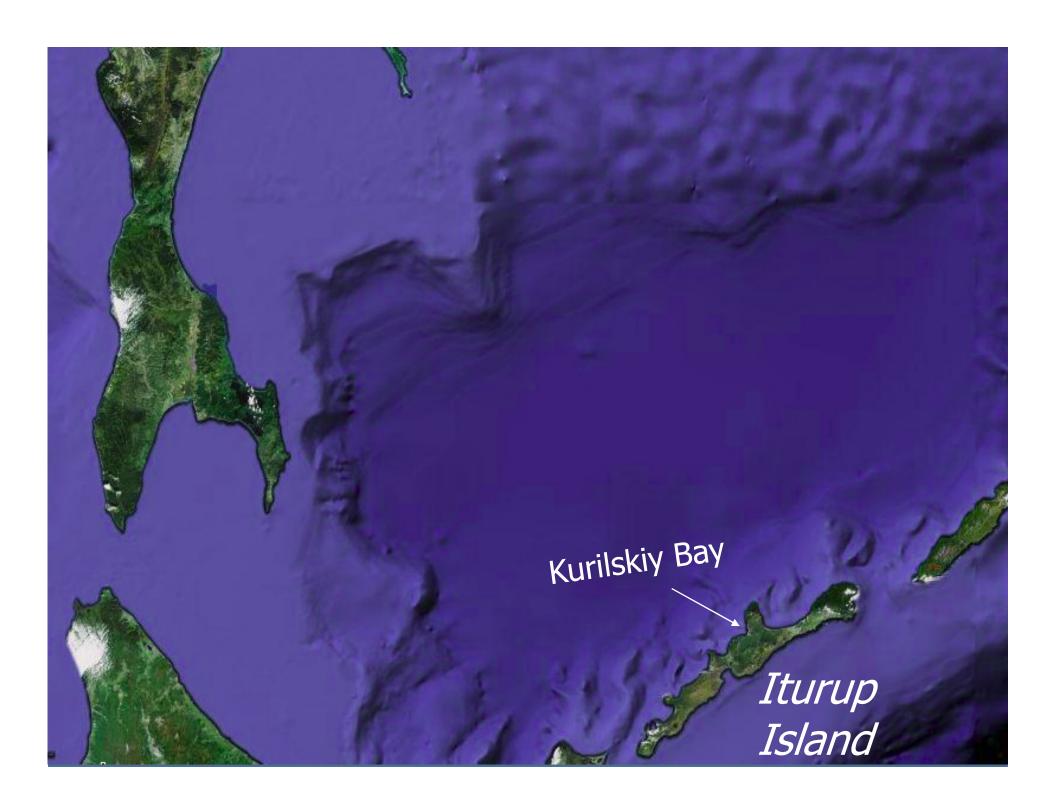
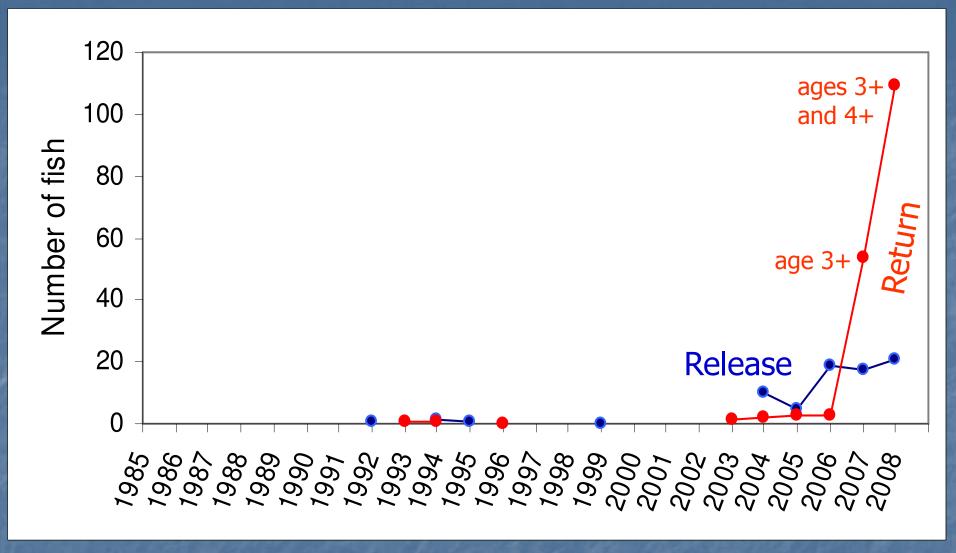


- Konstantin Afanasiev
- Galina Rubtsova
- Marina Shitova
- Ludmila Fedorova
- Tatiana Malinina
- Tatiana Rakitskaya
- Valentina Prokhorovskaya
- Mikhail Kruchinin
- Victor Pogodin







Abundance of chum salmon released from the Kurilskiy hatchery (blue, in 10<sup>6</sup>) and returned back in the Kurilskiy Bay (red, in 10<sup>4</sup>)

MS-locus	Allele structure		Size range	# alleles
Ssa197	(Sinto	We have studied		
Ssa20.19	Bet of B	37 samples from the  Kurilskiy River system and Rybatskaya River		
Ogo2				
Oki1-1				
Oki1-2				
Oke3		of ~50 fish each at ten DNA (microsatellite) markers		
Oke11	The state of			
One103				
One109	Property of	in 2004-2008		
Ots3	1000	$(TC)_n$	74-108	19

Olsen J.B. and Seeb J.E. 1998. Trans. Am. Fish. Soc. 127: 535.

Sanchez et al. 1996. Heredity 77: 423-432.

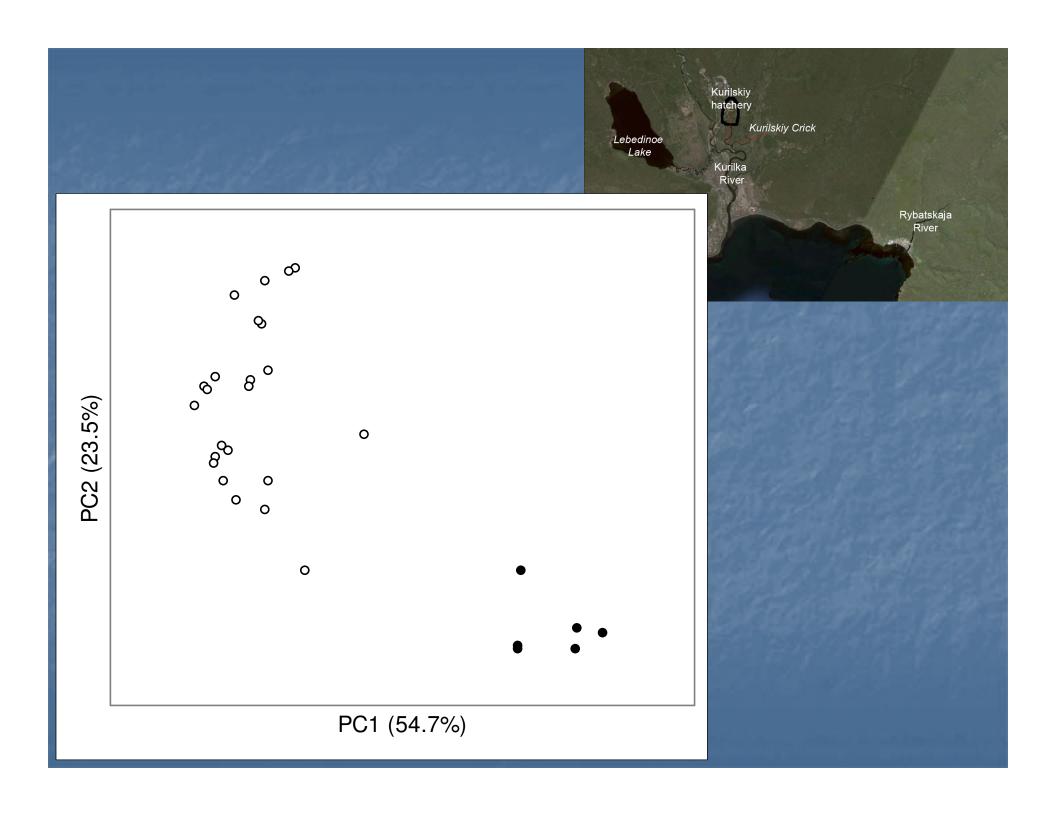
Olsen J.B. et al. 1998. Molecular Ecology 7: 1087-1089.

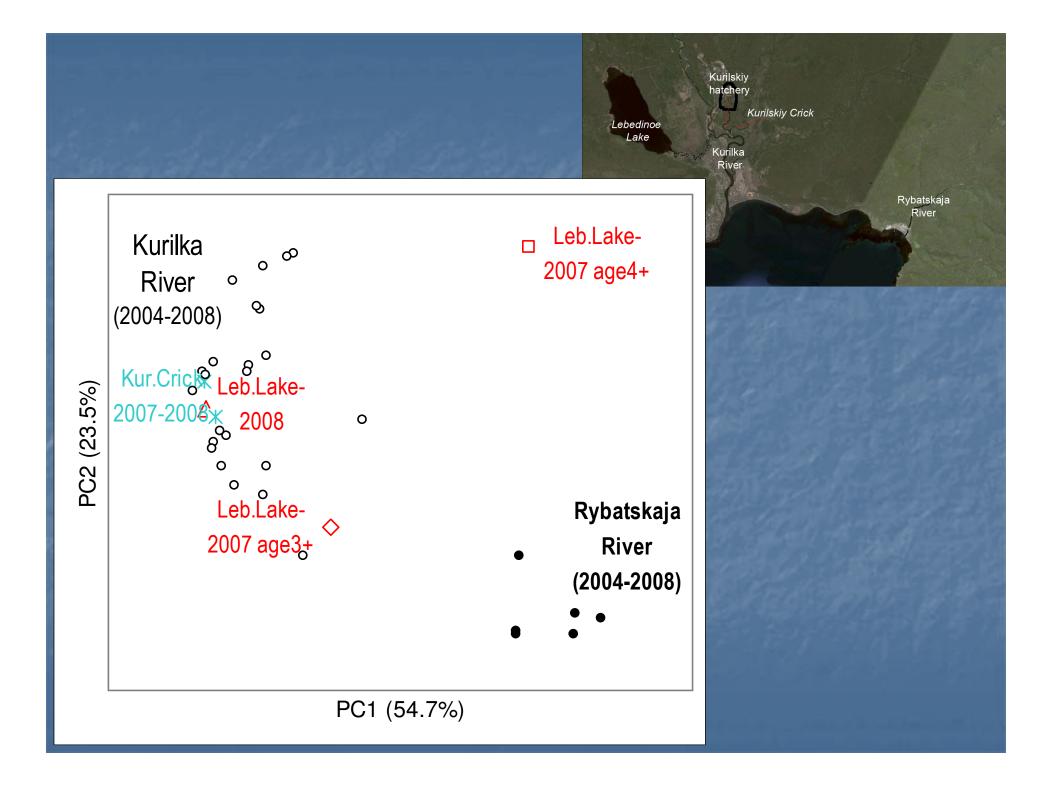
Smith C.T. et al. 1998. Molecular Ecology 7: 1614-1616.

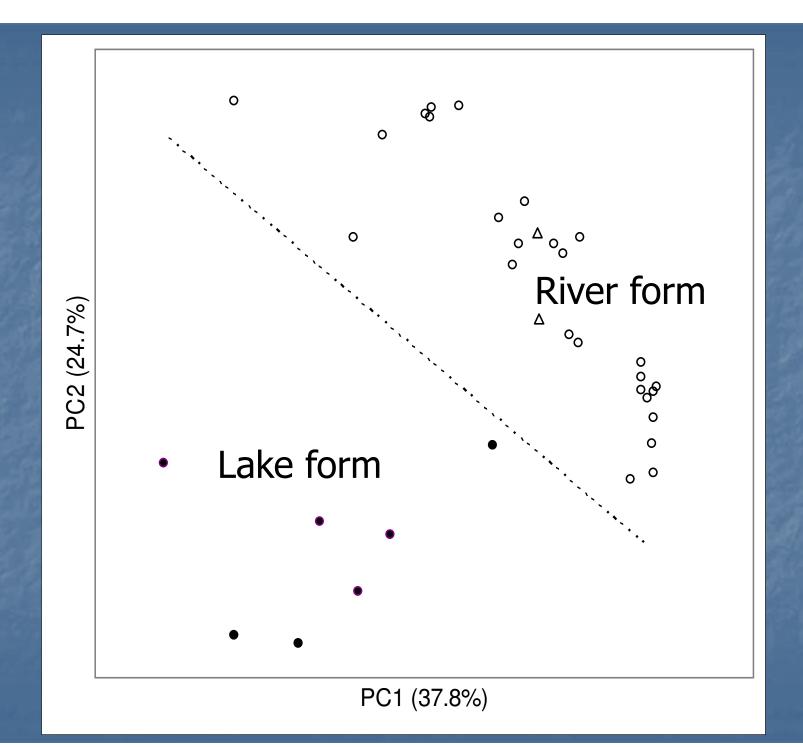
Buchholz W.G. et al. 2001. Animal Genetics 32: 162-165.

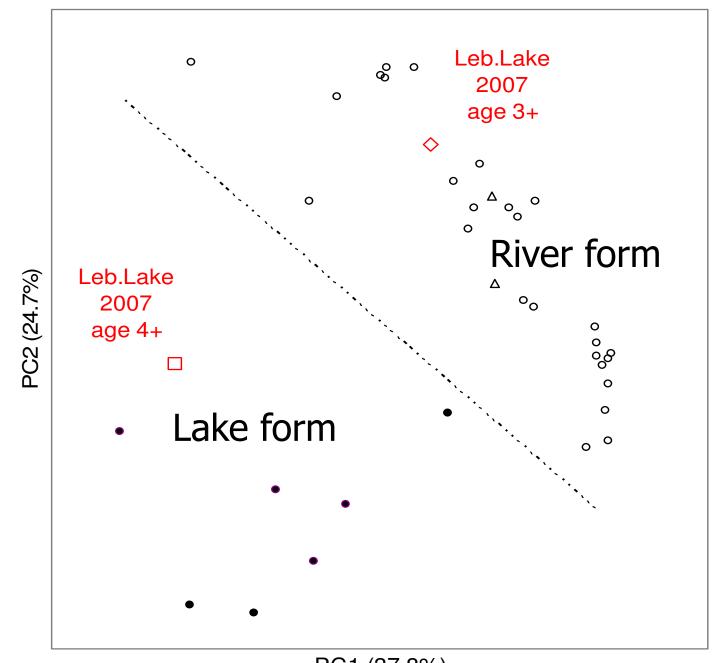
Olsen J.B. et al. 2000. Molecular Ecology 9: 2185-2187.

Small M.P. et al. 1998. Molecular Ecology 7: 141-155.









PC1 (37.8%)

## Conclusion

- Gene flow from increased the Kurilskiy hatchery stock of chum salmon seems to be distinguishable within the Kurilka River system, but does not visibly influence the neighboring Rybatskaya River stock probably due to low rate of gene flow.
- Nevertheless, even small gene flow from a large stock may change the genetics in a few generations. Thus, some measures should be taken in advance in order to prevent the wild chum salmon population of the Rybatskaya River in the future.