast of the Korea Peninsula before they migrate to their respective spawning plants, at least half of which lie in the coast along the Bohai Sea. Then, all of spawner shrimps for hatchery enhancement were transported alive by fishing vessel and sold to different shrimp larvae production plants along coast of the Bohai Sea in place of spawning migration at their last critical life phase, and that how much it would influence the released shrimp swimming ability or migratory habit is still needed to be clarified and paid more attention in the future. It was reported that two kinds of hatchery released fishes showed higher swimming ability but went with reduced survival rate in one kind than wild populations (Garlock et al., 2014; Taylor et al., 2017). Although present study did not prove hatchery released shrimp displayed higher swimming ability than its wild relative, it was a novel finding that the hatchery shrimp released in the Laizhou Bay did not just concentrate there but part of them could migrate northwest up along the west coast of the Bohai Sea, and based on history survey, some of them even swim up to the Bohai Bay until October when all of shrimp populations in the Bohai Sea initiate over-wintering migration (Wang et al., 2014). Due to the absent of samples captured from over-wintering plants and spawning plants, we still have no chance to clarify whether the released shrimps could complete a whole life cycle composed of three migrations as same as their wild relatives, which has been focused on as one of the next research items. Only if the released individuals were detected to swim back to their spawning plants, then whether the hatchery released shrimp accomplish a whole migration cycle and form replenishment population should be clarified. Hence, it is strongly suggested that the spawners should be only collected at their respective spawning plants.

Since hatchery release of Chinese shrimp were carried out in provinces along coast of the Bohai Seas, including Shandong, Hebei, Liaoning Provinces and Tianjin City in the spring of each year, shrimp-fishing was considered as a main source of revenue in autumn fishing season. However, no special shrimp-landing quota was distributed to fishing vessel, and the fishing disputes were inevitable. If the dynamic migration and distribution of hatchery released shrimp could be clarified, it would help to settle down the shrimp-fishing disputes.

References

Araki H, Schmid C. 2010. Is hatchery stocking a help or harm?: Evidence, limitations and future directions in ecological and genetic surveys. Aquaculture, 308(Suppl 1): S2–S11

Bell J D, Rothlisberg P C, Munro J L, et al. 2005. Restocking and stock enhancement of marine invertebrate fisheries. In: Southward A J, Young C M, Fuiman L A, eds. Advances in Marine Biology. San Diego, CA: Elsevier Academic Press, 49: 1–370

Bravington M V, Ward R D. 2004. Microsatellite DNA markers: evaluating their potential for estimating the proportion of hatchery-reared offspring in a stock enhancement programme. Molecular Ecology, 13(5): 1287–1297, doi: 10.1111/j.1365-294X.2004.02116.x

Deng Jingyao. 1983. Enhancement and releasing prawn resources. Marine Sciences (in Chinese), (6): 55–58

Deng Jingyao. 1998. The research status of shrimp fishery research. Chinese Bulletin of Life Sciences (in Chinese), 10(4): 191–194, 197

Deng Jingyao, Ye Changchen, Liu Yongchang. 1990. Penaeid Shrimp—Its Biology and Management in the Yellow-Bohai Seas (in Chinese). Beijing: China Ocean Press, 256–258

Garlock T M, Monk C T, Lorenzen K, et al. 2014. Effects of hatchery rearing on Florida largemouth bass *Micropterus floridanus* resource allocation and performance under semi-natural conditions. Journal of Fish Biology, 85(6): 1830–1842, doi: 10.1111/jfb.12514

Gu Dexian, Wang Ting, Liu Guoshan, et al. 2014. Analysis on resources of Chinese shrimp *Fenneropenaeus orientali* in Tianjin sea area. Fishery Modernization (in Chinese), 41(2): 57–62

Klima E F. 1965. Evaluation of Biological Stains, Inks, and Fluorescent Pigments as Marks for Shrimp. Washington: US Department of the Interior, Bureau of Commercial Fisheries

Li Weiya, Wang Weiji, Kong Jie, et al. 2012. Establishment of the microsatellite quadruple PCR technology for *Fenneropenaeus chinensis* and its application in the evaluation on the effect of releasing simulation. Haiyang Xuebao (in Chinese), 34(5): 213–220

Li Kezhen, Wang Chengguo, Liang Haiyong, et al. 2019. Research on contribution rate of resources on proliferation and releasing of *Penaeus Chinensis* in southern Shandong Peninsula. Journal of Yantai University: Natural Science and Engineering Edition (in Chinese), 32(2): 165–170

Liu Ping, Meng Xianhong, He Yuying, et al. 2004. Genetic diversity in three wild populations of shrimp *Fenneropenaeus chinensis* in Yellow and Bohai Seas as revealed by microsatellite DNA. Oceanologia et Limnologia Sinica (in Chinese), 35(3): 252–257

Liu Zhiliang, Xu Yongjiang, Liu Xuezhou, et al. 2013. Tagging of Japanese flounder using T-bar tags. Progress in Fishery Sciences (in Chinese), 34(6): 80–86

Luo Kun, Zhang Tianshi, Kong Jie, et al. 2008. Study on techniques of internal tagging by visible implant fluorescent elastomer in *Fenneropenaeus chinensis*. Marine Fisheries Research (in Chinese), 29(3): 48–52

Marullo F, Emliani D A, Caillouet C W, et al. 1976. A vinyl streamer tag for shrimp (Penaeus spp.). Transactions of the American Fisheries Society, 105(6): 658–663, doi: 10.1577/1548-8659(1976)105<658:AVSTFS>2.0.CO;2

Ozerov M Y, Gross R, Bruneaux M, et al. 2016. Genomewide introgressive hybridization patterns in wild Atlantic salmon influenced by inadvertent gene flow from hatchery releases. Molecular Ecology, 25(6): 1275–1293, doi: 10.1111/mec.13570

Taylor M D, Laffan S W, Fairfax A V, et al. 2017. Finding their way in the world: using acoustic telemetry to evaluate relative movement patterns of hatchery-reared fish in the period following release. Fisheries Research, 186: 538–543, doi: 10.1016/j.fishres.2016.07.003

Wang Qingyin, Zhuang Zhimeng, Deng Jingyao, et al. 2006. Stock enhancement and translocation of the shrimp *Penaeus chinensis* in China. Fisheries Research, 80(1): 67–79, doi: 10.1016/j.fishres.2006.03.015

Wang Weiji. 2008. Genetic mapping of the Chinese shrimp *Fenneropenaeus chinensis* using AFLP markers and commercial traits QTL mapping. II Genetic linkage mapping using AFLP markers and primarily study on sex-determination of bluegill sunfish (*Lepomis macrochirus*) (in Chinese)[dissertation]. Qingdao: Ocean University of China

Wang Mosang, Wang Weiji, Xiao Guangxia, et al. 2016. Genetic diversity analysis of spawner and recaptured populations of Chinese shrimp (*Fenneropenaeus chinensis*) during stock enhancement in the Bohai Bay based on an SSR marker. Acta Oceanologica Sinica, 35(8): 51–56, doi: 10.1007/s13131-016-0830-0

Wang Weiji, Zhang Kai, Luo Kun, et al. 2014. Assessment of recapture rates after hatchery release of Chinese shrimp *Fenneropenaeus chinensis* in Jiaozhou Bay and Bohai Bay in 2012 using pedigree tracing based on SSR markers. Fisheries Science, 80(4): 749–755, doi: 10.1007/s12562-014-0743-9

Xu Qiang, Gao Fei, Zhang Libin, et al. 2017. A new tagging method and its early stress effect on the sea cucumber *Apostichopus japonicus*. Aquaculture, 468: 156–161, doi: 10.1016/j.aquaculture.2016.10.002

Ye Changchen, Yang Wei, Lin Yuan. 2005. Glory and recession of Chinese shrimp industry. Tianjin Fisheries (in Chinese), (1): 9–14

Zhang Kai, Wang Weiji, Kong Jie, et al. 2014. Accuracy of short sequence repeats on single-parent parentage identification in Chinese shrimp *Fenneropenaeus chinensis*. Aquatic Biology, 20(1): 45–51, doi: 10.3354/ab00547

Zhuang Zhimeng, Shi Tuo, Kong Jie, et al. 2001. Genetic diversity in *Penaeus chinensis* shrimp as revealed by RAPD technique. Progress in Natural Science, 11(6): 432–438