Japanese Bibliography in 2017 for NPAFC Science Plan

by

Shunpei Sato, Masa-aki Fukuwaka, and Shigehiko Urawa

Hokkaido National Fisheries Research Institute
Japan Fisheries Research and Education Agency
2-2 Nakanoshima, Toyohira-ku, Sapporo 062-0922, Japan

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Shunpei Sato, Masa-aki Fukuwaka, and Shigehiko Urawa

Hokkaido National Fisheries Research Institute, Japan Fisheries Research and Education Agency, 2-2 Nakanoshima, Toyohira-ku, Sapporo 062-0922, Japan

ABSTRACT: This bibliography listed original papers and documents published in 2017 by Japanese scientists and/or their collaborators to review Japanese national researches for the 2016-2020 NPAFC Science Plan. The bibliography includes 33 articles with abstracts, corresponding to five research themes of the NPAFC Science Plan.

Key Words: bibliography, Japanese science plan, NPAFC science plan, Japanese scientists

BACKGROUND

In 2016, the Science Sub-Committee (SSC) of the North Pacific Anadromous Fish Commission (NPAFC) developed a new five-year Science Plan 2016-2020 (SSC 2016). The SSC identified its primary goal "Understand Variations in Pacific Salmon Productivity in a Changing Climate" with five research themes: 1) Status of Pacific salmon and steelhead trout; 2) Pacific salmon and steelhead trout in a changing North Pacific Ocean; 3) New technologies; 4) Management systems; and 5) Integrated information systems. The new NPAFC Science plan is approximately consistent with the International Year of Salmon initiative (IYS-WG 2016).

The national research plan by Japan was established in July 2016 to correspond to the new NPAFC Science Plan (Fisheries Agency of Japan 2016). It is a high priority for Japanese salmon research to explain and forecast the annual variation of salmon production, corresponding to the new Science Plan themes. To review Japanese national researches for the NPAFC Science Plan, this bibliography listed original papers and documents published in 2017 by Japanese scientist and/or their collaborators. The current issue supplemented 33 articles published in 2017. The bibliography includes abstracts for most articles.

REFERENCES

Fisheries Agency of Japan. 2016. Japanese salmon research under the NPAFC Science Plan 2016-2020. NPAFC Doc. 1673. 2 pp. (Available at www.npafc.org).

International Year of the Salmon Working Group (IYS-WG). 2016.Outline proposal for an International Year of Salmon (IYS) 'Salmon and People in a Changing World'. NPAFC Doc. 1663. 9 pp. (Available at www.npafc.org).

The Science Sub-Committee (SSC). 2016. North Pacific Anadromous Fish Commission Science Plan 2016-2020. NPAFC Doc. 1665. 8 pp. (Available at www.npafc.org).

BIBLIOGRAPHY

Theme 1. Status of Pacific Salmon and Steelhead Trout

Ando, D., M. Murooka, K. Shimoda, H. Hayano, Y. Sasaki, Y. Miyakoshi and M. Nakajima. 2017. Estimation of heritability of vertebral number in chum salmon *Oncorhynchus keta*. Fish. Sci. 83: 413-423.

Hereditary causes of variation in the vertebral number of chum salmon were analyzed to estimate heritability for populations in the Chitose and Shikiu Rivers, Hokkaido Island, northern Japan. A total of 70 families were produced by diallel cross mating and then heritability was estimated using two statistical tests: a two-way ANOVA and a parent-offspring regression. Heritability estimates ranged from 0.26 to 1.91 and showed a strong correlation between the values from the two different tests. Estimates from female components were substantially higher than those from male components, which can be attributed to the maternal effect. Heritability in the Shikiu River population was shown to be higher than that in the Chitose River population. These results indicate that the heritability of vertebral number in chum salmon is generally high, and also that vertebral number is controlled by hereditary causes.

Ando, D., T. Watanabe and K. Shimoda. 2017. Geographical variation in vertebral number of chum salmon fry on Hokkaido Island, Japan. Aquacult. Sci. 65: 89-91 (In Japanese with English abstract).

Chum salmon eggs were collected from five local populations on Hokkaido Island during two different spawning periods, representing early and late spawning populations. Eggs from all populations and both spawning periods were maintained under similar laboratory conditions to detect variation in vertebral number of fry. Mean vertebral number varied according to both population and spawning period. Mean vertebral number observed in the late spawning population was lower than that of the early spawning population. Mean vertebral number was similar between salmon from neighboring rivers. These results suggest that the vertebral number of chum salmon varies between populations and is governed by hereditary factors.

Aoyama, T., Y. Shinriki, H. Ohmori and K. Takeuchi. 2017. Distribution and densities of wild masu salmon juveniles in the Assabu River system, southwestern Hokkaido, Japan (Note). Sci. Rep. Hokkaido Fish. Res. Inst. 92: 59-63 (In Japanese, no abstract).

Iida, M., S. Imai and S. Katayama. 2017. Effect of riverbed conditions on survival of planted eyed eggs in chum salmon *Oncorhynchus keta*. Fish. Sci. 83: 291-300.

Wild stocks of chum salmon *Oncorhynchus keta* are supplemented by hatchery fry enhancement programs in northern Honshu, Japan. To maintain these programs, there is a need to reduce expenses and labor. Eyed egg planting is more cost effective than hatchery production of fry. Therefore, we evaluated the effect of environmental conditions on survival of chum salmon eyed eggs planted using Whitlock-Vibert boxes. We measured the percent cumulative weight of fine sediments, Fredle index (FI) as a measure of permeability, vertical hydraulic gradient, water depth (WD), and flow velocity at planting locations. Egg-to-fry survival averaged 92.7% (range: 57.2-100%) in 2013 (N = 19) and 71.5% (range: 6.4-100%) in 2014 (N = 23). Survival was significantly positively correlated with FI and flow velocity, negatively associated with percent

cumulative weight of fine sediments and WD. Vertical hydraulic gradient had no effect on survival. Our results suggest that a higher FI (i.e., low amount of fine material and larger particle size), higher flow velocity, and shallower WD reduce the mortality of planted chum salmon eyed eggs. This is likely a result of increased permeability in the substrate and restriction of fine sediment intrusion into the incubation zone.

Chen, E. Y., J. B. Leonard, and H. Ueda. 2017. The behavioural homing response of adult chum salmon *Oncorhynchus keta* to amino-acid profiles. J. Fish Biol. 90: 1257-1264.

Adult chum salmon Oncorhynchus keta homing behaviour in a two-choice test tank (Y-maze) was monitored using a passive integrated transponder (PIT)-tag system in response to river-specific dissolved free amino-acid (DFAA) profiles and revealed that the majority of *O. keta* showed a preference for artificial natal-stream water and tended to stay in this maze arm for a longer period; natal-stream water was chosen over a nearby tributary's water, but not when the *O. keta* were presented with a non-tributary water. The results demonstrate the ability of *O. keta* to discriminate artificial stream waters containing natural levels of DFAA.

Iijima, A. 2017. Stock assessment of masu salmon in the coastal area of southwestern Hokkaido in the Sea of Japan by standardized CPUE. Sci. Rep. Hokkaido Fish. Res. Inst. 92: 13-20 (In Japanese with English abstract).

In this study, I used yearly catch and effort data to standardize catch per unit effort (CPUE) of masu salmon by coastal fishery in southwestern Hokkaido in the Sea of Japan, from 2003-2014, using the generalized linear models (GLM) approach. By examining the validity of the best model selected by Akaike information criterion (AIC), good fit was observed and the error structure assumed in the GLM procedure appeared appropriate. Because the standardized model accurately predicts the catch, the method used in the present study appeared effective for the stock assessment of masu salmon, which have been caught with various fishing gears widely over a long period. When annual trend of the standardized CPUE was calculated by the least squares mean, the standardized CPUE did not show a decreasing trend, suggesting that catch of masu salmon would have decreased because of decrease in the number of fishermen engaged in line fishing in this area.

Kitanishi, S., T. Yamamoto, H. Ishii, Y. Yamaguchi and T. Kobayashi. 2017. Dispersal patterns of anadromous and freshwater resident masu salmon at different spatial scales in mid-western Hokkaido, Japan. Ichthyol. Res. 64: 111-115.

To evaluate the influences of spatial scale on dispersal, the dispersal patterns of masu salmon *Oncorhynchus masou masou* were investigated at among-river (ca. <43 km) and within-river levels in mid-western Hokkaido, Japan. A genetic differentiation (F ST) and assignment test showed that among-river dispersal was much less common (2.9 % of 339 individuals) than within-river dispersal (7.4 % of 190 individuals). We also found that there was no bias in dispersal at the among-river level, while anadromous males were more likely to disperse at the within-river level, suggesting that the dispersal patterns may be scale dependent.

Koyama, T., K. Shimoda, T. Aoyama, A. Iijima, H. Urabe, M. Fujiwara and Y. Miyakoshi. 2017. Age composition of chum salmon returning to rivers on the Sea of Japan side of Hokkaido from 2010 to 2016(Note). Sci. Rep. Hokkaido Fish. Res. Inst. 92: 47-58 (In Japanese, no abstract).

Miyakoshi, Y., H. Hayano, H. Omori, M. Fujiwara, K. Takeuchi and M. Nagata. 2017. Overwinter survival and smolt run of masu salmon stocked in upper old-growth and lower clear-cut reaches of a river in northern Hokkaido. Sci. Rep. Hokkaido Fish. Res. Inst. 91: 9-18 (In Japanese with English abstract).

In this study, we compared the overwinter survivals of the juvenile masu salmon (*Oncorhynchus masou*) stocked in the upper old-growth and lower clear-cut reaches of the Masuhoro River in northern Hokkaido, Japan. Two size groups of the hatchery-reared masu salmon (mean weights were 13.9 g for the large-sized group and 9.3 g for the small-sized group) were stocked in the Masuhoro River in October 1998. In the spring of 1999, the numbers of the downward-migrating smolts and resident-type parr were surveyed for each group, and their overwinter survivals were estimated. The overwinter survivals of the large-sized groups (19.2% in the upper and 14.1% in the lower reaches) were higher than those of the small-sized groups (9.4% in the upper and 10.2% in the lower reaches) in both reaches of the river. The average survival rate of the fish stocked in the upper reach (14.3%) was slightly higher than that of the fish stocked in the lower reach (12.2%). The mean smolt size of the fish stocked in the lower reach (13.0 cm) was larger than that in the upper reach (12.5 cm). These results indicate that the instream habitat conditions, such as the abundance of instream cover, affected the overwinter survival of the juvenile masu salmon, and the canopy conditions affected the growth of smolts in spring.

Morita, K., and J. Tsuboi. 2017. Sexual size dimorphism in a landlocked Pacific salmon in relation to breeding habitat features. Evol. Ecol. 31: 653-661.

Many animal species exhibit size dimorphism between sexes. Sexual selection, whereby male-male competition favors larger body sizes, has been considered a likely cause of sexual size dimorphism. Habitat features in breeding areas could affect the outcome of male-male competition, yet few attempts have been made to relate breeding habitat features with interpopulation variation in sexual size dimorphism. In this study, we examined interpopulation variation in sexual size dimorphism by studying the landlocked amago salmon (*Oncorhynchus masou ishikawae*) at a microgeographic scale. We found that female body size was independent of stream size but that male body size decreased with smaller stream sizes. A likely explanation is that the relationship between reproductive success and the size of males is influenced by the availability of refuges that are only available to small-bodied males. Sexual differences in body size increased with decreasing stream sizes, supporting the hypothesis that the reproductive success of larger males is reduced in smaller streams. In contrast, the maturation-length threshold increased with stream size for both sexes. The stream-size-based interpopulation variation in sexual size dimorphism and size at maturity in landlocked amago salmon may therefore have arisen through a combination of sexual and natural selection.

Saito, T. 2017. Estimating the origins of adult chum salmon *Oncorhynchus keta* in the Okhotsk and Sea of Japan regions using discriminant analysis of scale characteristics. Fish. Sci. 83: 383-400.

Linear discriminant analysis (LDA) based on scale patterns was used to develop a methodology of estimating regional origins of chum salmon. Age-4 fish were sampled in 2004-2006 from 12 river stocks of the Okhotsk and Sea of Japan (SJ) regions from Hokkaido to Honshu. The scale radius at the first annulus of each fish was separated into i intervals and the

radius of each interval was divided by the number of scale circuli within the interval to quantify scale patterns. The *i* variables and five other morphometric measurements were used in a stepwise LDA to classify the following regional groups: Hokkaido and Honshu (I), Okhotsk and SJ (II), Okhotsk, Hokkaido SJ and Honshu SJ (III). Percentages of correctly classified fish (hit rates) improved with increased *i* but tended to be close to asymptotic values in all cases. Hit rates for each river stock in case (I) ranged from 74.3% to 100% (mean 97.2%), estimated by direct maximum likelihood methods using predictor variable sets from the best models for LDAs. Hit rates were lower in cases (II) and (III). This study demonstrated that scale patterns are useful for classifying the origins of chum salmon, at least between Hokkaido and Honshu.

Sasaki, K., K. Hasegawa and M. Yatsuya. 2017. Escape of cultured coho salmon into a stream, coastal Iwate Prefecture, Japan. Nippon Suisan Gakkaishi 83: 1005-1007. (In Japanese, no abstract).

Sasaki, K., T. Kurokawa, H. Nikaido, D. Muraoka and Y. Okada. 2017. Did farmed coho salmon *Oncorhynchus kisutch* that escaped during the earthquake and tsunami disaster in 2011 interbreed with native masu salmon *Oncorhynchus masou*? Bull. Jap. Fish. Res. Edu. Agen. 45: 63-67.

During the Great East Japan Earthquake on March 11, 2011, several million individuals of farmed coho salmon (*Oncorhynchus kisutch*) escaped from aquaculture facilities in the Northeast Pacific Ocean, Tohoku, Japan. In fall of the same year, sexually mature coho salmon migrated up rivers in this area. Farmed coho salmon that migrate up rivers to breed may affect the genetic material of native salmon species and result in weakened populations. Especially, there is a strong concern that coho salmon may cross with the native masu salmon (*Oncorhynchus masou*); it is known that hybrids of these species have survivability. In this study, we surveyed masu salmon landed at a local fish market, using genetic and morphological methods in order to determine whether there are hybrids. As a result, hybrids were not found in this survey. Therefore, at this moment the impact on the genetic resources of masu salmon is considered to be low.

Shiraishi, K. 2017. Variation in the numbers of adult returns and released fry for chum salmon *Oncorhynchus keta* caused by the Great East Japan Earthquake in Miyagi Prefecture. Aquacult. Sci. 65: 161-163 (In Japanese with English abstract).

I compared contrasts of the numbers of released fry chum salmon from hatcheries and their returns before and after the 2011 Great East Japan Earthquake. Numbers of released fry in 2010 and 2011 brood years and adult returns in 2014-2015 were lower than those of previous year groups because of the negative effect of the earthquake, whereas their return rate showed no change. This result suggests that the decrease in adult return may be caused by the number of released fry in the 2010 brood year.

Susuki, K., M. Ban, M. Ichimura, and H. Kudo. 2017. Comparative anatomy of the dorsal hump in mature Pacific salmon. J. Morphol. 278: 948-959.

Mature male Pacific salmon (Genus *Oncorhynchus*) demonstrate prominent morphological changes, such as the development of a dorsal hump. The degree of dorsal hump formation depends on the species in Pacific salmon. It is generally accepted that mature males of sockeye (*O. nerka*) and pink (*O. gorbuscha*) salmon develop most pronounced dorsal humps. The internal structure of the dorsal hump in pink salmon has been confirmed in detail. In this study, the dorsal

hump morphologies were analyzed in four Pacific salmon species inhabiting Japan, masu (*O. masou*), sockeye, chum (*O. keta*), and pink salmon. The internal structure of the dorsal humps also depended on the species; sockeye and pink salmon showed conspicuous development of connective tissue and growth of bone tissues in the dorsal tissues. Masu and chum salmon exhibited less-pronounced increases in connective tissues and bone growth. Hyaluronic acid was clearly detected in dorsal hump connective tissue by histochemistry, except for in masu salmon. The lipid content in dorsal hump connective tissue was richer in masu and chum salmon than in sockeye and pink salmon. These results revealed that the patterns of dorsal hump formation differed among species, and especially sockeye and pink salmon develop pronounced dorsal humps through both increases in the amount of connective tissue and the growth of bone tissues. In contrast, masu and chum salmon develop their dorsal humps by the growth of bone tissues, rather than the development of connective tissue.

Tago, Y., N. Iida, N. Yamazaki, S. Azuma, S. Inoue and A. Nitta. 2017. Depth distribution of over-summered masu salmons in a large pool just below the Jin-san Dam in the Jinzu River. Aquacult. Sci. 65: 311-320 (In Japanese with English abstract).

Dept distribution of masu salmon, *Oncorhynchus masou masou*, in a large pool (Max. 13.7 m depth) just below the Jin-san Dam in the Jinzu River, was investigated by using the telemetry system and archival tags from summer until the spawning period in 2009. The dissolved oxygen in the pool was adequate enough from top to bottom for the masu salmon's survival. Turbidity of the pool was moderate. Water temperature in the bottom layer was 1.1-1.4 ℃ lower than that in the surface layer. In such condition, it was unexpectedly found that masu salmons tend to be in the surface layer (Ca. 1.0 m below the surface with current less than 0.35 m/s) in the day time, or in the middle layer (Ca. 2-4 m) in the night. It was also found that masu salmons sometimes dive to the bottom (Max. 13.6 m depth) regardless of day or night, and that masu salmons tend to select shallow depths with the approach of the spawning season. These results suggest that masu salmons prefer the surface layer rather than the layers near to the bottom, if the current, water temperature, oxygen and turbidity are apt for the masu salmon's inhabitation.

Theme 2. Pacific Salmon and Steelhead Trout in a Changing North Pacific Ocean

Beacham, T. D., C. Wallace, S. Sato, and S. Urawa. 2017. Microsatellite identification of sockeye salmon rearing in the Bering Sea during summer 2016. NPAFC Doc. 1683. 12pp. Fisheries and Oceans Canada, Pacific Biological Station, and Hokkaido National Fisheries Research Institute, Japan Fisheries Research and Education Agency (Available at http://www.npafc.org).

Stock composition of Sockeye Salmon (*Oncorhynchus nerka*) caught in the southern central Bering Sea during a Japanese research cruise in the summer of 2016 was estimated through an analysis of microsatellite variation. Variation at 14 microsatellites was analyzed for immature Sockeye Salmon, and a 415-population baseline spanning Japan, Russia, Alaska, Canada, and Washington State was used to determine the stock composition of the fish sampled. Alaskan-origin Sockeye Salmon were the most abundant in the catch of immature individuals, comprising 85.3% of all Sockeye Salmon caught, with the catch dominated by Sockeye Salmon of Bristol Bay origin (80.0%). Canadian-origin salmon accounted for an average of 3.3% of the

catch, while Russian-origin Sockeye Salmon accounted for 11.3% of the catch, with 382 individuals of the catch genotyped.

Honda, K., T. Kawakami, K. Suzuki, K. Watanabe and T. Saito. 2017. Growth rate characteristics of juvenile chum salmon *Oncorhynchus keta* originating from the Pacific coast of Japan and reaching Konbumori, eastern Hokkaido. Fish. Sci. 83: 987-996.

Juvenile chum salmon *Oncorhynchus keta* originating from rivers along the Pacific coast of Japan migrate northwards to the Sea of Okhotsk, typically passing off Konbumori, near the easternmost part of Hokkaido Island. We used daily-increment analysis of otoliths to back-calculate the growth rates [mean daily growth rate in fork length (FL)] of 369 juveniles (56-146 mm FL) originating from various rivers southwest of Konbumori, and sampled at Konbumori between 2005 and 2014. We examined differences in growth rate in terms of differences in distance from the source of juveniles, their river or region of origin, to Konbumori, and FL at time of collection. The results show that juvenile chum salmon originating from distant sources tended to grow faster than those from more proximal sources, likely contributing to larger FLs in the former. Growth rates of larger fish ($\geq$ 90 mm FL) differed little (medians: 0.64-0.68 mm/day) among regions of origin, whereas those of smaller fish tended to be low among fish originating from more proximal regions (20-126 km from Konbumori). These results suggest that fish migrating from more distant rivers were better able to survive and to reach Konbumori by achieving or exceeding a certain growth rate.

Honda, K., S. Sato, T. Sato, T. Morishita, M. Ogawa, and K. Suzuki. 2017. The summer 2016 Japanese salmon research cruise of the R/V *Hokko maru*. NPAFC Doc. 1697. 15 pp. Hokkaido National Fisheries Research Institute, Japan Fisheries Research and Education Agency (Available at http://www.npafc.org).

A summer high-seas research cruise to investigate the biology of Pacific salmon was conducted during August 4-10 in the Bering Sea aboard the Japanese research vessel Hokko maru. Research cruise activities included the collection of data on oceanography, zooplankton, micronekton, salmonids, and other organisms. In addition, seawater samples were collected for environmental DNA analysis. A total of 2,124 salmonids were caught by surface trawls and angling at 13 monitoring stations. Chum salmon was the most abundant species (79.8%), followed by sockeye salmon (18.5%), Chinook salmon (1.60%), and pink salmon (0.09%). Salmonids were measured with respect to fork length and body and gonad weights by sex, and the scales were removed for age determination. Isotope, genetic, otolith, stomach, and seawater samples were obtained for future study. There were 12 chum salmon tagged with disk tags and released in the Bering Sea. Among them, two large chum salmon were released with an archival tag. Age-specific catch per unit effort by surface trawl and annual mean body weight of each ocean age of chum salmon during 2007-2016 are documented here.

Hoshi, N., K. Sakaoka, Y. Kajiwara, M. Ohwada, T. Sato, K. Imai, Y. Inagaki, and S. Takagi. 2017. Results of 2016 salmon research by the *Oshoro-maru*. NPAFC Doc. 1692. 9 pp. T/V "*Oshoro maru*", Graduate School of Fisheries Sciences and Faculty of Fisheries, Hokkaido University (Available at http://www.npafc.org).

In order to accumulate oceanographic and biological data (including salmonids) and to clarify the oceanic structure and marine ecosystem, the T/V *Oshoro maru* conducted oceanographic observations and fishing surveys in the western North Pacific (along the 155°E longitude line and 47°N 160°E). The survey was conducted during the Cruise #025 in May, and

the Cruise #026-Leg2 June to July 2016. Eleven oceanographic observations and three drift gillnet surveys were conducted along the 155°E during the Cruise #025 in May. The Polar Front was observed in the vicinity of 44°N which were shifted north than the location in previous years and the Subarctic Boundary was located in the north side of 41°N also shifted north rather than last year. A total of 474 salmonids was caught by gillnet surveys, including 439 Pink, 32 Chum, two Steelhead and one Sockeye salmon. Pink salmon was the dominant species. The fork lengths (F.L.) of chum salmon collected by C-gear gillnet ranged between 454-586 mm F.L., and those of pink salmon ranged between 300-430 mm F.L., 90.6% of chum salmon caught along 155°E were adult fish. To collect salmon samples extensively and to collect fresh salmon blood and various tissues, three hook-and-line gear samplings were conducted during the Cruise #026-Leg2. Almost all of caught by these gears were Pink salmon. A total of eight Chum, and 237 Pink salmon were collected during the Cruise #026-Leg2.

Watanabe, K. 2017. Multi-timescale interactions between pink and chum salmon catch per unit effort in the Bering Sea. Fish. Oceanogr. 26: 498-506.
Based on generalized linear models, interspecific interactions were identified between chum and pink salmon. In addition, the effects of sea surface temperature and location on the variability of catch per unit effort (CPUE) of chum salmon from gill-net surveys carried out between 1972 and 2010 were investigated. In the optimal model, interspecific interactions between CPUEs of chum and pink salmon on a year scale were positive for approximately half of all years in the central Bering Sea. In addition, interspecific interactions on a multi-year scale were positive in even-numbered years. The effects of location on the CPUE of chum salmon were significant variables in the optimal model. The CPUEs of chum salmon located near the continental shelf in the Bering Sea were higher than those of other locations. This study provides new evidence of positive interspecific interactions between the CPUEs of chum and pink salmon. The results also suggest that the standardized CPUE of chum salmon from the gill-net surveys reflects relative chum salmon abundance in the North Pacific Ocean in the following year.

Theme 3: New Technologies

Azumaya, T., S. Sato, S. Urawa, and T. Nagasawa. 2017. Homing migration route of Japanese chum salmon estimated by a data storage magnetic tag. NPAFC Doc. 1699. 15 pp. Hokkaido National Fisheries Research Institute, Japan Fisheries Research and Education Agency (Available at http://www.npafc.org).
Archival tagging operations of chum salmon (*Oncorhynchus keta*), which record the geomagnetic intensity and inclination fields, were carried out in the Bering Sea in 2012. Data storage tags were attached to the body of chum salmon on board the research ship. Tagged chum salmon was recaptured near the coast of Hokkaido, Japan in 2012. The tags stored temperature, depth, geomagnetic intensity, inclination, compass heading vector and tilt of the fish during the homing migration. Data by archival tag on chum salmon indicated it moved from the Bering Sea to the coast of Japan in 74 days. To determine the ocean location of tagged fish after release, we estimated the homing migration route using a progressive vector which is the product of the swimming speed and compass heading vector of the tag. It was found that the estimated homing migration route was approximately along the isoline of the magnetic intensity at the recapture site. Simple homing migration model reproduced the homing migration route in the open sea. From

these results it was found that although both the geomagnetic intensity and inclination play more important roles on homing migration of chum salmon, with the effect of geomagnetic intensity for the homing migration in the open sea was larger than the geomagnetic inclination.

Iida, M., K. Tokano and S. Katayama. 2017. Effects of incubation substrate and rearing density on the growth and survival of masu salmon *Oncorhynchus masou* alevins. J. Fish. Technol. 9: 71-75 (In Japanese with English abstract).

We investigated the impacts of incubation substrate and rearing density on the growth and survival of masu salmon (*Oncorhynchus masou*) alevins. Eyed eggs of masu salmon were stocked in incubation tanks at different egg densities with or without gravel substrate. The survival rate from eggs to emergent fry did not differ depending on the presence of gravel substrate, nor on the rearing density. The mean body weight of emergent fry reared with the gravel substrate was significantly heavier than that of fry at the same rearing density without gravel substrate. In the absence of gravel substrate, the mean body weight of emergent fry reared at a high density was significantly heavier than that of fry reared at a low density. These results indicate that the growth of masu salmon alevins is affected by the presence of incubation substrate as well as rearing density. The incubation substrate may restrain alevins from actively moving, promoting their efficient absorption of yolk nutrient for growth.

Kaneto, Y., S. Katayama and M. Iida. 2017. Age determination of chum salmon using scales and otoliths. Nippon Suisan Gakkaishi 83: 758-763 (In Japanese with English abstract).

Age determination of chum salmon using scales becomes difficult as sexual maturation progresses. We examined and compared the working efficiency and accuracy of aging methods using scales, otolith surface, and otolith section with chum salmon. The percentage of age estimated correctly, cross-checked with known age by the otolith thermal mark and release protocol, was under 80% for the otolith surface and the common otolith sectioning methods in which otoliths are sliced to around 150 mu m thickness. The accuracies were 100% using scales and thinner otolith sections of around 80 mu m thickness. We therefore recommend employing the more accurate aging methods using scales and thinner otolith sections in line with the working efficiency and maturational conditions.

Kitanishi, S., T. Ikeda, and T. Yamamoto. 2017. Short-term temporal instability in fine-scale genetic structure of masu salmon. Freshwart. Biol. 62: 1655-1664.

1. Identifying spatial extent and temporal patterns of population genetic structure is important for understanding evolutionary relationships among local populations and for designing conservation programmes. However, little attention has been devoted to understand whether genetic structure is temporally stable or unstable, and how genetic characteristics may change over time. The goal of this study was to assess the temporal stability of the genetic structure of masu salmon (*Oncorhynchus masou*). 2. To examine the temporal component of genetic variation in genetic structuring within a river system, we used 810 masu salmon collected from eight tributaries of the Atsuta River, Hokkaido, Japan, over three consecutive years (i.e. 200709). We assessed the temporal stability of the genetic structure in 15 microsatellite loci by comparing genetic diversity, effective population size and the relationships between genetic and geographical distances among samples collected from different tributaries and over time. 3. Significant genetic differences were observed among most of the temporal samples collected from the same tributary, and analysis of molecular variance indicated that the temporal

component explained about 10 times more of the genetic variation (1.98%) than did the spatial component (0.18%). 4. Isolation by distance (IBD) was detected only in 2009. In addition, a significant correlation in population genetic structure was observed between samples collected in 2008 and those in 2009. In 2007, decomposed pairwise regression analysis identified one population as an outlier population and, following exclusion of the outlier sample, IBD was observed in 2007. This population is small and physically isolated by waterfall, in which the effective population size or effective number of breeders would be expected to be small. 5. We found that fine-scale genetic structure in masu salmon populations was temporally unstable, due perhaps to genetic drift in small isolated populations, temporal changes in environmental conditions (e.g. drought), and a combination of these factors. This study also highlights that the genetic structure among populations could easily be affected by temporal and/or sampling issues. Studies focused on temporal genetic structuring are likely to be important for conservation of species inhabiting unstable or isolated habitats such as freshwater fish.

Sakaguchi, S. O., S. Shimamura, Y. Shimizu, G. Ogawa, Y. Yamada, K. Shimizu, H. Kasai, H. Kitazato, Y. Fujiwara, K. Fujikura and K. Takishita. 2017. Comparison of morphological and DNA-based techniques for stomach content analyses in juvenile chum salmon *Oncorhynchus keta*: a case study on diet richness of juvenile fishes. Fish. Sci. 83: 47-56.

To identify the stomach contents of marine organisms, morphological observations are commonly conducted. However, the results obtained by this traditional method are frequently biased, as it is difficult to detect partially digested, soft-bodied organisms. To resolve this, recent studies have used DNA-based (DNA barcoding) analyses to examine the diet breadth of marine organisms. Here, we compared the prey richness of juvenile fishes using morphological observations and DNA-based analyses, with a focus on juvenile chum salmon *Oncorhynchus keta*. A higher number of prey taxa were successfully identified using DNA-based analyses than morphological observations. However, we also noticed several shortcomings of the DNA-based analyses, as reported in other diet-analysis studies that used molecular techniques. For example, the degree of digestion among prey taxa might have resulted in differential sensitivity to DNA detection. Additionally, several prey taxa could not be precisely identified, as the sequence data for some of the targeted organismal groups are unavailable in public gene databases. Remarkably, it is also possible that DNA-based analyses detected secondary prey, and therefore, the richness of prey taxa was likely overestimated. Thus, dietary analyses of juvenile fishes need to be carefully conducted, considering the respective advantages and disadvantages of DNA-based and morphological techniques.

Sakaguchi, S. O., T. Ikuta, G. Ogawa, K. Yamane, N. Shiga, H. Kitazato, K. Fujikura and K. Takishita. 2017. Morphological identity of a taxonomically unassigned cytochrome c oxidase subunit I sequence from stomach contents of juvenile chum salmon determined using polymerase chain reaction. Fish. Sci. 83. 757-765.

In a previous report, we analyzed the stomach contents of juvenile chum salmon *Oncorhynchus keta* by morphological observation and also by molecular identification using the mitochondrial cytochrome c oxidase subunit I (COI) region. However, one of the most frequently detected COI sequences could not be assigned to any specific taxon, even at the phylum level. In the present study, we conducted in situ hybridization (ISH) on the stomach contents of juvenile chum salmon using the COI sequence and polymerase chain reaction amplification of a 18S

ribosomal RNA gene from the tissue sections where ISH signals were detected. As a result, the organism that was enigmatic at the phylum level was found to be an appendicularian. Moreover, *Oikopleura longicauda* collected from the bay where the juvenile chum salmon samples were obtained was shown to have the same COI sequences as this taxonomic "orphan" COI sequence from the stomach contents. The present results suggest that the COI sequences previously deposited in public databases for "*Oikopleura*" are actually derived from taxonomic groups other than appendicularians, and that this may have hampered our understanding of prey richness in the stomach or gut of certain marine animals based on DNA barcoding.

Sato, S. and S. Urawa. 2017. Genetic variation of Japanese pink salmon populations inferred from nucleotide sequence analysis of the mitochondrial DNA control region. Environ. Biol. Fish. 100: 1355-1372.

To estimate genetic variation and structure of pink salmon (*Oncorhynchus gorbuscha*) populations in Hokkaido, Japan, we analyzed the nucleotide sequence of about 500 bp in a variable portion of the 5' end of the mitochondrial DNA control region for even- and odd-year broodlines. Sixty-seven haplotypes were detected in the examined individuals. Among these, 25 haplotypes were unique to the even-year broodline, while another 30 haplotypes were unique to the odd-year broodline. Five and three length-heteroplasmic haplotypes were detected in the even-year broodline and odd-year broodline, respectively. The distribution pattern of the 67 haplotypes was different among populations between both broodlines, while not different among populations within the same broodline. The haplotype and nucleotide diversity were higher for even-year broodline populations than for odd-year broodline populations, suggesting greater genetic variation within populations of the even-year broodline. Analysis of molecular variance and pairwise fixation index estimates also demonstrated strong genetic differentiation between even- and odd-year broodlines, although there was no genetic differentiation among populations within the same year broodline. The neutrality tests and mismatch distribution analysis indicate that the demographic history of pink salmon in Japan differs between even- and odd-year populations. Together, these results suggest strong reproductive isolation between the even- and odd-year broodlines of pink salmon, and high gene flow with broodlines due to straying.

Torao, M. 2017. Counting of salmon escapements from aerial video images captured using a drone. Aquacult. Sci. 65: 157-159 (In Japanese with English summary).

The effectiveness of the number estimation using drone-captured video of the salmon spawning escapements in the rivers of eastern Hokkaido was verified by counting with those by visual counting from the ground. It was possible to discriminate adult pink and chum salmons on the video images. A significantly strong correlation was observed between ground level visual counts and aerial video counts ($P < 0.001$, $r = 0.992$). Thus, these findings confirmed that counting using drone-captured video images is an effective alternative to visual counting, along with the application of the area under the curve method, for estimating salmon escapements.

Torao, M and T. Yanagimoto. 2017. Mitochondrial DNA analysis of population structure in odd-year pink salmon (*Oncorhynchus gorbuscha*) from the Nemuro Strait, Hokkaido Japan. Sci. Rep. Hokkaido Fish. Res. Inst. 91: 1-7 (In Japanese with English abstract).

In this study, we evaluated the genetic structure of the odd-year brood line of pink salmon *Oncorhynchus gorbuscha* populations sampled from the eight rivers in the Nemuro Strait, eastern Hokkaido, in 2015. Pink salmon sampled from the Sashirui, Rausu, Shunkari-kotan, Kunbetsu,

Ichani, Shibetsu, Touhoro, and Nishibetsu rivers were examined using the three mitochondrial DNA (mtDNA) regions (COI, ND5, and D-Loop). We observed no significant genetic differences in the three mtDNA regions among the pink salmon populations from the eight rivers. However, genetic differences were observed between the odd- and even-year lineages of the pink salmon populations that returned in 2014. Moreover, when comparing COI and ND5 regions with the previously reported data of the Rusha River facing the Okhotsk Sea in 2008 and 2009, significant differences were observed only between different lineage groups. These results suggest that the genetic structure of the pink salmon populations in the Nemuro Strait region have similarities within the even- or odd-year lineages. Moreover, the two-year life cycle of pink salmon has resulted in the odd- and even-year lineages being genetically isolated in eastern Hokkaido. In addition, the haplotype and nucleotide diversities indicated greater differentiation within the even-year than within the odd-year lineage in the Nemuro Strait population.

Tarpey, C. M., J. E. Seeb, G. J. McKinney, W. D. Templin, A. Bugaev, S. Sato, and L. W. Seeb. 2017. Single-nucleotide polymorphism data describe contemporary population structure and diversity in allochronic lineages of pink salmon (*Oncorhynchus gorbuscha*). Can. J. Fish. Aquat. Sci. DOI: dx.doi.org/10.1139/cjfas-2017-0023.
        Pink salmon, the most abundant Pacific salmon, have an obligate 2-year life cycle that leads to reproductively isolated even- and odd-year lineages. Using new and existing data, we examined the genetic structure of both lineages across their distributional range by genotyping 16 681 single-nucleotide polymorphisms for 383 individuals originating from seven pairs of even- and odd-year populations. Distinct differences in standing pools of genetic variation were identified between the lineages; we observed higher levels of heterozygosity, allelic richness, and significantly more private alleles in the odd-year lineage. However, the patterns of population structure were concordant between lineages: the Asian and northern Alaska populations displayed little differentiation but differed significantly from populations in southcentral Alaska and the Pacific Northwest. Our population structure results, in the context of known paleoecological information, suggest that both lineages occupied a northern Beringial refugium as well as a Cascadian refugium in North America during the Last Glacial Maximum. These results highlight the influence of historical patterns of habitat availability on contemporary population structure and support the hypothesis of a pre-glacial origin of the lineages.

Tsukagoshi, H., S. Terui, S. Sato, and S. Abe. 2017. Development and characterization of 13 polymorphic microsatellite DNA markers for pink salmon (*Oncorhynchus gorbuscha*) using next-generation sequencing approach. J. Appl. Ichthyol. 33: 1204-1207 (No abstract).

Theme 4: Management Systems

Aoyama, J. 2017. Natural spawning of chum salmon *Oncorhynchus keta* within a hatchery stock enhancement program: a case in the Otsuchi River at the Sanriku coast. Coastal Marine Sci. 40: 1-6.
        Natural spawning of chum salmon, *Oncorhynchus keta*, in the Otsuchi River within a hatchery-based stock enhancement program was assessed for the first time in the 2014-2015 spawning season. Adult chum salmon, their spawning redds and carcasses were visually counted biweekly by walking along the river 1.0 to 4.0 km from the river mouth, during 15 September

2014 to 27 January 2015. A total of 160 spawning redds and 808 carcasses were found and at least 904 adults were counted upstream of the hatchery weir, suggesting that chum salmon spawn naturally in the Otsuchi River within a hatchery stock enhancement program. The majority of spawning redds (91.3%) were found in the area of 2.0-2.5 km from the river mouth and the main spawning area appears to have shifted more than 500 m upstream compared to the previous description in 1962. Retention of carcasses in the Otsuchi River (less than 14 days) was significantly shorter than Hokkaido (30-40 days during autumn and 70-80 days during winter). Warm water temperatures and relatively rapid flow by the steep gradient of the river in Sanriku Ria likely made carcasses quickly decomposed or washed away. This study suggested a possible contribution of naturally spawning chum salmon for returning adults in the Otsuchi River and a particular ecological role of salmon carcasses in the riverine ecosystem in Sanriku Ria.

Theme 5: Integrated Information Systems

No publication.