

ON DEVELOPMENT OF A DNA DATABASE FOR
REPRODUCTION, IDENTIFICATION AND CERTIFICATION OF POPULATIONS OF
PACIFIC SALMON: AN EXAMPLE FROM CHUM SALMON OF ITURUP ISLAND

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RESUME

Sustainable reproduction, stock identification, and ecological certification of fishery need knowledge of inherited features of populations. This requires a database that includes genetic data on stocks involved. One of the leading aims of such a database is a possibility to genetically distinguish populations. Then the following principal questions arise: What genetic markers should be used; Do these markers allow to distinguish geographically closed stocks and their components; How to sample for the purposes of such a database? As an example, we studied two stocks of chum salmon (*Oncorhynchus keta* W.), one from the Kurilka River and the other from the Reidovaya River system, the Iturup Island, during the period of spawning run. It was shown that the stocks are well distinguished from each other using microsatellite markers. In turn, these stocks differ from

other chum salmon populations of Iturup Island. The results of the study suggest the following requirements for DNA databases on Pacific salmon to establish genetic differentiation:

- microsatellites are suitable markers for distinguishing populations;
- in a given river basin, biological samples ought to be taken from natural spawning locations, and from enhanced components of the stock as well (hatcheries, etc.), following the spatial and temporal structure of the stock;
- at each location of collecting biological material, more than one population sample ought to be taken (at least, in the beginning, in the middle, and in the end of the spawning run);
- the size of each sample should be not less than 50-100 fish;
- additionally to genotyping, determining the age, sex and other biological characters of fish sampled is important for detailed population-genetic analysis.

On the establishment of a DNA-database for resolution of the issue of Reproduction,
Identification and Certification of the Population of Pacific Salmon

For Chum on Iturup Island.

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In order to resolve the issue of sustainable reproduction of salmon, group identification and ecological certification, it is important to know the hereditary specifics of each population. For this, it is necessary to establish a database, containing the genetic characteristics for the fish of these groups. One of the issues arising from this question, is to develop the genetic methodology able to differentiate one population from the others. To resolve this, we need to answer the following basic questions: what genetic markers to use, whether these markers can be used to differentiate geographically close groups and the population components of these groups, how to collect biological material for such a database? As an example, studying the chum groups (*Oncorhynchus keta*) in the river areas of Reidovo and Kuriljka on Iturup Island during the entire run, we have shown that they are well differentiated by micro-satellite markers. In addition, they differ from other groups of chum on Iturup Island. The requirements for genetic differentiation of populations for Pacific Salmon in a DNA database of are :

Specifically:

- Micro-satellite appears to be a good genetic marker for differentiation of the populations;
- Selection should be done on natural, un-restored areas, as well as areas near hatcheries, considering the distribution and the timing structure of the group;
- each location of selection should be characterized by a few samples (at least, at the beginning, middle and end of the run),
- Size of the sampling must be no less than 50-100 individuals;
- Selection of samples for genetic-typing is important to carryout together with biological analysis of the studied fish—to determine the sex, age, and other characteristics.

Conclusions

Groups of Chum from Reidovo and Kuriljka Salmon Hatcheries are clearly differentiated by micro-satellite markers, confirming their individuality as populations. In turn, they are clearly differentiated from chum in other areas studied on Iturup. This is a basis for identification in the mixed ocean harvests and for certification of activities for reproduction and harvests. Further clarification must be to enlarge the number and study of the focal point, as population specific

Differentiation, as revealed, of geographically close populations is most likely attributed to the highly developed homing sense of chum. For this reason, it follows that sockeye and Chinook are expected to have a good differentiation between various populations. On pinks, accounting for the high straying (Glubokovskiy, Zhivotovskiy, 1986) this species is not expected to have a high genetic differentiation as with the chums, moreover pinks have many micro-satellite Zero-allays (??), which complicates the interpretation of the genetic data acquired (A. Gharrett, personal info). This dictates the necessity of careful selection of the analytical methods of micro-satellite locus for pinks, so that it provides the likelihood to differentiate, at least, large regional groups of this species.

Our research determined the following concluding principals for the genetic-population studies of Pacific salmonoids for creation of a DNA population database for the reproduction, genetic identification and certification of salmon.

- 1). Each population must be characterized by the samples taken with consideration of the area and timing of the group structure, during the run (sampling, at least from the beginning, middle and end of the run), river and lakes forms, seasonal forms, in areas of hatcheries and spawning grounds etc.
- 2). Size of each sample must be not less than 50-100 individuals
- 3) Genetic-typical sampling must be done in conjunction with its biological analysis, at least with the determination of sex and age.
- 4) The best genetic markers for differentiation of population is micro-satellite. Specifically, it follows to create a reference genetic database for Pacific Salmon; upon which the study of other types of genetic polyformisms (mono-celled –SNP, restructured fragment and nucleotide issuing of mitochondrial DNA and atomic genes, Fingerprinting, aplozimov) may contribute additional important information.
- 5) With the aim of creating a constructive base of genetic data for salmon groups, it follows to enlarge the number of genetic locus, especially for each population group differentiated may have its own specific collection of markers.