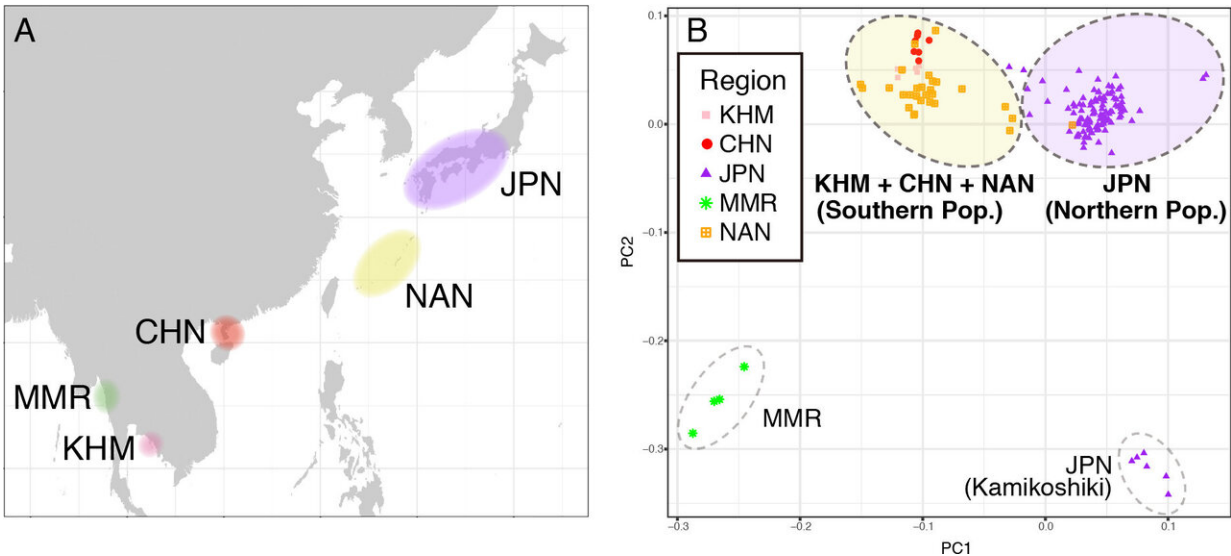


Pearls of wisdom

January 10 2020, by Anna Aaronson



Population structure of the pearl oyster, *Pinctada fucata*, in the western Pacific. (A) Sampling localities. JPN: mainland Japan including Honshu, Shikoku, and Kyushu. NAN: Nansei Islands. CHN: China. KHM: Cambodia. MMR: Myanmar. (B) PCA (principal component analysis) using genome-wide SNP data revealed that the northern population (mainland Japan) genetically diverged from southern population (Cambodia, China, and Nansei Islands). Individuals from Myanmar in the Indian Ocean are distinguishable from others in the Pacific because of a geographical barrier. In addition, the population in Kamikoshiki Island, Japan is genetically unique because they live in a local lagoon isolated from ocean by a sand bank. Credit: OIST

Since the late 19th century, pearl aquaculture has been a revered industry in Japan, enabling widespread cultivation and commercialization of

beautiful pearls. From a genetic and evolutionary perspective, scientists have known little about the source of these pearls—the Japanese pearl oyster, *Pinctada fucata*, until now.

Researchers in the Marine Genomics Unit at the Okinawa Institute of Science and Technology Graduate University (OIST), in collaboration with scientists from Mie Prefecture, Japan, have, using genome-wide genetic data from specimens collected across the western Pacific, elucidated how [pearl oyster](#) populations vary genetically and geographically. Their analyses provide insight into how these pearl oysters have adapted to [environmental changes](#) over time. Understanding the genetic structure of these populations will be crucial for developing effective and targeted conservation strategies for the species in light of climate change, the researchers said.

"In particular we wanted to understand the [population](#) structure of *P. fucata* and how these pearl oysters moved from the southwestern Pacific (of which Okinawa is a part), north, to mainland Japan," said Dr. Takeshi Takeuchi, the first author of the new study, published in *Evolutionary Applications*. "*P. fucata* is a good model for understanding genetic differentiation because the species is so widespread across the western Pacific."

Cracking the pearl oyster genome

After a century of success, Japanese pearl production plummeted during the 1990s due to detrimental algal blooms and an outbreak of bacterial disease, both of which damaged pearl oyster populations. Additionally, during this time, pearl farmers introduced Chinese pearl oysters into Japanese waters, threatening the genetic diversity of the *P. fucata* population.

To better understand and conserve these animals, the scientists analyzed

about 200 individual *P. fucata* specimens from across mainland Japan, the southern Nansei Archipelago, including sites near Okinawa, along with China, Myanmar, and Cambodia. In order to minimize the effect of recent intermingling between Japanese and Chinese populations, they used frozen specimens collected between 2000 and 2003. They sequenced the genomes of the specimens and analyzed 36,203 single nucleotide polymorphism (SNP) sites. SNPs are tiny differences in DNA's building blocks that help scientists study genetic variation.

Takeuchi and his colleagues found that pearl oysters in mainland Japan (the northern population) are genetically distant from the southern population in the Nansei Islands, China, and Cambodia.



The Japanese pearl oyster, *P. fucata*. Credit: Okinawa Institute of Science and Technology

However, the researchers could not understand why pearl oysters in the Japanese mainland and Nansei Islands were genetically distinct, since they weren't separated by a land barrier. Due to the strong Kuroshio Current, the oysters could easily be propelled from Nansei to the mainland, mixing the populations.

To solve this mystery, the scientists looked at environmental factors that might influence genetic diversification, including [sea surface temperature](#), oxygen, [carbon dioxide](#), phosphate, and nitrate levels in the water, as well as ocean salinity.

Through statistical analyses, they found that sea surface temperature and oxygen concentration strongly correlated with genetic variation. The mainland and Nansei populations are likely distinct because they adapted to local environmental conditions, the researchers said.

Traveling back in time

These findings then helped the researchers piece together *P. fucata*'s history. During the Last Glacial Maximum (about 20,000 years ago), ocean surface temperatures were much lower than present day, and *P. fucata* populations were absent in the Japanese mainland. After the last glacial period, however, temperatures in Japan increased and peaked 6,000 years ago at two to three degrees higher than present, and the pearl oyster populations moved north to mainland Japan.

Moving forward, the researchers hope to continue studying the pearl

oysters' genes, since climate change and increasing ocean temperatures may affect *P. fucata*'s distribution.

"Using genome-wide data, we revealed population structure of the pearl oyster in the western Pacific," said Takeuchi. "We are now developing DNA markers to distinguish the Japanese population from others. This will be useful for conserving the unique genetic resources of the Japanese pearl oysters," said Takeuchi.

More information: Takeshi Takeuchi et al, Divergent northern and southern populations and demographic history of the pearl oyster in the western Pacific revealed with genomic SNPs, *Evolutionary Applications* (2019). [DOI: 10.1111/eva.12905](https://doi.org/10.1111/eva.12905)

Provided by Okinawa Institute of Science and Technology

Citation: Pearls of wisdom (2020, January 10) retrieved 23 May 2024 from <https://phys.org/news/2020-01-pearls-wisdom.html>

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